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Transcriptomics analysis reveals the high biodegradation efficiency of white-rot fungus *Phanerochaete sordida* YK-624 on native lignin

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Short title: RNA-Seq of lignin degradation in *P. sordida* YK-624

Abstract

Lignocellulosic biomass is an organic matrix composed of cellulose, hemicellulose, and lignin. In nature, lignin degradation by basidiomycetes is the key step in lignocellulose decay. The white-rot fungus *Phanerochaete sordida* YK-624 (YK-624) has been extensively studied due to its high lignin degradation ability. It was demonstrated that YK-624 can secrete lignin peroxidase and manganese peroxidase for lignin degradation. However, the underlying mechanism for lignin degradation by YK-624 remains unknown. Here, we analyzed YK-624 gene expression following growth under ligninolytic and nonligninolytic conditions and compared the differentially expressed genes in YK-624 to those in the model white-rot fungus *P. chrysosporium* by next-generation sequencing. More ligninolytic enzymes and lignin-degrading auxiliary enzymes were upregulated in YK-624. This might explain the high degradation efficiency of YK-624. In addition, the genes involved in energy metabolism pathways, such as the TCA cycle, lipid metabolism, carbon metabolism and glycolysis, were upregulated under ligninolytic conditions in YK-624. The first differential gene expression analysis of YK-624 under ligninolytic and nonligninolytic conditions was reported in this study. The results obtained in this study indicated that YK-624 produces more enzymes involved in lignin degradation and energy metabolism.

Introduction

To create renewable clean energy resources, one of the most feasible methods is the development of biorefineries to produce biofuels and renewable chemicals (1, 2). Lignocellulosic biomass is the most abundant carbon-neutral source and composed primarily of lignin, cellulose, and hemicellulose. Due to the high abundance and low cost of lignocellulosic substrates, they are considered attractive feedstocks for second generation biofuel production. Furthermore, unlike first-generation biofuel feedstocks, they do not compete with food and are therefore widely used as waste or byproducts from agricultural industries and forestry (3). However, lignocellulose recalcitrance presents the largest obstacle in the biotechnological conversion of biomass during degradation of the aromatic polymer lignin.

Lignin is the second most abundant biopolymer and a major component of lignocellulosic biomass, constituting ~25% of woody plant cell walls. Because of its water insoluble, heterogeneous and optically inactive nature, lignin is highly resistant to chemobiological degradation (4). In nature, lignin degradation by basidiomycetes is the key step in lignocellulose decay. It is known that some microorganisms can degrade lignin, but only white-rot fungi can degrade it to carbon dioxide and water (5). This biodegradation process is initiated by one-electron oxidation and is mediated by some ligninolytic enzymes, including lignin peroxidase (LiP), manganese peroxidase (MnP), laccase and versatile peroxidase (VP). LiP and MnP were first reported in *Phanerochaete chrysosporium* (6, 7). LiP was able to attack lignin by oxidative cleavage of nonphenolic aromatic substrates (8). MnP can oxidize Mn^{2+} to Mn^{3+} to degrade lignin via lipid peroxidation reactions (6). VPs are LiP-MnP hybrid peroxidases (9). Laccases, which are widely distributed in plants, insects and fungi, are blue multicopper oxidases, and they can oxidize substituted phenols by reducing molecular oxygen to H_2O (10, 11). In addition, other extracellular enzymes involved in lignin degradation have been reported, including aryl-alcohol oxidase, glyoxal oxidase, and aryl-alcohol dehydrogenases (12). The white-rot fungus *Phanerochaete sordida* YK-624 (YK-624) exhibited higher ligninolytic activity than the model white-rot fungi *P. chrysosporium* or *Trametes versicolor* (13). We have previously demonstrated that YK-624 could secrete LiP and MnP for lignin degradation (14, 15, 16). However, the underlying mechanism responsible for the lignin degradation of this white-rot fungus remains unknown.

Here, we report the first transcriptomic data of the hyper lignin-degrading white-rot fungus YK-624. In this paper, we aimed to investigate the key genes for lignin degradation and to elucidate the underlying mechanism of the high ligninolytic activity of YK-624. We analyzed YK-624 gene expression following growth under ligninolytic and nonligninolytic conditions and compared differential gene expression to *P. chrysosporium* by next-generation sequencing (RNA-Seq).

Material and methods

Decay test

Wise method was used in this study for removing lignin from beech wood meal (17), in which a sodium chlorite/acetic acid mixture was used at 70~80°C in a water bath, and sodium chlorite and acetic acid were added every 1 h for up to 8 h. After the reaction, the slurry was filtered, and the solids were washed with cold distilled water and acetone. The solids were used as holocellulose medium (the Klason lignin was below 1%) after air-drying.

After YK-624 and *P. chrysosporium* were incubated on PDA plates at 30°C for 3 days, the growing edge of the 10-mm-diameter mycelium disks was punched out. One disk was inoculated into 0.5 g extractive-free beech wood meal (ligninolytic) or holocellulose meal (nonligninolytic) (60~80 mesh) and 1.25 mL Kirk medium (consisting of Kirk salt solution and 2,2-dimethylsuccinic acid) as described by Tien and Kirk (7). The weight loss and lignin content of each condition were determined after 5, 10, 15, and 20 days of incubation using our previous method (13).

RNA extraction, cDNA library preparation and sequencing

Based on the incubation method described as the *decay test*, total RNA was extracted from biological triplicates of YK-624 and *P. chrysosporium* on 1 g wood and holocellulose media. After 10 days of incubation, each sample was ground into a fine powder in liquid nitrogen. Extraction of total RNA was conducted using Concert Plant RNA Reagent (Invitrogen, United States) and further purified with the Qiagen RNeasy Mini Kit (Hilden, Germany). RNA quantity and quality were determined based on the method described by Garg et al. (18). RNA quality was assessed by agarose gel electrophoresis and the OD260/OD280 ratio.

The subsequent cDNA library construction method was described in our previous study (19). Briefly, total RNA samples were treated and purified with a DNase I and Qiagen RNeasy Mini Kit, respectively. First-strand cDNA was synthesized using an oligo-dT primer and PrimeScript reverse transcriptase (Takara). Then, libraries for strand-specific RNA sequencing were performed in two individual sequencing runs. Paired-end sequences of 75 bp were obtained using an Illumina MiSeq system.

Transcriptome assembly and functional annotation

RNA-Seq and differential expression genes (DEGs) analyses were performed as previously described (19). The paired-end reads were assembled into contigs (unigenes) by Trinity (20) after quality trimming of the adapter sequences using cutadapt ver. 1.8.1. The data sets supporting the results of this article are available in the DDBJ Sequence Read Archive (DRA) (accession numbers for the sequences of *P. sordida* YK-624 and *P. chrysosporium* are DRA009154 and DRA009155, respectively). The *P*-value was determined by the false discovery rate (FDR). DEGs were set at >1-fold up- or downregulated (FDR < 0.05) in this study. Functional annotation of the unigenes was performed in the Swiss-Prot and Uniref 90 databases by a local BLASTX algorithm (21). KEGG pathways and GO annotation were performed and assigned to unigenes using the KEGG automatic annotation server (KAAS) and InterproScan (22, 23).

Biomass in wood cultures detection

P. chrysosporium and YK-624 DNA were extracted from 10-day beech wood cultures. Wood cultures were well mixed to uniformly and then 100 mg of wet culture was collected (approximately 30 dry mg). The cultures were bead beat for 45 sec × 2 times followed 12.5 ng of EGFP (Enhanced Green Fluorescent Protein) gene was added as internal standard. After that, crude DNA was extracted by using ISOPLANT II (Nippon Gene Co., LTD.) according to the manufacture's protocol. equivalent volume of solution containing 2M NaCl, 1% polyvinylpyrrolidone, and 1% cetyl trimethyl ammonium bromide was added to the crude DNA solution, then heat at 60 ºC for 20 min. DNA was extracted with chloroform, following by isopropanol precipitation. Precipitates were dissolved in water, and used as templates for quantitative PCR (qPCR). The qPCR reagent employed was TB Green Premix Ex Taq II (Tli RNase H Plus, TaKaRa Bio Inc.), and specific primers for the genes EGFP (AAGCTGACCCTGAAGTTCATCTGC / CTTGTAGTTGCCGTCGTCCTTGAA) and internal transcribed spacers 1 (fungal ITS universal primers (24), GGAAGTAAAAGTCGTAACAAGG / GCTGCGTTCTTCATCGATGC) were used. Reaction conditions for qPCR were as follows: preincubation, 95 °C for 60 s; amplification, 45 cycles of 95 °C for 10 s, 55 °C for 30 s, 72 ºC for 30 s. The amounts of mycelia containing with wood culture was estimated from ΔCq (differences of threshold cycle (Cq)) values of EGFP and ITS. Calibration curves of both strains were prepared from mycelia obtained from potato dextrose broth cultures (Fig. S1).

Results and discussion

Lignin degradation

Firstly, time courses of wood weight loss by YK-624 and *P. chrysosporium* were investigated. As shown in Fig. S2, both fungi started wood decay after 10 days incubation. Therefore, we focused on 10-day wood cultures to elucidate the ligninolytic mechanism at early decay stage, newly 10-day wood cultures of both fungi were prepared to measured mycelial growth and ligninolytic activity in addition of weight loss. In the present study, qPCR was used for speculating the mycelial weight of YK-624 and *P. chrysosporium* in the wood cultures. It revealed that mycelia contents in 10-day wood cultures (dry bases) of YK-624 and *P. chrysosporium* were 20.2±0.7 mg/g and 11.1±0.3 mg/g, respectively. The ligninolytic properties of the two strains were investigated. YK-624 showed 32.7%

ligninolytic activity and 13.9% weight loss (Fig. 1). *P. chrysosporium* showed only 6.7% ligninolytic activity and 4.6% weight loss (Fig. 1). Although the amount of YK-624 mycelium in 10-day wood culture was 1.8 times larger than that of *P. chrysosporium*, YK-624 showed 4.9 and 3.0 times higher rates of lignin degradation and wood decay, respectively. Therefore, it can be said that YK-624 exhibits clearly higher ligninolytic activity per mycelia than *P. chrysosporium* in early wood decay stage. These results are in good agreement with those of our previous study, in which YK-624 had significantly higher ligninolytic activity (13).

Sequence assembly

Total RNA was extracted from biological triplicates of YK-624 and *P. chrysosporium* on wood meal and holocellulose meal after an incubation period of 10 days (termed YKwood, YKholo, PCwood, and PCholo). cDNA libraries were constructed after purification of mRNA for sequencing by MiSeq. Raw paired-end (2 × 76 bp) sequences from mRNAs were obtained: 33,539,967 and 32,722,656 reads for YK-624 and *P. chrysosporium*, respectively. The high-quality reads (quality values >30) were assembled into 44,250 (N50 length = 1,020 bp) and 33,340 (N50 length = 1,426 bp) unigenes. Furthermore, ribosomal RNA (rRNA) and genes were obtained from mitochondrial sequences that matched entries in the SILVA (version 111) rRNA database (25) and were excluded from Trinity unigenes.

Functional annotations

The unigenes were searched against the Swiss-Prot and Uniref 90 databases by local BLASTX and annotated with gene ontology (GO) terms for functional annotation (Table S1; Table S2). Differentially expressed genes (DEGs) between the ligninolytic and nonligninolytic conditions were identified in this study. There were 985 upregulated genes and 1,085 downregulated genes in YK-624 (Table S1). In *P. chrysosporium*, 1,257 genes were upregulated, while 1,296 genes were downregulated (Table S2).

The role of the ligninolytic enzymes LiP and MnP in lignin degradation has been extensively documented (26). The *P. chrysosporium* genome contains ten LiPs and five MnPs, that *P. carnosa* encodes four LiPs and seven MnPs (27). In the present study, three LiPs and five MnPs were upregulated in YK-624, while only two LiPs and one MnP were upregulated in *P. chrysosporium* under ligninolytic conditions. The number of LiP- and MnP-encoding genes in YK-624 were three times more abundance than those encoded by *P. chrysosporium* (Fig. 2, Tables S3 and S4). This may explain the high degradation efficiency of YK-624. In addition, some lignin-degrading auxiliary enzymes, including glucose oxidase (c21424_g1_i1), and aryl-alcohol dehydrogenase (c17439_g4_i2, c21326_g1_i1), were also detected under ligninolytic conditions. Glucose oxidase are involved in the oxidative generation of H_2O_2 (28). Aryl-alcohol dehydrogenase is produced during the ligninolytic growth phase of the fungus (29). Moreover, ATPase, ATP synthase and NADH-cytochrome b_5 reductases were upregulated in YK-624, suggesting that it generated more energy than *P. chrysosporium* under ligninolytic conditions.

GO enrichment analysis of the two white-rot fungi was performed in the present study. We found 19 upregulated and 12 downregulated GO terms in YK-624. The most enriched GO terms were “ATPase activity” in the molecular functions category, “transport” and “transmembrane transport” in the biological processes category, and “ribosome” in the cellular components category under ligninolytic conditions (Table 1). These results further demonstrated that YK-624 produced more energy for lignin degradation. In contrast, only "hydrogen ion transmembrane transporter activity" in molecular functions and "ATP synthesis coupled proton transport" in biological processes were significantly enriched in *P. chrysosporium* (Table 2). It was reported that the transportation of lignin-derived aromatic molecules is very important for biomass applications (30). This transportation activity was detected in both fungi.

To explore the underlying mechanisms for the high lignin degradation of YK-624, we mapped all upregulated genes in YK-624 and *P. chrysosporium* to Kyoto Encyclopedia of Genes and Genomes (KEGG) metabolic pathways. Our results suggested that the metabolic pathways (ko01100) and their biosynthesis of secondary metabolites (ko01110) were the most frequently represented pathways. We compared the DEGs in YK-624 and *P. chrysosporium* under ligninolytic conditions according to the KEGG pathway assignments. A summary of transcripts involved in the lignin-degrading pathways of YK-624 is shown (Fig. 2) and the pathways include carbon metabolism, the tricarboxylic acid cycle (TCA cycle) and xenobiotic biodegradation. The TCA cycle involves important biochemical reactions in energy production. In YK-624, citrate synthase (c9786_g2_i1, c9786_g1_i1, c18209_g1_i1), aconitate hydratase (c2247_g2_i1, c2247_g1_i1), isocitrate lyase (c19877_g1_i1), which are involved in the process, were upregulated (Fig. 3; Table S5). At the same time, pyruvate dehydrogenase E1 component beta subunit (c18339_g1_i1) and acetyl-CoA synthetase (c11906_g1_i1, c932_g1_i1, c15471_g1_i1) were also upregulated, and the products of the metabolic pathways that they are involved in will go further into the TCA cycle. The other 4 upregulated genes were malonate-semialdehyde dehydrogenase (acetylating)/methylmalonate-semialdehyde dehydrogenase (c18180_g1_i1), fructose-1,6-

bisphosphatase I (c11615_g2_i1, c11615_g1_i2), glycine hydroxymethyltransferase (c10791_g1_i1, c10791_g2_i1) and catalase (c798_g2_i1), which are responsible for lipid metabolism, glycolysis, and carbon metabolism; thus, YK-624 generated more ATP for lignin degradation. All the energy generated by accelerating metabolic pathways as described above will be used for lignin biodegradation (Fig. 3 and Table S5). Aldehyde dehydrogenase (NAD^+) (c22536_g1_i1, c16100_g1_i2, c16100_g4_i1, c16100_g3_i1, c24243_g1_i1, c14166_g1_i3, c14166_g1_i3, c16100_g2_i2, c10926_g2_i1, c10926_g2_i1, c18318_g1_i1, c18396_g1_i1, c3080_g1_i1, c9139_g1_i1), salicylate hydroxylase (c7235_g1_i1, c14217_g2_i1, c16040_g1_i1, c17093_g1_i1, c19987_g1_i1, c16570_g2_i2), carboxymethylenebutenolidase (c13613_g1_i1), amidase (c9043_g1_i1, c16877_g3_i1), nitrilase (c5973_g1_i2) and phenol 2-monooxygenase (c12326_g2_i1, c12326_g1_i1, c11376_g1_i1, c11376_g2_i1), which are involved in xenobiotic biodegradation, were also upregulated in YK-624 (Table S5). It was reported that the addition of alkali lignin (Sigma 45-471003) can increase energy production in the bacterium *Enterobacter lignolyticus* SCF1 (31). ATP-dependent mechanisms play an important role in aromatic compounds derived from lignin degradation (30). Hereby, these results showed that more ligninolytic enzymes (LiPs and MnPs) are upregulated in YK-624 under ligninolytic conditions. Furthermore, the genes related to energy production that accelerate metabolic pathways such as the TCA cycle, lipid metabolism, carbon metabolism, and glycolysis are upregulated in YK-624. All the energy generated might be used for degrading lignin. Therefore, YK-624 can biodegrade lignin more efficiently. This study may provide new insights into genetic engineering for lignin biodegradation in the future.

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Figure Legends

Fig. 1 Ligninolytic properties of *P. sordida* YK-624 (black) and *P. chrysosporium* (white). The values are presented as the mean ± standard deviation of triplicate samples.

Fig. 2 Upregulated DEGs encoded lignin peroxidases and manganese peroxidases of *P. sordida* YK-624 and *P. chrysosporium*. The details of these DEGs were shown in Table S3 and Table S4. Pc-LiP: lignin peroxidases of *P. chrysosporium*; Pc-MnP: manganese peroxidases of *P. chrysosporium*; YK-LiP: lignin peroxidases of *P. sordida* YK-624; Pc-MnP: manganese peroxidases of *P. sordida* YK-624.

Fig. 3 Summary of upregulated DEGs of *P. sordida* YK-624 under ligninolytic condition involved in lignin degradation. The details of these DEGs were shown in Table S5. **PDHB**: pyruvate dehydrogenase E1 component beta subunit; **ACSS**: acetyl-CoA synthetase; mmsA: malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase; **FBP**: fructose-1,6-bisphosphatase I; **glyA:** glycine hydroxymethyltransferase; **katE:** catalase; **CS**: citrate synthase; **ACO**: aconitate hydratase; **ICL**: isocitrate lyase; **LiP**: lignin peroxidase; MnP: manganese peroxidase; **GOD**: glucose oxidase; **AAD**: aryl-alcohol dehydrogenase.

Supplementary data

The following is the Supplementary data to this article:

Table S1 Data for *P. sordida* YK-624 transcripts.

Table S2 Data for *P. chrysosporium* transcripts.

Table S3 Details of lignin peroxidases and manganese peroxidases of *P. sordida* YK-624 under ligninolytic condition.

Table S4 Details of lignin peroxidases and manganese peroxidases of *P. chrysosporium* under ligninolytic condition.

Table S5. Details of DEGs of *P. sordida* YK-624 summarized in figure 3.

Fig. S1 The calibration curves of biomass and ΔCq for *P. sordida* YK-624 and *P. chrysosporium* by qPCR.

Fig. S2 Time course for the weight loss of *P. sordida* YK-624 and *P. chrysosporium*.

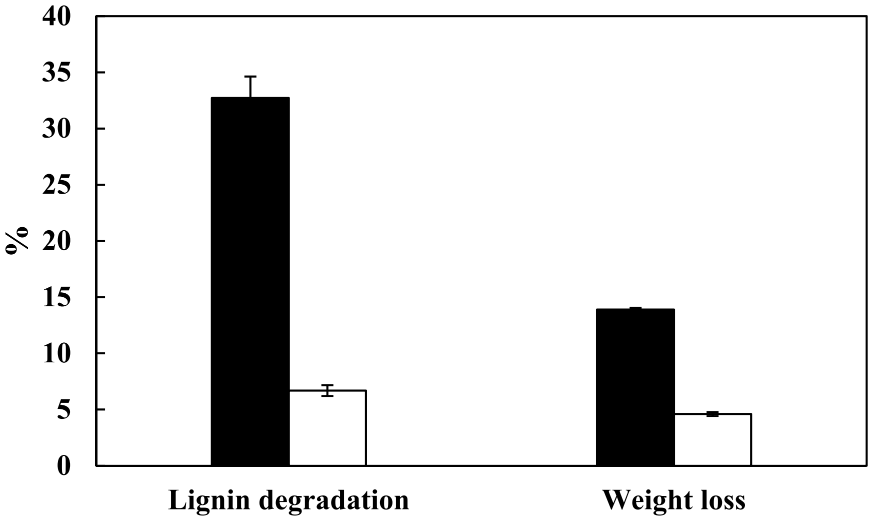

Fig. 1 Ligninolytic properties of *P. sordida* YK-624 (black) and *P. chrysosporium* (white). The values are presented as the mean ± standard deviation of triplicate samples.

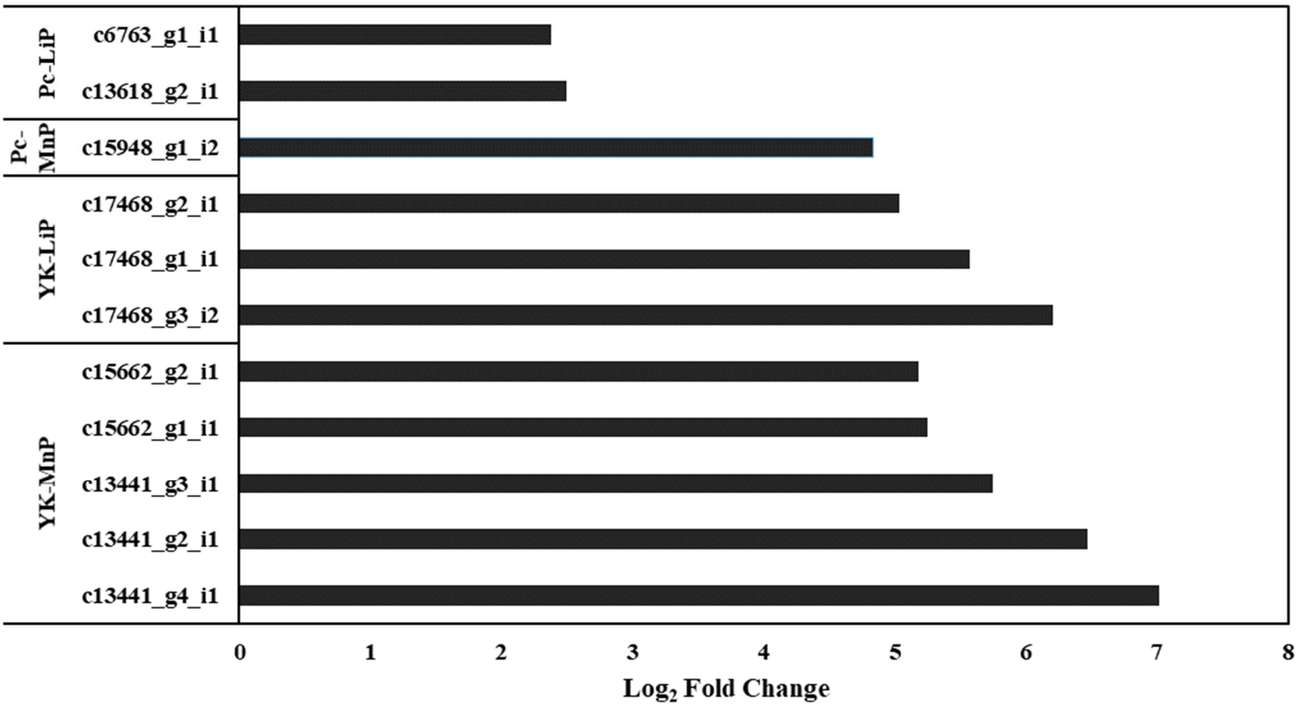

Fig. 2 Upregulated DEGs encoded lignin peroxidases and manganese peroxidases of *P. sordida* YK-624 and *P. chrysosporium*. The details of these DEGs were shown in Table S3 and Table S4. Pc-LiP: lignin peroxidases of *P. chrysosporium*; Pc-MnP: manganese peroxidases of *P. chrysosporium*; YK-LiP: lignin peroxidases of *P. sordida* YK-624; Pc-MnP: manganese peroxidases of *P. sordida* YK-624.

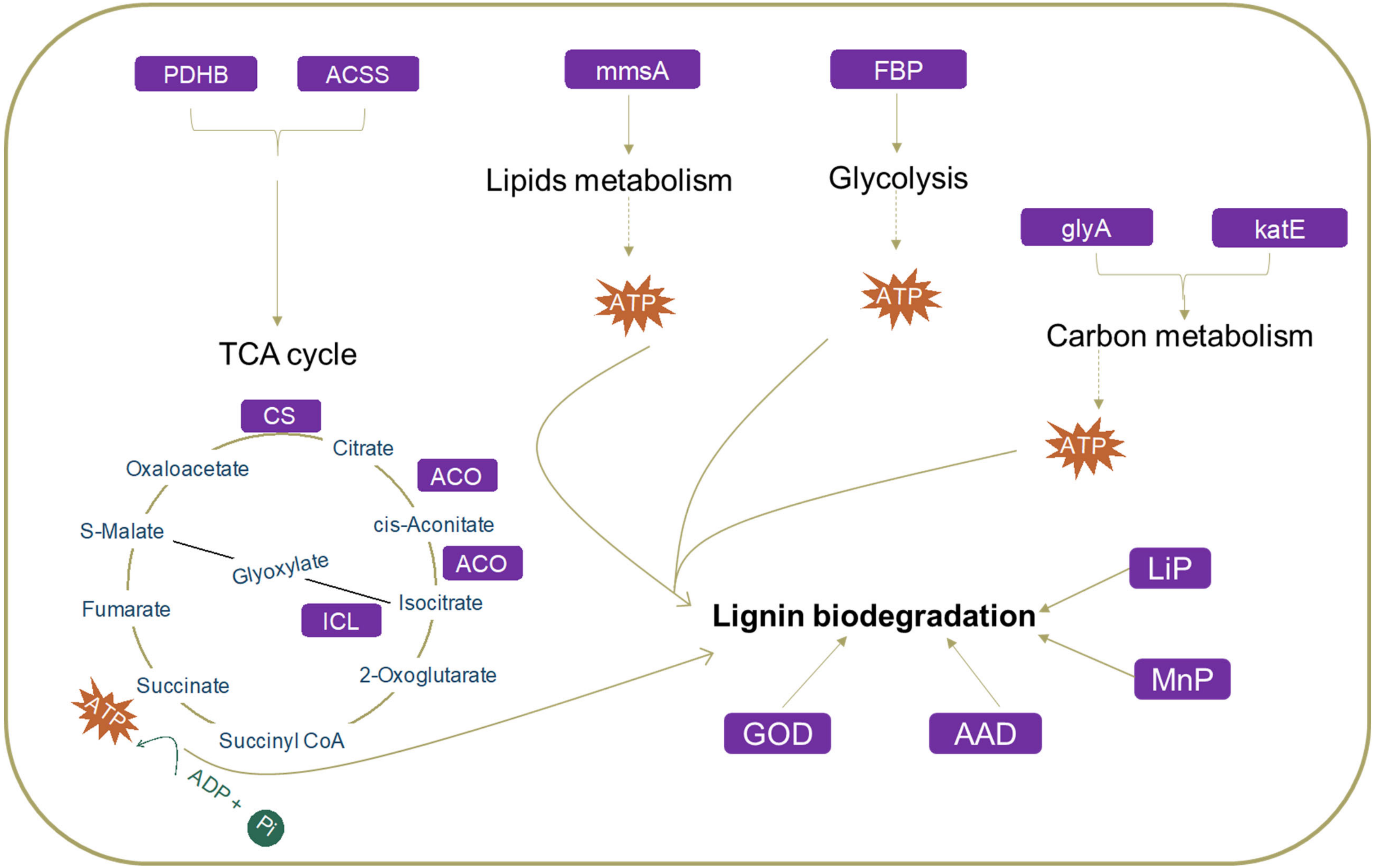
PDHB
ACSS
mmsA
FBP
Lipids metabolism
Glycolysis
glyA
katE
ATP
ATP
Carbon metabolism
TCA cycle
CS
Citrate
Oxaloacetate
ACO
cis-Aconitate
S-Malate
Glyoxylate
ACO
Isocitrate
Fumarate
ICL
ATP
Succinate
2-Oxoglutarate
Succinyl CoA
ADP +
Pi
ATP
LiP
Lignin biodegradation
MnP
GOD
AAD

Fig. 3 Summary of upregulated DEGs of *P. sordida* YK-624 under ligninolytic condition involved in lignin degradation. The details of these DEGs were shown in Table S5. **PDHB**: pyruvate dehydrogenase E1 component beta subunit; **ACSS**: acetyl-CoA synthetase; mmsA: malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase; **FBP**: fructose-1,6-bisphosphatase I; **glyA:** glycine hydroxymethyltransferase; **katE:** catalase; **CS**: citrate synthase; **ACO**: aconitate hydratase; **ICL**: isocitrate lyase; **LiP**: lignin peroxidase; MnP: manganese peroxidase; **GOD**: glucose oxidase; **AAD**: aryl-alcohol dehydrogenase.

Table 1 Enrichment of gene ontology terms in differentially expressed sequences in *P. sordida* YK-624 detected by PAGE

GO_name	**Description**	**GO_id**	**Number of sequences**	***Z* core**	***P*-value**	**FDR**
BP	transport	GO:0006810	128	6.478	9.32E-11	4.02E-09
BP	transmembrane transport	GO:0055085	407	5.933	2.98E-09	1.07E-07
MF	ATPase activity, coupled to transmembrane movement of substances	GO:0042626	57	5.326	1.01E-07	3.1E-06
MF	metal ion transmembrane transporter activity	GO:0046873	16	5.011	5.42E-07	1.37E-05
BP	metal ion transport	GO:0030001	22	4.128	3.67E-05	0.0007
CC	ribosome	GO:0005840	110	3.822	0.0001	0.0019
MF	structural constituent of ribosome	GO:0003735	112	3.782	0.0002	0.0021
BP	glycolytic process	GO:0006096	12	3.685	0.0002	0.0029
BP	translation	GO:0006412	109	3.576	0.0003	0.0042
CC	membrane	GO:0016020	276	3.336	0.0008	0.0097

MF	ATPase activity	GO:0016887	106	3.158	0.0016	0.0171
BP	DNA replication	GO:0006260	44	3.123	0.0018	0.0184
BP	response to oxidative stress	GO:0006979	21	3.039	0.0024	0.0223
MF	serine-type endopeptidase activity	GO:0004252	17	3.001	0.0027	0.0242
MF	transporter activity	GO:0005215	21	2.930	0.0034	0.0293
MF	threonine-type endopeptidase activity	GO:0004298	16	2.848	0.0044	0.0339
CC	proteasome core complex	GO:0005839	16	2.848	0.0044	0.0339
BP	proteolysis involved in cellular protein catabolic process	GO:0051603	16	2.848	0.0044	0.0339
MF	transferase activity, transferring acyl groups	GO:0016746	25	2.737	0.0062	0.0432
MF	cation binding	GO:0043169	14	-2.768	0.0056	0.0406
MF	nucleic acid binding	GO:0003676	218	-2.781	0.0054	0.0404
MF	nutrient reservoir activity	GO:0045735	11	-3.062	0.0022	0.0216
MF	protein kinase activity	GO:0004672	260	-3.961	7.46E-05	0.0012

BP	protein phosphorylation	GO:0006468	263	-3.998	6.39E-05	0.0011
MF	structural constituent of cell wall	GO:0005199	13	-4.293	1.76E-05	0.0003
CC	fungal-type cell wall	GO:0009277	13	-4.293	1.76E-05	0.0003
MF	protein binding	GO:0005515	990	-5.000	5.73E-07	1.37E-05
BP	carbohydrate metabolic process	GO:0005975	216	-8.000	1.33E-15	7.19E-14
MF	hydrolase activity, hydrolyzing *O*-glycosyl compounds	GO:0004553	155	-8.027	8.88E-16	6.39E-14
CC	extracellular region	GO:0005576	39	-10.671	0	0
MF	cellulose binding	GO:0030248	33	-10.816	0	0

GO gene ontology, PAGE parametric analysis of gene set enrichment, BP biological process, MF molecular function, CC cellular component, FDR False discovery rate. Overall mean of log Fold Change values and the standard deviation were used to calculate *Z* scores. Log Fold change value of each GO term upregulated in ligninolytic condition is represented by positive number and downregulated is represented by negative number.

Table 2 Enrichment of gene ontology terms in differentially expressed sequences in *P. chrysosporium* detected by PAGE

GO_name	**Description**	**GO_id**	**Number of sequences**	***Z* core**	***P*-value**	**FDR**
MF	hydrogen ion transmembrane transporter activity	GO:0015078	13	5.096	3.47E-07	1.43E-05
BP	ATP synthesis coupled proton transport	GO:0015986	10	4.551	5.35E-06	0.0002
BP	carbohydrate metabolic process	GO:0005975	201	-8.175	2.22E-16	1.15E-14
MF	hydrolase activity, hydrolyzing *O*-glycosyl compounds	GO:0004553	139	-10.242	0	0
CC	extracellular region	GO:0005576	34	-15.308	0	0
MF	cellulose binding	GO:0030248	28	-17.335	0	0

GO gene ontology, PAGE parametric analysis of gene set enrichment, BP biological process, MF molecular function, CC cellular component, FDR False discovery rate. Overall mean of log Fold Change values and the standard deviation were used to calculate *Z* scores. Log Fold change value of each GO term upregulated in ligninolytic condition is represented by positive number and downregulated is represented by negative number.

Table S1 Data for *P. sordida* YK-624 transcripts.

id	**logFC**	**logCPM**	**PValue**	**FDR**	**Swissprot**	**Uniref90**	**GO**
c2536_g1_i1	7.766631	6.172585	1.81E-16	4.51E-13	RecName: Full=Aspartic protease; Flags: Precursor [Xanthophyllomyces dendrorhous]	NA	GO:0004190|GO:0006508
c23118_g1_i1	7.630286	2.13146	8.66E-12	5.94E-09	NA	NA	NA
c13441_g4_i1	7.020386	6.751793	1.90E-24	3.32E-20	RecName: Full=Manganese peroxidase H4; AltName: Full=MP-I; AltName: Full=Peroxidase manganese-dependent H4; Flags: Precursor [Phanerochaete chrysosporium]	NA	NA
c2536_g2_i1	6.488611	5.436299	1.72E-12	1.50E-09	NA	NA	NA
c13441_g2_i1	6.467584	5.557523	2.28E-23	1.75E-19	RecName: Full=Manganese peroxidase H4; AltName: Full=MP-I; AltName: Full=Peroxidase manganese-dependent H4; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c17468_g3_i1	6.208726	11.86809	3.74E-21	2.18E-17	NA	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c17468_g3_i2	6.208726	11.86809	3.74E-21	2.18E-17	RecName: Full=Ligninase LG6; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c17468_g3_i3	6.208726	11.86809	3.74E-21	2.18E-17	NA	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c7367_g1_i1	6.184459	0.981013	2.27E-06	0.000259	NA	NA	NA
c15869_g1_i1	5.844483	4.296198	8.24E-19	2.62E-15	RecName: Full=Aldo-keto reductase yakc [Schizosaccharomyces pombe 972h-]	NA	NA
c15869_g1_i2	5.844483	4.296198	8.24E-19	2.62E-15	NA	NA	NA
c13441_g3_i1	5.750339	5.729756	1.14E-20	5.70E-17	RecName: Full=Manganese peroxidase 1; Short=MnP-1; Short=MnP1; AltName: Full=Manganese peroxidase isozyme 1; AltName: Full=Peroxidase manganese-dependent 1; AltName: Full=Peroxidase manganese-dependent I; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c17468_g1_i1	5.571735	8.843674	1.31E-20	5.74E-17	RecName: Full=Ligninase LG6; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	NA	NA

c4317_g1_i1	5.507593	7.925298	2.06E-09	7.41E-07	NA	NA	NA
c22277_g1_i1	5.443824	0.505728	6.08E-05	0.003618	NA	NA	NA
c3819_g2_i1	5.386135	0.462274	0.000676	0.021984	NA	NA	NA
c11710_g2_i1	5.298277	0.408971	0.00151	0.040125	RecName: Full=Probable intron-encoded endonuclease 3 (mitochondrion) [Neurospora crassa OR74A]	NA	NA
c15355_g2_i1	5.264012	2.43569	1.07E-09	4.05E-07	NA	NA	NA
c15662_g1_i1	5.255081	3.24243	1.10E-12	1.02E-09	RecName: Full=Manganese peroxidase H4; AltName: Full=MP-I; AltName: Full=Peroxidase manganese-dependent H4; Flags: Precursor [Phanerochaete chrysosporium]	NA	NA
c15228_g1_i1	5.252486	0.394749	0.000133	0.006471	RecName: Full=Cytochrome b; AltName: Full=Complex III subunit 3; AltName: Full=Complex III subunit III; AltName: Full=Cytochrome b-c1 complex subunit 3; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome b subunit (mitochondrion) [Schizophyllum commune]	NA	GO:0009055|GO:0016020|GO:0016491
c4883_g1_i1	5.186924	4.475872	2.23E-20	8.68E-17	NA	UniRef90_K5VUF8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUF8_PHACS	NA
c15662_g2_i1	5.178091	3.423881	6.36E-14	7.42E-11	RecName: Full=Manganese peroxidase H4; AltName: Full=MP-I; AltName: Full=Peroxidase manganese-dependent H4; Flags: Precursor [Phanerochaete chrysosporium]	NA	NA
c26950_g1_i1	5.155824	0.342405	0.000708	0.022771	NA	NA	NA
c17468_g2_i1	5.038693	7.741133	6.08E-07	9.32E-05	RecName: Full=Ligninase LG6; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	NA	NA
c15869_g7_i1	4.896192	3.941092	1.32E-11	8.41E-09	RecName: Full=Aldo-keto reductase yakc [Schizosaccharomyces pombe 972h-]	NA	NA
c8963_g1_i1	4.701114	6.124813	3.51E-26	1.23E-21	NA	NA	NA
c26549_g1_i1	4.673695	5.607505	1.02E-16	2.75E-13	RecName: Full=Centromere protein V; Short=CENP-V; AltName: Full=Proline-rich protein 6 [Mus musculus]	NA	GO:0008152|GO:0016846
c8963_g2_i1	4.672163	4.994493	4.47E-24	5.21E-20	NA	NA	NA
c11984_g2_i1	4.628303	2.616321	1.36E-07	2.65E-05	RecName: Full=Lysozyme M1; AltName: Full=1,4-beta-N-acetylmuramidase M1; Flags: Precursor [Streptomyces globisporus]	NA	GO:0003796|GO:0009253|GO:0016998
c17020_g1_i1	4.324698	1.036425	3.22E-05	0.002197	NA	NA	NA

c22490_g1_i1	4.262676	2.102261	0.001088	0.031828	RecName: Full=Fruiting body protein SC3; AltName: Full=Hydrophobin SC3; Flags: Precursor [Schizophyllum commune]	UniRef90_A0A067TLC6 Uncharacterized protein n=1 Tax=Galerina marginata CBS 339.88 RepID=A0A067TLC6_9AGAR	GO:0005199|GO:0009277
c21550_g1_i1	4.254494	5.542718	3.00E-14	3.89E-11	NA	NA	NA
c21090_g1_i1	4.219139	8.897173	2.64E-10	1.17E-07	NA	NA	NA
c14424_g1_i1	4.210421	5.116589	1.54E-17	4.48E-14	RecName: Full=High affinity potassium transporter [Schwanniomyces occidentalis]	NA	GO:0015079|GO:0016020|GO:0071805
c15355_g1_i1	4.204835	3.333505	1.26E-08	3.65E-06	RecName: Full=Sterigmatocystin 8-O-methyltransferase; Flags: Precursor [Aspergillus flavus]	NA	GO:0008171
c71_g2_i1	4.170209	1.513004	1.94E-06	0.00023	NA	NA	NA
c22989_g1_i1	4.156276	2.495165	9.71E-06	0.000861	NA	NA	NA
c15007_g1_i1	4.151152	3.510355	4.81E-15	8.01E-12	NA	NA	NA
c642_g2_i1	4.150907	5.651171	9.17E-05	0.004926	RecName: Full=Zinc-regulated transporter 1; AltName: Full=High-affinity zinc transport protein zrt1 [Schizosaccharomyces pombe 972h-]	UniRef90_UPI0004418422 ZIP-like iron-zinc transporter n=1 Tax=Punctularia strigosozonata (strain HHB-11173) RepID=UPI0004418422	NA
c19828_g1_i1	4.105695	7.85493	4.51E-20	1.58E-16	NA	NA	NA
c5019_g1_i1	4.10196	1.478749	4.22E-05	0.002708	NA	NA	NA
c20738_g1_i1	4.089679	3.45483	6.07E-15	9.65E-12	NA	NA	NA
c14424_g3_i1	4.082097	2.887809	5.74E-12	4.10E-09	NA	NA	NA
c642_g1_i1	4.054939	7.248535	7.91E-05	0.004363	RecName: Full=Zinc-regulated transporter 1; AltName: Full=High-affinity zinc transport protein ZRT1 [Saccharomyces cerevisiae S288c]	UniRef90_K5UKJ6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UKJ6_PHACS	GO:0016020|GO:0030001|GO:0046873|GO:0055085
c17493_g6_i1	4.037331	6.664265	2.07E-16	4.83E-13	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]	NA	GO:0004190|GO:0006508
c23071_g1_i1	3.992285	0.810724	0.000272	0.011062	NA	NA	NA
c25806_g1_i1	3.978506	2.934634	2.05E-07	3.81E-05	NA	NA	NA
c14516_g1_i1	3.969658	5.854878	4.75E-10	2.05E-07	NA	NA	NA

c14516_g1_i2	3.969658	5.854878	4.75E-10	2.05E-07	RecName: Full=ADP,ATP carrier protein; AltName: Full=ADP/ATP translocase; AltName: Full=Adenine nucleotide translocator; Short=ANT [Neurospora crassa OR74A]	UniRef90_K5V5K6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V5K6_PHACS	NA
c5236_g2_i1	3.833109	6.529366	1.10E-12	1.02E-09	RecName: Full=Galactinol synthase 4; Short=AtGolS4; Short=GolS-4 [Arabidopsis thaliana]	UniRef90_K5WJY7 Glycosyltransferase family 8 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJY7_PHACS	GO:0016757
c14424_g2_i1	3.808773	4.271397	1.44E-15	2.51E-12	RecName: Full=High affinity potassium transporter [Schwanniomyces occidentalis]	NA	GO:0015079|GO:0016020|GO:0071805
c20202_g1_i1	3.798684	6.76534	1.50E-06	0.000187	RecName: Full=Glucan endo-1,6-beta-glucosidase B; AltName: Full=Beta-1,6-glucanase B; AltName: Full=Endo-1,6-beta-D-glucanase B; AltName: Full=Endo-1,6-beta-glucanase B; Flags: Precursor [Aspergillus nidulans FGSC A4]	NA	GO:0004553|GO:0005975
c8923_g1_i1	3.786663	4.03395	5.83E-09	1.90E-06	NA	NA	NA
c6004_g1_i1	3.785721	5.253268	3.91E-16	8.55E-13	NA	UniRef90_K5V2H6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V2H6_PHACS	NA
c4038_g1_i1	3.724549	0.654041	0.000166	0.007527	NA	NA	NA
c17355_g1_i1	3.694874	2.695365	1.01E-10	4.93E-08	NA	NA	NA
c22857_g1_i1	3.688429	6.721265	0.000356	0.013453	RecName: Full=Zinc-regulated transporter 2; AltName: Full=Low-affinity zinc transport protein ZRT2 [Saccharomyces cerevisiae S288c]	UniRef90_K5UKJ6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UKJ6_PHACS	GO:0016020|GO:0030001|GO:0046873|GO:0055085
c9107_g2_i1	3.669988	4.604581	1.06E-12	1.02E-09	NA	NA	NA
c14175_g1_i1	3.656163	4.033502	6.64E-10	2.76E-07	NA	NA	NA
c14175_g1_i2	3.656163	4.033502	6.64E-10	2.76E-07	NA	NA	NA
c21110_g1_i1	3.626854	8.694213	7.80E-13	8.02E-10	NA	NA	NA
c17443_g2_i1	3.615276	4.35965	1.00E-11	6.73E-09	NA	NA	NA
c13909_g1_i1	3.614132	3.817808	0.000126	0.006229	RecName: Full=Zinc homeostasis factor 1 [Schizosaccharomyces pombe 972h-]	NA	GO:0006812|GO:0008324|GO:0016021|GO:0055085
c13909_g1_i2	3.614132	3.817808	0.000126	0.006229	NA	NA	GO:0006812|GO:0008324|GO:0016021|GO:0055085

c259_g2_i1	3.605184	9.167249	6.45E-07	9.80E-05	RecName: Full=Inositol-3-phosphate synthase; Short=MIP synthase; AltName: Full=Myo-inositol 1-phosphate synthase; Short=IPS; Short=MI-1-P synthase [Candida albicans SC5314]	UniRef90_K5W3D7 Uncharacterized protein n=2 Tax=Phanerochaetaceae RepID=K5W3D7_PHACS	GO:0004512|GO:0006021|GO:0008654
c12640_g1_i1	3.534161	3.180372	2.98E-12	2.37E-09	NA	NA	NA
c12640_g1_i2	3.534161	3.180372	2.98E-12	2.37E-09	NA	NA	NA
c2435_g1_i1	3.517831	5.868505	0.000245	0.010167	RecName: Full=Uncharacterized membrane protein YFL054C [Saccharomyces cerevisiae S288c]	NA	GO:0005215|GO:0006810|GO:0016020
c74_g1_i1	3.506535	2.711464	7.62E-10	3.14E-07	NA	UniRef90_K5VZI4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZI4_PHACS	NA
c13311_g2_i1	3.488353	1.973282	2.24E-06	0.000256	NA	NA	NA
c10786_g2_i1	3.468032	0.506918	0.000692	0.022413	NA	NA	NA
c10786_g2_i2	3.468032	0.506918	0.000692	0.022413	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	NA	GO:0004190|GO:0006508
c4114_g1_i1	3.462324	1.926037	4.73E-06	0.000479	NA	NA	GO:0008080
c2547_g1_i1	3.449896	2.15433	7.73E-09	2.35E-06	NA	NA	NA
c2547_g1_i2	3.449896	2.15433	7.73E-09	2.35E-06	NA	NA	NA
c26166_g1_i1	3.426606	7.710422	1.61E-07	3.07E-05	RecName: Full=Sterigmatocystin 8-O-methyltransferase; AltName: Full=Aflatoxin biosynthesis protein P; Flags: Precursor [Aspergillus parasiticus]	NA	GO:0008171
c25270_g1_i1	3.417457	1.937527	5.80E-06	0.00057	NA	NA	NA
c11714_g3_i1	3.412539	3.09448	8.91E-09	2.66E-06	NA	NA	NA
c8697_g1_i1	3.411871	0.981945	4.11E-05	0.002658	RecName: Full=Probable intron-encoded endonuclease aI2; Contains: RecName: Full=Truncated non-functional cytochrome oxidase 1; Contains: RecName: Full=Intron-encoded endonuclease aI2; Flags: Precursor (mitochondrion) [Ustilago maydis 521]	NA	GO:0004129|GO:0005506|GO:0009055|GO:0009060|GO:0016021|GO:0020037|GO:0055114
c3917_g1_i1	3.373359	0.447594	0.001337	0.036824	NA	NA	NA
c8417_g2_i1	3.300131	6.492474	4.61E-16	9.49E-13	NA	NA	NA
c4361_g1_i1	3.272229	1.758827	0.000209	0.009031	RecName: Full=50S ribosomal protein L15 [Dinoroseobacter shibae DFL 12 = DSM 16493]	NA	NA
c259_g1_i1	3.272215	6.950944	7.12E-07	0.000106	NA	NA	NA
c9107_g1_i1	3.268209	6.668865	3.00E-14	3.89E-11	NA	NA	NA

c26849_g1_i1	3.24138	0.86324	0.000872	0.026883	NA	NA	NA
c3995_g1_i1	3.239427	3.384949	0.001662	0.042731	RecName: Full=Zinc/cadmium resistance protein [Saccharomyces cerevisiae S288c]	NA	GO:0006812|GO:0008324|GO:0016021|GO:0055085
c962_g1_i1	3.230143	1.253946	4.03E-05	0.002619	NA	NA	NA
c15266_g2_i1	3.222901	0.869288	0.000124	0.006161	RecName: Full=ABC transporter C family member 12; AltName: Full=ABC transporter ABCC.12 [Dictyostelium discoideum]	NA	NA
c11714_g4_i1	3.212697	3.162827	1.50E-08	4.22E-06	NA	NA	NA
c17469_g4_i1	3.197786	4.094636	9.73E-10	3.78E-07	RecName: Full=6-hydroxynicotinate 3-monooxygenase; Flags: Precursor [Pseudomonas fluorescens]	NA	NA
c17515_g2_i1	3.193873	5.379364	1.93E-10	8.74E-08	RecName: Full=2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2; Short=BPG-dependent PGAM 2; Short=PGAM 2; Short=Phosphoglyceromutase 2; Short=dPGM 2 [Gloeobacter violaceus PCC 7421]	UniRef90_K5WNI9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNI9_PHACS	NA
c17515_g2_i2	3.193873	5.379364	1.93E-10	8.74E-08	NA	NA	NA
c20129_g1_i1	3.16206	1.206122	0.000296	0.011746	NA	NA	NA
c16231_g4_i1	3.152324	1.471725	2.50E-06	0.000278	NA	UniRef90_K5XCP3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XCP3_PHACS	NA
c9107_g3_i1	3.120011	5.069266	1.90E-14	2.77E-11	NA	NA	NA
c22988_g1_i1	3.118025	9.341359	1.19E-12	1.07E-09	RecName: Full=Uncharacterized protein C3H7.13 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WB92 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WB92_PHACS	GO:0005515
c19202_g1_i1	3.091766	2.751153	7.78E-08	1.66E-05	RecName: Full=ATP synthase subunit 9, mitochondrial; AltName: Full=Lipid-binding protein (mitochondrion) [Ustilago maydis 521]	NA	GO:0015078|GO:0015991|GO:0033177
c27014_g1_i1	3.091692	0.784039	0.000435	0.015808	NA	NA	NA
c16746_g1_i1	3.079069	3.415992	1.33E-07	2.60E-05	NA	NA	NA
c16746_g1_i2	3.079069	3.415992	1.33E-07	2.60E-05	NA	NA	NA
c16746_g1_i3	3.079069	3.415992	1.33E-07	2.60E-05	NA	NA	NA
c8993_g2_i1	3.072114	5.059353	1.18E-11	7.64E-09	RecName: Full=N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D; Short=N-acyl phosphatidylethanolamine	NA	NA

					phospholipase D; Short=NAPE-PLD; Short=NAPE-hydrolyzing phospholipase D [Mus musculus]		
c17469_g1_i1	3.051579	1.413282	0.00119	0.033772	NA	NA	NA
c14399_g4_i1	3.042448	5.17917	3.14E-12	2.44E-09	RecName: Full=Uncharacterized ATPase YjoB [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0005524
c16562_g2_i1	3.035619	1.621227	1.08E-06	0.000149	NA	NA	NA
c14399_g1_i1	3.029244	3.208559	1.13E-09	4.26E-07	NA	NA	NA
c23014_g1_i1	3.003307	4.37153	2.78E-09	9.61E-07	NA	UniRef90_K5UPN2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UPN2_PHACS	NA
c9043_g1_i1	3.000907	6.184448	4.58E-12	3.34E-09	RecName: Full=Amidase 1; Short=AtAMI1; AltName: Full=Translocon at the outer membrane of chloroplasts 64-I; Short=AtTOC64-I [Arabidopsis thaliana]	NA	GO:0016884
c24711_g1_i1	2.959112	3.736989	1.21E-08	3.51E-06	NA	NA	NA
c16409_g1_i1	2.956344	4.456282	1.12E-05	0.000959	RecName: Full=Putative uncharacterized oxidoreductase YDR541C [Saccharomyces cerevisiae S288c]	UniRef90_K5UP09 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UP09_PHACS	GO:0003824|GO:0003854|GO:0016616|GO:0050662|GO:0055114
c23647_g1_i1	2.955377	5.929224	1.97E-12	1.68E-09	NA	NA	NA
c17694_g1_i1	2.952302	8.06709	0.000323	0.012476	NA	UniRef90_K5UPM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UPM7_PHACS	NA
c8417_g3_i1	2.92866	8.348174	2.14E-12	1.78E-09	RecName: Full=Uncharacterized protein TC_0114	NA	NA
c23706_g1_i1	2.920918	2.94989	8.84E-11	4.42E-08	NA	NA	GO:0008762|GO:0016491|GO:0050660|GO:0055114
c3698_g1_i1	2.919199	1.309265	2.82E-05	0.001982	NA	NA	NA
c17245_g4_i1	2.906246	6.251977	0.000208	0.009031	RecName: Full=Exoglucanase 1; AltName: Full=1,4-beta-cellobiohydrolase; AltName: Full=Exocellobiohydrolase I; AltName: Full=Exoglucanase I; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004553|GO:0005975
c19128_g1_i1	2.901735	1.719128	0.000152	0.007144	NA	NA	NA
c9043_g3_i1	2.899399	5.259558	3.73E-12	2.83E-09	NA	NA	NA

c3922_g1_i1	2.895931	5.855102	1.46E-07	2.79E-05	RecName: Full=Inositol oxygenase; AltName: Full=Myo-inositol oxygenase; Short=MI oxygenase [Dictyostelium discoideum]	NA	GO:0005506|GO:0005737|GO:0019310|GO:0050113|GO:0055114
c3922_g1_i2	2.895931	5.855102	1.46E-07	2.79E-05	NA	NA	GO:0005506|GO:0005737|GO:0019310|GO:0050113|GO:0055114
c16183_g2_i1	2.890591	3.541017	2.43E-07	4.37E-05	NA	NA	NA
c16183_g2_i2	2.890591	3.541017	2.43E-07	4.37E-05	NA	NA	NA
c71_g1_i1	2.882969	4.498755	1.81E-08	5.02E-06	RecName: Full=Quinidine resistance protein 2 [Saccharomyces cerevisiae S288c]	UniRef90_K5VS05 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VS05_PHACS	NA
c8417_g1_i1	2.866814	4.385292	7.73E-10	3.14E-07	NA	NA	NA
c17340_g3_i1	2.861654	1.530954	0.00022	0.009391	NA	NA	NA
c11908_g2_i1	2.861563	1.495501	0.000166	0.007527	NA	NA	NA
c22322_g1_i1	2.852615	3.188014	1.33E-08	3.83E-06	NA	UniRef90_K5V002 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V002_PHACS	NA
c6658_g1_i1	2.851417	0.980187	0.00072	0.023043	NA	NA	NA
c27310_g1_i1	2.850444	2.520648	6.61E-05	0.00385	NA	NA	NA
c14585_g1_i1	2.834235	3.172433	7.00E-09	2.17E-06	NA	NA	NA
c14585_g1_i2	2.834235	3.172433	7.00E-09	2.17E-06	NA	NA	NA
c14585_g1_i3	2.834235	3.172433	7.00E-09	2.17E-06	NA	NA	NA
c15269_g1_i1	2.821457	3.758011	7.57E-07	0.000111	NA	NA	NA
c15269_g1_i2	2.821457	3.758011	7.57E-07	0.000111	NA	NA	NA
c11237_g1_i1	2.819533	3.38535	6.60E-07	9.99E-05	NA	NA	NA
c18487_g1_i1	2.817512	1.517475	0.001255	0.035208	NA	NA	NA
c10867_g2_i1	2.80057	2.995835	1.08E-07	2.20E-05	RecName: Full=Allantoate permease [Saccharomyces cerevisiae S288c]	NA	GO:0016021|GO:0055085
c632_g1_i1	2.786232	9.912544	1.35E-09	5.00E-07	RecName: Full=Probable tripeptidyl-peptidase SED3; AltName: Full=Sedolisin-C; Flags: Precursor [Trichophyton verrucosum HKI 0517]	UniRef90_K5W588 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W588_PHACS	GO:0004252|GO:0006508

c9456_g1_i1	2.783151	2.355738	6.62E-08	1.47E-05	NA	UniRef90_K5WCL6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCL6_PHACS	NA
c22977_g1_i1	2.782631	1.463083	5.93E-05	0.003555	NA	NA	NA
c4843_g2_i1	2.781609	3.083983	2.87E-07	5.14E-05	NA	UniRef90_A0A0C3NNY4 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NNY4_PHLGI	NA
c22176_g1_i1	2.768632	1.980559	9.84E-07	0.000139	NA	NA	NA
c14873_g1_i1	2.762164	7.565166	1.68E-11	1.03E-08	NA	UniRef90_K5W405 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W405_PHACS	NA
c14253_g1_i1	2.756438	6.42996	2.82E-08	7.40E-06	NA	NA	GO:0008152|GO:0008168
c14253_g1_i2	2.756438	6.42996	2.82E-08	7.40E-06	RecName: Full=Trans-aconitate 3-methyltransferase [Saccharomyces cerevisiae YJM789]	NA	GO:0008152|GO:0008168
c11246_g1_i1	2.756432	3.464473	4.04E-06	0.000415	NA	NA	NA
c19955_g1_i1	2.754773	3.236271	1.35E-10	6.38E-08	RecName: Full=Uncharacterized FAD-linked oxidoreductase YvdP; AltName: Full=Spore coat protein YvdP [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0016491|GO:0050660|GO:0055114
c10969_g1_i1	2.748819	3.384065	0.00012	0.006043	NA	NA	NA
c13160_g2_i1	2.747025	5.440778	8.59E-11	4.36E-08	NA	NA	NA
c25622_g1_i1	2.744978	2.050384	0.000572	0.019535	NA	NA	NA
c25595_g1_i1	2.734985	5.344277	2.04E-10	9.16E-08	RecName: Full=Pentachlorophenol 4-monooxygenase; AltName: Full=Pentachlorophenol hydroxylase [Sphingobium chlorophenolicum]	NA	GO:0016491|GO:0055114
c14873_g2_i1	2.717802	5.391544	2.42E-11	1.43E-08	NA	NA	NA
c14873_g2_i2	2.717802	5.391544	2.42E-11	1.43E-08	NA	NA	NA
c17925_g1_i1	2.716797	2.698002	1.65E-07	3.10E-05	NA	UniRef90_K5WVX6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WVX6_PHACS	NA
c18810_g1_i1	2.714214	1.186406	0.001315	0.036385	RecName: Full=Short-chain dehydrogenase reductase 2a; Short=AtSDR2a [Arabidopsis thaliana]	NA	GO:0008152|GO:0016491
c5843_g1_i1	2.701985	9.292928	0.000107	0.005575	NA	NA	NA

c15744_g2_i1	2.69556	3.645547	8.55E-08	1.78E-05	RecName: Full=Uncharacterized transporter C417.10 [Schizosaccharomyces pombe 972h-]	NA	NA
c15754_g1_i1	2.694046	3.243824	1.66E-06	0.000204	RecName: Full=Putative aryl-alcohol dehydrogenase C977.14c [Schizosaccharomyces pombe 972h-]	NA	NA
c7354_g1_i1	2.690774	3.57115	1.02E-09	3.90E-07	NA	NA	NA
c632_g2_i1	2.687453	9.431438	9.09E-08	1.88E-05	RecName: Full=Tripeptidyl-peptidase SED2; AltName: Full=Sedolisin-B; Flags: Precursor [Arthroderma otae CBS 113480]	UniRef90_K5W588 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W588_PHACS	GO:0008236
c6763_g2_i1	2.68473	5.651421	5.08E-09	1.69E-06	RecName: Full=Stabilin-2; AltName: Full=Fasciclin, EGF-like, laminin-type EGF-like and link domain-containing scavenger receptor 2; Short=FEEL-2; AltName: Full=Hyaluronan receptor for endocytosis; Contains: RecName: Full=175 kDa stabilin-2; AltName: Full=175 kDa hyaluronan receptor for endocytosis; Flags: Precursor, partial [Rattus norvegicus]	NA	NA
c12398_g1_i1	2.68299	2.725422	3.00E-08	7.72E-06	RecName: Full=N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D; Short=N-acyl phosphatidylethanolamine phospholipase D; Short=NAPE-PLD; Short=NAPE-hydrolyzing phospholipase D [Rattus norvegicus]	UniRef90_K5W3Z7 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3Z7_PHACS	NA
c16667_g1_i1	2.677377	3.434653	7.82E-11	4.14E-08	NA	NA	NA
c17340_g1_i1	2.672891	2.373126	4.59E-06	0.000469	NA	NA	GO:0005515
c27321_g1_i1	2.665889	1.754221	0.000102	0.005359	NA	NA	NA
c6543_g2_i1	2.663314	3.792165	1.88E-05	0.001441	RecName: Full=Peptidyl-Lys metalloendopeptidase; Short=MEP; AltName: Full=GfMEP; Flags: Precursor [Grifola frondosa]	NA	GO:0004222|GO:0006508
c16888_g2_i1	2.655037	5.307042	5.18E-05	0.003183	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	NA	GO:0004190|GO:0006508
c19971_g1_i1	2.654837	7.485506	5.15E-07	8.26E-05	NA	NA	NA
c5195_g2_i1	2.651713	2.701103	1.12E-06	0.000152	RecName: Full=Putative cytochrome P450 cyp-13B1 [Caenorhabditis elegans]	UniRef90_G5EJV2 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJV2_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c10867_g1_i1	2.642565	3.740787	1.76E-08	4.93E-06	RecName: Full=Allantoate permease [Saccharomyces cerevisiae S288c]	NA	NA
c21461_g1_i1	2.624959	1.555244	8.51E-05	0.00462	NA	NA	NA
c6666_g1_i1	2.608002	1.095312	0.001943	0.04751	NA	NA	NA

c16915_g1_i1	2.596626	5.483511	4.52E-08	1.06E-05	RecName: Full=Mitochondrial sorting homolog [Caenorhabditis elegans]	NA	GO:0005524
c15754_g2_i1	2.582824	4.103526	2.89E-08	7.55E-06	NA	NA	NA
c15754_g2_i2	2.582824	4.103526	2.89E-08	7.55E-06	RecName: Full=Putative aryl-alcohol dehydrogenase YPL088W [Saccharomyces cerevisiae S288c]	NA	NA
c11298_g1_i1	2.580581	0.817389	0.001032	0.030623	NA	NA	NA
c12255_g1_i1	2.578054	0.825103	0.000942	0.028606	NA	UniRef90_K5W9A7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W9A7_PHACS	NA
c15634_g2_i1	2.574085	5.172936	1.66E-07	3.11E-05	RecName: Full=Glutathione S-transferase omega-2; Short=GSTO-2; AltName: Full=Glutathione S-transferase omega 2-2; Short=GSTO 2-2; AltName: Full=Glutathione-dependent dehydroascorbate reductase; AltName: Full=Monomethylarsonic acid reductase; Short=MMA(V) reductase [Rattus norvegicus]	NA	GO:0005515
c11714_g1_i1	2.563511	4.912239	4.47E-08	1.06E-05	NA	NA	NA
c13160_g1_i1	2.563139	6.353313	1.41E-11	8.79E-09	NA	NA	NA
c17264_g3_i1	2.557366	5.811131	3.82E-08	9.28E-06	NA	NA	NA
c26006_g1_i1	2.555271	1.788907	0.000896	0.027433	RecName: Full=Uncharacterized transporter mfs2 [Schizosaccharomyces pombe 972h-]	NA	NA
c14343_g1_i1	2.541961	2.323328	1.08E-05	0.000931	NA	NA	NA
c14343_g1_i2	2.541961	2.323328	1.08E-05	0.000931	NA	NA	NA
c16915_g4_i1	2.540513	5.729783	7.74E-07	0.000113	NA	NA	NA
c19032_g1_i1	2.539841	1.938714	2.47E-06	0.000277	NA	NA	NA
c10024_g2_i1	2.537779	5.176446	1.83E-06	0.00022	NA	UniRef90_K5WTC9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WTC9_PHACS	NA
c15544_g3_i1	2.536039	1.288215	0.000306	0.012066	NA	NA	NA
c12063_g1_i1	2.531627	3.467101	5.32E-07	8.38E-05	RecName: Full=3-hydroxybenzoate 6-hydroxylase 1; AltName: Full=Constitutive 3-hydroxybenzoate 6-hydroxylase [Pseudomonas alcaligenes]	NA	NA
c12063_g1_i2	2.531627	3.467101	5.32E-07	8.38E-05	NA	NA	NA
c23648_g1_i1	2.525316	4.126038	1.02E-06	0.000143	NA	NA	NA

c19546_g1_i1	2.524146	6.327613	1.17E-07	2.31E-05	RecName: Full=Phenylalanine ammonia-lyase [Amanita muscaria]	NA	NA
c23124_g1_i1	2.519412	1.051467	0.000312	0.012225	NA	NA	NA
c14343_g3_i1	2.519055	2.794528	1.20E-06	0.00016	NA	NA	NA
c16084_g3_i1	2.517945	3.977012	3.10E-10	1.35E-07	RecName: Full=Multidrug resistance protein 1B; AltName: Full=ATP-binding cassette sub-family B member 1B; AltName: Full=P-glycoprotein 1; AltName: CD_antigen=CD243 [Mus musculus]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c8601_g2_i1	2.517253	4.29836	4.72E-06	0.000479	RecName: Full=MFS antiporter QDR2 [Candida albicans SC5314]	NA	GO:0016021|GO:0055085
c5236_g1_i1	2.51674	2.723616	2.20E-05	0.001633	NA	NA	NA
c12709_g3_i1	2.50539	4.871397	1.61E-05	0.001277	RecName: Full=Sterigmatocystin 8-O-methyltransferase; AltName: Full=Aflatoxin biosynthesis protein P; Flags: Precursor [Aspergillus parasiticus]	UniRef90_K5WNG4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNG4_PHACS	NA
c15062_g1_i1	2.502633	2.300879	5.17E-05	0.003183	NA	NA	NA
c9060_g1_i1	2.501802	4.277349	6.64E-06	0.000633	RecName: Full=Sphingoid long-chain base transporter RSB1 [Saccharomyces cerevisiae EC1118]	NA	GO:0006950|GO:0016021
c17281_g1_i1	2.494865	6.67956	5.87E-09	1.90E-06	NA	NA	GO:0003824|GO:0008152|GO:0050662
c17281_g1_i2	2.494865	6.67956	5.87E-09	1.90E-06	RecName: Full=L-aminoadipate-semialdehyde dehydrogenase large subunit; AltName: Full=Alpha-aminoadipate reductase; Short=Alpha-AR [Candida glabrata CBS 138]	NA	GO:0003824|GO:0008152|GO:0050662
c14894_g1_i1	2.494535	5.233353	0.000156	0.007221	RecName: Full=Putative alpha-ketoglutarate-dependent sulfonate dioxygenase [Schizosaccharomyces pombe 972h-]	UniRef90_K5WLC8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLC8_PHACS	GO:0016491|GO:0055114
c14894_g1_i2	2.494535	5.233353	0.000156	0.007221	NA	NA	GO:0016491|GO:0055114
c12709_g2_i1	2.489863	4.185421	1.37E-06	0.000175	NA	UniRef90_K5WNG4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNG4_PHACS	NA
c9276_g1_i1	2.487861	5.300668	3.00E-06	0.000327	RecName: Full=Condensin complex subunit 3; AltName: Full=CAPG homolog; AltName: Full=p100 [Schizosaccharomyces pombe 972h-]	NA	NA
c24667_g1_i1	2.475809	2.402451	0.000145	0.006852	NA	NA	GO:0005525
c16925_g1_i1	2.474375	1.566257	0.000671	0.021925	NA	NA	GO:0006725|GO:0016853

c13774_g1_i1	2.472457	1.766451	0.000322	0.012476	RecName: Full=Sugar transporter STL1 [Saccharomyces cerevisiae S288c]	NA	GO:0016021|GO:0022857|GO:0055085
c17439_g4_i1	2.471208	8.253943	4.73E-07	7.81E-05	NA	NA	NA
c17439_g4_i2	2.471208	8.253943	4.73E-07	7.81E-05	RecName: Full=Aryl-alcohol dehydrogenase [NADP(+)]; Short=AAD [Phanerochaete chrysosporium]	NA	NA
c11416_g1_i1	2.470054	3.310703	1.14E-07	2.29E-05	NA	NA	NA
c13298_g1_i1	2.468647	2.417584	9.92E-06	0.000878	RecName: Full=Anthocyanidin 3-O-glucosyltransferase; AltName: Full=Bronze-1; AltName: Full=Bz-McC allele; AltName: Full=Flavonol 3-O-glucosyltransferase; AltName: Full=UDP-glucose flavonoid 3-O-glucosyltransferase [Zea mays]	NA	GO:0008152|GO:0016758
c17426_g1_i1	2.458742	8.142968	8.12E-11	4.24E-08	NA	NA	GO:0016021|GO:0055085
c17426_g1_i2	2.458742	8.142968	8.12E-11	4.24E-08	NA	NA	NA
c17426_g1_i3	2.458742	8.142968	8.12E-11	4.24E-08	RecName: Full=Uncharacterized MFS-type transporter C530.15c [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c17426_g1_i4	2.458742	8.142968	8.12E-11	4.24E-08	NA	NA	GO:0016021|GO:0055085
c17426_g1_i5	2.458742	8.142968	8.12E-11	4.24E-08	NA	NA	GO:0016021|GO:0055085
c17426_g1_i6	2.458742	8.142968	8.12E-11	4.24E-08	NA	NA	GO:0016021|GO:0055085
c10221_g1_i1	2.453001	1.584218	0.000288	0.011519	NA	NA	NA
c17020_g2_i1	2.451417	4.937882	5.22E-07	8.29E-05	NA	NA	NA
c17020_g2_i2	2.451417	4.937882	5.22E-07	8.29E-05	NA	NA	NA
c17020_g2_i3	2.451417	4.937882	5.22E-07	8.29E-05	NA	NA	NA
c17020_g2_i4	2.451417	4.937882	5.22E-07	8.29E-05	NA	NA	NA
c17020_g2_i5	2.451417	4.937882	5.22E-07	8.29E-05	NA	NA	NA
c14097_g1_i1	2.451277	2.108104	2.77E-05	0.001954	NA	NA	NA
c18003_g1_i1	2.450839	3.327733	1.06E-06	0.000148	NA	NA	NA
c14941_g1_i1	2.447413	2.563184	2.37E-05	0.001734	NA	UniRef90_K5WHY2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WHY2_PHACS	NA
c19808_g1_i1	2.442348	7.922406	8.72E-06	0.000786	RecName: Full=Testicular acid phosphatase homolog; Flags: Precursor [Xenopus laevis]	NA	GO:0003993
c17123_g5_i1	2.438217	1.905132	0.000487	0.017141	NA	NA	NA
c7334_g2_i1	2.437613	1.740138	7.51E-05	0.004201	NA	NA	NA

c678_g2_i1	2.436471	5.264499	9.64E-06	0.000858	RecName: Full=Rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] reductase; AltName: Full=3-ketoacyl-acyl carrier protein reductase [Pseudomonas aeruginosa PAO1]	UniRef90_K5VXS2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXS2_PHACS	GO:0008152|GO:0016491
c9551_g1_i1	2.436008	4.277188	5.33E-08	1.22E-05	NA	UniRef90_K5V3A6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3A6_PHACS	NA
c15792_g2_i1	2.418169	1.864946	0.000362	0.01363	NA	NA	NA
c26718_g1_i1	2.407389	1.216482	0.001116	0.032444	NA	NA	NA
c4241_g1_i1	2.402429	2.989868	9.35E-07	0.000133	NA	NA	NA
c4241_g1_i2	2.402429	2.989868	9.35E-07	0.000133	NA	NA	NA
c14986_g2_i1	2.390798	4.760899	3.30E-08	8.18E-06	RecName: Full=High affinity potassium transporter [Schwanniomyces occidentalis]	NA	GO:0015079|GO:0016020|GO:0071805
c12791_g1_i1	2.382758	2.05642	1.76E-05	0.001374	RecName: Full=UPF0659 protein C216.03 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WKC9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKC9_PHACS	NA
c23628_g1_i1	2.381893	2.749747	1.44E-05	0.001164	NA	NA	NA
c18107_g1_i1	2.379127	4.770643	3.19E-09	1.10E-06	NA	NA	NA
c10338_g4_i1	2.378078	3.435825	2.33E-06	0.000264	NA	NA	NA
c10338_g4_i2	2.378078	3.435825	2.33E-06	0.000264	NA	NA	NA
c10138_g3_i1	2.372643	3.383286	5.94E-07	9.23E-05	NA	NA	NA
c2245_g1_i1	2.363017	1.526261	3.73E-05	0.002467	NA	NA	NA
c14635_g1_i1	2.362476	2.640179	1.00E-05	0.000885	NA	UniRef90_K5WI05 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WI05_PHACS	GO:0003824|GO:0008152
c25695_g1_i1	2.360077	2.802047	6.63E-05	0.003855	NA	NA	NA
c20419_g1_i1	2.358609	2.509671	4.48E-07	7.43E-05	RecName: Full=NmrA-like family domain-containing protein 1 [Gallus gallus]	NA	NA
c9741_g1_i1	2.35785	2.412014	9.52E-06	0.000851	NA	NA	NA
c17653_g1_i1	2.356353	4.764891	3.36E-07	5.90E-05	NA	NA	NA
c4594_g1_i1	2.35312	5.108807	1.26E-05	0.001045	RecName: Full=Probable pyridoxal 5'-phosphate synthase subunit PDX1; Short=PLP synthase subunit PDX1 [Schizosaccharomyces pombe 972h-]	NA	GO:0009228|GO:0036355|GO:0042823

c15358_g1_i1	2.341603	3.702297	1.27E-06	0.000167	NA	NA	NA
c21437_g1_i1	2.33989	2.992717	3.41E-07	5.93E-05	NA	NA	NA
c9463_g2_i1	2.33541	2.531253	0.00011	0.005665	NA	UniRef90_K5VL46 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VL46_PHACS	NA
c26843_g1_i1	2.33126	1.159242	0.000403	0.014861	NA	NA	NA
c26987_g1_i1	2.328287	1.995839	0.000109	0.005644	NA	NA	NA
c16167_g1_i1	2.32581	3.257149	3.07E-06	0.000333	NA	NA	NA
c16167_g1_i2	2.32581	3.257149	3.07E-06	0.000333	NA	NA	NA
c16167_g1_i3	2.32581	3.257149	3.07E-06	0.000333	NA	NA	NA
c16167_g1_i4	2.32581	3.257149	3.07E-06	0.000333	NA	NA	NA
c16167_g1_i5	2.32581	3.257149	3.07E-06	0.000333	NA	NA	NA
c12061_g2_i1	2.323188	6.280456	2.73E-08	7.22E-06	NA	NA	NA
c16667_g2_i1	2.322183	5.917719	8.03E-10	3.23E-07	RecName: Full=Vitellogenic carboxypeptidase; Flags: Precursor [Aedes aegypti]	NA	GO:0004185|GO:0006508
c16667_g2_i2	2.322183	5.917719	8.03E-10	3.23E-07	NA	NA	GO:0004185|GO:0006508
c16667_g2_i3	2.322183	5.917719	8.03E-10	3.23E-07	NA	NA	GO:0004185|GO:0006508
c16667_g2_i4	2.322183	5.917719	8.03E-10	3.23E-07	NA	NA	GO:0004185|GO:0006508
c2989_g1_i1	2.31372	1.77731	0.000579	0.019728	RecName: Full=Uncharacterized transporter C1529.01 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0022857|GO:0055085
c9381_g1_i1	2.313138	2.39659	0.000274	0.011097	RecName: Full=Zinc-type alcohol dehydrogenase-like protein C2E1P3.01 [Schizosaccharomyces pombe 972h-]	UniRef90_K5W3Z2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3Z2_PHACS	GO:0008270|GO:0016491|GO:0055114
c9381_g1_i2	2.313138	2.39659	0.000274	0.011097	NA	NA	GO:0008270|GO:0016491|GO:0055114
c10138_g1_i1	2.311902	7.265796	1.31E-05	0.001078	RecName: Full=Probable tripeptidyl-peptidase SED2; AltName: Full=Sedolisin-B; Flags: Precursor [Trichophyton verrucosum HKI 0517]	NA	GO:0008236
c18715_g1_i1	2.309318	1.631827	0.000155	0.0072	NA	NA	NA
c15978_g1_i1	2.307374	4.852514	1.49E-06	0.000187	RecName: Full=Trichodiene oxygenase; AltName: Full=Cytochrome P450 58 [Fusarium sporotrichioides]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c23735_g1_i1	2.305324	2.887846	2.87E-06	0.000315	NA	NA	NA
c1537_g1_i1	2.290144	1.983903	2.95E-05	0.002043	NA	NA	GO:0016746
c1537_g1_i2	2.290144	1.983903	2.95E-05	0.002043	RecName: Full=Putative mitochondrial carnitine O-acetyltransferase [Saccharomyces cerevisiae S288c]	NA	GO:0016746
c15930_g1_i1	2.288758	4.540743	9.12E-07	0.000131	RecName: Full=Uncharacterized MFS-type transporter C409.08 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0022857|GO:0055085
c16237_g1_i1	2.287756	3.516984	0.000167	0.007558	NA	NA	NA
c16237_g1_i2	2.287756	3.516984	0.000167	0.007558	NA	NA	NA
c16237_g1_i3	2.287756	3.516984	0.000167	0.007558	NA	NA	NA
c17139_g1_i1	2.28464	1.61233	0.001066	0.031448	NA	NA	NA
c8601_g3_i1	2.281988	4.83903	1.12E-05	0.000956	RecName: Full=Quinidine resistance protein 2 [Saccharomyces cerevisiae S288c]	NA	GO:0016021|GO:0022857|GO:0055085
c16984_g2_i1	2.281256	4.72852	9.26E-09	2.74E-06	RecName: Full=Chitin deacetylase; Flags: Precursor [Cryptococcus neoformans var. grubii H99]	NA	NA
c8396_g1_i1	2.280548	3.657089	1.76E-06	0.000214	RecName: Full=Enoyl reductase LovC [Aspergillus terreus]	NA	GO:0008270|GO:0016491|GO:0055114
c19896_g1_i1	2.280499	4.332409	2.32E-08	6.34E-06	NA	NA	NA
c19529_g1_i1	2.278153	6.436863	3.29E-08	8.18E-06	NA	NA	NA
c13018_g1_i1	2.277082	7.332174	1.63E-06	0.000201	RecName: Full=Serine-type carboxypeptidase F; Short=Proteinase F; AltName: Full=CPD-II; Flags: Precursor [Aspergillus niger]	NA	GO:0004185|GO:0006508
c24805_g1_i1	2.267555	4.119025	5.54E-08	1.25E-05	NA	NA	NA
c16911_g1_i1	2.266162	4.722525	1.83E-05	0.001415	NA	NA	NA
c10138_g4_i1	2.261115	7.374204	3.92E-06	0.000404	RecName: Full=Tripeptidyl-peptidase sed2; AltName: Full=Sedolisin-B; Flags: Precursor [Aspergillus fumigatus Af293]	NA	GO:0004252|GO:0006508
c14625_g1_i1	2.25406	1.278083	0.000554	0.019018	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V788 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V788_PHACS	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c23181_g1_i1	2.245173	5.678689	1.35E-05	0.001104	NA	NA	NA
c16790_g2_i1	2.238228	5.221403	5.18E-09	1.71E-06	RecName: Full=Serine/threonine-protein kinase ppk27 [Schizosaccharomyces pombe 972h-]	NA	GO:0004672|GO:0005524|GO:0006468
c15522_g5_i1	2.237426	4.566578	0.000438	0.015878	NA	NA	NA

c16488_g2_i1	2.236618	3.522466	1.48E-08	4.19E-06	NA	NA	GO:0004185|GO:0006508
c16488_g2_i2	2.236618	3.522466	1.48E-08	4.19E-06	RecName: Full=Carboxypeptidase Y homolog A; Flags: Precursor [Blastomyces dermatitidis SLH14081]	UniRef90_K5VR04 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VR04_PHACS	GO:0004185|GO:0006508
c16488_g2_i3	2.236618	3.522466	1.48E-08	4.19E-06	NA	NA	GO:0004185|GO:0006508
c11876_g2_i1	2.235991	3.896326	1.19E-07	2.33E-05	RecName: Full=P-type cation-transporting ATPase; AltName: Full=Cadmium resistance protein 2; AltName: Full=Cadmium-translocating P-type ATPase; AltName: Full=Cd(2+)-exporting ATPase [Saccharomyces cerevisiae S288c]	NA	GO:0030001|GO:0046872
c23510_g1_i1	2.231694	5.55021	0.000439	0.01588	NA	UniRef90_K5VPV7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPV7_PHACS	NA
c22264_g1_i1	2.223242	5.051423	2.78E-06	0.000306	RecName: Full=NADP-specific glutamate dehydrogenase; Short=NADP-GDH; AltName: Full=NADP-dependent glutamate dehydrogenase [Hebeloma cylindrosporum]	UniRef90_K5WPC5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WPC5_PHACS	GO:0006520|GO:0016491|GO:0055114
c23694_g1_i1	2.223014	2.409299	0.001333	0.036745	NA	NA	NA
c17111_g1_i1	2.221712	4.240098	4.95E-07	8.02E-05	NA	NA	GO:0008152|GO:0016846
c17111_g1_i2	2.221712	4.240098	4.95E-07	8.02E-05	RecName: Full=Centromere protein V; Short=CENP-V; AltName: Full=Nuclear protein p30; AltName: Full=Proline-rich protein 6 [Homo sapiens]	NA	GO:0008152|GO:0016846
c17111_g1_i3	2.221712	4.240098	4.95E-07	8.02E-05	NA	NA	GO:0008152|GO:0016846
c22025_g1_i1	2.215456	1.826253	2.82E-05	0.001982	NA	UniRef90_K5WDQ1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDQ1_PHACS	NA
c23180_g1_i1	2.210338	3.114173	5.94E-05	0.003555	NA	NA	NA
c21703_g1_i1	2.20266	1.591613	0.001135	0.032884	NA	NA	NA
c24701_g1_i1	2.201599	2.3884	6.83E-06	0.000647	NA	NA	NA
c14771_g1_i1	2.192515	2.915113	3.37E-06	0.000358	NA	UniRef90_K5VM35 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VM35_PHACS	NA
c9652_g1_i1	2.188568	2.274154	0.000772	0.024386	RecName: Full=L-aminoadipate-semialdehyde dehydrogenase large subunit; AltName: Full=Alpha-aminoadipate reductase; Short=Alpha-AR [Ashbya gossypii ATCC 10895]	UniRef90_A0A0C3NE97 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NE97_PHLGI	GO:0003824|GO:0050662

c8754_g1_i1	2.186217	2.96334	5.45E-05	0.003325	NA	NA	NA
c15445_g3_i1	2.18531	3.364047	9.20E-08	1.89E-05	NA	NA	NA
c15445_g3_i2	2.18531	3.364047	9.20E-08	1.89E-05	NA	NA	NA
c15957_g1_i1	2.180335	5.491176	0.000685	0.022219	NA	NA	NA
c15957_g1_i2	2.180335	5.491176	0.000685	0.022219	NA	NA	NA
c15957_g1_i3	2.180335	5.491176	0.000685	0.022219	NA	NA	GO:0016491|GO:0055114
c15957_g1_i4	2.180335	5.491176	0.000685	0.022219	NA	NA	GO:0016491|GO:0055114
c14900_g1_i1	2.178519	5.550832	6.91E-08	1.51E-05	RecName: Full=Anthocyanidin 3-O-glucosyltransferase 5; AltName: Full=Flavonol 3-O-glucosyltransferase 5; AltName: Full=UDP-glucose flavonoid 3-O-glucosyltransferase 5 [Manihot esculenta]	UniRef90_K5XFM7 Glycosyltransferase family 1 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XFM7_PHACS	GO:0008152|GO:0016758
c14900_g1_i2	2.178519	5.550832	6.91E-08	1.51E-05	NA	NA	GO:0008152|GO:0016758
c16183_g1_i1	2.172949	3.780742	3.54E-05	0.002351	NA	NA	NA
c15358_g2_i1	2.172787	3.667235	2.06E-06	0.00024	RecName: Full=Uncharacterized N-acetyltransferase C550.08 [Schizosaccharomyces pombe 972h-]	NA	GO:0008080|GO:0016747
c15573_g2_i1	2.170958	2.511103	0.000146	0.00689	NA	NA	NA
c15573_g2_i2	2.170958	2.511103	0.000146	0.00689	NA	NA	NA
c16612_g1_i1	2.169157	2.938431	3.19E-05	0.002185	NA	NA	NA
c16612_g1_i2	2.169157	2.938431	3.19E-05	0.002185	NA	NA	NA
c16588_g1_i1	2.167721	2.476058	0.001535	0.040582	NA	NA	NA
c17653_g5_i1	2.16323	8.616789	1.27E-05	0.00105	NA	NA	NA
c17653_g5_i2	2.16323	8.616789	1.27E-05	0.00105	NA	NA	NA
c17653_g5_i3	2.16323	8.616789	1.27E-05	0.00105	NA	UniRef90_A0A060SG59 Uncharacterized protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060SG59_PYCCI	NA
c21462_g1_i1	2.162501	1.056924	0.001803	0.045131	NA	NA	NA
c22202_g1_i1	2.15925	2.159505	0.000575	0.019597	RecName: Full=Cytochrome P450 67; AltName: Full=CYPLXVII; AltName: Full=Planta-induced rust protein 16, partial [Uromyces viciae-fabae]	UniRef90_K5VUV0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUV0_PHACS	NA
c17520_g1_i1	2.158094	5.639545	2.40E-06	0.000272	NA	NA	NA
c17520_g1_i2	2.158094	5.639545	2.40E-06	0.000272	NA	UniRef90_A0A0C3SEU4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SEU4_PHLGI	NA

c10338_g3_i1	2.151624	2.252484	0.001553	0.040839	NA	NA	NA
c25133_g1_i1	2.14869	6.103222	9.71E-07	0.000138	NA	NA	NA
c19877_g1_i1	2.147588	7.092094	1.41E-05	0.001145	RecName: Full=Isocitrate lyase; Short=ICL; Short=Isocitrase; Short=Isocitratase [Coprinopsis cinerea okayama7#130]	NA	GO:0004451|GO:0019752
c13621_g1_i1	2.145847	4.412436	1.31E-06	0.00017	NA	NA	GO:0008270
c13621_g1_i2	2.145847	4.412436	1.31E-06	0.00017	NA	NA	GO:0008270
c9741_g2_i1	2.142012	2.504573	0.000316	0.012335	NA	NA	NA
c16003_g1_i1	2.140449	3.960412	1.38E-07	2.66E-05	NA	NA	NA
c10138_g2_i1	2.135301	7.356829	4.36E-05	0.002754	RecName: Full=Probable tripeptidyl-peptidase SED2; AltName: Full=Sedolisin-B; Flags: Precursor [Trichophyton verrucosum HKI 0517]	NA	NA
c14625_g3_i1	2.134355	1.652624	0.000143	0.006797	RecName: Full=Multiple drug resistance-associated protein-like transporter 1; Short=MRP-like transporter 1; AltName: Full=Vacuolar multi-drug resistance ABC transporter MTL1 [Candida albicans SC5314]	UniRef90_K5WFW7 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFW7_PHACS	NA
c20247_g1_i1	2.133397	2.952541	1.93E-06	0.000229	NA	NA	NA
c15930_g2_i1	2.124787	2.982738	7.37E-06	0.000682	RecName: Full=Uncharacterized MFS-type transporter C530.15c [Schizosaccharomyces pombe 972h-]	NA	NA
c21326_g1_i1	2.1247	6.216892	0.000252	0.010387	RecName: Full=Aryl-alcohol dehydrogenase [NADP(+)]; Short=AAD [Phanerochaete chrysosporium]	NA	NA
c21466_g1_i1	2.109859	5.685016	0.000107	0.005597	RecName: Full=Oxygen-dependent choline dehydrogenase; Short=CDH; Short=CHD; AltName: Full=Betaine aldehyde dehydrogenase; Short=BADH [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]	NA	GO:0016614|GO:0055114
c16160_g4_i1	2.103599	3.480028	3.38E-07	5.92E-05	NA	NA	NA
c16160_g4_i2	2.103599	3.480028	3.38E-07	5.92E-05	NA	NA	NA
c26272_g1_i1	2.103473	7.22645	0.000208	0.009031	NA	NA	NA
c10775_g1_i1	2.099124	1.502938	0.000668	0.021876	NA	NA	NA
c26796_g1_i1	2.0976	2.597832	2.49E-06	0.000278	NA	NA	NA
c6146_g1_i1	2.094928	3.332869	1.74E-05	0.001361	NA	UniRef90_K5VXE7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXE7_PHACS	NA

c16372_g3_i1	2.085662	5.212226	3.55E-06	0.000373	RecName: Full=Probable tripeptidyl-peptidase SED2; AltName: Full=Sedolisin-B; Flags: Precursor [Trichophyton verrucosum HKI 0517]	UniRef90_Q281W2 Family S53 protease n=1 Tax=Phanerochaete chrysosporium RepID=Q281W2_PHACH	GO:0008236
c14175_g2_i1	2.077979	5.164526	7.45E-05	0.004201	NA	NA	NA
c14175_g2_i2	2.077979	5.164526	7.45E-05	0.004201	NA	NA	NA
c9074_g1_i1	2.076333	4.338978	0.001257	0.03523	NA	NA	NA
c15792_g1_i1	2.075678	4.004367	1.28E-06	0.000168	NA	NA	NA
c15792_g1_i2	2.075678	4.004367	1.28E-06	0.000168	NA	NA	NA
c17473_g2_i1	2.071616	5.790441	0.00017	0.007681	NA	NA	NA
c19786_g1_i1	2.068759	2.236153	0.000174	0.007762	NA	NA	NA
c9652_g2_i1	2.062977	2.639694	0.000993	0.029716	NA	UniRef90_K5WI05 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WI05_PHACS	NA
c8423_g2_i1	2.062943	3.922701	7.35E-08	1.60E-05	NA	NA	NA
c19897_g1_i1	2.061071	3.246835	2.46E-05	0.001776	NA	NA	NA
c23133_g1_i1	2.058218	1.938167	0.001914	0.047002	NA	UniRef90_K5W149 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W149_PHACS	NA
c14290_g2_i1	2.044188	5.794366	0.000136	0.006551	NA	NA	NA
c14290_g2_i2	2.044188	5.794366	0.000136	0.006551	RecName: Full=Copper transport protein ctr6; Short=Copper transporter 6 [Schizosaccharomyces pombe 972h-]	NA	GO:0005375|GO:0016021|GO:0035434
c2245_g2_i1	2.031614	6.588725	2.46E-06	0.000277	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	NA	GO:0004190|GO:0006508
c14941_g2_i1	2.031166	4.048416	2.23E-05	0.001656	NA	NA	NA
c14941_g2_i2	2.031166	4.048416	2.23E-05	0.001656	NA	UniRef90_K5WHY2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WHY2_PHACS	NA
c17380_g1_i1	2.027981	5.06994	5.96E-07	9.23E-05	NA	NA	NA
c17380_g1_i2	2.027981	5.06994	5.96E-07	9.23E-05	NA	NA	NA
c17380_g1_i3	2.027981	5.06994	5.96E-07	9.23E-05	NA	NA	NA
c17123_g1_i1	2.024109	4.041673	2.07E-06	0.00024	NA	NA	NA
c17123_g1_i2	2.024109	4.041673	2.07E-06	0.00024	NA	NA	NA

c17676_g2_i1	2.023965	1.803815	0.000127	0.00629	RecName: Full=Bifunctional protein Aas; Includes: RecName: Full=2-acylglycerophosphoethanolamine acyltransferase; AltName: Full=2-acyl-GPE acyltransferase; AltName: Full=Acyl-[acyl-carrier-protein]--phospholipid O-acyltransferase; Includes: RecName: Full=Acyl-[acyl-carrier-protein] synthetase; AltName: Full=Acyl-ACP synthetase; AltName: Full=Long-chain-fatty-acid--[acyl-carrier-protein] ligase [Citrobacter koseri ATCC BAA-895]	UniRef90_K5XAI9 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XAI9_PHACS	GO:0003824|GO:0008152
c13018_g2_i1	2.021294	5.325654	2.98E-05	0.002058	RecName: Full=Carboxypeptidase cpdS; Flags: Precursor [Aspergillus phoenicis]	NA	GO:0004185|GO:0006508
c12015_g1_i1	2.015364	6.089742	5.41E-05	0.003309	RecName: Full=L-aminoadipate-semialdehyde dehydrogenase large subunit; AltName: Full=Alpha-aminoadipate reductase; Short=Alpha-AR [Penicillium chrysogenum]	NA	NA
c12015_g1_i2	2.015364	6.089742	5.41E-05	0.003309	NA	NA	NA
c21438_g1_i1	2.000855	3.68536	2.13E-05	0.001602	NA	NA	NA
c21089_g1_i1	1.99508	1.776577	0.000585	0.019829	NA	NA	NA
c11908_g1_i1	1.994973	3.333282	0.000153	0.00715	NA	NA	NA
c16084_g1_i1	1.991799	3.176041	1.68E-06	0.000205	RecName: Full=ABC transporter B family member 2; AltName: Full=ABC transporter ABCB.2 [Dictyostelium discoideum]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c16899_g2_i1	1.99171	5.131716	6.05E-05	0.00361	RecName: Full=Uncharacterized ATPase YjoB [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0005524
c17255_g2_i1	1.990371	8.653726	1.13E-06	0.000153	RecName: Full=Uncharacterized MFS-type transporter C409.08 [Schizosaccharomyces pombe 972h-]	NA	NA
c17255_g2_i2	1.990371	8.653726	1.13E-06	0.000153	NA	NA	NA
c1099_g1_i1	1.989506	2.248229	0.000161	0.007432	NA	UniRef90_K5VZD9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZD9_PHACS	GO:0003924|GO:0005525
c8530_g1_i1	1.986961	1.859039	0.000497	0.017411	NA	NA	NA
c17108_g1_i1	1.985762	7.482541	5.04E-06	0.000504	RecName: Full=Aldo-keto reductase yakc [Schizosaccharomyces pombe 972h-]	NA	NA
c17108_g1_i2	1.985762	7.482541	5.04E-06	0.000504	NA	NA	NA
c12061_g3_i1	1.984085	6.965585	1.79E-06	0.000217	NA	NA	NA

c201_g1_i1	1.971596	5.51057	0.000441	0.015944	NA	UniRef90_K5W743 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W743_PHACS	NA
c11876_g3_i1	1.967585	2.609533	1.86E-05	0.001432	RecName: Full=P-type cation-transporting ATPase; AltName: Full=Cadmium resistance protein 2; AltName: Full=Cadmium-translocating P-type ATPase; AltName: Full=Cd(2+)-exporting ATPase [Saccharomyces cerevisiae S288c]	NA	GO:0000166|GO:0046872
c17301_g2_i1	1.966588	6.340582	3.69E-06	0.000383	NA	NA	NA
c17301_g2_i2	1.966588	6.340582	3.69E-06	0.000383	NA	NA	NA
c27148_g1_i1	1.965142	1.511305	0.001905	0.046848	NA	NA	NA
c19856_g1_i1	1.963847	2.156695	0.000629	0.020921	NA	NA	NA
c19565_g1_i1	1.961926	10.37279	3.48E-08	8.56E-06	NA	NA	NA
c13302_g2_i1	1.957779	4.661116	4.06E-08	9.78E-06	NA	NA	NA
c15501_g4_i1	1.953727	4.907835	1.48E-05	0.001187	NA	NA	NA
c15501_g4_i2	1.953727	4.907835	1.48E-05	0.001187	NA	NA	NA
c24824_g1_i1	1.952079	2.792449	4.31E-05	0.002735	NA	NA	NA
c15485_g2_i1	1.951695	7.250652	2.05E-05	0.001558	RecName: Full=Beta-etherase; AltName: Full=Beta-aryl ether cleaving enzyme [Sphingomonas paucimobilis]	NA	GO:0005515
c14771_g2_i1	1.949396	3.085484	9.04E-05	0.004868	NA	NA	NA
c14771_g2_i2	1.949396	3.085484	9.04E-05	0.004868	NA	UniRef90_K5VM35 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VM35_PHACS	NA
c13890_g2_i1	1.936882	2.421804	4.26E-05	0.002723	NA	NA	NA
c13890_g2_i2	1.936882	2.421804	4.26E-05	0.002723	NA	NA	NA
c13890_g2_i3	1.936882	2.421804	4.26E-05	0.002723	NA	NA	NA
c17354_g2_i1	1.935731	4.400997	7.14E-07	0.000106	RecName: Full=Uncharacterized protein C17A5.05c [Schizosaccharomyces pombe 972h-]	NA	NA
c17354_g2_i2	1.935731	4.400997	7.14E-07	0.000106	NA	NA	NA
c12841_g3_i1	1.932649	3.89805	2.14E-05	0.001605	NA	UniRef90_K5VPU8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPU8_PHACS	NA
c11413_g1_i1	1.929336	3.215112	0.000379	0.014135	NA	NA	GO:0008152|GO:0016846

c20615_g1_i1	1.925887	1.249082	0.001601	0.041613	NA	NA	NA
c22815_g1_i1	1.925679	2.580764	0.00032	0.012414	NA	UniRef90_K5VSK8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSK8_PHACS	NA
c5973_g1_i1	1.923446	8.244286	0.001199	0.033985	NA	NA	GO:0006807|GO:0016810
c5973_g1_i2	1.923446	8.244286	0.001199	0.033985	RecName: Full=Bifunctional nitrilase/nitrile hydratase NIT4B; Short=TNIT4B; AltName: Full=Cyanoalanine nitrilase B; AltName: Full=Nitrilase 4B [Nicotiana tabacum]	UniRef90_K5VE18 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VE18_PHACS	GO:0006807|GO:0016810
c16124_g2_i1	1.92234	5.165179	2.95E-05	0.002043	RecName: Full=Protein bimA [Aspergillus nidulans FGSC A4]	NA	NA
c16124_g2_i2	1.92234	5.165179	2.95E-05	0.002043	NA	NA	NA
c9551_g2_i1	1.92035	7.506018	5.00E-05	0.003098	RecName: Full=Anthranilate--CoA ligase [Pseudomonas aeruginosa PAO1]	UniRef90_K5V3A6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3A6_PHACS	GO:0003824|GO:0008152
c9551_g2_i2	1.92035	7.506018	5.00E-05	0.003098	NA	NA	GO:0003824|GO:0008152
c10395_g2_i1	1.920196	5.497804	2.15E-06	0.000248	NA	NA	NA
c15992_g3_i1	1.918191	2.263002	7.71E-05	0.004288	NA	NA	NA
c15992_g3_i2	1.918191	2.263002	7.71E-05	0.004288	RecName: Full=Aflatoxin B1 aldehyde reductase member 3; AltName: Full=AFB1 aldehyde reductase 2; Short=AFB1-AR 2 [Homo sapiens]	NA	NA
c15992_g3_i3	1.918191	2.263002	7.71E-05	0.004288	NA	NA	NA
c16084_g4_i1	1.915678	4.740182	2.42E-07	4.37E-05	RecName: Full=Multidrug resistance protein 1B; AltName: Full=ATP-binding cassette sub-family B member 1B; AltName: Full=P-glycoprotein 1; AltName: CD_antigen=CD243 [Mus musculus]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c12398_g2_i1	1.915281	5.491039	2.33E-05	0.001711	RecName: Full=Bifunctional epoxide hydrolase 2; Includes: RecName: Full=Cytosolic epoxide hydrolase 2; Short=CEH; AltName: Full=Epoxide hydratase; AltName: Full=Soluble epoxide hydrolase; Short=SEH; Includes: RecName: Full=Lipid-phosphate phosphatase [Rattus norvegicus]	UniRef90_K5WTB3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WTB3_PHACS	NA
c5227_g1_i1	1.910774	3.660824	1.67E-05	0.001315	RecName: Full=Porphobilinogen deaminase; Short=PBG; AltName: Full=Hydroxymethylbilane synthase; Short=HMBS; AltName: Full=Pre-uroporphyrinogen synthase [Synechococcus sp. CC9311]	UniRef90_A0A0C3S6D9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S6D9_PHLGI	GO:0004418|GO:0033014
c13395_g1_i1	1.908287	2.40677	3.23E-05	0.002201	NA	NA	NA

c10893_g1_i1	1.906599	4.555213	4.82E-07	7.86E-05	NA	NA	NA
c10893_g1_i2	1.906599	4.555213	4.82E-07	7.86E-05	NA	NA	NA
c9455_g1_i1	1.904931	3.717446	0.000587	0.019861	NA	NA	NA
c9455_g1_i2	1.904931	3.717446	0.000587	0.019861	NA	UniRef90_A0A067QQA1 Uncharacterized protein n=1 Tax=Jaapia argillacea MUCL 33604 RepID=A0A067QQA1_9HOMO	NA
c8154_g1_i1	1.904295	5.062941	1.06E-06	0.000147	NA	NA	NA
c8154_g1_i2	1.904295	5.062941	1.06E-06	0.000147	NA	NA	NA
c22536_g1_i1	1.90405	2.155214	0.000109	0.005644	RecName: Full=Aldehyde dehydrogenase, mitochondrial; AltName: Full=ALDH class 2; AltName: Full=P51; Flags: Precursor [Leishmania tarentolae]	UniRef90_A0A0C3SCG1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SCG1_PHLGI	GO:0008152|GO:0016491|GO:0055114
c26893_g1_i1	1.90343	4.55678	0.000133	0.006471	RecName: Full=Sorbitol dehydrogenase; AltName: Full=L-iditol 2-dehydrogenase [Homo sapiens]	NA	GO:0008270|GO:0016491|GO:0055114
c6240_g1_i1	1.903043	3.683948	0.000272	0.011062	NA	NA	NA
c17512_g2_i1	1.902174	3.093245	1.27E-05	0.001047	NA	NA	NA
c17512_g2_i2	1.902174	3.093245	1.27E-05	0.001047	NA	NA	NA
c17133_g5_i1	1.900477	6.264362	0.000546	0.018806	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17133_g5_i2	1.900477	6.264362	0.000546	0.018806	RecName: Full=Ent-kaurene oxidase; AltName: Full=Cytochrome P450 503A1; AltName: Full=Cytochrome P450-4 [Fusarium fujikuroi]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17551_g1_i1	1.900098	6.769724	3.34E-05	0.002268	NA	NA	GO:0005524|GO:0006298|GO:0030983
c17551_g1_i2	1.900098	6.769724	3.34E-05	0.002268	NA	NA	GO:0005524|GO:0006298|GO:0030983
c17551_g1_i3	1.900098	6.769724	3.34E-05	0.002268	NA	NA	GO:0005524|GO:0006298|GO:0030983
c17551_g1_i4	1.900098	6.769724	3.34E-05	0.002268	RecName: Full=Mismatch repair endonuclease PMS2; AltName: Full=DNA mismatch repair protein PMS2; AltName: Full=PMS1 protein homolog 2 [Homo sapiens]	UniRef90_K5WQ81 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQ81_PHACS	GO:0005524|GO:0006298|GO:0030983

c12326_g2_i1	1.898586	5.289225	4.79E-06	0.000483	RecName: Full=Phenol 2-monooxygenase; AltName: Full=Phenol hydroxylase [Trichosporon cutaneum]	UniRef90_K5XCV5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XCV5_PHACS	NA
c12326_g2_i2	1.898586	5.289225	4.79E-06	0.000483	NA	NA	NA
c3657_g1_i1	1.898501	4.818119	3.69E-07	6.36E-05	NA	NA	NA
c14935_g1_i1	1.898409	2.015508	0.001301	0.036076	NA	NA	NA
c14935_g1_i2	1.898409	2.015508	0.001301	0.036076	NA	NA	NA
c15983_g1_i1	1.897106	4.46306	1.40E-05	0.001136	NA	NA	GO:0008080|GO:0016747
c15983_g1_i2	1.897106	4.46306	1.40E-05	0.001136	RecName: Full=Uncharacterized N-acetyltransferase C550.08 [Schizosaccharomyces pombe 972h-]	NA	GO:0008080|GO:0016747
c12662_g1_i1	1.895282	4.313632	5.60E-06	0.000552	NA	UniRef90_K5WJ20 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJ20_PHACS	GO:0007155|GO:0030246
c26671_g1_i1	1.89283	1.899588	0.000168	0.007595	NA	NA	NA
c15501_g1_i1	1.89232	4.440322	5.91E-06	0.000576	NA	NA	NA
c17573_g1_i1	1.891412	5.532854	4.70E-05	0.002945	RecName: Full=Probable urea active transporter 1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WJK6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJK6_PHACS	GO:0005215|GO:0006810|GO:0016020|GO:0055085
c21689_g1_i1	1.883374	1.903932	0.00032	0.012414	NA	NA	NA
c17133_g6_i1	1.876388	5.107005	0.000116	0.005916	RecName: Full=Ent-kaurene oxidase; AltName: Full=Cytochrome P450 503A1; AltName: Full=Cytochrome P450-4 [Fusarium fujikuroi]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c13142_g1_i1	1.873261	5.076483	1.13E-06	0.000153	NA	NA	NA
c18054_g1_i1	1.867841	3.409353	1.51E-05	0.001207	NA	NA	NA
c21992_g1_i1	1.867637	4.041447	7.66E-05	0.004265	NA	UniRef90_A0A060S7Z5 Uncharacterized protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060S7Z5_PYCCI	NA
c2858_g2_i1	1.861528	4.68827	0.000112	0.005746	RecName: Full=5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase; AltName: Full=Cobalamin-independent methionine synthase; AltName: Full=Methionine synthase, vitamin-B12 independent isozyme [Candida albicans SC5314]	NA	GO:0003871|GO:0008270|GO:0009086

c16039_g2_i1	1.859938	4.321531	0.000293	0.011667	NA	NA	NA
c10424_g1_i1	1.85764	1.684662	0.000409	0.015059	RecName: Full=Uncharacterized methyltransferase sll0829 [Synechocystis sp. PCC 6803 substr. Kazusa]	NA	GO:0008152|GO:0008168
c17747_g1_i1	1.856732	4.218262	0.001136	0.032884	NA	UniRef90_K5WEU8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEU8_PHACS	NA
c9120_g2_i1	1.854954	1.909973	0.000739	0.023596	NA	NA	NA
c21991_g1_i1	1.853557	3.628894	0.000116	0.005898	RecName: Full=Polyamine transporter 3 [Saccharomyces cerevisiae S288c]	UniRef90_K5UYU6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UYU6_PHACS	GO:0016021|GO:0022857|GO:0055085
c3916_g1_i1	1.852675	2.5258	0.000447	0.016087	NA	NA	NA
c3916_g1_i2	1.852675	2.5258	0.000447	0.016087	RecName: Full=Putative monoglyceride lipase; Short=MGL; AltName: Full=Monoacylglycerol hydrolase; Short=MAG hydrolase; Short=MGH; AltName: Full=Monoacylglycerol lipase; Short=MAG lipase; Short=MAGL [Schizosaccharomyces pombe 972h-]	NA	NA
c2609_g1_i1	1.847	2.700465	0.000106	0.005553	NA	NA	NA
c22810_g1_i1	1.832329	7.330048	0.00126	0.035246	RecName: Full=ATP-citrate synthase; AltName: Full=ATP-citrate (pro-S-)-lyase; AltName: Full=Citrate cleavage enzyme [Bos taurus]	UniRef90_K5V2S1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V2S1_PHACS	GO:0003824|GO:0008152|GO:0044262|GO:0046912|GO:0048037
c23600_g1_i1	1.83164	2.273199	0.001093	0.031913	NA	NA	NA
c13622_g2_i1	1.831635	2.71561	0.000112	0.005746	NA	NA	NA
c13622_g2_i2	1.831635	2.71561	0.000112	0.005746	NA	NA	NA
c13142_g2_i1	1.831151	4.85339	3.57E-06	0.000374	NA	NA	NA
c8509_g1_i1	1.829449	4.107015	3.58E-05	0.002374	NA	NA	NA
c27351_g1_i1	1.827051	1.869805	0.00084	0.026083	NA	NA	NA
c16562_g1_i1	1.826368	5.322539	3.27E-06	0.00035	RecName: Full=Manganese transporter pdt1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WR84 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WR84_PHACS	GO:0005215|GO:0006810|GO:0016020
c16562_g1_i2	1.826368	5.322539	3.27E-06	0.00035	NA	NA	GO:0005215|GO:0006810|GO:0016020
c16877_g2_i1	1.824343	3.567554	8.34E-05	0.004542	NA	NA	NA

c4594_g2_i1	1.822427	3.394507	0.000482	0.017031	RecName: Full=Pyridoxal 5'-phosphate synthase subunit PDX1; Short=PLP synthase subunit PDX1; AltName: Full=Singlet oxygen resistance protein 1 [Cercospora nicotianae]	NA	GO:0042823
c9705_g2_i1	1.822092	5.976661	0.001246	0.03501	RecName: Full=Glucosamine-6-phosphate isomerase; AltName: Full=Glucosamine-6-phosphate deaminase; Short=GNPDA; Short=GlcN6P deaminase [Aedes aegypti]	UniRef90_K5UXU1 Glucosamine-6-phosphate isomerase n=2 Tax=Phanerochaetaceae RepID=K5UXU1_PHACS	GO:0005975
c9705_g2_i2	1.822092	5.976661	0.001246	0.03501	NA	NA	GO:0005975
c18180_g1_i1	1.813551	7.640385	8.11E-07	0.000118	RecName: Full=Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial; Short=MMSDH; Short=Malonate-semialdehyde dehydrogenase [acylating]; AltName: Full=Aldehyde dehydrogenase family 6 member A1; Flags: Precursor [Bos taurus]	NA	GO:0008152|GO:0016491|GO:0055114
c11262_g1_i1	1.812829	4.293244	4.11E-05	0.002658	RecName: Full=Phenylalanine ammonia-lyase [Amanita muscaria]	NA	GO:0009058|GO:0016841
c6010_g1_i1	1.810379	4.553447	5.36E-05	0.003285	NA	UniRef90_K5WHN8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WHN8_PHACS	NA
c2733_g1_i1	1.807218	3.818932	2.65E-06	0.000294	NA	NA	NA
c26741_g1_i1	1.804401	5.242597	5.33E-06	0.00053	RecName: Full=Major facilitator superfamily domain-containing protein 7-b [Xenopus (Silurana) tropicalis]	NA	GO:0016021|GO:0022857|GO:0055085
c9616_g1_i1	1.803775	1.950417	0.000585	0.019829	NA	UniRef90_K5VZM2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZM2_PHACS	GO:0016614|GO:0050660|GO:0055114
c2772_g2_i1	1.802404	5.329257	0.000113	0.00579	NA	NA	NA
c21109_g1_i1	1.801133	6.031811	0.00165	0.042542	RecName: Full=Glucan endo-1,3-alpha-glucosidase agn1; AltName: Full=Endo-1,3-alpha-glucanase agn1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	NA
c23736_g1_i1	1.80104	2.622972	0.000227	0.009613	NA	NA	NA
c15985_g2_i1	1.797572	3.690571	8.00E-05	0.004407	NA	NA	NA
c9567_g1_i1	1.79686	2.451423	0.000334	0.012814	RecName: Full=Chorismate mutase; Short=CM [Saccharomyces cerevisiae S288c]	UniRef90_K5V7A1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V7A1_PHACS	NA
c4714_g1_i1	1.79396	2.014817	0.000305	0.01206	NA	NA	NA

c12841_g4_i1	1.79378	4.178429	2.71E-05	0.001921	NA	UniRef90_A0A0C3PUC0 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PUC0_PHLGI	NA
c17123_g4_i1	1.792433	3.939401	8.20E-05	0.004485	NA	NA	NA
c17123_g4_i2	1.792433	3.939401	8.20E-05	0.004485	NA	NA	NA
c21606_g1_i1	1.791448	6.997791	5.43E-07	8.51E-05	NA	NA	NA
c3795_g1_i1	1.789399	2.348811	0.000394	0.014599	NA	NA	NA
c2858_g1_i1	1.779613	6.914038	0.000453	0.016233	RecName: Full=5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase; AltName: Full=Cobalamin-independent methionine synthase; AltName: Full=Methionine synthase, vitamin-B12 independent isozyme [Dictyostelium discoideum]	NA	GO:0003871|GO:0008270|GO:0008652|GO:0009086
c2851_g1_i1	1.779031	2.496152	0.001426	0.038596	NA	NA	NA
c11758_g3_i1	1.778751	8.284008	8.53E-06	0.000773	NA	NA	NA
c17999_g1_i1	1.778194	5.558882	0.000101	0.005327	NA	NA	NA
c11745_g1_i1	1.776978	2.267702	0.000458	0.016379	NA	NA	NA
c13916_g3_i1	1.774489	2.072561	0.000581	0.019777	NA	NA	NA
c16870_g5_i1	1.774232	3.51714	0.000456	0.016341	NA	NA	NA
c16870_g5_i2	1.774232	3.51714	0.000456	0.016341	NA	NA	NA
c16870_g5_i3	1.774232	3.51714	0.000456	0.016341	NA	NA	NA
c16789_g2_i1	1.769476	4.321223	2.38E-05	0.001734	RecName: Full=Glucoamylase 1; AltName: Full=1,4-alpha-D-glucan glucohydrolase; AltName: Full=Glucan 1,4-alpha-glucosidase; Flags: Precursor [Candida albicans SC5314]	NA	GO:0004553|GO:0005975
c12326_g1_i1	1.768708	4.002332	0.000163	0.007484	RecName: Full=Phenol 2-monooxygenase; AltName: Full=Phenol hydroxylase [Trichosporon cutaneum]	UniRef90_J4HVY8 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4HVY8_FIBRA	GO:0008033|GO:0016491|GO:0050660|GO:0055114
c23045_g1_i1	1.763168	5.671574	6.70E-06	0.000637	NA	NA	NA
c10791_g1_i1	1.762801	2.211258	0.000133	0.006471	RecName: Full=Serine hydroxymethyltransferase; Short=SHMT; AltName: Full=Glycine hydroxymethyltransferase; AltName: Full=Maternal effect lethal protein 32; AltName: Full=Serine methylase [Caenorhabditis briggsae]	NA	GO:0004372|GO:0006544|GO:0006563
c14419_g1_i1	1.761336	3.610431	1.79E-05	0.001392	NA	NA	NA

c14419_g1_i2	1.761336	3.610431	1.79E-05	0.001392	NA	NA	NA
c14625_g2_i1	1.760905	2.005065	0.00115	0.0331	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	UniRef90_J4I966 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4I966_FIBRA	GO:0005524|GO:0016887
c17495_g4_i1	1.758121	3.405484	6.20E-06	0.000599	RecName: Full=ABC transporter C family member 10; AltName: Full=ABC transporter ABCC.10 [Dictyostelium discoideum]	NA	GO:0005524|GO:0016887
c16889_g1_i1	1.755739	6.30063	2.61E-05	0.001868	NA	NA	GO:0008152|GO:0016491
c16889_g1_i2	1.755739	6.30063	2.61E-05	0.001868	NA	NA	GO:0008152|GO:0016491
c16889_g1_i3	1.755739	6.30063	2.61E-05	0.001868	RecName: Full=Uncharacterized oxidoreductase C736.13 [Schizosaccharomyces pombe 972h-]	NA	GO:0008152|GO:0016491
c16789_g4_i1	1.754407	1.522257	0.001623	0.042035	RecName: Full=Alpha-glucosidase; AltName: Full=Maltase; Contains: RecName: Full=Alpha-glucosidase subunit 1; Contains: RecName: Full=Alpha-glucosidase subunit 2; Flags: Precursor [Pseudozyma tsukubaensis]	NA	GO:0004553|GO:0005975
c3324_g1_i1	1.748255	4.476245	0.000655	0.021594	RecName: Full=Pantothenate transporter liz1 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c16906_g2_i1	1.741913	2.657972	0.000294	0.011693	NA	NA	NA
c16372_g2_i1	1.741209	5.481964	0.000134	0.0065	RecName: Full=Tripeptidyl-peptidase SED4; AltName: Full=Sedolisin-D; Flags: Precursor [Arthroderma otae CBS 113480]	UniRef90_Q281W2 Family S53 protease n=1 Tax=Phanerochaete chrysosporium RepID=Q281W2_PHACH	GO:0004252|GO:0006508
c15247_g1_i1	1.740558	3.946092	7.90E-06	0.000727	NA	NA	NA
c19848_g1_i1	1.73801	1.92252	0.001599	0.041611	NA	NA	NA
c14430_g1_i1	1.735307	3.960161	0.000123	0.006148	NA	NA	NA
c14430_g1_i2	1.735307	3.960161	0.000123	0.006148	NA	UniRef90_K5WXK3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WXK3_PHACS	NA
c8423_g3_i1	1.735	3.923942	2.00E-06	0.000236	NA	NA	NA
c24804_g1_i1	1.731408	2.314811	0.000475	0.016873	RecName: Full=Guanine nucleotide-binding protein alpha-4 subunit [Ustilago maydis 521]	NA	GO:0003924|GO:0004871|GO:0007186|GO:0019001|GO:0031683
c21276_g1_i1	1.728355	6.342752	1.35E-05	0.001107	NA	NA	NA

c14805_g4_i1	1.727389	5.150141	6.91E-06	0.000653	NA	UniRef90_K5V2C8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V2C8_PHACS	GO:0046983
c12571_g2_i1	1.723245	2.570015	0.000122	0.006135	NA	UniRef90_K5WAE4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAE4_PHACS	NA
c19611_g1_i1	1.711317	5.583345	6.20E-05	0.003677	RecName: Full=Probable transport protein YPL264C [Saccharomyces cerevisiae S288c]	NA	GO:0016020
c6737_g1_i1	1.709948	3.455935	1.07E-05	0.000921	NA	NA	NA
c17301_g3_i1	1.708894	6.131153	0.000375	0.014001	RecName: Full=Linoleate 10R-lipoxygenase; AltName: Full=Cyclooxygenase-like fatty acid oxygenase; AltName: Full=Fatty acid oxygenase ppoC; AltName: Full=Linoleate 10R-dioxygenase; Short=10R-DOX; AltName: Full=Psi-producing oxygenase C; Short=AfPpoC [Aspergillus fumigatus Af293]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17301_g3_i2	1.708894	6.131153	0.000375	0.014001	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c21443_g1_i1	1.706335	2.323652	0.001522	0.040313	RecName: Full=Fatty acid synthase subunit alpha; AltName: Full=p190/210; Includes: RecName: Full=Acyl carrier; Includes: RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase; AltName: Full=Beta-ketoacyl reductase; Includes: RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase; AltName: Full=Beta-ketoacyl synthase [Schizosaccharomyces pombe 972h-]	NA	GO:0000287|GO:0008897|GO:0009059
c9319_g1_i1	1.704259	6.024985	4.21E-05	0.002706	RecName: Full=MFS antiporter QDR2 [Candida albicans SC5314]	UniRef90_K5VPF9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPF9_PHACS	NA
c13302_g1_i1	1.703097	5.502709	1.31E-06	0.00017	RecName: Full=Probable aspartic-type endopeptidase CTSD; Flags: Precursor, partial [Arthroderma otae CBS 113480]	NA	GO:0004190|GO:0006508
c5895_g1_i1	1.703094	2.017252	0.001595	0.041577	RecName: Full=Carbamoyl-phosphate synthase arginine-specific large chain; AltName: Full=Arginine-specific carbamoyl-phosphate synthetase, ammonia chain [Schizosaccharomyces pombe 972h-]	UniRef90_K5VPP4 Uncharacterized protein n=2 Tax=Phanerochaetaceae RepID=K5VPP4_PHACS	NA
c15971_g1_i1	1.702162	7.060526	0.000962	0.028991	NA	NA	GO:0003824|GO:0003854|GO:0006694|GO:001661

							6|GO:0050662|GO:0055114
c15971_g1_i2	1.702162	7.060526	0.000962	0.028991	RecName: Full=Putative uncharacterized oxidoreductase C513.07 [Schizosaccharomyces pombe 972h-]	NA	GO:0003824|GO:0003854|GO:0006694|GO:0016616|GO:0050662|GO:0055114
c24901_g1_i1	1.699635	6.965259	3.77E-05	0.002489	NA	NA	NA
c14020_g2_i1	1.698423	5.198995	8.12E-06	0.000744	NA	NA	NA
c14020_g2_i2	1.698423	5.198995	8.12E-06	0.000744	NA	NA	NA
c11789_g1_i1	1.698043	3.607487	1.47E-05	0.001185	RecName: Full=Inosine triphosphate pyrophosphatase; Short=ITPase; Short=Inosine triphosphatase; AltName: Full=Non-canonical purine NTP pyrophosphatase; AltName: Full=Non-standard purine NTP pyrophosphatase; AltName: Full=Nucleoside-triphosphate diphosphatase; AltName: Full=Nucleoside-triphosphate pyrophosphatase; Short=NTPase [Cryptococcus neoformans var. neoformans JEC21]	NA	GO:0016787
c14419_g2_i1	1.696851	2.864944	0.000174	0.007762	NA	NA	NA
c12944_g2_i1	1.695384	4.686642	1.66E-05	0.001313	RecName: Full=Solute carrier family 28 member 3; AltName: Full=Concentrative Na(+)-nucleoside cotransporter 3; Short=CNT 3; Short=rCNT3 [Rattus norvegicus]	NA	NA
c2775_g1_i1	1.695321	4.586457	3.14E-06	0.000338	NA	NA	NA
c12061_g1_i1	1.695156	6.692822	2.64E-05	0.001882	RecName: Full=Oleate activated transcription factor 3 [Saccharomyces cerevisiae S288c]	NA	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c15949_g4_i1	1.695097	2.226247	0.001486	0.03964	RecName: Full=Bifunctional epoxide hydrolase 2; Includes: RecName: Full=Cytosolic epoxide hydrolase 2; Short=CEH; AltName: Full=Epoxide hydratase; AltName: Full=Soluble epoxide hydrolase; Short=SEH; Includes: RecName: Full=Lipid-phosphate phosphatase [Rattus norvegicus]	NA	NA
c16304_g2_i1	1.689628	3.65202	4.45E-05	0.002808	NA	UniRef90_A0A0C3RYK4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RYK4_PHLGI	NA
c15544_g2_i1	1.688808	1.772491	0.001596	0.041577	NA	NA	NA

c15544_g2_i2	1.688808	1.772491	0.001596	0.041577	NA	NA	NA
c2247_g2_i1	1.68637	8.441041	2.87E-05	0.00201	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; AltName: Full=Homocitrate dehydratase; Flags: Precursor [Aspergillus nidulans FGSC A4]	NA	GO:0008152
c14633_g2_i1	1.680229	4.441173	3.67E-06	0.000382	RecName: Full=Exopolysaccharide phosphotransferase SCO6023; AltName: Full=Stealth protein SCO6023 [Streptomyces coelicolor A3(2)]	UniRef90_K5WHN3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WHN3_PHACS	GO:0016772
c12005_g2_i1	1.679512	4.380939	1.04E-05	0.000904	RecName: Full=Glucan 1,3-beta-glucosidase; AltName: Full=1,3-beta-D-glucanohydrolase; AltName: Full=Exo-beta 1,3 glucanase; Flags: Precursor [Bipolaris zeicola]	NA	NA
c15869_g6_i1	1.679237	5.958383	2.48E-05	0.001791	NA	NA	NA
c15869_g6_i2	1.679237	5.958383	2.48E-05	0.001791	RecName: Full=Aldo-keto reductase yakc [Schizosaccharomyces pombe 972h-]	NA	NA
c15869_g6_i3	1.679237	5.958383	2.48E-05	0.001791	NA	NA	NA
c6202_g2_i1	1.676393	4.772841	0.00016	0.007396	NA	UniRef90_K5W8F1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8F1_PHACS	NA
c18986_g1_i1	1.675732	3.976848	0.000695	0.022477	NA	NA	NA
c16925_g2_i1	1.674183	3.470967	0.001631	0.042212	RecName: Full=Probable 2-oxoglutarate-dependent dioxygenase DIN11; AltName: Full=Protein DARK-INDUCIBLE 11 [Arabidopsis thaliana]	NA	GO:0016491|GO:0016706|GO:0055114
c1575_g1_i1	1.673603	3.014206	5.68E-05	0.003449	NA	NA	NA
c1575_g1_i2	1.673603	3.014206	5.68E-05	0.003449	NA	NA	NA
c11023_g1_i1	1.671904	6.847851	3.51E-06	0.00037	RecName: Full=Hydantoin utilization protein C; AltName: Full=ORF4 [Pseudomonas sp. NS671]	NA	GO:0004719|GO:0006464|GO:0008152|GO:0008168|GO:0016787
c11023_g1_i2	1.671904	6.847851	3.51E-06	0.00037	NA	NA	GO:0004719|GO:0006464|GO:0008152|GO:0008168|GO:0016787
c11023_g1_i3	1.671904	6.847851	3.51E-06	0.00037	NA	NA	GO:0004719|GO:0006464|GO:0008152|GO:0008168|GO:0016787

c18000_g1_i1	1.671824	3.601986	0.000177	0.007864	NA	NA	NA
c13148_g1_i1	1.670218	4.844656	0.001392	0.03793	RecName: Full=ATP-dependent RNA helicase chl1; AltName: Full=Chromosome loss protein 1 [Schizosaccharomyces pombe 972h-]	NA	GO:0003676|GO:0005524|GO:0006139|GO:0008026|GO:0016818
c8992_g2_i1	1.669167	6.138505	6.72E-05	0.003899	NA	NA	NA
c17721_g1_i1	1.667257	5.28888	0.001701	0.043472	NA	UniRef90_K5WYY4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYY4_PHACS	NA
c21847_g1_i1	1.659574	5.929427	1.98E-05	0.001508	RecName: Full=Uncharacterized transporter C417.10 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c15985_g1_i1	1.658783	5.301284	0.000672	0.021925	NA	NA	NA
c11758_g1_i1	1.658762	7.361203	2.41E-05	0.001745	NA	NA	NA
c21424_g1_i1	1.65853	8.813752	0.00067	0.021925	RecName: Full=Glucose oxidase; AltName: Full=Beta-D-glucose:oxygen 1-oxido-reductase; AltName: Full=Glucose oxyhydrase; Short=GOD [Penicillium amagasakiense]	NA	GO:0016614|GO:0050660|GO:0055114
c17133_g2_i1	1.656036	4.18824	0.000967	0.029105	NA	NA	NA
c11745_g2_i1	1.655425	2.344994	0.000334	0.012814	NA	NA	NA
c3194_g1_i1	1.655206	4.420125	3.31E-06	0.000352	NA	NA	NA
c16083_g1_i1	1.653485	4.84435	1.36E-05	0.001109	RecName: Full=Beta-hexosaminidase 2; AltName: Full=Beta-GlcNAcase 2; AltName: Full=Beta-N-acetylhexosaminidase 2; AltName: Full=Beta-hexosaminidase 3; Short=AtHEX3; AltName: Full=N-acetyl-beta-glucosaminidase 2; Flags: Precursor [Arabidopsis thaliana]	NA	GO:0004553|GO:0005975
c14869_g1_i1	1.649866	5.116427	0.000432	0.015746	NA	UniRef90_K5UV81 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UV81_PHACS	NA
c6708_g1_i1	1.648189	1.842317	0.000809	0.025372	RecName: Full=Ankyrin repeat, PH and SEC7 domain containing protein secG [Dictyostelium discoideum]	NA	GO:0005515
c4710_g1_i1	1.646911	3.783734	7.31E-06	0.000678	NA	NA	NA
c4710_g1_i2	1.646911	3.783734	7.31E-06	0.000678	NA	NA	NA
c16154_g2_i1	1.646794	4.853933	5.80E-05	0.00349	RecName: Full=Oligomycin resistance ATP-dependent permease YOR1 [Saccharomyces cerevisiae S288c]	NA	NA

c8688_g1_i1	1.645825	4.004534	0.001419	0.038492	NA	NA	NA
c8688_g1_i2	1.645825	4.004534	0.001419	0.038492	NA	NA	NA
c10893_g2_i1	1.645139	3.490421	2.41E-05	0.001745	NA	NA	NA
c12290_g2_i1	1.642281	4.239982	0.000209	0.009039	NA	UniRef90_A0A0C3PQH6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PQH6_PHLGI	NA
c17254_g2_i1	1.642016	4.078574	1.88E-05	0.001441	NA	NA	NA
c17254_g2_i2	1.642016	4.078574	1.88E-05	0.001441	NA	NA	GO:0003333|GO:0015171|GO:0016020
c17254_g2_i3	1.642016	4.078574	1.88E-05	0.001441	RecName: Full=Uncharacterized amino-acid permease C15C4.04c [Schizosaccharomyces pombe 972h-]	NA	GO:0003333|GO:0015171|GO:0016020
c17254_g2_i4	1.642016	4.078574	1.88E-05	0.001441	NA	NA	GO:0003333|GO:0006810|GO:0015171|GO:0016020|GO:0055085
c17254_g2_i5	1.642016	4.078574	1.88E-05	0.001441	NA	NA	GO:0003333|GO:0015171|GO:0016020
c15501_g5_i1	1.640579	3.351223	0.001269	0.035355	NA	NA	NA
c7677_g1_i1	1.638625	3.795079	0.000247	0.010214	NA	NA	NA
c7677_g1_i2	1.638625	3.795079	0.000247	0.010214	NA	NA	NA
c16877_g3_i1	1.637498	5.25962	6.26E-05	0.003707	RecName: Full=Amidase [Rhodococcus erythropolis]	NA	GO:0016884
c16877_g3_i2	1.637498	5.25962	6.26E-05	0.003707	NA	NA	GO:0016884
c17255_g1_i1	1.635033	7.767589	7.50E-05	0.004201	RecName: Full=Uncharacterized MFS-type transporter C409.08 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0022857|GO:0055085
c2247_g1_i1	1.632785	8.086558	7.51E-05	0.004201	RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor [Bos taurus]	NA	GO:0008152
c12732_g1_i1	1.627353	2.271978	0.000718	0.022998	NA	UniRef90_K5VB84 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VB84_PHACS	NA
c2760_g2_i1	1.626315	7.620512	0.000445	0.01604	NA	NA	NA
c24661_g1_i1	1.624928	8.558911	0.000136	0.006559	NA	NA	NA

c12444_g2_i1	1.621302	4.664288	0.001165	0.033394	RecName: Full=Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type; AltName: Full=Calcium pump [Anopheles gambiae]	UniRef90_K5VVT4 Calcium-transporting ATPase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVT4_PHACS	NA
c23638_g1_i1	1.619967	3.274784	0.000238	0.009892	RecName: Full=Guanine nucleotide-binding protein alpha-4 subunit [Ustilago maydis 521]	NA	GO:0003924|GO:0004871|GO:0005525|GO:0007186|GO:0019001|GO:0031683
c19354_g1_i1	1.618326	13.89939	2.32E-05	0.001707	NA	NA	NA
c13042_g2_i1	1.616966	2.07476	0.001449	0.039067	NA	NA	NA
c12124_g1_i1	1.616046	2.798304	0.000214	0.009222	NA	NA	GO:0008152|GO:0016787
c2424_g1_i1	1.614308	7.716741	0.000453	0.016233	RecName: Full=Suppressor of hairless homolog; AltName: Full=RBP-Jkappa [Halocynthia roretzi]	NA	NA
c5006_g2_i1	1.613387	2.590257	0.002013	0.048781	NA	UniRef90_J7SBW4 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J7SBW4_FIBRA	NA
c26884_g1_i1	1.612964	7.85851	8.96E-05	0.004835	NA	NA	NA
c798_g2_i1	1.612511	7.70208	8.16E-06	0.000745	RecName: Full=Catalase [Schizosaccharomyces pombe 972h-]	UniRef90_K5WSG9 Catalase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WSG9_PHACS	GO:0004096|GO:0020037|GO:0055114
c4972_g1_i1	1.609669	4.652289	2.94E-05	0.002042	NA	UniRef90_K5UKA3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UKA3_PHACS	NA
c16746_g2_i1	1.606845	4.042515	0.000604	0.020323	RecName: Full=Cytochrome P450 704C1; AltName: Full=Cytochrome P450 CYPD [Pinus taeda]	NA	GO:0005506|GO:0008080|GO:0016705|GO:0020037|GO:0055114
c10805_g2_i1	1.6049	5.901395	0.000367	0.013765	RecName: Full=Uncharacterized amino-acid permease C15C4.04c [Schizosaccharomyces pombe 972h-]	NA	GO:0003333|GO:0006810|GO:0015171|GO:0016020|GO:0055085
c9339_g2_i1	1.604278	1.987037	0.001239	0.034879	RecName: Full=Putative reductase 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5WFD6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFD6_PHACS	NA
c16031_g1_i1	1.599986	2.763455	0.000213	0.0092	RecName: Full=Carboxypeptidase Y homolog A; Flags: Precursor [Microsporum gypseum CBS 118893]	NA	GO:0004185|GO:0006508

c17525_g1_i1	1.599593	5.044945	1.14E-05	0.000969	NA	NA	NA
c17525_g1_i2	1.599593	5.044945	1.14E-05	0.000969	NA	UniRef90_A0A0C3PDI5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PDI5_PHLGI	NA
c17525_g1_i3	1.599593	5.044945	1.14E-05	0.000969	NA	NA	NA
c17525_g1_i4	1.599593	5.044945	1.14E-05	0.000969	NA	NA	NA
c17525_g1_i5	1.599593	5.044945	1.14E-05	0.000969	NA	NA	NA
c17525_g1_i6	1.599593	5.044945	1.14E-05	0.000969	NA	NA	NA
c17525_g1_i7	1.599593	5.044945	1.14E-05	0.000969	NA	NA	NA
c17525_g1_i8	1.599593	5.044945	1.14E-05	0.000969	NA	NA	NA
c2424_g2_i1	1.597962	4.667687	0.000135	0.006518	NA	NA	NA
c21574_g1_i1	1.597607	7.343277	1.19E-05	0.000998	RecName: Full=Urea-proton symporter DUR3; Short=AtDUR3; AltName: Full=High-affinity urea active transporter DUR3 [Arabidopsis thaliana]	NA	GO:0005215|GO:0006810|GO:0016020|GO:0055085
c5195_g1_i1	1.595995	4.241717	5.11E-05	0.003152	NA	UniRef90_K5W9M8 Sulfurtransferase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W9M8_PHACS	NA
c13955_g1_i1	1.595856	4.809604	1.20E-05	0.001	NA	NA	NA
c15501_g3_i1	1.594496	3.455787	0.001541	0.040582	NA	NA	NA
c17476_g4_i1	1.593398	3.361077	0.000516	0.017947	NA	NA	NA
c17476_g4_i2	1.593398	3.361077	0.000516	0.017947	NA	NA	NA
c17476_g4_i3	1.593398	3.361077	0.000516	0.017947	RecName: Full=Zeaxanthin epoxidase, chloroplastic; Short=AtZEP; AltName: Full=Protein ABA DEFICIENT 1; Short=AtABA1; AltName: Full=Protein IMPAIRED IN BABA-INDUCED STERILITY 3; AltName: Full=Protein LOW EXPRESSION OF OSMOTIC STRESS-RESPONSIVE GENES 6; AltName: Full=Protein NON-PHOTOCHEMICAL QUENCHING 2; Flags: Precursor [Arabidopsis thaliana]	NA	NA
c15266_g3_i1	1.593341	4.3392	8.13E-06	0.000744	NA	NA	NA
c617_g1_i1	1.592913	3.016502	0.000133	0.006471	RecName: Full=Putative mitochondrial carnitine O-acetyltransferase [Saccharomyces cerevisiae S288c]	UniRef90_K5VTP3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VTP3_PHACS	GO:0016746

c14859_g1_i1	1.5913	2.952962	0.000215	0.009224	NA	UniRef90_A0A0C3S478 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S478_PHLGI	NA
c19468_g1_i1	1.591287	7.229564	0.000154	0.007167	RecName: Full=Putative oxidoreductase YteT; Flags: Precursor [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0008152|GO:0016491|GO:0055114
c14136_g1_i1	1.590744	3.586797	3.90E-05	0.00255	NA	NA	NA
c14136_g1_i2	1.590744	3.586797	3.90E-05	0.00255	NA	NA	NA
c14136_g1_i3	1.590744	3.586797	3.90E-05	0.00255	NA	NA	NA
c27221_g1_i1	1.589095	2.85068	0.000307	0.012083	NA	NA	NA
c20461_g1_i1	1.5869	4.026706	0.000121	0.006087	RecName: Full=Glucan 1,3-beta-glucosidase; AltName: Full=1,3-beta-D-glucanohydrolase; AltName: Full=Exo-beta 1,3 glucanase; Flags: Precursor [Bipolaris zeicola]	NA	NA
c13830_g2_i1	1.585058	2.39674	0.000831	0.025953	RecName: Full=Cytochrome P450 67; AltName: Full=CYPLXVII; AltName: Full=Planta-induced rust protein 16, partial [Uromyces viciae-fabae]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c11609_g1_i1	1.584754	3.302396	0.0017	0.043472	RecName: Full=Trichodiene synthase; AltName: Full=Sesquiterpene cyclase; Short=TS [Trichoderma harzianum]	NA	GO:0016106|GO:0045482
c11849_g2_i1	1.573317	3.277382	0.000289	0.011555	NA	NA	NA
c9365_g2_i1	1.571989	5.215113	2.11E-05	0.001594	NA	UniRef90_K5W544 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W544_PHACS	NA
c23044_g1_i1	1.571403	6.739316	8.41E-05	0.004572	NA	NA	NA
c17720_g1_i1	1.569105	6.963294	0.002041	0.049186	NA	UniRef90_A0A0C3NLU2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NLU2_PHLGI	NA
c15971_g2_i1	1.565458	5.026454	3.39E-05	0.002283	RecName: Full=NADPH-dependent methylglyoxal reductase GRE2; AltName: Full=3-methylbutanal reductase; AltName: Full=Genes de respuesta a estres protein 2; AltName: Full=Isovaleraldehyde reductase [Saccharomyces cerevisiae S288c]	NA	GO:0003824|GO:0003854|GO:0006694|GO:0009058|GO:0016616|GO:0050662|GO:0055114
c16816_g2_i1	1.561402	4.701373	0.001402	0.03814	RecName: Full=L-threo-3-deoxy-hexylosonate aldolase; AltName: Full=L-threo-3-deoxy-hexulosonate aldolase [Aspergillus niger]	NA	GO:0008152|GO:0016829
c9495_g1_i1	1.559257	3.051432	0.000569	0.019466	NA	NA	NA
c17362_g1_i1	1.554283	5.7091	0.001178	0.033618	NA	NA	GO:0016021|GO:0055085

c17362_g1_i2	1.554283	5.7091	0.001178	0.033618	RecName: Full=Uncharacterized transporter C11D3.18C [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c17362_g1_i3	1.554283	5.7091	0.001178	0.033618	NA	NA	GO:0016021|GO:0055085
c17362_g1_i4	1.554283	5.7091	0.001178	0.033618	NA	NA	GO:0016021|GO:0055085
c13009_g1_i1	1.553066	3.240276	0.000766	0.024228	NA	NA	GO:0004061|GO:0019441
c17669_g7_i1	1.552732	3.626808	0.000114	0.005805	NA	NA	NA
c17669_g7_i2	1.552732	3.626808	0.000114	0.005805	NA	NA	NA
c14807_g2_i1	1.552306	5.742584	2.17E-05	0.001622	NA	NA	NA
c13774_g2_i1	1.552158	3.317012	6.92E-05	0.003986	NA	NA	GO:0016021|GO:0022857|GO:0055085
c13774_g2_i2	1.552158	3.317012	6.92E-05	0.003986	RecName: Full=Sugar transporter STL1 [Saccharomyces cerevisiae S288c]	NA	GO:0016021|GO:0022857|GO:0055085
c11262_g2_i1	1.548831	7.120182	0.001379	0.037709	RecName: Full=Phenylalanine ammonia-lyase [Amanita muscaria]	NA	GO:0009058|GO:0016841
c21469_g1_i1	1.544556	4.028247	0.000952	0.028841	RecName: Full=Pyranose dehydrogenase; Short=PDH; AltName: Full=Pyranose:quinone oxidoreductase 1; Flags: Precursor [Agaricus xanthodermus]	NA	GO:0016491|GO:0016614|GO:0050660|GO:0055114
c11906_g1_i1	1.540573	5.037281	0.00012	0.006054	RecName: Full=Acetoacetyl-CoA synthetase [Gallus gallus]	NA	GO:0003824|GO:0008152
c17481_g5_i1	1.540434	7.82094	9.97E-05	0.0053	NA	NA	NA
c15266_g4_i1	1.539308	3.58534	8.31E-05	0.004533	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c14083_g2_i1	1.538914	3.020891	0.00049	0.017223	NA	NA	NA
c14083_g2_i2	1.538914	3.020891	0.00049	0.017223	NA	NA	NA
c9675_g1_i1	1.538299	5.383965	0.000977	0.029382	NA	NA	NA
c9675_g1_i2	1.538299	5.383965	0.000977	0.029382	NA	NA	NA
c9675_g1_i3	1.538299	5.383965	0.000977	0.029382	NA	UniRef90_A0A0C3QY40 Uncharacterized protein n=1 Tax=Tulasnella calospora MUT 4182 RepID=A0A0C3QY40_9HOMO	NA
c9675_g1_i4	1.538299	5.383965	0.000977	0.029382	NA	NA	NA
c9656_g1_i1	1.53572	4.025591	0.000266	0.01089	NA	NA	NA
c11662_g2_i1	1.535428	7.094415	0.000136	0.006554	NA	NA	NA

c4138_g1_i1	1.535156	2.40656	0.001196	0.033905	NA	NA	NA
c4967_g1_i1	1.534307	3.301424	0.000115	0.005854	RecName: Full=Ribonucleoside-diphosphate reductase large chain; AltName: Full=Ribonucleotide reductase [Schizosaccharomyces pombe 972h-]	UniRef90_K5VY69 Ribonucleoside-diphosphate reductase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VY69_PHACS	GO:0006260|GO:0055114
c26906_g1_i1	1.532498	6.892176	0.000289	0.011555	RecName: Full=Protoplast secreted protein 2; Flags: Precursor [Saccharomyces cerevisiae S288c]	NA	GO:0010181|GO:0016491
c23003_g1_i1	1.532188	7.131439	0.000941	0.028585	NA	NA	NA
c19352_g1_i1	1.530913	10.56389	0.000476	0.016875	RecName: Full=Regulator of rDNA transcription protein 15 [Saccharomyces cerevisiae S288c]	NA	NA
c10805_g3_i1	1.529071	4.731599	0.000798	0.025066	RecName: Full=Uncharacterized amino-acid permease PB24D3.02c [Schizosaccharomyces pombe 972h-]	NA	NA
c8698_g4_i1	1.527667	5.017306	0.000118	0.005994	RecName: Full=Histone H2B [Agaricus bisporus]	NA	GO:0003677
c16767_g1_i1	1.525909	4.12543	0.000569	0.019466	NA	NA	NA
c23059_g1_i1	1.522578	9.642279	0.001803	0.045131	RecName: Full=S-adenosylmethionine synthase; Short=AdoMet synthase; AltName: Full=Methionine adenosyltransferase; Short=MAT [Schizosaccharomyces pombe 972h-]	UniRef90_A0A067Q470 S-adenosylmethionine synthase n=1 Tax=Jaapia argillacea MUCL 33604 RepID=A0A067Q470_9HOMO	GO:0004478|GO:0006556
c17123_g2_i1	1.521021	4.739695	0.000155	0.007192	NA	NA	NA
c8509_g2_i1	1.520708	5.36483	0.00032	0.012414	NA	NA	NA
c8509_g2_i2	1.520708	5.36483	0.00032	0.012414	NA	NA	NA
c10291_g1_i1	1.519665	4.21913	0.000185	0.008167	NA	NA	GO:0005515
c10291_g1_i2	1.519665	4.21913	0.000185	0.008167	NA	NA	GO:0005515
c16906_g3_i1	1.51894	5.848328	6.35E-05	0.003734	NA	NA	NA
c16906_g3_i2	1.51894	5.848328	6.35E-05	0.003734	NA	NA	NA
c24790_g1_i1	1.51859	6.067542	2.63E-05	0.001877	RecName: Full=Aorsin; Flags: Precursor [Aspergillus oryzae RIB40]	NA	GO:0004252|GO:0006508
c15953_g5_i1	1.517444	4.582881	0.000248	0.010237	RecName: Full=DUF21 domain-containing protein At4g33700; AltName: Full=CBS domain-containing protein CBSDUF6 [Arabidopsis thaliana]	NA	NA
c12319_g2_i1	1.517336	4.175864	3.36E-05	0.002268	NA	UniRef90_A0A0C3RRW4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RRW4_PHLGI	NA

c16406_g5_i1	1.517154	2.46667	0.001327	0.036627	NA	UniRef90_A0A067QK71 Uncharacterized protein n=1 Tax=Jaapia argillacea MUCL 33604 RepID=A0A067QK71_9HOMO	NA
c11376_g1_i1	1.514992	4.516778	0.0013	0.036076	RecName: Full=Phenol 2-monooxygenase; AltName: Full=Phenol hydroxylase [Trichosporon cutaneum]	NA	NA
c17611_g4_i1	1.514686	3.866227	4.03E-05	0.002619	RecName: Full=3-O-alpha-D-mannopyranosyl-alpha-D-mannopyranose xylosylphosphotransferase; AltName: Full=Xylosylphosphotransferase 1 [Cryptococcus neoformans var. grubii]	UniRef90_K5WHN3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WHN3_PHACS	NA
c11758_g2_i1	1.51439	8.048123	0.000163	0.007484	NA	NA	NA
c17301_g6_i1	1.513811	3.07748	0.000955	0.028918	RecName: Full=Psi-producing oxygenase A; AltName: Full=Fatty acid oxygenase ppoA; Includes: RecName: Full=Linoleate 8R-lipoxygenase; Includes: RecName: Full=9,12-octadecadienoate 8-hydroperoxide 8R-isomerase [Aspergillus fumigatus A1163]	NA	NA
c16124_g1_i1	1.503977	5.966315	0.000344	0.013111	NA	NA	GO:0005515
c16124_g1_i2	1.503977	5.966315	0.000344	0.013111	NA	NA	GO:0005515
c16124_g1_i3	1.503977	5.966315	0.000344	0.013111	NA	NA	GO:0005515
c16124_g1_i4	1.503977	5.966315	0.000344	0.013111	RecName: Full=Anaphase-promoting complex subunit 3; AltName: Full=20S cyclosome/APC complex protein apc3; AltName: Full=Nuclear alteration protein 2; AltName: Full=Nuclear scaffold-like protein p76 [Schizosaccharomyces pombe 972h-]	NA	GO:0005515
c14525_g1_i1	1.50108	4.323991	0.000396	0.014633	NA	NA	NA
c14525_g1_i2	1.50108	4.323991	0.000396	0.014633	NA	UniRef90_K5VWK1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWK1_PHACS	NA
c26710_g1_i1	1.499358	7.571613	4.61E-05	0.002901	RecName: Full=Bleomycin hydrolase; Short=BH; Short=BLM hydrolase; Short=BMH [Rattus norvegicus]	NA	GO:0004197|GO:0006508
c21407_g1_i1	1.499341	2.2845	0.001096	0.031926	NA	NA	NA
c15953_g2_i1	1.495729	5.558218	7.59E-05	0.004235	RecName: Full=DUF21 domain-containing protein At4g33700; AltName: Full=CBS domain-containing protein CBSDUF6 [Arabidopsis thaliana]	NA	NA
c10370_g2_i1	1.495356	7.310944	0.001462	0.039267	NA	NA	NA

c10395_g1_i1	1.49459	6.866154	0.000343	0.013079	RecName: Full=Cytokinesis protein sepH; AltName: Full=Serine/threonine-protein kinase sepH [Aspergillus nidulans FGSC A4]	NA	GO:0004672|GO:0005524|GO:0006468|GO:0035556
c16401_g3_i1	1.491228	4.18338	2.17E-05	0.001622	NA	NA	NA
c16401_g3_i2	1.491228	4.18338	2.17E-05	0.001622	NA	NA	NA
c16401_g3_i3	1.491228	4.18338	2.17E-05	0.001622	NA	NA	NA
c16401_g3_i4	1.491228	4.18338	2.17E-05	0.001622	NA	NA	NA
c13999_g2_i1	1.491186	3.142107	0.000833	0.025984	NA	NA	GO:0004672|GO:0005524|GO:0006468|GO:0009103|GO:0016020|GO:0016773
c13999_g2_i2	1.491186	3.142107	0.000833	0.025984	RecName: Full=Serine/threonine-protein kinase CHK1; AltName: Full=Checkpoint kinase 1 [Ustilago maydis 521]	NA	GO:0004672|GO:0005524|GO:0006468
c17611_g3_i1	1.489726	4.960755	0.001769	0.044429	RecName: Full=3-O-alpha-D-mannopyranosyl-alpha-D-mannopyranose xylosylphosphotransferase; AltName: Full=Xylosylphosphotransferase 1 [Cryptococcus gattii WM276]	UniRef90_K5VS69 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VS69_PHACS	NA
c13605_g2_i1	1.489661	4.721893	0.000112	0.005746	NA	NA	NA
c6737_g2_i1	1.486552	4.430421	0.000234	0.009841	NA	NA	NA
c16791_g1_i1	1.485826	8.060967	4.48E-05	0.002821	NA	NA	NA
c16791_g1_i2	1.485826	8.060967	4.48E-05	0.002821	NA	NA	NA
c9083_g1_i1	1.478959	6.070703	0.000281	0.011318	NA	NA	NA
c9319_g3_i1	1.477693	5.616094	0.000186	0.008185	RecName: Full=MFS antiporter QDR2 [Candida albicans SC5314]	UniRef90_K5VPF9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPF9_PHACS	NA
c9463_g1_i1	1.476822	2.913528	0.000586	0.019849	NA	UniRef90_K5VL46 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VL46_PHACS	NA
c12944_g1_i1	1.475788	6.415835	4.17E-05	0.002691	NA	NA	NA
c12944_g1_i2	1.475788	6.415835	4.17E-05	0.002691	RecName: Full=Solute carrier family 28 member 3; AltName: Full=Concentrative Na(+)-nucleoside cotransporter 3; AltName: Full=hfCNT [Eptatretus stoutii]	NA	NA
c4902_g1_i1	1.475548	3.630064	0.000173	0.007753	NA	NA	NA

c23634_g1_i1	1.474236	4.793469	6.79E-05	0.003928	NA	NA	NA
c34_g1_i1	1.471886	6.883202	0.001599	0.041611	RecName: Full=Enolase; AltName: Full=2-phospho-D-glycerate hydro-lyase; AltName: Full=2-phosphoglycerate dehydratase [Neocallimastix frontalis]	UniRef90_F8PCM1 Enolase n=18 Tax=Agaricomycetes RepID=F8PCM1_SERL9	GO:0000015|GO:0000287|GO:0004634|GO:0006096
c24789_g1_i1	1.468181	5.881552	0.000155	0.007192	RecName: Full=Tripeptidyl-peptidase sed1; AltName: Full=Sedolisin-A; Flags: Precursor [Aspergillus fumigatus Af293]	NA	GO:0008236
c6405_g1_i1	1.465257	2.098898	0.001891	0.046639	NA	NA	NA
c6405_g1_i2	1.465257	2.098898	0.001891	0.046639	NA	NA	NA
c8509_g3_i1	1.463434	5.096173	0.001067	0.031456	RecName: Full=Tripeptidyl aminopeptidase; Short=Tap; Flags: Precursor [Streptomyces coelicolor A3(2)]	NA	NA
c16100_g1_i1	1.462738	3.718321	0.000105	0.005547	NA	NA	GO:0008152|GO:0016491|GO:0055114
c16100_g1_i2	1.462738	3.718321	0.000105	0.005547	RecName: Full=Aldehyde dehydrogenase; Short=ALDDH; Short=ALDH [Agaricus bisporus]	NA	GO:0008152|GO:0016491|GO:0055114
c12190_g3_i1	1.459588	6.942732	4.32E-05	0.002735	RecName: Full=Oligopeptide transporter 3; Short=AtOPT3 [Arabidopsis thaliana]	UniRef90_M9PA63 Oligopeptide transporter 11 n=1 Tax=Phanerochaete chrysosporium RepID=M9PA63_PHACH	GO:0055085
c488_g1_i1	1.459533	5.250947	0.000117	0.005916	RecName: Full=Probable quinate permease; AltName: Full=Quinate transporter [Aspergillus fumigatus Af293]	UniRef90_K5V441 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V441_PHACS	GO:0016021|GO:0022857|GO:0055085
c15173_g1_i1	1.456585	4.071815	0.001505	0.040011	NA	NA	NA
c616_g2_i1	1.456151	5.087266	0.000123	0.006151	RecName: Full=NADH-cytochrome b5 reductase 1; AltName: Full=Microsomal cytochrome b reductase [Kluyveromyces lactis NRRL Y-1140]	UniRef90_K5WGX1 NADH-cytochrome b5 reductase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGX1_PHACS	NA
c14161_g1_i1	1.453803	4.964003	0.000961	0.028991	NA	NA	NA
c2877_g2_i1	1.451289	10.59278	0.000414	0.015177	RecName: Full=Protein TAR1 [Kluyveromyces lactis NRRL Y-1140]	NA	NA
c11183_g1_i1	1.45062	2.521341	0.001707	0.043499	RecName: Full=Poly [ADP-ribose] polymerase 2; Short=PARP-2; AltName: Full=NAD(+) ADP-ribosyltransferase 2; Short=ADPRT-2; AltName: Full=Poly[ADP-ribose] synthase 2 [Arabidopsis thaliana]	NA	GO:0003950|GO:0006471

c248_g1_i1	1.448275	5.59386	0.000474	0.01684	RecName: Full=Endoplasmin; AltName: Full=94 kDa glucose-regulated protein; Short=GRP-94; AltName: Full=Heat shock protein 90 kDa beta member 1; Flags: Precursor [Bos taurus]	UniRef90_K5V8M0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V8M0_PHACS	NA
c13708_g1_i1	1.446981	6.400388	0.000112	0.005746	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c4251_g1_i1	1.446445	2.874678	0.000744	0.0237	RecName: Full=Transmembrane protein 97 [Mus musculus]	NA	NA
c15174_g2_i1	1.445747	4.013375	0.001188	0.033751	NA	NA	NA
c12888_g1_i1	1.444007	5.477465	0.001956	0.047757	NA	NA	NA
c12888_g1_i2	1.444007	5.477465	0.001956	0.047757	NA	NA	NA
c19803_g1_i1	1.442644	5.703353	0.00078	0.024604	NA	NA	NA
c13405_g1_i1	1.439154	3.797349	5.95E-05	0.003557	RecName: Full=Probable very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase; AltName: Full=3-hydroxyacyl-CoA dehydratase; Short=HACD [Schizosaccharomyces pombe 972h-]	NA	NA
c13405_g1_i2	1.439154	3.797349	5.95E-05	0.003557	NA	NA	NA
c24063_g1_i1	1.438174	4.486104	0.000335	0.012828	NA	NA	NA
c27475_g1_i1	1.437931	3.983366	7.22E-05	0.004116	NA	NA	NA
c9906_g1_i1	1.436042	3.015642	0.001716	0.043629	NA	UniRef90_K5XAE4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XAE4_PHACS	NA
c11501_g3_i1	1.433501	3.542183	0.000623	0.020836	NA	NA	GO:0016829|GO:0042597
c9537_g1_i1	1.432176	6.029709	8.22E-05	0.004489	NA	UniRef90_A0A0C3SFR0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SFR0_PHLGI	NA
c13142_g3_i1	1.427647	4.449023	0.00034	0.012988	NA	NA	NA
c11615_g2_i1	1.422242	5.646458	0.000168	0.00761	RecName: Full=Fructose-1,6-bisphosphatase, cytosolic; Short=FBPase; AltName: Full=CY-F1; AltName: Full=D-fructose-1,6-bisphosphate 1-phosphohydrolase [Solanum tuberosum]	NA	GO:0005975|GO:0042132|GO:0042578
c13291_g2_i1	1.420986	7.158375	0.001471	0.039363	RecName: Full=Putative agmatinase 1; AltName: Full=Agmatine ureohydrolase 1; Short=AUH 1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	GO:0046872

c3152_g1_i1	1.419315	6.263174	0.001074	0.031527	NA	NA	NA
c21340_g1_i1	1.41901	5.345042	0.000182	0.008055	NA	NA	NA
c7402_g1_i1	1.417506	4.717532	0.000227	0.009624	NA	NA	NA
c16035_g2_i1	1.417087	4.608984	0.000737	0.023571	NA	NA	NA
c12841_g2_i1	1.416805	5.366422	0.00047	0.016777	NA	NA	NA
c284_g1_i1	1.414783	7.443091	0.00036	0.013573	RecName: Full=Uncharacterized membrane protein C3B8.06 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V9B9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V9B9_PHACS	NA
c248_g2_i1	1.410038	5.558777	0.000595	0.02009	RecName: Full=Endoplasmin; AltName: Full=Heat shock 108 kDa protein; Short=HSP 108; Short=HSP108; AltName: Full=Heat shock protein 90 kDa beta member 1; AltName: Full=Transferrin-binding protein; Flags: Precursor [Gallus gallus]	UniRef90_K5V8M0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V8M0_PHACS	GO:0005524|GO:0006457|GO:0006950|GO:0051082
c9786_g1_i1	1.408071	5.661358	0.000129	0.00635	RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor [Neurospora crassa OR74A]	UniRef90_K5WYH4 Citrate synthase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYH4_PHACS	GO:0044262|GO:0046912
c7664_g1_i1	1.403967	4.535677	0.001705	0.043499	RecName: Full=Uncharacterized protein aq_928 [Aquifex aeolicus VF5]	NA	GO:0010181|GO:0016491|GO:0042602|GO:0055114
c13396_g2_i1	1.400239	2.659474	0.000674	0.021932	NA	NA	NA
c13396_g2_i2	1.400239	2.659474	0.000674	0.021932	NA	NA	NA
c798_g1_i1	1.398873	8.997391	0.000314	0.012296	RecName: Full=Peroxisomal catalase [Candida albicans SC5314]	UniRef90_A0A0C3P0I8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P0I8_PHLGI	GO:0004096|GO:0020037|GO:0055114
c4599_g2_i1	1.39395	3.624159	0.000446	0.016062	NA	NA	NA
c24823_g1_i1	1.39394	3.538101	0.001378	0.037691	NA	NA	NA
c9319_g2_i1	1.392617	5.189298	0.000142	0.006766	RecName: Full=Quinidine resistance protein 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5VPF9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPF9_PHACS	GO:0016021|GO:0022857|GO:0055085
c15501_g2_i1	1.388124	3.356666	0.00155	0.040768	NA	NA	NA
c21313_g1_i1	1.385751	7.199493	0.001802	0.045131	RecName: Full=Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial; AltName: Full=Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex; AltName: Full=Pyruvate	NA	GO:0008152|GO:0016746

					dehydrogenase complex component E2; Short=PDC-E2; Short=PDCE2; Flags: Precursor [Schizosaccharomyces pombe 972h-]		
c13302_g3_i1	1.385632	5.097645	8.13E-05	0.004456	NA	NA	GO:0004190|GO:0006508
c13302_g3_i2	1.385632	5.097645	8.13E-05	0.004456	NA	NA	GO:0004190|GO:0006508
c3152_g2_i1	1.385038	5.4357	0.001146	0.033049	NA	NA	NA
c242_g1_i1	1.384249	7.746862	0.000194	0.008524	NA	NA	NA
c17154_g1_i1	1.38235	3.960132	0.000268	0.010931	NA	NA	NA
c17154_g1_i2	1.38235	3.960132	0.000268	0.010931	NA	NA	NA
c17154_g1_i3	1.38235	3.960132	0.000268	0.010931	NA	NA	NA
c2468_g1_i1	1.382099	5.695657	0.00013	0.006359	NA	NA	NA
c6063_g1_i1	1.380361	5.368749	0.000128	0.006318	RecName: Full=Xanthine phosphoribosyltransferase 1; Short=XPRT [Saccharomyces cerevisiae S288c]	UniRef90_A0A067QG11 Uncharacterized protein n=1 Tax=Jaapia argillacea MUCL 33604 RepID=A0A067QG11_9HOMO	NA
c15853_g2_i1	1.379425	4.295607	0.001965	0.047952	RecName: Full=Uncharacterized protein CC613.01 [Schizosaccharomyces pombe 972h-]	NA	NA
c8698_g2_i1	1.377882	7.360491	0.00028	0.011306	RecName: Full=Histone H2B [Agaricus bisporus]	NA	GO:0003677|GO:0005622|GO:0043565
c4673_g1_i1	1.377351	6.685164	0.000531	0.018385	NA	NA	NA
c15173_g3_i1	1.373823	3.725061	0.000848	0.026275	RecName: Full=GTPase Der; AltName: Full=GTP-binding protein EngA [Janthinobacterium sp. Marseille]	NA	GO:0005524|GO:0005525|GO:0015093|GO:0015684|GO:0016021|GO:0016887
c14288_g3_i1	1.373684	2.887197	0.000878	0.026968	RecName: Full=Tripeptidyl aminopeptidase; Short=Tap; Flags: Precursor [Streptomyces coelicolor A3(2)]	NA	NA
c8996_g1_i1	1.373118	3.95221	9.34E-05	0.005003	NA	NA	NA
c8996_g1_i2	1.373118	3.95221	9.34E-05	0.005003	NA	NA	NA
c9465_g1_i1	1.366611	3.679132	0.000959	0.02898	NA	NA	NA
c826_g2_i1	1.364477	6.62128	0.000164	0.007494	RecName: Full=Lysine-specific permease [Saccharomyces cerevisiae S288c]	UniRef90_A0A0C3S1V1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S1V1_PHLGI	GO:0006810|GO:0016020|GO:0055085

c21733_g1_i1	1.36325	3.56437	0.000423	0.015488	RecName: Full=Protein LUTEIN DEFICIENT 5, chloroplastic; AltName: Full=Cytochrome P450 97A3; Flags: Precursor [Arabidopsis thaliana]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c4102_g1_i1	1.359963	2.198498	0.001954	0.047754	RecName: Full=Phosphatidyl-N-methylethanolamine N-methyltransferase; Short=PLMT; AltName: Full=Overproducer of inositol protein 3; AltName: Full=Unsaturated phospholipid methyltransferase [Saccharomyces cerevisiae S288c]	NA	NA
c21575_g1_i1	1.357861	6.400629	0.000901	0.027574	RecName: Full=Probable urea active transporter 1 [Schizosaccharomyces pombe 972h-]	NA	GO:0005215|GO:0006810|GO:0016020|GO:0055085
c16374_g2_i1	1.35686	6.162095	0.00025	0.010289	RecName: Full=[Pyruvate dehydrogenase (acetyl-transferring)] kinase, mitochondrial; Short=Pyruvate dehydrogenase kinase; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_K5X522 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X522_PHACS	NA
c20388_g1_i1	1.354581	4.009371	0.000402	0.014826	RecName: Full=Argininosuccinate synthase; AltName: Full=Citrulline--aspartate ligase [Schizosaccharomyces pombe 972h-]	NA	GO:0004055|GO:0005524|GO:0006526
c14060_g1_i1	1.353658	2.523103	0.001706	0.043499	NA	NA	NA
c13297_g2_i1	1.352624	3.465511	0.000346	0.013147	RecName: Full=Carbamoyl-phosphate synthase arginine-specific large chain; AltName: Full=Arginine-specific carbamoyl-phosphate synthetase, ammonia chain [Trichosporon cutaneum]	NA	NA
c558_g1_i1	1.35179	4.040386	0.000202	0.008844	NA	NA	NA
c8404_g1_i1	1.350857	4.223416	0.000354	0.013422	NA	NA	NA
c17374_g1_i1	1.350694	2.781652	0.001019	0.030364	NA	NA	NA
c17374_g1_i2	1.350694	2.781652	0.001019	0.030364	NA	NA	NA
c7082_g1_i1	1.350453	3.665721	0.001607	0.041679	NA	NA	GO:0008152|GO:0016846
c9212_g2_i1	1.349443	7.33495	0.000261	0.010702	NA	NA	GO:0055085
c9212_g2_i2	1.349443	7.33495	0.000261	0.010702	RecName: Full=Glutathione transporter 1 [Schizosaccharomyces pombe 972h-]	NA	GO:0055085
c16083_g3_i1	1.348664	3.70057	0.001079	0.031614	RecName: Full=Beta-hexosaminidase 2; AltName: Full=Beta-GlcNAcase 2; AltName: Full=Beta-N-acetylhexosaminidase 2; AltName: Full=Beta-hexosaminidase 3; Short=AtHEX3; AltName: Full=N-acetyl-beta-glucosaminidase 2; Flags: Precursor [Arabidopsis thaliana]	NA	GO:0004553|GO:0005975

c16083_g3_i2	1.348664	3.70057	0.001079	0.031614	NA	NA	NA
c16231_g3_i1	1.34605	4.602524	0.001085	0.031775	NA	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c16231_g3_i2	1.34605	4.602524	0.001085	0.031775	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V788 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V788_PHACS	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c15467_g3_i1	1.34433	5.03026	0.000812	0.025428	NA	NA	NA
c15467_g3_i2	1.34433	5.03026	0.000812	0.025428	NA	NA	NA
c158_g1_i1	1.343627	3.296508	0.001875	0.046402	NA	UniRef90_J4G919 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4G919_FIBRA	NA
c158_g1_i2	1.343627	3.296508	0.001875	0.046402	NA	NA	NA
c13633_g1_i1	1.343581	4.562918	0.001062	0.031403	RecName: Full=Acetamidase [Aspergillus nidulans FGSC A4]	NA	GO:0016884
c13291_g1_i1	1.339263	6.874567	0.000966	0.02909	RecName: Full=Putative agmatinase 1; AltName: Full=Agmatine ureohydrolase 1; Short=AUH 1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	GO:0046872
c23595_g1_i1	1.33913	4.237442	0.000541	0.018663	NA	NA	NA
c4852_g2_i1	1.338958	6.316729	0.000203	0.008845	NA	UniRef90_B8R4Q7 Delta-12 desaturase n=2 Tax=Phanerochaete chrysosporium RepID=B8R4Q7_PHACH	NA
c6753_g1_i1	1.337828	5.85233	0.000108	0.005616	RecName: Full=Sugar phosphatase YfbT [Escherichia coli K-12]	NA	NA
c4940_g1_i1	1.336339	6.328769	0.000597	0.020096	RecName: Full=Delta-1-pyrroline-5-carboxylate dehydrogenase; Short=P5C dehydrogenase; AltName: Full=L-glutamate gamma-semialdehyde dehydrogenase [Agaricus bisporus]	UniRef90_K5XAP6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XAP6_PHACS	GO:0008152|GO:0016491|GO:0055114
c16253_g2_i1	1.332082	3.119162	0.000912	0.027873	NA	UniRef90_K5UW00 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UW00_PHACS	GO:0005515
c11501_g2_i1	1.332048	4.047428	0.000238	0.009892	NA	NA	GO:0016829|GO:0042597

c15043_g1_i1	1.330761	3.257748	0.00041	0.015059	NA	NA	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c15043_g1_i2	1.330761	3.257748	0.00041	0.015059	NA	NA	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c15430_g1_i1	1.330711	3.0577	0.000617	0.02069	NA	NA	GO:0003924|GO:0004871|GO:0007186|GO:0019001|GO:0031683
c15430_g1_i2	1.330711	3.0577	0.000617	0.02069	RecName: Full=Guanine nucleotide-binding protein alpha-2 subunit; AltName: Full=GP2-alpha [Neurospora crassa OR74A]	NA	GO:0003924|GO:0004871|GO:0007186|GO:0019001|GO:0031683
c16084_g2_i1	1.330263	7.561639	0.000229	0.009631	RecName: Full=Leptomycin B resistance protein pmd1 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c16084_g2_i2	1.330263	7.561639	0.000229	0.009631	NA	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c16084_g2_i3	1.330263	7.561639	0.000229	0.009631	NA	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c26273_g1_i1	1.329534	6.332516	0.00037	0.013844	NA	NA	NA
c23793_g1_i1	1.328648	4.710337	0.001151	0.033109	NA	NA	NA
c16154_g1_i1	1.327284	3.631128	0.001607	0.041679	RecName: Full=Oligomycin resistance ATP-dependent permease YOR1 [Saccharomyces cerevisiae S288c]	NA	GO:0005524|GO:0016887
c2876_g1_i1	1.324029	11.86383	0.001861	0.046211	RecName: Full=Uncharacterized protein YLR154C-G [Saccharomyces cerevisiae S288c]	NA	NA
c2650_g1_i1	1.323868	3.33	0.001174	0.033607	NA	NA	NA

c826_g1_i1	1.323465	7.973339	0.000737	0.023571	RecName: Full=Dicarboxylic amino acid permease [Saccharomyces cerevisiae S288c]	UniRef90_K5UKF2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UKF2_PHACS	GO:0003333|GO:0006810|GO:0015171|GO:0016020|GO:0055085
c6181_g2_i1	1.320926	6.983185	0.002025	0.04895	RecName: Full=Uncharacterized glycosidase Rv0584; Flags: Precursor [Mycobacterium tuberculosis H37Rv]	UniRef90_K5W0L8 Glycoside hydrolase family 92 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W0L8_PHACS	NA
c36_g1_i1	1.31983	6.794857	0.000326	0.012556	RecName: Full=Proline-specific permease; AltName: Full=Proline transport protein [Aspergillus nidulans FGSC A4]	UniRef90_A0A0C3RSN8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RSN8_PHLGI	GO:0003333|GO:0006810|GO:0015171|GO:0016020|GO:0055085
c25130_g1_i1	1.319818	6.01477	0.000417	0.015279	NA	NA	NA
c9589_g1_i1	1.319126	3.162307	0.000916	0.027943	RecName: Full=26S proteasome non-ATPase regulatory subunit 7 homolog B; AltName: Full=26S proteasome regulatory subunit RPN8b; Short=AtRPN8b; AltName: Full=Protein MATERNAL EFFECT EMBRYO ARREST 34 [Arabidopsis thaliana]	UniRef90_K5WX77 Uncharacterized protein n=2 Tax=Phanerochaetaceae RepID=K5WX77_PHACS	NA
c10791_g2_i1	1.316996	5.256031	0.000206	0.008941	RecName: Full=Serine hydroxymethyltransferase 2; Short=SHMT 2; AltName: Full=Glycine hydroxymethyltransferase 2; AltName: Full=Serine methylase 2 [Dictyostelium discoideum]	NA	GO:0004372|GO:0006544|GO:0006563
c692_g2_i1	1.315683	6.020343	0.000658	0.021662	RecName: Full=Dihydroxy-acid dehydratase; Short=DAD [Rhodopirellula baltica SH 1]	UniRef90_K5W5L6 Uncharacterized protein n=2 Tax=Phanerochaetaceae RepID=K5W5L6_PHACS	GO:0003824|GO:0008152
c13388_g2_i1	1.314171	5.221699	0.000233	0.009815	NA	NA	NA
c17275_g5_i1	1.3129	3.704853	0.000367	0.013765	NA	NA	NA
c17275_g5_i2	1.3129	3.704853	0.000367	0.013765	NA	NA	NA
c17275_g5_i3	1.3129	3.704853	0.000367	0.013765	NA	NA	NA
c16816_g1_i1	1.309549	5.29458	0.001143	0.032972	RecName: Full=L-threo-3-deoxy-hexylosonate aldolase; AltName: Full=L-threo-3-deoxy-hexulosonate aldolase [Aspergillus niger]	NA	GO:0008152|GO:0016829
c16368_g2_i1	1.309505	6.815832	0.000755	0.023984	NA	NA	GO:0016491|GO:0055114
c16368_g2_i2	1.309505	6.815832	0.000755	0.023984	RecName: Full=Polyamine oxidase; Flags: Precursor [Zea mays]	UniRef90_K5VM77 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VM77_PHACS	GO:0016491|GO:0055114
c14524_g2_i1	1.308701	4.15354	0.000237	0.009892	RecName: Full=Putative hydroxymethylpyrimidine/phosphomethylpyrimidine kinase 2; AltName: Full=Hydroxymethylpyrimidine kinase 2; Short=HMP kinase 2; AltName: Full=Hydroxymethylpyrimidine phosphate	UniRef90_K5VWZ9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWZ9_PHACS	NA

					kinase 2; Short=HMP-P kinase 2; Short=HMP-phosphate kinase 2; Short=HMPP kinase 2 [Schizosaccharomyces pombe 972h-]		
c10378_g2_i1	1.30695	7.097524	0.000173	0.007758	NA	NA	NA
c10378_g2_i2	1.30695	7.097524	0.000173	0.007758	NA	NA	NA
c2433_g2_i1	1.305311	6.57386	0.000628	0.020921	RecName: Full=Hydroxyacid-oxoacid transhydrogenase, mitochondrial; Short=HOT; AltName: Full=Alcohol dehydrogenase iron-containing protein 1; Short=ADHFe1; Flags: Precursor [Mus musculus]	NA	GO:0016491|GO:0046872|GO:0055114
c36_g2_i1	1.304409	4.939022	0.000633	0.020973	RecName: Full=Cationic amino acid transporter 1 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3RSN8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RSN8_PHLGI	GO:0003333|GO:0006810|GO:0015171|GO:0016020|GO:0055085
c9184_g2_i1	1.30384	6.903127	0.001762	0.044328	NA	NA	NA
c9184_g2_i2	1.30384	6.903127	0.001762	0.044328	NA	NA	NA
c21609_g1_i1	1.303412	6.847595	0.000486	0.017141	NA	NA	NA
c16039_g4_i1	1.297829	2.480614	0.002077	0.049806	NA	NA	NA
c4876_g1_i1	1.296171	4.920859	0.001608	0.041682	RecName: Full=N-alpha-acetyltransferase 30; AltName: Full=N-terminal acetyltransferase C complex catalytic subunit mak3 homolog; AltName: Full=NatC catalytic subunit [Schizosaccharomyces pombe 972h-]	UniRef90_K5URW0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5URW0_PHACS	GO:0008080
c20240_g1_i1	1.289747	5.626268	0.001075	0.031527	NA	NA	NA
c16228_g1_i1	1.285851	4.565239	0.000981	0.029431	RecName: Full=Probable 26S proteasome regulatory subunit rpn6 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3S4S2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S4S2_PHLGI	NA
c16873_g2_i1	1.284287	4.291947	0.001943	0.04751	RecName: Full=Probable transporter MCH4 [Saccharomyces cerevisiae S288c]	NA	GO:0016021|GO:0055085
c6212_g1_i1	1.283815	8.027228	0.00184	0.045868	RecName: Full=Peroxiredoxin-6 [Gallus gallus]	NA	GO:0016209|GO:0016491|GO:0051920|GO:0055114
c9812_g1_i1	1.283614	4.000598	0.00092	0.028048	NA	UniRef90_K5W879 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W879_PHACS	NA
c16100_g4_i1	1.282698	4.11623	0.000389	0.014422	RecName: Full=Aldehyde dehydrogenase; Short=ALDDH; Short=ALDH [Agaricus bisporus]	NA	GO:0008152|GO:0016491|GO:0055114

c5620_g1_i1	1.281354	4.148656	0.001972	0.048047	RecName: Full=Porphobilinogen deaminase; Short=PBG; AltName: Full=Hydroxymethylbilane synthase; Short=HMBS; AltName: Full=Pre-uroporphyrinogen synthase [Yarrowia lipolytica CLIB122]	UniRef90_K5W8W7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8W7_PHACS	GO:0004418|GO:0033014
c20299_g1_i1	1.281047	2.900588	0.001513	0.040168	NA	NA	NA
c26821_g1_i1	1.280879	4.860185	0.001494	0.039789	RecName: Full=Golgi apparatus membrane protein TVP38 [Coprinopsis cinerea okayama7#130]	NA	NA
c12543_g2_i1	1.27967	4.124951	0.000877	0.026968	RecName: Full=ARF guanine-nucleotide exchange factor GNOM; AltName: Full=Pattern formation protein EMB30; AltName: Full=Protein EMBRYO DEFECTIVE 30; AltName: Full=Protein MIZU-KUSSEI2; AltName: Full=Protein VASCULAR NETWORK 7 [Arabidopsis thaliana]	UniRef90_K5VVQ9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVQ9_PHACS	NA
c11662_g1_i1	1.274413	6.782786	0.001143	0.032972	NA	NA	NA
c24641_g1_i1	1.273906	5.983499	0.001372	0.037587	NA	NA	NA
c23160_g1_i1	1.273812	5.979118	0.001257	0.03523	NA	UniRef90_K5WW84 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WW84_PHACS	NA
c22937_g1_i1	1.273277	5.473482	0.001059	0.031317	NA	UniRef90_K5WGX1 NADH-cytochrome b5 reductase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGX1_PHACS	NA
c834_g1_i1	1.271438	6.20434	0.001739	0.043941	NA	UniRef90_K5VN87 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VN87_PHACS	NA
c834_g1_i2	1.271438	6.20434	0.001739	0.043941	NA	NA	NA
c692_g1_i1	1.267582	6.336598	0.000373	0.013933	RecName: Full=Dihydroxy-acid dehydratase; Short=DAD [Flavobacterium psychrophilum JIP02/86]	UniRef90_K5W5L6 Uncharacterized protein n=2 Tax=Phanerochaetaceae RepID=K5W5L6_PHACS	GO:0003824|GO:0008152
c11501_g1_i1	1.267233	4.67989	0.000663	0.021767	NA	NA	NA
c616_g1_i1	1.26394	5.718051	0.000387	0.014371	RecName: Full=NADH-cytochrome b5 reductase 1; AltName: Full=Microsomal cytochrome b reductase [Cryptococcus neoformans var. neoformans B-3501A]	UniRef90_UPI000441824E ferredoxin reductase-like C-terminal NADP-linked domain-containing protein n=1 Tax=Punctularia strigosozonata (strain HHB-11173) RepID=UPI000441824E	GO:0016491|GO:0055114
c13929_g1_i1	1.262743	7.748691	0.00063	0.020941	NA	NA	NA
c13929_g1_i2	1.262743	7.748691	0.00063	0.020941	NA	NA	NA
c13929_g1_i3	1.262743	7.748691	0.00063	0.020941	NA	NA	NA

c13929_g1_i4	1.262743	7.748691	0.00063	0.020941	NA	NA	NA
c6532_g2_i1	1.262314	7.052219	0.001457	0.03918	NA	NA	NA
c17669_g2_i1	1.261665	4.879749	0.00103	0.030615	NA	NA	NA
c17669_g2_i2	1.261665	4.879749	0.00103	0.030615	NA	NA	NA
c17669_g2_i3	1.261665	4.879749	0.00103	0.030615	NA	NA	NA
c11407_g2_i1	1.260745	3.596231	0.001785	0.044799	NA	NA	NA
c11407_g2_i2	1.260745	3.596231	0.001785	0.044799	NA	NA	NA
c4902_g2_i1	1.25482	5.201812	0.00104	0.030849	NA	NA	NA
c13438_g1_i1	1.254552	9.774464	0.000473	0.01682	RecName: Full=Alkali-sensitive linkage protein 1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	NA
c13438_g1_i2	1.254552	9.774464	0.000473	0.01682	NA	NA	NA
c13438_g1_i3	1.254552	9.774464	0.000473	0.01682	NA	NA	NA
c17512_g3_i1	1.254148	4.214073	0.000466	0.01663	NA	NA	NA
c17512_g3_i2	1.254148	4.214073	0.000466	0.01663	NA	UniRef90_K5UNU9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UNU9_PHACS	NA
c17512_g3_i3	1.254148	4.214073	0.000466	0.01663	NA	NA	NA
c17512_g3_i4	1.254148	4.214073	0.000466	0.01663	NA	NA	NA
c17512_g3_i5	1.254148	4.214073	0.000466	0.01663	NA	NA	NA
c15010_g2_i1	1.253555	3.410308	0.000701	0.022628	RecName: Full=Uncharacterized acyltransferase C1718.04 [Schizosaccharomyces pombe 972h-]	NA	NA
c14895_g1_i1	1.253333	4.691136	0.001135	0.032884	NA	UniRef90_A0A0C3S8F9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S8F9_PHLGI	NA
c15010_g3_i1	1.25223	3.344587	0.001114	0.032418	NA	NA	NA
c15010_g3_i2	1.25223	3.344587	0.001114	0.032418	NA	NA	NA
c10405_g1_i1	1.251237	8.070005	0.001133	0.032873	RecName: Full=Uncharacterized transporter C3H1.06c [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c16374_g1_i1	1.250624	6.960172	0.000568	0.019466	NA	NA	NA
c16374_g1_i2	1.250624	6.960172	0.000568	0.019466	RecName: Full=[Pyruvate dehydrogenase (acetyl-transferring)] kinase, mitochondrial; Short=Pyruvate dehydrogenase kinase; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_K5X522 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X522_PHACS	NA

c17598_g1_i1	1.24944	8.073141	0.000471	0.016782	NA	NA	NA
c17598_g1_i2	1.24944	8.073141	0.000471	0.016782	NA	NA	NA
c17598_g1_i3	1.24944	8.073141	0.000471	0.016782	RecName: Full=Pentachlorophenol 4-monooxygenase; AltName: Full=Pentachlorophenol hydroxylase [Sphingobium chlorophenolicum]	UniRef90_K5UZT8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UZT8_PHACS	NA
c17598_g1_i4	1.24944	8.073141	0.000471	0.016782	NA	NA	NA
c17980_g1_i1	1.249011	6.409874	0.00172	0.04367	NA	UniRef90_K5VDL8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VDL8_PHACS	NA
c241_g2_i1	1.248245	7.07978	0.001142	0.032972	NA	NA	NA
c16817_g1_i1	1.246296	6.677375	0.001384	0.037816	NA	NA	GO:0030554
c16817_g1_i2	1.246296	6.677375	0.001384	0.037816	RecName: Full=Uncharacterized protein C4B3.03c; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	NA
c2236_g1_i1	1.239695	9.202787	0.000386	0.014371	NA	NA	NA
c16201_g1_i1	1.239083	4.874661	0.001555	0.04085	NA	UniRef90_K5WCU0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCU0_PHACS	NA
c279_g2_i1	1.234592	6.289432	0.000838	0.026065	NA	UniRef90_A0A067NG89 Uncharacterized protein n=1 Tax=Pleurotus ostreatus PC15 RepID=A0A067NG89_PLEOS	GO:0004222|GO:0005615|GO:0008270
c16301_g2_i1	1.232231	3.623859	0.001536	0.040582	NA	NA	NA
c16301_g2_i2	1.232231	3.623859	0.001536	0.040582	NA	UniRef90_K5UKN0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UKN0_PHACS	NA
c242_g2_i1	1.230372	10.87384	0.001094	0.031913	RecName: Full=Plasma membrane ATPase 2; AltName: Full=Proton pump 2, partial [Solanum lycopersicum]	UniRef90_A0A0C3RPV4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RPV4_PHLGI	NA
c22889_g1_i1	1.230232	6.867743	0.000708	0.022771	RecName: Full=UDP-glucuronic acid decarboxylase 1; AltName: Full=UDP-glucuronate decarboxylase 1; Short=UGD; Short=UXS-1 [Homo sapiens]	UniRef90_K5W6N1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6N1_PHACS	GO:0003824|GO:0003854|GO:0006694|GO:0008831|GO:0016616|GO:0045226|GO:0050662|GO:0055114
c21895_g1_i1	1.22858	3.825607	0.001995	0.04844	NA	NA	NA

c26773_g1_i1	1.227684	4.145725	0.001356	0.037305	RecName: Full=Uncharacterized zinc-type alcohol dehydrogenase-like protein YbdR [Escherichia coli K-12]	NA	GO:0008270|GO:0016491|GO:0055114
c10365_g1_i1	1.227292	5.630931	0.000432	0.015746	RecName: Full=Uncharacterized ATPase YjoB [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0005524
c12959_g2_i1	1.224837	5.248807	0.000476	0.016875	NA	NA	NA
c20549_g1_i1	1.223956	3.385489	0.001719	0.04367	NA	NA	NA
c23567_g1_i1	1.214867	6.771033	0.001728	0.043789	RecName: Full=Aldehyde reductase 1; Short=ALR 1; AltName: Full=Alcohol dehydrogenase [NADP(+)]; AltName: Full=Aldehyde reductase I [Sporidiobolus salmonicolor]	NA	NA
c8381_g1_i1	1.207445	4.209119	0.001474	0.039373	NA	NA	NA
c16777_g2_i1	1.20345	4.101585	0.000662	0.021743	NA	NA	NA
c16777_g2_i2	1.20345	4.101585	0.000662	0.021743	NA	NA	NA
c16777_g2_i3	1.20345	4.101585	0.000662	0.021743	NA	NA	NA
c8981_g1_i1	1.20307	3.551247	0.002049	0.049331	NA	NA	GO:0003677
c8981_g1_i2	1.20307	3.551247	0.002049	0.049331	RecName: Full=Homeobox protein 10; Short=DdHbx-10 [Dictyostelium discoideum]	NA	GO:0003677
c8981_g1_i3	1.20307	3.551247	0.002049	0.049331	NA	NA	GO:0003677
c6757_g1_i1	1.198911	5.379477	0.000988	0.029612	NA	NA	NA
c21771_g1_i1	1.198666	5.253058	0.000984	0.029521	RecName: Full=26S proteasome non-ATPase regulatory subunit 4 homolog; AltName: Full=26S proteasome regulatory subunit RPN10; Short=AtRPN10; AltName: Full=26S proteasome regulatory subunit S5A homolog; AltName: Full=Multiubiquitin chain-binding protein 1; Short=AtMCB1 [Arabidopsis thaliana]	NA	NA
c488_g2_i1	1.196551	5.683928	0.001204	0.034092	RecName: Full=Probable quinate permease; AltName: Full=Quinate transporter [Neosartorya fischeri NRRL 181]	UniRef90_A0A0C3RZF2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RZF2_PHLGI	GO:0016021|GO:0022857|GO:0055085
c16492_g1_i1	1.19553	5.691098	0.001187	0.033737	NA	NA	GO:0006810|GO:0016021|GO:0055085
c16492_g1_i2	1.19553	5.691098	0.001187	0.033737	NA	NA	GO:0006810|GO:0016021|GO:0055085

c16492_g1_i3	1.19553	5.691098	0.001187	0.033737	RecName: Full=Uncharacterized solute carrier family 35 member C320.08 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VT45 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VT45_PHACS	GO:0006810|GO:0016021|GO:0055085
c17308_g2_i1	1.191931	4.680086	0.001687	0.043247	RecName: Full=Ubiquitin carboxyl-terminal hydrolase 2 [Schizosaccharomyces pombe 972h-]	NA	GO:0004843|GO:0005622|GO:0006511
c17308_g2_i2	1.191931	4.680086	0.001687	0.043247	NA	NA	GO:0004843|GO:0005622|GO:0006511
c3599_g1_i1	1.190334	4.687969	0.001163	0.033394	NA	NA	GO:0051287|GO:0055114
c19618_g1_i1	1.189328	3.865651	0.001733	0.043852	RecName: Full=Leucine aminopeptidase 1; AltName: Full=Leucyl aminopeptidase 1; Short=LAP1; Flags: Precursor [Metarhizium robertsii ARSEF 23]	NA	GO:0008152|GO:0016787
c2326_g1_i1	1.189247	6.897904	0.001388	0.037848	NA	NA	NA
c19988_g1_i1	1.186947	5.750878	0.000715	0.022951	RecName: Full=Putative phosphatidate cytidylyltransferase; AltName: Full=CDP-DAG synthase; AltName: Full=CDP-DG synthase; AltName: Full=CDP-diacylglycerol synthase; Short=CDS; AltName: Full=CDP-diglyceride pyrophosphorylase; AltName: Full=CDP-diglyceride synthase; AltName: Full=CTP:phosphatidate cytidylyltransferase [Schizosaccharomyces pombe 972h-]	NA	GO:0016020|GO:0016772
c10365_g2_i1	1.185443	5.268862	0.00111	0.032313	NA	NA	NA
c15200_g2_i1	1.18462	3.200991	0.001904	0.046848	NA	NA	NA
c23568_g1_i1	1.182448	5.973639	0.001849	0.04602	NA	NA	NA
c22757_g1_i1	1.180971	9.029697	0.001604	0.041664	NA	UniRef90_K5V8P8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V8P8_PHACS	NA
c3486_g1_i1	1.178158	9.434659	0.001009	0.030157	NA	NA	NA
c3486_g1_i2	1.178158	9.434659	0.001009	0.030157	NA	NA	NA
c19397_g1_i1	1.173055	6.12279	0.000622	0.020818	RecName: Full=60S acidic ribosomal protein P0 [Schizosaccharomyces pombe 972h-]	NA	GO:0003735|GO:0005622|GO:0005840|GO:0006414
c19396_g1_i1	1.170949	6.801786	0.001461	0.039265	RecName: Full=60S acidic ribosomal protein P0 [Podospora anserina]	NA	NA
c15808_g2_i1	1.1701	4.552592	0.001092	0.031913	RecName: Full=Condensin complex subunit 1; AltName: Full=Chromosome assembly protein XCAP-D2; AltName:	NA	NA

					Full=Chromosome condensation-related SMC-associated protein 1; AltName: Full=Chromosome-associated protein D2; AltName: Full=Eg7; AltName: Full=Non-SMC condensin I complex subunit D2 [Xenopus laevis]		
c6796_g2_i1	1.169073	8.860649	0.001069	0.031484	RecName: Full=Protein priA; Flags: Precursor [Lentinula edodes]	NA	NA
c14817_g2_i1	1.166555	4.453603	0.001261	0.035246	RecName: Full=Ribonucleoside-diphosphate reductase small chain; AltName: Full=Ribonucleotide reductase small subunit [Neurospora crassa OR74A]	UniRef90_K5WJT3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJT3_PHACS	GO:0009186|GO:0055114
c17553_g2_i1	1.16555	5.674574	0.001489	0.039682	NA	NA	NA
c17553_g2_i2	1.16555	5.674574	0.001489	0.039682	NA	UniRef90_K5URB8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5URB8_PHACS	NA
c5102_g1_i1	1.159896	6.669711	0.000819	0.025639	RecName: Full=Probable 2-methylcitrate dehydratase [Saccharomyces cerevisiae S288c]	UniRef90_K5W6B4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6B4_PHACS	GO:0019543|GO:0047547
c16670_g1_i1	1.15562	4.517805	0.001722	0.043684	RecName: Full=Probable 4-coumarate--CoA ligase 3; Short=4CL 3; Short=Os4CL3; AltName: Full=4-coumaroyl-CoA synthase 3 [Oryza sativa Japonica Group]	NA	GO:0003824|GO:0008152
c16670_g1_i2	1.15562	4.517805	0.001722	0.043684	NA	NA	GO:0003824|GO:0008152
c6182_g1_i1	1.150474	4.936932	0.001452	0.039103	NA	NA	NA
c13388_g1_i1	1.149855	4.46687	0.001586	0.041394	NA	NA	NA
c13388_g1_i2	1.149855	4.46687	0.001586	0.041394	NA	NA	NA
c6434_g1_i1	1.144263	5.036143	0.001738	0.043932	RecName: Full=26S proteasome regulatory subunit 4 homolog B; AltName: Full=26S proteasome AAA-ATPase subunit RPT2b; AltName: Full=26S proteasome subunit 4 homolog B; AltName: Full=Regulatory particle triple-A ATPase subunit 2b [Arabidopsis thaliana]	NA	GO:0005524
c15952_g3_i1	1.143743	8.274839	0.001124	0.032638	NA	NA	GO:0004553|GO:0005975
c15952_g3_i2	1.143743	8.274839	0.001124	0.032638	RecName: Full=Probable endo-1,3(4)-beta-glucanase AFUA_2G14360; AltName: Full=Mixed-linked glucanase AFUA_2G14360; Flags: Precursor [Aspergillus fumigatus Af293]	NA	GO:0004553|GO:0005975
c26603_g1_i1	1.143727	6.739621	0.001319	0.036433	RecName: Full=Oxysterol-binding protein-like protein 1 [Schizosaccharomyces pombe 972h-]	NA	NA

c22404_g1_i1	1.142767	4.063084	0.001044	0.030936	NA	UniRef90_K5WL86 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WL86_PHACS	NA
c11603_g1_i1	1.138325	3.915764	0.00206	0.049512	NA	NA	GO:0016757
c9365_g3_i1	1.132799	6.664829	0.001404	0.03817	RecName: Full=Pentatricopeptide repeat-containing protein 5, mitochondrial; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3SEJ1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SEJ1_PHLGI	GO:0045454
c23065_g1_i1	1.13234	8.771416	0.001094	0.031913	NA	NA	NA
c6182_g2_i1	1.128176	10.05551	0.000925	0.028128	RecName: Full=Subtilisin-like serine protease pepC; Flags: Precursor [Aspergillus niger]	UniRef90_A0A0C3PPR6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PPR6_PHLGI	GO:0004252|GO:0006508
c12199_g1_i1	1.120046	5.681703	0.001585	0.041388	NA	UniRef90_K5V238 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V238_PHACS	NA
c15991_g4_i1	1.116337	5.135949	0.001836	0.045834	NA	NA	NA
c19698_g1_i1	1.114433	3.869184	0.002028	0.048968	RecName: Full=40S ribosomal protein S7 [Schizosaccharomyces pombe 972h-]	NA	GO:0003735|GO:0005622|GO:0005840|GO:0006412
c17825_g1_i1	1.10794	5.996587	0.001464	0.039283	NA	NA	NA
c11286_g2_i1	1.094922	6.818703	0.001498	0.039873	NA	NA	NA
c16767_g4_i1	1.091062	4.488055	0.001864	0.046224	RecName: Full=Swarming motility protein YbiA [Escherichia coli K-12]	NA	NA
c16767_g4_i2	1.091062	4.488055	0.001864	0.046224	NA	NA	NA
c17027_g1_i1	1.080932	5.18923	0.002006	0.048673	RecName: Full=Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial; Short=KAT/AadAT; AltName: Full=2-aminoadipate aminotransferase; AltName: Full=2-aminoadipate transaminase; AltName: Full=Alpha-aminoadipate aminotransferase; Short=AadAT; AltName: Full=Kynurenine aminotransferase II; AltName: Full=Kynurenine--oxoglutarate aminotransferase II; AltName: Full=Kynurenine--oxoglutarate transaminase 2; AltName: Full=Kynurenine--oxoglutarate transaminase II; Flags: Precursor [Mus musculus]	NA	GO:0009058|GO:0030170
c17027_g1_i2	1.080932	5.18923	0.002006	0.048673	NA	NA	GO:0009058|GO:0030170

c24733_g1_i1	1.062587	7.703273	0.001984	0.048274	RecName: Full=Uncharacterized amino-acid permease C11D3.08c [Schizosaccharomyces pombe 972h-]	NA	GO:0003333|GO:0006810|GO:0015171|GO:0016020|GO:0055085
c16576_g1_i1	1.061256	4.771193	0.002026	0.04895	NA	UniRef90_K5UXA5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UXA5_PHACS	NA
c16576_g1_i2	1.061256	4.771193	0.002026	0.04895	NA	NA	NA
c20001_g1_i1	1.05386	7.691594	0.00205	0.049336	RecName: Full=Saccharopepsin; AltName: Full=Aspartate protease; Short=PrA; Short=Proteinase A; AltName: Full=Carboxypeptidase Y-deficient protein 4; AltName: Full=Proteinase YSCA; Flags: Precursor [Saccharomyces cerevisiae S288c]	NA	GO:0004190|GO:0006508
c18037_g1_i1	-7.57932	8.287857	2.51E-23	1.75E-19	RecName: Full=Cellulose-growth-specific protein; Flags: Precursor [Agaricus bisporus]	NA	NA
c11924_g1_i1	-7.48407	7.59398	2.02E-14	2.83E-11	RecName: Full=Probable endo-beta-1,4-glucanase D; Short=Endoglucanase D; AltName: Full=Carboxymethylcellulase D; AltName: Full=Cellulase D; Flags: Precursor [Aspergillus niger CBS 513.88]	NA	NA
c17725_g1_i1	-7.18698	11.31525	2.88E-13	3.05E-10	RecName: Full=Exoglucanase 1; AltName: Full=1,4-beta-cellobiohydrolase; AltName: Full=Exocellobiohydrolase I; AltName: Full=Exoglucanase I; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_K5ULV7 Glucanase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5ULV7_PHACS	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c17608_g3_i1	-6.73095	1.383199	5.20E-07	8.29E-05	NA	NA	NA
c21547_g1_i1	-6.53101	3.557742	1.07E-11	7.08E-09	RecName: Full=Probable 1,4-beta-D-glucan cellobiohydrolase B; AltName: Full=Beta-glucancellobiohydrolase B; AltName: Full=Exocellobiohydrolase B; AltName: Full=Exoglucanase B; Flags: Precursor [Aspergillus terreus NIH2624]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c11363_g1_i1	-5.67018	8.877446	3.40E-11	1.92E-08	NA	NA	NA
c17064_g1_i1	-5.62064	0.600019	1.73E-05	0.001358	NA	NA	NA
c15134_g1_i1	-5.61876	7.007971	4.25E-14	5.31E-11	RecName: Full=Manganese peroxidase H4; AltName: Full=MP-I; AltName: Full=Peroxidase manganese-dependent H4; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c22848_g1_i1	-5.37537	0.458796	1.37E-04	0.006559	NA	NA	NA

c999_g1_i1	-5.36835	3.97319	1.86E-10	8.54E-08	NA	UniRef90_K5WLD2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLD2_PHACS	NA
c24899_g1_i1	-5.34731	0.441779	2.99E-04	0.011864	NA	NA	NA
c17734_g1_i1	-5.27925	0.403642	0.000284	0.011416	NA	UniRef90_K5W069 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W069_PHACS	NA
c5209_g1_i1	-5.17423	0.342376	0.001557	0.040851	NA	NA	GO:0046872
c13426_g2_i1	-5.02222	3.496374	1.13E-07	2.27E-05	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]	NA	GO:0004190|GO:0006508
c18036_g1_i1	-4.9679	3.657577	8.60E-14	9.70E-11	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c14289_g2_i1	-4.93828	2.127284	1.26E-05	0.001045	NA	NA	NA
c21987_g1_i1	-4.79787	0.151466	0.001976	0.048118	NA	NA	NA
c23490_g1_i1	-4.73998	6.334609	8.66E-12	5.94E-09	RecName: Full=Probable xyloglucan-specific endo-beta-1,4-glucanase A; AltName: Full=Xyloglucanase A; AltName: Full=Xyloglucanendohydrolase A; Flags: Precursor [Aspergillus niger CBS 513.88]	UniRef90_K5VCY6 Glycoside hydrolase family 12 protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCY6_PHACS	GO:0000272|GO:0008810
c12820_g2_i1	-4.62386	7.788321	2.45E-09	8.71E-07	NA	UniRef90_K5V246 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V246_PHACS	NA
c5016_g2_i1	-4.40518	1.071004	4.98E-06	0.000501	NA	UniRef90_A0A0C3P2T4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P2T4_PHLGI	NA
c2432_g1_i1	-4.38308	9.329374	1.16E-05	0.00098	RecName: Full=Probable endo-beta-1,4-glucanase D; Short=Endoglucanase D; AltName: Full=Carboxymethylcellulase D;	NA	NA

					AltName: Full=Cellulase D; Flags: Precursor [Aspergillus niger CBS 513.88]		
c8937_g2_i1	-4.36933	2.684709	8.35E-11	4.29E-08	NA	NA	NA
c13426_g3_i1	-4.30029	4.57929	2.38E-08	6.40E-06	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]	NA	GO:0004190|GO:0006508
c5699_g1_i1	-4.28134	0.990603	2.94E-06	0.000321	NA	NA	NA
c10012_g2_i1	-4.27577	2.038776	1.04E-06	0.000145	RecName: Full=Exoglucanase 1; AltName: Full=1,4-beta-cellobiohydrolase; AltName: Full=Exocellobiohydrolase I; Short=CBHI; AltName: Full=Exoglucanase I; Flags: Precursor [Trichoderma harzianum]	UniRef90_Q66NB8 Cellulose binding iron reductase n=2 Tax=Phanerochaete chrysosporium RepID=Q66NB8_PHACH	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c17406_g4_i1	-4.26399	6.861	1.21E-15	2.22E-12	NA	NA	GO:0005199|GO:0009277
c17406_g4_i2	-4.26399	6.861	1.21E-15	2.22E-12	NA	NA	NA
c17406_g4_i3	-4.26399	6.861	1.21E-15	2.22E-12	NA	NA	NA
c17406_g4_i4	-4.26399	6.861	1.21E-15	2.22E-12	NA	NA	NA
c1515_g1_i1	-4.23401	2.976196	6.47E-05	0.003786	NA	NA	NA
c1515_g1_i2	-4.23401	2.976196	6.47E-05	0.003786	NA	NA	NA
c12820_g1_i1	-4.15476	7.100007	1.21E-10	5.81E-08	NA	UniRef90_A0A067ML58 Uncharacterized protein n=1 Tax=Botryobasidium botryosum FD-172 SS1 RepID=A0A067ML58_9HOMO	NA
c12832_g1_i1	-4.11515	7.832609	1.69E-14	2.57E-11	NA	UniRef90_C0KTY1 Hydrophobin n=3 Tax=Phlebiopsis gigantea RepID=C0KTY1_PHLGI	GO:0005199|GO:0009277
c12832_g2_i1	-4.04341	7.873079	4.61E-06	0.00047	RecName: Full=Fruiting body protein SC3; AltName: Full=Hydrophobin SC3; Flags: Precursor [Schizophyllum commune]	UniRef90_UPI00044110EA fungal hydrophobin n=1 Tax=Dichomitus squalens (strain LYAD-421) RepID=UPI00044110EA	GO:0005199|GO:0009277
c4493_g1_i1	-4.04297	0.82707	3.09E-05	0.002127	NA	NA	NA
c6813_g1_i1	-4.03896	4.27214	5.67E-14	6.83E-11	NA	NA	NA
c7352_g1_i1	-4.01232	0.798148	1.96E-04	8.59E-03	NA	NA	NA

c10012_g1_i1	-4.00115	6.449325	2.53E-08	6.75E-06	RecName: Full=Cellobiose dehydrogenase; Short=CDH; AltName: Full=Cellobiose-quinone oxidoreductase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_Q66NB8 Cellulose binding iron reductase n=2 Tax=Phanerochaete chrysosporium RepID=Q66NB8_PHACH	NA
c2784_g1_i1	-3.98827	6.702365	1.34E-06	0.000172	RecName: Full=Aldose 1-epimerase; AltName: Full=Galactose mutarotase [Sus scrofa]	NA	GO:0005975|GO:0016853
c14602_g1_i1	-3.91836	7.050269	1.01E-12	1.01E-09	RecName: Full=Oxalate decarboxylase OxdC [Bacillus subtilis subsp. subtilis str. 168]	UniRef90_A0A0C3NZZ2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NZZ2_PHLGI	GO:0045735
c11799_g3_i1	-3.8897	8.203554	2.60E-09	9.10E-07	NA	NA	NA
c10012_g3_i1	-3.80124	5.081266	7.81E-07	0.000114	RecName: Full=Cellobiose dehydrogenase; Short=CDH; AltName: Full=Cellobiose-quinone oxidoreductase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_Q66NB8 Cellulose binding iron reductase n=2 Tax=Phanerochaete chrysosporium RepID=Q66NB8_PHACH	NA
c11131_g2_i1	-3.77679	2.73333	1.31E-06	0.00017	NA	NA	NA
c11799_g1_i1	-3.75673	8.281788	6.63E-09	2.09E-06	NA	NA	NA
c17009_g4_i1	-3.75602	3.865326	9.45E-11	4.66E-08	RecName: Full=Endo-1,4-beta-xylanase C; Short=Xylanase C; AltName: Full=1,4-beta-D-xylan xylanohydrolase C; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004553|GO:0005975
c2432_g2_i1	-3.75086	7.583742	9.07E-05	0.004879	RecName: Full=Probable 1,4-beta-D-glucan cellobiohydrolase B; AltName: Full=Beta-glucancellobiohydrolase B; AltName: Full=Exocellobiohydrolase B; AltName: Full=Exoglucanase B; Flags: Precursor [Aspergillus fumigatus Af293]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c17724_g1_i1	-3.74565	0.641639	2.36E-04	0.009881	NA	NA	NA
c26145_g1_i1	-3.70366	8.05957	7.51E-05	0.004201	RecName: Full=Para-nitrobenzyl esterase; AltName: Full=Intracellular esterase B; AltName: Full=PNB carboxy-esterase; Short=PNBCE [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0008152|GO:0016787
c17189_g3_i1	-3.62885	5.186541	5.59E-07	8.73E-05	NA	NA	NA
c17856_g1_i1	-3.62834	8.290953	2.57E-12	2.09E-09	RecName: Full=Allergen Asp f 7; AltName: Allergen=Asp f 7; Flags: Precursor [Aspergillus fumigatus Af293]	UniRef90_K5WQU9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQU9_PHACS	NA
c10106_g1_i1	-3.60879	0.564085	8.66E-04	0.026767	NA	NA	NA
c24668_g1_i1	-3.60639	3.109851	0.000842	0.026129	NA	NA	NA
c17009_g5_i1	-3.59002	4.188504	1.77E-11	1.07E-08	NA	NA	NA
c7348_g1_i1	-3.57222	1.456131	4.41E-07	7.37E-05	NA	NA	NA

c7348_g1_i2	-3.57222	1.456131	4.41E-07	7.37E-05	NA	NA	NA
c25333_g1_i1	-3.54621	5.531599	6.61E-16	1.28E-12	NA	NA	NA
c24512_g1_i1	-3.53259	10.57665	6.35E-09	2.04E-06	RecName: Full=Nuclease S1; AltName: Full=Deoxyribonuclease S1; AltName: Full=Endonuclease S1; AltName: Full=Single-stranded-nucleate endonuclease; Flags: Precursor [Aspergillus oryzae RIB40]	NA	GO:0003676|GO:0004519|GO:0006308
c3312_g1_i1	-3.53166	4.611032	5.08E-10	2.16E-07	NA	NA	NA
c14217_g3_i1	-3.52777	1.041492	9.71E-05	0.005178	NA	NA	NA
c13078_g3_i1	-3.51914	5.013967	1.26E-13	1.38E-10	NA	NA	NA
c19343_g1_i1	-3.51503	7.106234	7.65E-08	1.65E-05	NA	NA	NA
c5058_g1_i1	-3.51022	1.974942	4.42E-07	7.37E-05	NA	UniRef90_A0A0C3PR69 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PR69_PHLGI	GO:0008080
c5058_g1_i2	-3.51022	1.974942	4.42E-07	7.37E-05	NA	NA	NA
c13428_g3_i1	-3.50428	0.513094	0.001073	0.031527	NA	NA	NA
c5695_g1_i1	-3.49778	0.502399	0.000673	0.021932	NA	NA	NA
c16657_g1_i1	-3.47897	3.324411	5.41E-08	1.23E-05	NA	NA	NA
c2784_g2_i1	-3.47535	7.417396	4.76E-06	4.81E-04	RecName: Full=Aldose 1-epimerase; AltName: Full=Galactose mutarotase; AltName: Full=Type-1 mutarotase [Escherichia coli K-12]	NA	GO:0005975|GO:0016853
c11799_g2_i1	-3.4639	6.987342	9.43E-08	1.93E-05	NA	NA	NA
c14109_g2_i1	-3.43342	3.43586	4.28E-11	2.38E-08	NA	NA	NA
c17245_g7_i1	-3.41524	1.349434	2.09E-06	0.000241	NA	NA	NA
c2666_g1_i1	-3.4004	0.449184	0.001262	0.035246	NA	NA	NA
c11799_g4_i1	-3.38282	7.124023	3.24E-06	0.000347	NA	NA	NA
c13650_g1_i1	-3.37363	2.21909	1.67E-06	0.000204	NA	NA	NA
c16619_g3_i1	-3.33961	2.378776	6.98E-07	0.000105	NA	NA	NA
c8661_g1_i1	-3.33529	1.596412	8.78E-07	0.000126	NA	NA	NA
c8661_g1_i2	-3.33529	1.596412	8.78E-07	0.000126	NA	NA	NA
c8661_g1_i3	-3.33529	1.596412	8.78E-07	0.000126	NA	NA	NA
c14072_g1_i1	-3.30414	2.068573	0.000113	0.005768	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A;	NA	GO:0004190|GO:0006508

					Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]		
c1287_g2_i1	-3.2401	6.003488	4.83E-05	0.003021	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c4583_g1_i1	-3.21442	5.843475	5.63E-11	3.08E-08	NA	NA	NA
c5020_g1_i1	-3.21351	1.203369	7.51E-05	0.004201	NA	NA	NA
c5020_g1_i2	-3.21351	1.203369	7.51E-05	0.004201	NA	NA	NA
c768_g1_i1	-3.20951	2.675616	3.16E-08	8.07E-06	NA	NA	NA
c17471_g1_i1	-3.19977	4.532816	4.80E-08	1.11E-05	NA	NA	NA
c17471_g1_i2	-3.19977	4.532816	4.80E-08	1.11E-05	NA	NA	NA
c17471_g1_i3	-3.19977	4.532816	4.80E-08	1.11E-05	NA	NA	NA
c17471_g1_i4	-3.19977	4.532816	4.80E-08	1.11E-05	NA	NA	NA
c17497_g3_i1	-3.19892	3.990723	1.13E-07	2.27E-05	NA	NA	NA
c25334_g1_i1	-3.18662	4.904779	6.80E-11	3.66E-08	NA	NA	NA
c20359_g1_i1	-3.17112	1.470435	0.00017	0.007681	NA	NA	NA
c2716_g1_i1	-3.16871	2.506233	2.28E-05	0.001687	NA	NA	NA
c22035_g1_i1	-3.16009	1.459921	1.01E-05	0.000886	NA	NA	NA
c11983_g1_i1	-3.15238	2.749731	4.05E-07	6.84E-05	NA	NA	GO:0005199|GO:0009277
c11983_g1_i2	-3.15238	2.749731	4.05E-07	6.84E-05	NA	NA	GO:0005199|GO:0009277
c11983_g1_i3	-3.15238	2.749731	4.05E-07	6.84E-05	NA	NA	GO:0005199|GO:0009277
c19693_g1_i1	-3.1423	5.329275	7.01E-06	6.57E-04	NA	NA	NA
c270_g1_i1	-3.13644	2.985239	3.98E-07	6.79E-05	NA	NA	NA
c11327_g1_i1	-3.12388	3.505053	3.26E-08	8.18E-06	RecName: Full=Cystathionine gamma-lyase; AltName: Full=Gamma-cystathionase [Dictyostelium discoideum]	NA	GO:0030170
c20360_g1_i1	-3.11327	3.852582	1.74E-10	8.10E-08	NA	NA	NA
c2628_g1_i1	-3.10729	3.900175	3.22E-11	1.85E-08	NA	NA	NA
c2628_g1_i2	-3.10729	3.900175	3.22E-11	1.85E-08	NA	NA	NA
c26256_g1_i1	-3.0924	1.127404	2.85E-05	0.001999	NA	NA	NA

c11564_g1_i1	-3.07333	1.123763	0.001723	0.043684	RecName: Full=Glutathione S-transferase PM239X14; AltName: Full=GST class-phi [Arabidopsis thaliana]	NA	GO:0005515
c2810_g1_i1	-3.05095	9.884024	6.89E-08	1.51E-05	NA	NA	NA
c11686_g1_i1	-3.04805	6.311251	0.000153	0.00715	NA	NA	NA
c17561_g3_i1	-3.01405	5.280308	5.22E-10	2.20E-07	RecName: Full=Small heat shock protein C4 [Rickettsia felis URRWXCal2]	UniRef90_K5WAF9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAF9_PHACS	NA
c24599_g1_i1	-3.00018	7.775745	3.94E-05	0.002567	RecName: Full=Aflatoxin B1 aldehyde reductase member 4; AltName: Full=AFB1 aldehyde reductase 3; Short=AFB1-AR 3; AltName: Full=Aldoketoreductase 7-like [Homo sapiens]	NA	NA
c9330_g1_i1	-2.99974	4.76608	7.87E-08	1.66E-05	RecName: Full=Aldehyde dehydrogenase; Short=ALDDH; Short=ALDH [Agaricus bisporus]	UniRef90_K5W5U6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5U6_PHACS	GO:0008152|GO:0016491|GO:0055114
c9330_g1_i2	-2.99974	4.76608	7.87E-08	1.66E-05	NA	NA	GO:0008152|GO:0016491|GO:0055114
c17659_g4_i1	-2.99952	5.28998	3.84E-05	0.002531	NA	UniRef90_K5WL35 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WL35_PHACS	NA
c13710_g1_i1	-2.98756	3.585718	0.00049	0.017237	NA	NA	GO:0004553|GO:0005975
c13710_g1_i2	-2.98756	3.585718	0.00049	0.017237	RecName: Full=Probable arabinan endo-1,5-alpha-L-arabinosidase A; AltName: Full=Endo-1,5-alpha-L-arabinanase A; Short=ABN A; Flags: Precursor [Aspergillus niger CBS 513.88]	NA	GO:0004553|GO:0005975
c13710_g1_i3	-2.98756	3.585718	4.90E-04	0.017237	NA	NA	GO:0004553|GO:0005975
c27585_g1_i1	-2.98187	0.701828	0.001446	0.039006	NA	NA	NA
c357_g2_i1	-2.97519	0.703128	1.77E-03	4.44E-02	NA	NA	NA
c25755_g1_i1	-2.96997	1.540888	1.56E-03	4.10E-02	NA	NA	NA
c1486_g1_i1	-2.94763	2.113063	0.000147	0.006924	NA	NA	NA
c1486_g1_i2	-2.94763	2.113063	0.000147	0.006924	NA	NA	NA
c9122_g2_i1	-2.93881	6.769295	4.31E-05	2.73E-03	NA	NA	NA
c14015_g1_i1	-2.93857	3.679347	7.27E-05	0.004129	RecName: Full=Probable endo-beta-1,4-glucanase D; Short=Endoglucanase D; AltName: Full=Carboxymethylcellulase D;	NA	NA

					AltName: Full=Cellulase D; Flags: Precursor [Aspergillus terreus NIH2624]		
c12882_g1_i1	-2.92606	1.024961	2.71E-04	0.011034	NA	NA	NA
c24721_g1_i1	-2.91902	1.521098	5.85E-06	0.000573	NA	NA	NA
c17952_g1_i1	-2.89891	3.694363	3.04E-11	1.77E-08	NA	UniRef90_UPI0004622054 hypothetical protein TRAVEDRAFT_24130 n=1 Tax=Trametes versicolor (strain FP-101664) RepID=UPI0004622054	NA
c16481_g2_i1	-2.89675	1.885861	0.001169	0.033482	NA	UniRef90_A0A060SDE2 Glycoside Hydrolase Family 131 protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060SDE2_PYCCI	NA
c9469_g1_i1	-2.88764	2.025524	1.82E-05	1.41E-03	NA	NA	NA
c9469_g1_i2	-2.88764	2.025524	1.82E-05	0.001409	NA	NA	NA
c17546_g3_i1	-2.88326	2.548369	5.06E-06	0.000504	RecName: Full=Lipase 1; Flags: Precursor [Candida rugosa]	UniRef90_K5WPW0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WPW0_PHACS	GO:0008152|GO:0016787
c11447_g1_i1	-2.88121	1.50899	1.01E-04	0.005335	NA	NA	NA
c17579_g1_i1	-2.87888	4.445533	3.24E-08	8.18E-06	NA	NA	NA
c17579_g1_i2	-2.87888	4.445533	3.24E-08	8.18E-06	NA	NA	NA
c1634_g1_i1	-2.87128	4.006363	1.18E-05	0.000989	NA	NA	NA
c21277_g1_i1	-2.86592	5.774323	2.93E-07	5.20E-05	RecName: Full=WSC domain-containing protein 2 [Danio rerio]	NA	NA
c17491_g2_i1	-2.86418	2.158892	1.82E-06	0.00022	NA	NA	NA
c17491_g2_i2	-2.86418	2.158892	1.82E-06	2.20E-04	NA	NA	NA
c16434_g2_i1	-2.86274	0.978296	0.000315	0.012335	NA	NA	NA
c16434_g2_i2	-2.86274	0.978296	0.000315	0.012335	NA	NA	NA
c21392_g1_i1	-2.86166	6.69255	2.24E-06	0.000256	NA	NA	NA
c13494_g1_i1	-2.85733	4.70942	6.07E-07	9.32E-05	NA	NA	NA
c13494_g1_i2	-2.85733	4.70942	6.07E-07	9.32E-05	NA	NA	NA
c15489_g1_i1	-2.84293	5.719333	2.48E-06	0.000278	NA	NA	NA
c15489_g1_i2	-2.84293	5.719333	2.48E-06	0.000278	NA	NA	NA
c15489_g1_i3	-2.84293	5.719333	2.48E-06	0.000278	NA	NA	NA
c17357_g3_i1	-2.82523	3.725226	0.000288	0.011519	NA	NA	NA

c17497_g2_i1	-2.81102	3.247737	7.27E-06	0.000676	NA	NA	NA
c17497_g2_i2	-2.81102	3.247737	7.27E-06	0.000676	NA	NA	NA
c9706_g1_i1	-2.8094	2.89989	2.19E-08	6.03E-06	NA	UniRef90_K5W9P2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W9P2_PHACS	NA
c26380_g1_i1	-2.80401	0.947564	0.000347	0.01317	NA	NA	NA
c13225_g1_i1	-2.79884	1.424157	0.000484	0.017091	NA	NA	NA
c13225_g1_i2	-2.79884	1.424157	0.000484	0.017091	NA	NA	NA
c483_g1_i1	-2.79826	6.814845	0.000872	0.026883	NA	UniRef90_A0A0C3S1L8 Carbohydrate-binding module family 13 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S1L8_PHLGI	NA
c19694_g1_i1	-2.79424	7.252752	2.09E-07	3.86E-05	RecName: Full=Oxalate decarboxylase OxdC [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0045735
c15484_g2_i1	-2.79372	3.916887	1.04E-05	0.000904	RecName: Full=Arabinogalactan endo-beta-1,4-galactanase; AltName: Full=Endo-1,4-beta-galactanase; Short=Galactanase [Humicola insolens]	NA	GO:0015926
c15484_g2_i2	-2.79372	3.916887	1.04E-05	0.000904	NA	NA	GO:0015926
c17491_g1_i1	-2.7742	4.821233	1.64E-07	3.10E-05	NA	NA	NA
c17491_g1_i2	-2.7742	4.821233	1.64E-07	3.10E-05	NA	NA	NA
c17491_g1_i3	-2.7742	4.821233	1.64E-07	3.10E-05	NA	NA	NA
c23704_g1_i1	-2.77127	5.709991	6.20E-07	9.47E-05	RecName: Full=Aldehyde dehydrogenase; Short=ALDDH; Short=ALDH [Agaricus bisporus]	NA	GO:0008152|GO:0016491|GO:0055114
c14668_g1_i1	-2.7699	1.948396	6.50E-05	0.003792	RecName: Full=Zinc-binding alcohol dehydrogenase domain-containing protein cipB; AltName: Full=Concanamycin-induced protein B [Aspergillus nidulans FGSC A4]	UniRef90_K5WGV0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGV0_PHACS	GO:0016491|GO:0055114
c14668_g1_i2	-2.7699	1.948396	6.50E-05	0.003792	NA	NA	GO:0016491|GO:0055114
c11162_g1_i1	-2.76948	0.916388	0.000826	0.025808	NA	NA	NA
c11162_g1_i2	-2.76948	0.916388	0.000826	0.025808	NA	NA	NA
c24511_g1_i1	-2.76776	9.60526	3.98E-12	2.96E-09	RecName: Full=Probable 2-oxoglutarate-dependent dioxygenase At3g49630 [Arabidopsis thaliana]	NA	GO:0016491|GO:0016706|GO:0055114

c16463_g3_i1	-2.76629	3.322084	6.89E-09	2.15E-06	NA	UniRef90_K5VVY4 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVY4_PHACS	GO:0004659|GO:0016021
c16463_g3_i2	-2.76629	3.322084	6.89E-09	2.15E-06	NA	NA	GO:0004659|GO:0016021
c17113_g2_i1	-2.7599	7.528184	2.47E-09	8.71E-07	NA	NA	NA
c23847_g1_i1	-2.75279	1.941368	5.57E-06	5.50E-04	NA	NA	NA
c22280_g1_i1	-2.74889	0.91552	0.000597	0.020096	NA	NA	NA
c791_g1_i1	-2.74824	3.228805	0.000228	0.009631	RecName: Full=Probable ATP-dependent RNA helicase kurz [Drosophila melanogaster]	UniRef90_K5VCV6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCV6_PHACS	NA
c710_g2_i1	-2.74641	7.765741	4.50E-04	0.016189	RecName: Full=Cellulose-growth-specific protein; Flags: Precursor [Agaricus bisporus]	UniRef90_A0A060SY86 Auxilliary Activities Family 9 / Carbohydrate-Binding Module Family 1 protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060SY86_PYCCI	NA
c21985_g1_i1	-2.72508	5.30499	9.46E-10	3.71E-07	NA	NA	NA
c22310_g1_i1	-2.71768	4.390681	1.41E-09	5.20E-07	NA	UniRef90_K5WKN9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKN9_PHACS	NA
c17009_g1_i1	-2.70995	2.831765	3.34E-06	0.000355	RecName: Full=Endo-1,4-beta-xylanase C; Short=Xylanase C; AltName: Full=1,4-beta-D-xylan xylanohydrolase C; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004553|GO:0005975
c16240_g2_i1	-2.7091	4.585957	4.91E-08	1.13E-05	NA	UniRef90_B8PJD8 Predicted protein n=1 Tax=Postia placenta (strain ATCC 44394 / Madison 698-R) RepID=B8PJD8_POSPM	NA
c16240_g2_i2	-2.7091	4.585957	4.91E-08	1.13E-05	NA	NA	NA
c15587_g3_i1	-2.70871	4.529918	1.93E-06	0.000229	NA	NA	NA
c15587_g3_i2	-2.70871	4.529918	1.93E-06	0.000229	NA	NA	NA
c17220_g1_i1	-2.68763	5.270916	7.14E-09	2.19E-06	NA	NA	NA
c17220_g1_i2	-2.68763	5.270916	7.14E-09	2.19E-06	NA	NA	NA
c17220_g1_i3	-2.68763	5.270916	7.14E-09	2.19E-06	NA	NA	NA
c17220_g1_i4	-2.68763	5.270916	7.14E-09	2.19E-06	NA	NA	NA
c17220_g1_i5	-2.68763	5.270916	7.14E-09	2.19E-06	NA	NA	NA

c17220_g1_i6	-2.68763	5.270916	7.14E-09	2.19E-06	NA	NA	NA
c8793_g1_i1	-2.68681	2.137538	2.66E-06	2.94E-04	NA	NA	NA
c8793_g1_i2	-2.68681	2.137538	2.66E-06	0.000294	NA	NA	NA
c8793_g1_i3	-2.68681	2.137538	2.66E-06	0.000294	NA	NA	NA
c24658_g1_i1	-2.68598	0.867924	0.000755	0.023984	NA	NA	NA
c2878_g1_i1	-2.68526	7.362862	4.94E-05	0.003073	RecName: Full=Major facilitator superfamily domain-containing protein 1 [Danio rerio]	NA	GO:0016021|GO:0055085
c17176_g1_i1	-2.65656	8.384528	1.81E-09	6.59E-07	NA	NA	NA
c17176_g1_i2	-2.65656	8.384528	1.81E-09	6.59E-07	NA	NA	NA
c17176_g1_i3	-2.65656	8.384528	1.81E-09	6.59E-07	NA	NA	NA
c17176_g1_i4	-2.65656	8.384528	1.81E-09	6.59E-07	NA	NA	NA
c14602_g2_i1	-2.65619	1.128986	0.001806	0.045181	NA	NA	NA
c776_g1_i1	-2.65075	5.567703	1.21E-06	0.000161	NA	NA	NA
c14072_g2_i1	-2.64418	2.369657	1.84E-05	0.001424	NA	NA	GO:0004190|GO:0006508
c14072_g2_i2	-2.64418	2.369657	1.84E-05	0.001424	NA	NA	GO:0004190|GO:0006508
c17459_g1_i1	-2.63992	3.818276	5.74E-08	1.29E-05	NA	NA	NA
c17459_g1_i2	-2.63992	3.818276	5.74E-08	1.29E-05	NA	NA	NA
c4420_g1_i1	-2.63737	2.220682	1.18E-03	3.37E-02	NA	NA	NA
c4420_g1_i2	-2.63737	2.220682	0.00118	0.033662	NA	NA	NA
c12120_g1_i1	-2.63224	5.279133	9.98E-05	0.0053	RecName: Full=Alpha-L-arabinofuranosidase A; Short=ABF A; Short=Arabinosidase A; AltName: Full=Arabinoxylan-arabinofuranohydrolase of 70 kDa; Short=AF-70; Flags: Precursor [Penicillium canescens]	NA	GO:0016798
c220_g1_i1	-2.62044	6.314322	0.000877	0.026968	NA	NA	NA
c220_g1_i2	-2.62044	6.314322	0.000877	0.026968	NA	NA	NA
c17471_g2_i1	-2.6121	3.001762	3.90E-05	0.00255	NA	NA	NA
c14867_g1_i1	-2.61115	2.297593	1.49E-06	0.000187	NA	NA	NA
c14867_g1_i2	-2.61115	2.297593	1.49E-06	0.000187	NA	NA	NA
c14867_g1_i3	-2.61115	2.297593	1.49E-06	0.000187	NA	NA	NA
c17610_g1_i1	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA

c17610_g1_i10	-2.61087	4.656163	3.42E-09	1.16E-06	NA	UniRef90_A0A0C3P027 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P027_PHLGI	NA
c17610_g1_i2	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA
c17610_g1_i3	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA
c17610_g1_i4	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA
c17610_g1_i5	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA
c17610_g1_i6	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA
c17610_g1_i7	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA
c17610_g1_i8	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA
c17610_g1_i9	-2.61087	4.656163	3.42E-09	1.16E-06	NA	NA	NA
c10309_g1_i1	-2.60118	6.374199	4.04E-06	0.000415	NA	NA	NA
c10309_g1_i2	-2.60118	6.374199	4.04E-06	0.000415	RecName: Full=4-O-methyl-glucuronoyl methylesterase; AltName: Full=Glucuronoyl esterase 2; Short=GE2; Flags: Precursor [Trichoderma reesei QM6a]	NA	Nc10310_g4_i1
c27047_g1_i1	-2.59572	5.391852	1.47E-05	0.001187	NA	NA	NA
c18586_g1_i1	-2.58715	1.49346	0.000131	0.006379	NA	NA	NA
c19849_g1_i1	-2.58249	3.365249	1.76E-05	0.001374	RecName: Full=Uncharacterized transporter C3H1.06c [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0022857|GO:0055085
c9469_g2_i1	-2.56987	6.045746	1.57E-06	0.000196	RecName: Full=Translation initiation factor IF-2 [Desulfitobacterium hafniense Y51]	UniRef90_K5WUJ9 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WUJ9_PHACS	NA
c16685_g2_i1	-2.56689	6.674697	1.25E-04	0.006209	NA	NA	NA
c17053_g2_i1	-2.56402	4.914173	3.90E-05	0.00255	NA	NA	NA
c17053_g2_i2	-2.56402	4.914173	3.90E-05	0.00255	NA	NA	NA
c17053_g2_i3	-2.56402	4.914173	3.90E-05	0.00255	NA	NA	NA
c15230_g1_i1	-2.56265	3.495506	3.86E-06	0.0004	NA	NA	NA
c19194_g1_i1	-2.56237	1.469424	3.18E-05	2.18E-03	NA	NA	NA
c16619_g1_i1	-2.55695	3.61391	1.08E-06	0.000149	NA	NA	NA
c13807_g3_i1	-2.55467	1.049404	0.000545	0.018785	NA	NA	NA
c18567_g1_i1	-2.54729	4.64314	3.59E-08	8.77E-06	RecName: Full=Exoglucanase 1; AltName: Full=1,4-beta-cellobiohydrolase; AltName: Full=Exocellobiohydrolase I;	NA	GO:0004553|GO:0005975

					AltName: Full=Exoglucanase I; Flags: Precursor [Phanerochaete chrysosporium]		
c12236_g1_i1	-2.54036	2.526901	2.07E-06	0.00024	NA	UniRef90_A0A0C3P2T4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P2T4_PHLGI	NA
c14593_g1_i1	-2.54	2.421002	0.00018	0.008005	NA	NA	NA
c14593_g1_i2	-2.54	2.421002	0.00018	0.008005	NA	UniRef90_K5V4W2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V4W2_PHACS	NA
c14593_g1_i3	-2.54	2.421002	0.00018	0.008005	NA	NA	NA
c6767_g1_i1	-2.53935	0.786295	1.64E-03	0.042276	NA	NA	NA
c11327_g2_i1	-2.532	4.120152	5.05E-06	0.000504	RecName: Full=Cystathionine gamma-lyase; AltName: Full=Cysteine-protein sulfhydrase; AltName: Full=Gamma-cystathionase [Homo sapiens]	NA	GO:0030170
c10797_g1_i1	-2.53107	5.586849	6.83E-05	0.003947	RecName: Full=WSC domain-containing protein 2 [Danio rerio]	NA	NA
c824_g1_i1	-2.52864	2.523532	4.38E-08	1.05E-05	RecName: Full=Mycosubtilin synthase subunit B; Includes: RecName: Full=ATP-dependent tyrosine adenylase; Short=TyrA; AltName: Full=Tyrosine activase; Includes: RecName: Full=ATP-dependent asparagine adenylase 2; Short=AsnA 2; AltName: Full=Asparagine activase 2; Includes: RecName: Full=ATP-dependent glutamine adenylase; Short=GlnA; AltName: Full=Glutamine activase; Includes: RecName: Full=ATP-dependent proline adenylase; Short=ProA; AltName: Full=Proline activase [Bacillus subtilis]	UniRef90_K5VZI9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZI9_PHACS	GO:0003824|GO:0008152
c731_g1_i1	-2.52319	2.909453	2.40E-07	4.37E-05	NA	NA	NA
c731_g1_i2	-2.52319	2.909453	2.40E-07	4.37E-05	NA	NA	GO:0005515
c17053_g4_i1	-2.51868	5.084956	3.41E-05	0.002295	NA	NA	NA
c17053_g4_i2	-2.51868	5.084956	3.41E-05	0.002295	NA	NA	NA
c17053_g4_i3	-2.51868	5.084956	3.41E-05	0.002295	NA	NA	NA
c27084_g1_i1	-2.51711	1.255611	0.000395	0.014606	NA	NA	NA
c5348_g1_i1	-2.51455	1.259161	0.000218	0.009329	NA	NA	NA
c5348_g1_i2	-2.51455	1.259161	0.000218	0.009329	NA	NA	NA

c17497_g1_i1	-2.50206	5.178287	3.47E-06	0.000367	NA	NA	NA
c17497_g1_i2	-2.50206	5.178287	3.47E-06	0.000367	NA	NA	NA
c18069_g1_i1	-2.50174	1.444936	5.10E-04	0.017783	NA	NA	NA
c16328_g2_i1	-2.49929	2.013869	1.55E-05	0.001237	NA	UniRef90_K5VRS8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRS8_PHACS	NA
c16328_g2_i2	-2.49929	2.013869	1.55E-05	0.001237	NA	NA	NA
c12787_g2_i1	-2.48933	4.552552	2.18E-05	0.001622	RecName: Full=Rhamnogalacturonase A; Short=RGase A; Short=RHG A; AltName: Full=Rhamnogalacturonan hydrolase A; Flags: Precursor [Aspergillus aculeatus]	UniRef90_K5VC60 Glycoside hydrolase family 28 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VC60_PHACS	GO:0004553|GO:0004650|GO:0005576|GO:0005975|GO:0030248
c270_g2_i1	-2.48822	5.279012	2.92E-05	0.00204	NA	NA	NA
c24722_g1_i1	-2.4869	1.979894	3.48E-04	0.013205	NA	NA	NA
c157_g1_i1	-2.4788	3.374657	1.44E-07	2.77E-05	NA	NA	NA
c16682_g1_i1	-2.47275	7.738752	6.31E-05	0.00372	RecName: Full=Lipase; AltName: Full=Triacylglycerol lipase; Flags: Precursor [Thermomyces lanuginosus]	NA	GO:0006629
c16902_g1_i1	-2.47198	5.474355	1.32E-06	0.00017	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c16902_g1_i2	-2.47198	5.474355	1.32E-06	0.00017	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c13426_g1_i1	-2.46583	4.499589	6.98E-06	0.000657	NA	NA	NA
c13426_g1_i2	-2.46583	4.499589	6.98E-06	0.000657	NA	NA	NA
c13426_g1_i3	-2.46583	4.499589	6.98E-06	0.000657	NA	NA	NA
c13426_g1_i4	-2.46583	4.499589	6.98E-06	0.000657	NA	NA	NA
c16948_g1_i1	-2.46269	4.433358	5.09E-07	8.21E-05	NA	NA	NA
c16948_g1_i2	-2.46269	4.433358	5.09E-07	8.21E-05	NA	NA	NA
c1866_g1_i1	-2.45217	1.582636	0.000296	0.011746	NA	NA	NA
c1866_g1_i2	-2.45217	1.582636	0.000296	0.011746	NA	NA	NA
c15824_g1_i1	-2.45144	1.740834	0.000629	0.020921	NA	NA	NA
c3033_g1_i1	-2.44827	5.498231	1.38E-06	0.000176	NA	NA	NA

c14506_g3_i1	-2.44158	2.48677	0.000165	0.007501	RecName: Full=Negative regulator of sexual conjugation and meiosis [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3S9M2 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S9M2_PHLGI	GO:0004672|GO:0005524|GO:0006468
c14506_g3_i2	-2.44158	2.48677	0.000165	0.007501	NA	NA	GO:0004672|GO:0005524|GO:0006468
c17336_g1_i1	-2.44071	4.301494	7.59E-05	0.004235	NA	NA	GO:0004719|GO:0006464|GO:0008152|GO:0008168|GO:0008171|GO:0008610
c17336_g1_i2	-2.44071	4.301494	7.59E-05	0.004235	RecName: Full=Sterol 24-C-methyltransferase; AltName: Full=Delta(24)-sterol C-methyltransferase [Debaryomyces hansenii CBS767]	NA	GO:0004719|GO:0006464|GO:0008152|GO:0008168|GO:0008171|GO:0008610
c17336_g1_i3	-2.44071	4.301494	7.59E-05	0.004235	NA	NA	GO:0004719|GO:0006464|GO:0008168|GO:0008610
c17336_g1_i4	-2.44071	4.301494	7.59E-05	0.004235	NA	NA	NA
c17336_g1_i5	-2.44071	4.301494	7.59E-05	0.004235	NA	NA	GO:0004719|GO:0006464|GO:0008152|GO:0008168|GO:0008171|GO:0008610
c9687_g1_i1	-2.43612	2.380061	2.07E-05	0.001568	NA	NA	NA
c9687_g1_i2	-2.43612	2.380061	2.07E-05	0.001568	NA	NA	NA
c19266_g1_i1	-2.43426	0.986169	8.25E-04	0.025808	NA	NA	NA
c12798_g1_i1	-2.43132	8.017092	1.56E-05	0.001249	RecName: Full=Spherulin-1A; Flags: Precursor [Physarum polycephalum]	UniRef90_A0A0C3PT82 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PT82_PHLGI	GO:0045735
c12798_g1_i2	-2.43132	8.017092	1.56E-05	0.001249	NA	NA	GO:0045735
c12414_g1_i1	-2.4288	6.263397	1.42E-06	0.000179	RecName: Full=Probable mitochondrial chaperone BCS1-B; AltName: Full=BCS1-like protein 2 [Dictyostelium discoideum]	UniRef90_K5VUW8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUW8_PHACS	NA
c12414_g1_i2	-2.4288	6.263397	1.42E-06	0.000179	NA	NA	NA
c273_g1_i1	-2.42796	6.368952	8.14E-10	3.23E-07	NA	NA	NA

c273_g1_i2	-2.42796	6.368952	8.14E-10	3.23E-07	NA	UniRef90_K5WUG7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WUG7_PHACS	NA
c22775_g1_i1	-2.41936	4.981624	3.95E-07	6.77E-05	RecName: Full=Protein psi1; AltName: Full=Protein psi [Schizosaccharomyces pombe 972h-]	UniRef90_K5X4S7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X4S7_PHACS	NA
c5681_g1_i1	-2.41571	6.568807	1.62E-06	0.000201	NA	UniRef90_K5VLL5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VLL5_PHACS	NA
c16816_g3_i1	-2.41467	1.184119	0.00061	0.020491	NA	NA	NA
c13546_g1_i1	-2.41338	5.345343	1.20E-06	0.00016	NA	NA	NA
c13546_g1_i2	-2.41338	5.345343	1.20E-06	0.00016	NA	NA	NA
c13546_g1_i3	-2.41338	5.345343	1.20E-06	0.00016	NA	NA	NA
c27523_g1_i1	-2.41205	1.181276	0.000616	0.020677	NA	NA	NA
c24584_g1_i1	-2.41193	1.545368	1.28E-04	0.006318	NA	NA	NA
c6232_g1_i1	-2.41118	2.607074	0.000111	0.005746	NA	NA	NA
c17471_g4_i1	-2.40652	2.613588	2.30E-07	4.21E-05	NA	NA	NA
c17471_g4_i2	-2.40652	2.613588	2.30E-07	4.21E-05	NA	NA	NA
c17471_g4_i3	-2.40652	2.613588	2.30E-07	4.21E-05	NA	NA	NA
c2878_g2_i1	-2.40384	2.933317	0.000146	0.006881	NA	NA	NA
c12073_g1_i1	-2.40211	5.048297	1.25E-06	1.66E-04	RecName: Full=Sulfite efflux pump SSU1 [Arthroderma benhamiae CBS 112371]	NA	GO:0016021|GO:0055085
c24943_g1_i1	-2.40166	5.313812	2.38E-08	6.40E-06	NA	NA	NA
c7570_g1_i1	-2.40064	2.260808	1.16E-05	0.00098	NA	NA	NA
c20189_g1_i1	-2.39655	1.354835	0.000638	0.021109	NA	NA	NA
c15899_g2_i1	-2.38305	3.088736	0.000281	0.011318	NA	NA	NA
c15899_g2_i2	-2.38305	3.088736	2.81E-04	1.13E-02	NA	NA	NA
c16292_g1_i1	-2.37767	2.243737	2.93E-05	0.00204	NA	NA	NA
c16292_g1_i2	-2.37767	2.243737	2.93E-05	0.00204	NA	NA	NA
c16292_g1_i3	-2.37767	2.243737	2.93E-05	0.00204	NA	UniRef90_A0A0C3SDW4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SDW4_PHLGI	NA

c17459_g2_i1	-2.37643	4.461921	4.91E-09	1.65E-06	NA	NA	NA
c23982_g1_i1	-2.37422	1.799169	1.40E-05	1.14E-03	NA	NA	NA
c554_g1_i1	-2.36938	2.416831	3.64E-07	6.30E-05	RecName: Full=Sugar phosphatase YfbT [Escherichia coli K-12]	UniRef90_K5WNE6 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNE6_PHACS	NA
c554_g1_i2	-2.36938	2.416831	3.64E-07	6.30E-05	NA	NA	NA
c849_g1_i1	-2.36749	3.12626	2.39E-05	0.001736	NA	NA	NA
c26638_g1_i1	-2.3642	6.260061	2.88E-07	5.14E-05	NA	NA	NA
c7662_g1_i1	-2.36418	9.486204	6.50E-09	2.07E-06	RecName: Full=Peptide methionine sulfoxide reductase B2, chloroplastic; Short=AtMSRB2; AltName: Full=Peptide-methionine (R)-S-oxide reductase; Flags: Precursor [Arabidopsis thaliana]	NA	GO:0033743|GO:0055114
c15604_g3_i1	-2.35569	5.602108	7.87E-08	1.66E-05	NA	NA	NA
c17516_g3_i1	-2.35413	5.186354	4.78E-07	7.85E-05	NA	UniRef90_K5V356 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V356_PHACS	NA
c23353_g1_i1	-2.35279	3.018881	4.31E-05	0.002735	RecName: Full=Oxidoreductase AflY; AltName: Full=Aflatoxin biosynthesis protein Y [Aspergillus parasiticus]	UniRef90_K5WLS1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLS1_PHACS	NA
c12427_g2_i1	-2.34121	5.76575	0.00191	0.04692	RecName: Full=Sorbitol dehydrogenase; AltName: Full=L-iditol 2-dehydrogenase [Bombyx mori]	UniRef90_K5XEB1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XEB1_PHACS	GO:0016491|GO:0055114
c25206_g1_i1	-2.34012	3.680391	6.28E-05	0.003707	NA	NA	NA
c12521_g1_i1	-2.33731	2.543386	7.02E-07	0.000105	RecName: Full=Uncharacterized permease C29B12.14c [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3RVF3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RVF3_PHLGI	GO:0015205|GO:0015851|GO:0016020
c12521_g1_i2	-2.33731	2.543386	7.02E-07	0.000105	NA	NA	GO:0015205|GO:0015851|GO:0016020
c16749_g3_i1	-2.32995	5.728068	0.000961	0.028991	NA	NA	NA
c16749_g3_i2	-2.32995	5.728068	0.000961	0.028991	NA	NA	NA
c16749_g3_i3	-2.32995	5.728068	0.000961	0.028991	RecName: Full=Xyloglucanase; Short=XG; AltName: Full=Cel74a; Flags: Precursor [Trichoderma reesei QM6a]	NA	NA
c16749_g3_i4	-2.32995	5.728068	0.000961	0.028991	NA	NA	NA

c16120_g1_i1	-2.32458	4.283448	4.00E-07	6.79E-05	NA	NA	NA
c16120_g1_i2	-2.32458	4.283448	4.00E-07	6.79E-05	NA	NA	NA
c16120_g1_i3	-2.32458	4.283448	4.00E-07	6.79E-05	NA	NA	NA
c16120_g1_i4	-2.32458	4.283448	4.00E-07	6.79E-05	NA	NA	NA
c16748_g1_i1	-2.32435	4.776012	7.87E-09	2.37E-06	NA	NA	NA
c26637_g1_i1	-2.32351	8.834241	4.54E-08	1.06E-05	NA	NA	NA
c27239_g1_i1	-2.31849	1.120398	0.000924	0.028119	NA	NA	NA
c16618_g1_i1	-2.31831	1.628143	5.93E-05	0.003555	NA	NA	NA
c18879_g1_i1	-2.31783	4.789411	3.72E-05	0.002461	NA	NA	NA
c8742_g1_i1	-2.31647	2.942483	4.97E-05	0.003089	NA	NA	NA
c8742_g1_i2	-2.31647	2.942483	4.97E-05	0.003089	NA	NA	NA
c8742_g1_i3	-2.31647	2.942483	4.97E-05	0.003089	NA	NA	NA
c12855_g1_i1	-2.31514	1.123523	0.000652	0.021542	NA	UniRef90_K5UL39 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UL39_PHACS	NA
c12855_g1_i2	-2.31514	1.123523	0.000652	0.021542	NA	NA	NA
c9545_g3_i1	-2.29688	6.098998	0.001224	0.03458	NA	UniRef90_K5XC08 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XC08_PHACS	NA
c15561_g3_i1	-2.29525	1.109275	1.87E-03	0.046364	NA	NA	NA
c24911_g1_i1	-2.29433	3.295735	1.35E-06	0.000173	NA	NA	NA
c4758_g1_i1	-2.29426	3.227409	4.10E-05	0.002658	RecName: Full=Endo-1,4-beta-xylanase A; Short=Xylanase A; AltName: Full=1,4-beta-D-xylan xylanohydrolase A; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c8763_g1_i1	-2.28857	1.96383	5.29E-05	0.003243	RecName: Full=Glutathione reductase; Short=GR; Short=GRase [Yarrowia lipolytica CLIB122]	NA	GO:0016491|GO:0055114
c24301_g1_i1	-2.28444	1.102585	0.001709	0.043499	RecName: Full=2-deoxyglucose-6-phosphate phosphatase 2; Short=2-DOG-6-P 2; Short=2-deoxyglucose-6-phosphatase 2 [Saccharomyces cerevisiae S288c]	NA	NA
c15901_g2_i1	-2.28015	4.091532	1.04E-08	3.07E-06	NA	NA	NA
c17406_g5_i1	-2.27912	6.484097	9.22E-06	0.000829	NA	NA	GO:0005199|GO:0009277
c17406_g5_i2	-2.27912	6.484097	9.22E-06	0.000829	NA	NA	GO:0005199|GO:0009277

c14269_g2_i1	-2.27774	4.229353	6.16E-08	1.37E-05	RecName: Full=Glyoxylase B2 [Dictyostelium discoideum]	NA	NA
c10654_g4_i1	-2.27573	1.100403	0.001073	0.031527	NA	NA	NA
c16220_g1_i1	-2.27506	2.265605	2.66E-05	1.89E-03	NA	NA	NA
c16220_g1_i2	-2.27506	2.265605	2.66E-05	1.89E-03	NA	NA	NA
c2001_g1_i1	-2.27481	1.86673	0.00079	0.024873	RecName: Full=Uncharacterized protein YcaC [Escherichia coli K-12]	NA	GO:0003824|GO:0008152
c5202_g1_i1	-2.26823	2.790024	0.000106	0.005553	NA	NA	NA
c14174_g2_i1	-2.26689	10.87545	8.22E-06	0.000748	NA	NA	NA
c2603_g1_i1	-2.2641	2.057312	5.61E-05	0.003411	NA	NA	NA
c2603_g1_i2	-2.2641	2.057312	5.61E-05	0.003411	NA	NA	NA
c16051_g1_i1	-2.26108	4.672849	1.10E-06	0.00015	RecName: Full=Copper-transporting ATPase RAN1; AltName: Full=Protein HEAVY METAL ATPASE 7; AltName: Full=Protein RESPONSIVE TO ANTAGONIST 1 [Arabidopsis thaliana]	NA	GO:0030001|GO:0046872
c16051_g1_i2	-2.26108	4.672849	1.10E-06	0.00015	NA	NA	GO:0030001|GO:0046872
c17532_g5_i1	-2.25728	5.922436	4.79E-08	1.11E-05	NA	UniRef90_A0A0C3NAR3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NAR3_PHLGI	NA
c25744_g1_i1	-2.25532	1.091695	1.30E-03	3.61E-02	NA	NA	NA
c15474_g1_i1	-2.25064	3.991266	7.26E-05	0.004129	NA	NA	NA
c15474_g1_i2	-2.25064	3.991266	7.26E-05	4.13E-03	NA	NA	NA
c15610_g1_i1	-2.24012	9.800263	8.03E-08	1.68E-05	NA	NA	GO:0005515
c15610_g1_i2	-2.24012	9.800263	8.03E-08	1.68E-05	NA	NA	GO:0005515
c15610_g1_i3	-2.24012	9.800263	8.03E-08	1.68E-05	NA	NA	GO:0005515
c15610_g1_i4	-2.24012	9.800263	8.03E-08	1.68E-05	NA	NA	GO:0005515
c15610_g1_i5	-2.24012	9.800263	8.03E-08	1.68E-05	RecName: Full=Serine-threonine kinase receptor-associated protein [Gallus gallus]	NA	GO:0005515
c14511_g1_i1	-2.2349	2.735706	6.96E-05	0.003994	RecName: Full=Uncharacterized oxidoreductase C162.03 [Schizosaccharomyces pombe 972h-]	UniRef90_K5UQC9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UQC9_PHACS	GO:0003824|GO:0008152|GO:0016491|GO:0050662
c16273_g2_i1	-2.23183	1.564126	0.000215	0.009244	NA	UniRef90_K5VZ01 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZ01_PHACS	NA

c25179_g1_i1	-2.22619	2.819028	1.58E-05	0.001258	NA	NA	NA
c24912_g1_i1	-2.22484	3.595803	2.99E-08	7.72E-06	NA	NA	NA
c17193_g2_i1	-2.21506	3.666507	6.31E-06	0.000606	NA	NA	NA
c4497_g1_i1	-2.21186	1.808459	3.47E-05	0.002316	NA	NA	NA
c4497_g1_i2	-2.21186	1.808459	3.47E-05	0.002316	NA	NA	NA
c1614_g1_i1	-2.21182	1.238041	1.87E-03	0.046323	NA	NA	NA
c26495_g1_i1	-2.20886	6.255489	2.27E-07	4.19E-05	RecName: Full=ABC transporter G family member 11; Short=ABC transporter ABCG.11; Short=AtABCG11; AltName: Full=Protein CUTICULAR DEFECT AND ORGAN FUSION 1; AltName: Full=Protein DESPERADO; AltName: Full=Protein PERMEABLE LEAVES 1; AltName: Full=White-brown complex homolog protein 11; Short=AtWBC11 [Arabidopsis thaliana]	NA	GO:0016020
c24262_g1_i1	-2.20744	2.209255	0.000266	0.010891	NA	NA	NA
c3709_g1_i1	-2.20663	1.6857	0.000102	0.005354	NA	NA	NA
c3709_g1_i2	-2.20663	1.6857	1.02E-04	0.005354	NA	NA	NA
c14506_g1_i1	-2.2056	1.40127	0.001453	0.039103	NA	NA	NA
c17116_g3_i1	-2.20316	4.62861	2.36E-04	0.009881	RecName: Full=Uncharacterized transporter C1002.16c [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c12303_g4_i1	-2.19918	1.05369	0.001211	0.034235	NA	UniRef90_K5V1S2 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V1S2_PHACS	NA
c12120_g2_i1	-2.19345	6.784034	1.31E-03	3.62E-02	RecName: Full=Probable alpha-L-arabinofuranosidase A; Short=ABF A; Short=Arabinosidase A; Flags: Precursor [Aspergillus terreus NIH2624]	NA	GO:0046373|GO:0046556
c2534_g2_i1	-2.18464	7.006473	5.98E-06	5.79E-04	RecName: Full=ABC transporter G family member 12; Short=ABC transporter ABCG.12; Short=AtABCG12; AltName: Full=Protein ECERIFERUM 5; AltName: Full=White-brown complex homolog protein 12; Short=AtWBC12 [Arabidopsis thaliana]	NA	GO:0005524|GO:0016887
c21872_g1_i1	-2.1822	4.403407	1.67E-06	0.000204	RecName: Full=TPR repeat-containing protein C19B12.01 [Schizosaccharomyces pombe 972h-]	NA	GO:0005515
c16626_g1_i1	-2.17637	5.806587	7.20E-07	0.000106	NA	NA	NA
c16626_g1_i2	-2.17637	5.806587	7.20E-07	0.000106	NA	NA	NA

c16626_g1_i3	-2.17637	5.806587	7.20E-07	0.000106	NA	NA	NA
c16626_g1_i4	-2.17637	5.806587	7.20E-07	0.000106	NA	NA	NA
c16626_g1_i5	-2.17637	5.806587	7.20E-07	0.000106	NA	NA	NA
c15078_g2_i1	-2.17559	3.450687	1.21E-05	0.001009	NA	NA	NA
c7927_g1_i1	-2.17526	5.667253	3.11E-07	5.50E-05	NA	NA	NA
c10164_g1_i1	-2.17495	1.886508	0.00017	0.007681	NA	NA	NA
c10164_g1_i2	-2.17495	1.886508	0.00017	0.007681	NA	NA	NA
c3033_g2_i1	-2.17184	6.014655	2.38E-05	0.001736	NA	NA	NA
c12535_g1_i1	-2.16587	1.781973	1.41E-04	0.006714	NA	UniRef90_K5UMG5 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UMG5_PHACS	NA
c7518_g1_i1	-2.16317	1.227444	1.54E-03	0.040582	NA	NA	NA
c743_g1_i1	-2.16148	2.602839	9.61E-05	0.005131	NA	UniRef90_K5VWE0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWE0_PHACS	NA
c26526_g1_i1	-2.1599	6.156812	0.001387	0.037846	NA	NA	NA
c15454_g1_i1	-2.15896	5.245015	0.000186	0.00818	NA	NA	NA
c15454_g1_i2	-2.15896	5.245015	0.000186	0.00818	RecName: Full=Alkali-sensitive linkage protein 1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	NA
c15454_g1_i3	-2.15896	5.245015	0.000186	0.00818	NA	NA	NA
c13711_g1_i1	-2.15649	1.995769	1.81E-04	0.00804	RecName: Full=Uncharacterized transporter C11D3.18C [Schizosaccharomyces pombe 972h-]	NA	NA
c24122_g1_i1	-2.15174	4.567582	7.62E-06	7.03E-04	NA	NA	NA
c13788_g3_i1	-2.15043	1.633107	0.00101	0.03017	NA	NA	NA
c24238_g1_i1	-2.13755	2.622066	0.00182	0.045486	NA	NA	NA
c17169_g1_i1	-2.13564	5.762505	7.26E-06	0.000676	NA	NA	NA
c17169_g1_i2	-2.13564	5.762505	7.26E-06	0.000676	NA	NA	NA
c15008_g1_i1	-2.12156	3.321387	0.00031	0.012196	NA	NA	NA
c15008_g1_i2	-2.12156	3.321387	0.00031	0.012196	NA	NA	NA
c15008_g1_i3	-2.12156	3.321387	3.10E-04	0.012196	NA	NA	NA
c1375_g1_i1	-2.11764	1.506256	0.000506	0.017685	NA	NA	GO:0016491|GO:0050660|GO:0055114

c1375_g1_i2	-2.11764	1.506256	5.06E-04	0.017685	NA	NA	GO:0016491|GO:0050660|GO:0055114
c9820_g1_i1	-2.11651	2.500069	0.000433	0.015766	NA	UniRef90_K5VZX4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZX4_PHACS	GO:0004671|GO:0006481|GO:0016021
c19663_g1_i1	-2.11619	1.966369	1.64E-04	7.50E-03	NA	NA	NA
c8869_g2_i1	-2.1127	2.230778	5.79E-05	0.00349	NA	NA	NA
c16839_g1_i1	-2.11118	3.622487	3.36E-05	0.002268	NA	NA	NA
c16839_g1_i2	-2.11118	3.622487	3.36E-05	0.002268	NA	NA	NA
c21393_g1_i1	-2.11066	5.491987	1.16E-05	0.000979	NA	NA	NA
c5296_g1_i1	-2.1017	1.950242	2.09E-04	0.009031	NA	NA	NA
c5296_g1_i2	-2.1017	1.950242	0.000209	0.009031	NA	NA	NA
c14174_g1_i1	-2.09853	5.490026	2.29E-05	0.001687	NA	NA	NA
c15657_g1_i1	-2.0983	5.188334	8.30E-07	0.00012	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15657_g1_i2	-2.0983	5.188334	8.30E-07	0.00012	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c16685_g1_i1	-2.09802	4.722459	8.89E-05	0.004814	NA	NA	NA
c16685_g1_i2	-2.09802	4.722459	8.89E-05	0.004814	NA	NA	NA
c2338_g1_i1	-2.09704	2.120786	3.43E-05	2.30E-03	NA	NA	NA
c18106_g1_i1	-2.09699	2.679471	7.18E-05	0.004106	NA	NA	NA
c26948_g1_i1	-2.09537	2.592819	0.001969	0.048003	NA	NA	NA
c21928_g1_i1	-2.09464	1.474655	0.00042	0.015377	NA	NA	NA
c14113_g2_i1	-2.08523	2.136448	0.000501	0.017527	NA	NA	NA
c14113_g2_i2	-2.08523	2.136448	5.01E-04	0.017527	NA	NA	NA
c19960_g1_i1	-2.08096	1.714946	0.000144	0.006851	NA	NA	NA
c14055_g1_i1	-2.07998	3.613751	0.001863	0.046224	RecName: Full=Manganese peroxidase H4; AltName: Full=MP-I; AltName: Full=Peroxidase manganese-dependent H4; Flags: Precursor [Phanerochaete chrysosporium]	NA	NA

c3484_g1_i1	-2.07748	2.187008	7.78E-05	0.004319	NA	NA	NA
c17116_g2_i1	-2.0723	6.059569	1.71E-04	0.007705	RecName: Full=Uncharacterized transporter C11D3.18C [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c26982_g1_i1	-2.06983	2.102522	0.00032	0.012414	NA	NA	NA
c14616_g1_i1	-2.06607	4.017522	5.80E-05	0.00349	NA	UniRef90_K5XA71 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XA71_PHACS	NA
c14616_g1_i2	-2.06607	4.017522	5.80E-05	0.00349	NA	NA	NA
c17037_g3_i1	-2.06084	2.014581	4.70E-05	0.002945	NA	NA	NA
c18231_g1_i1	-2.05993	4.362602	1.16E-05	9.79E-04	NA	NA	NA
c278_g1_i1	-2.05831	5.979676	9.94E-06	0.000878	NA	UniRef90_K5V0X7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V0X7_PHACS	NA
c16445_g2_i1	-2.05541	1.456242	4.49E-04	0.01615	NA	NA	NA
c16445_g2_i2	-2.05541	1.456242	4.49E-04	0.01615	NA	NA	NA
c1725_g1_i1	-2.04938	2.756257	0.000341	0.013005	NA	NA	NA
c25829_g1_i1	-2.0436	4.334932	6.94E-07	0.000105	NA	NA	NA
c20406_g1_i1	-2.04299	5.550174	0.000435	0.015808	NA	NA	NA
c12261_g2_i1	-2.04013	1.297506	0.001934	0.047394	NA	NA	NA
c12099_g1_i1	-2.037	1.795914	1.70E-03	4.34E-02	NA	NA	NA
c12099_g1_i2	-2.037	1.795914	1.70E-03	4.34E-02	NA	NA	NA
c18960_g1_i1	-2.03474	1.570962	6.54E-04	2.16E-02	NA	NA	NA
c15396_g2_i1	-2.03102	4.069219	5.27E-07	8.34E-05	NA	NA	NA
c15396_g2_i2	-2.03102	4.069219	5.27E-07	8.34E-05	NA	NA	NA
c15396_g2_i3	-2.03102	4.069219	5.27E-07	8.34E-05	NA	NA	NA
c9240_g1_i1	-2.02976	1.764918	2.03E-03	0.04895	NA	NA	NA
c11518_g1_i1	-2.0295	5.271456	1.41E-06	0.000179	RecName: Full=Heat shock protein 104; AltName: Full=Protein aggregation-remodeling factor hsp104 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006355|GO:0008134|GO:0016887|GO:0019538
c3975_g1_i1	-2.02852	4.892201	0.000106	0.005553	NA	NA	NA

c15705_g2_i1	-2.02667	6.404711	0.001064	0.03141	RecName: Full=NADP-dependent malic enzyme; Short=NADP-ME; AltName: Full=SrfA-induced gene A protein [Dictyostelium discoideum]	NA	GO:0004471|GO:0051287|GO:0055114
c16582_g1_i1	-2.02558	2.579533	1.06E-05	0.000916	NA	UniRef90_K5WR80 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WR80_PHACS	NA
c5238_g2_i1	-2.02345	2.582062	3.60E-06	0.000375	NA	NA	NA
c17449_g3_i1	-2.02298	3.346758	8.06E-05	0.004429	NA	NA	GO:0008762|GO:0016491|GO:0050660|GO:0055114
c17449_g3_i2	-2.02298	3.346758	8.06E-05	0.004429	RecName: Full=Bifunctional solanapyrone synthase; AltName: Full=Prosolanapyrone-II oxidase; AltName: Full=Prosolanapyrone-III cycloisomerase; Flags: Precursor [Alternaria solani]	NA	GO:0008762|GO:0016491|GO:0050660|GO:0055114
c10388_g1_i1	-2.02086	3.22371	0.000334	0.012814	NA	NA	GO:0018580|GO:0055114
c14951_g4_i1	-2.01844	3.646004	1.17E-07	2.31E-05	NA	UniRef90_K5WLE2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLE2_PHACS	NA
c14951_g4_i2	-2.01844	3.646004	1.17E-07	2.31E-05	NA	NA	NA
c16948_g2_i1	-2.0165	2.862497	0.000134	0.006486	NA	NA	NA
c16749_g4_i1	-2.01579	3.751508	0.002022	0.04895	RecName: Full=Xyloglucanase Xgh74A; Flags: Precursor [Ruminiclostridium thermocellum]	NA	NA
c16749_g4_i2	-2.01579	3.751508	2.02E-03	0.04895	NA	NA	NA
c17538_g1_i1	-2.01447	4.716593	1.89E-06	0.000226	NA	NA	NA
c17538_g1_i2	-2.01447	4.716593	1.89E-06	0.000226	NA	NA	NA
c17538_g1_i3	-2.01447	4.716593	1.89E-06	0.000226	NA	UniRef90_K5WKW8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKW8_PHACS	NA
c17538_g1_i4	-2.01447	4.716593	1.89E-06	0.000226	NA	NA	NA
c17538_g1_i5	-2.01447	4.716593	1.89E-06	0.000226	NA	NA	NA
c14616_g2_i1	-2.01147	4.897981	0.000357	0.013493	NA	UniRef90_K5XA71 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XA71_PHACS	NA

c21707_g1_i1	-2.01063	7.958028	7.89E-08	1.66E-05	NA	NA	NA
c13586_g1_i1	-2.01041	2.303655	3.33E-05	2.27E-03	NA	NA	NA
c13104_g1_i1	-2.00066	3.128716	1.01E-05	0.000886	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15651_g2_i1	-2.00011	2.386819	8.39E-04	0.026065	NA	NA	NA
c15651_g2_i2	-2.00011	2.386819	8.39E-04	0.026065	NA	NA	NA
c15651_g2_i3	-2.00011	2.386819	8.39E-04	0.026065	NA	NA	NA
c14695_g2_i1	-1.99144	2.98274	5.36E-06	0.000531	NA	UniRef90_K5VCY4 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCY4_PHACS	NA
c14695_g2_i2	-1.99144	2.98274	5.36E-06	0.000531	NA	NA	NA
c14695_g2_i3	-1.99144	2.98274	5.36E-06	0.000531	NA	NA	NA
c16619_g2_i1	-1.98906	5.487704	1.31E-06	0.00017	NA	NA	NA
c17064_g2_i1	-1.98811	4.58725	3.86E-04	0.014364	NA	NA	GO:0016021|GO:0055085
c17064_g2_i2	-1.98811	4.58725	3.86E-04	0.014364	NA	NA	GO:0016021|GO:0055085
c23853_g1_i1	-1.9812	1.532768	7.60E-04	2.41E-02	NA	NA	NA
c10067_g2_i1	-1.98113	5.300118	0.000228	0.009631	NA	UniRef90_A0A0C3NVI8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NVI8_PHLGI	NA
c16566_g1_i1	-1.97644	6.662738	4.23E-05	0.002709	NA	NA	GO:0003824
c16566_g1_i2	-1.97644	6.662738	4.23E-05	0.002709	RecName: Full=Protein phosphatase 2C homolog C10F6.17c; AltName: Full=Pyruvate dehydrogenase (Lipoamide) phosphatase C10F6.17c [Schizosaccharomyces pombe 972h-]	UniRef90_K5WVA5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WVA5_PHACS	GO:0003824
c14844_g4_i1	-1.97391	5.749563	7.29E-05	4.13E-03	RecName: Full=Putative chromatin-remodeling complex ATPase chain; AltName: Full=ISW2-like; AltName: Full=Sucrose nonfermenting protein 2 homolog [Arabidopsis thaliana]	UniRef90_A0A0C3PKL6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PKL6_PHLGI	GO:0003676|GO:0003677|GO:0005524
c20857_g1_i1	-1.97223	2.191556	0.000123	0.006151	NA	NA	NA
c2813_g1_i1	-1.96959	2.275941	5.52E-04	0.018962	NA	NA	NA
c2813_g1_i2	-1.96959	2.275941	0.000552	0.018962	NA	NA	NA

c694_g1_i1	-1.96666	6.113392	3.03E-05	0.002087	NA	UniRef90_A0A0C3NAV4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NAV4_PHLGI	NA
c10432_g3_i1	-1.96525	2.583765	0.000271	0.011033	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus parasiticus]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c13814_g3_i1	-1.96447	2.842681	0.00013	0.006359	RecName: Full=Probable RNA-directed DNA polymerase from transposon X-element; AltName: Full=Reverse transcriptase [Drosophila melanogaster]	NA	NA
c26699_g1_i1	-1.96427	3.015404	2.50E-05	0.001799	NA	NA	NA
c17532_g2_i1	-1.96313	1.524955	0.000837	0.026065	NA	NA	NA
c6550_g1_i1	-1.96282	1.51404	1.26E-03	0.035289	NA	NA	GO:0004672|GO:0005524|GO:0006468
c3302_g1_i1	-1.9586	2.113343	5.49E-05	0.003343	NA	NA	NA
c26377_g1_i1	-1.95661	3.064241	8.28E-06	0.000752	NA	NA	NA
c17113_g1_i1	-1.94796	6.518329	1.09E-06	0.00015	NA	NA	GO:0004671|GO:0006481|GO:0016020|GO:0016021
c3839_g1_i1	-1.94678	4.764286	4.41E-07	7.37E-05	NA	NA	NA
c17329_g2_i1	-1.94164	2.423272	0.001792	0.044948	NA	NA	NA
c8001_g1_i1	-1.93713	3.017426	0.000158	0.007318	NA	NA	NA
c8001_g1_i2	-1.93713	3.017426	0.000158	0.007318	NA	NA	NA
c16174_g2_i1	-1.93658	3.115026	4.20E-05	2.71E-03	NA	UniRef90_K5W259 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W259_PHACS	NA
c19661_g1_i1	-1.93515	2.542641	0.001013	0.030216	NA	NA	NA
c17490_g1_i1	-1.92595	2.382466	2.14E-04	0.009222	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName:	NA	GO:0004190|GO:0006508

					Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]		
c23864_g1_i1	-1.92257	2.144892	1.39E-03	3.80E-02	NA	NA	NA
c20503_g1_i1	-1.91999	5.543315	9.99E-05	0.0053	RecName: Full=Putative AAA family ATPase L572 [Acanthamoeba polyphaga mimivirus]	NA	GO:0005524
c14844_g2_i1	-1.91964	5.047893	0.000116	0.00589	NA	UniRef90_A0A0C3PKL6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PKL6_PHLGI	NA
c11787_g1_i1	-1.91935	1.490433	0.001474	0.039373	NA	NA	NA
c16685_g3_i1	-1.91818	5.597075	5.25E-04	0.018224	NA	NA	NA
c11332_g2_i1	-1.91701	2.08181	0.000311	0.012225	RecName: Full=Endo-1,4-beta-xylanase C; Short=Xylanase C; AltName: Full=1,4-beta-D-xylan xylanohydrolase C; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c16621_g1_i1	-1.9157	3.289211	2.78E-05	1.96E-03	NA	NA	NA
c16621_g1_i2	-1.9157	3.289211	2.78E-05	0.001963	NA	NA	NA
c13376_g1_i1	-1.91437	1.728213	0.000591	0.019994	NA	NA	NA
c12499_g2_i1	-1.90829	2.70643	7.10E-05	0.004072	NA	UniRef90_K5V9W9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V9W9_PHACS	NA
c19180_g1_i1	-1.89884	2.231067	1.02E-03	3.05E-02	NA	NA	NA
c16174_g1_i1	-1.89524	1.816085	0.001991	0.048382	NA	NA	NA
c16174_g1_i2	-1.89524	1.816085	0.001991	0.048382	NA	NA	NA
c20678_g1_i1	-1.89169	3.142658	6.87E-05	0.003965	NA	NA	NA
c9904_g1_i1	-1.88892	3.756513	1.65E-05	0.001309	NA	UniRef90_K5W1C2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1C2_PHACS	NA
c19662_g1_i1	-1.88717	1.784405	1.01E-03	3.02E-02	NA	NA	NA
c9363_g1_i1	-1.88667	4.453876	0.000363	0.013631	RecName: Full=Protein shq1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VDA6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VDA6_PHACS	NA
c9363_g1_i2	-1.88667	4.453876	3.63E-04	1.36E-02	NA	NA	NA
c9363_g1_i3	-1.88667	4.453876	0.000363	0.013631	NA	NA	NA

c58_g1_i1	-1.88313	1.703005	4.29E-04	1.57E-02	NA	UniRef90_A0A0C3P218 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P218_PHLGI	NA
c22878_g1_i1	-1.87967	1.579519	1.47E-03	0.039363	NA	NA	NA
c25180_g1_i1	-1.87899	4.211062	1.21E-05	0.001009	NA	NA	NA
c2278_g1_i1	-1.8745	4.84759	2.01E-06	0.000236	NA	NA	NA
c6842_g1_i1	-1.87448	5.894754	3.88E-05	0.00255	NA	NA	NA
c15838_g3_i1	-1.87433	3.719723	1.03E-05	0.000897	NA	NA	NA
c15838_g3_i2	-1.87433	3.719723	1.03E-05	0.000897	NA	NA	NA
c18105_g1_i1	-1.87337	8.7881	2.04E-05	0.001552	RecName: Full=Upstream activation factor subunit spp27; AltName: Full=Upstream activation factor 27 KDa subunit; Short=p27; AltName: Full=Upstream activation factor 30 KDa subunit; Short=p30; AltName: Full=Upstream activation factor subunit uaf30 [Schizosaccharomyces pombe 972h-]	NA	GO:0005515
c9596_g1_i1	-1.87199	1.797803	5.34E-04	0.018475	NA	NA	NA
c12162_g2_i1	-1.86812	4.547878	0.0013	0.036076	RecName: Full=Mannose-6-phosphate isomerase; AltName: Full=Phosphohexomutase; AltName: Full=Phosphomannose isomerase; Short=PMI [Cryptococcus neoformans var. neoformans JEC21]	NA	GO:0004476|GO:0005975|GO:0008270
c17037_g5_i1	-1.8656	3.365724	1.12E-05	0.000956	NA	NA	NA
c17037_g5_i2	-1.8656	3.365724	1.12E-05	0.000956	NA	NA	NA
c14269_g1_i1	-1.86031	5.454088	1.85E-06	0.000222	RecName: Full=Beta-lactamase hydrolase-like protein [Xylella fastidiosa Temecula1]	NA	NA
c14092_g1_i1	-1.85957	2.142168	1.44E-03	3.89E-02	NA	NA	NA
c14092_g1_i2	-1.85957	2.142168	1.44E-03	3.89E-02	NA	NA	NA
c12633_g1_i1	-1.85722	3.851122	0.00148	0.039506	NA	UniRef90_K5V6K3 Glycoside hydrolase family 79 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V6K3_PHACS	NA
c16321_g2_i1	-1.85507	2.767575	1.40E-04	0.006679	NA	NA	NA
c16321_g2_i2	-1.85507	2.767575	1.40E-04	0.006679	NA	UniRef90_K5UVX2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UVX2_PHACS	NA

c16321_g2_i3	-1.85507	2.767575	0.00014	0.006679	NA	NA	NA
c17377_g2_i1	-1.85019	2.691647	8.93E-05	0.004826	NA	NA	NA
c17406_g1_i1	-1.84556	1.456422	0.001761	0.044328	NA	NA	NA
c7071_g1_i1	-1.84536	4.375709	2.04E-06	0.000239	NA	NA	NA
c10005_g1_i1	-1.84367	1.459246	0.001756	0.044232	NA	UniRef90_K5WKY8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKY8_PHACS	NA
c14291_g1_i1	-1.83503	6.44682	5.02E-05	0.003106	NA	NA	NA
c14291_g1_i2	-1.83503	6.44682	5.02E-05	0.003106	NA	NA	NA
c2804_g1_i1	-1.83464	1.655656	0.001047	0.031	NA	NA	NA
c15561_g1_i1	-1.83448	2.162575	0.000672	0.021925	NA	NA	NA
c15869_g5_i1	-1.83412	6.028494	1.88E-05	0.001441	RecName: Full=GTPase-activating protein gyp10 [Schizosaccharomyces pombe 972h-]	NA	GO:0005097|GO:0032313
c9103_g1_i1	-1.83392	6.222587	2.58E-05	0.001852	NA	NA	NA
c19882_g1_i1	-1.82968	3.298676	2.24E-05	0.001662	NA	NA	NA
c16927_g1_i1	-1.82598	3.722629	7.01E-06	0.000657	NA	NA	NA
c16927_g1_i2	-1.82598	3.722629	7.01E-06	0.000657	NA	NA	NA
c16333_g1_i1	-1.81985	5.076173	8.56E-06	0.000773	NA	NA	NA
c16333_g1_i2	-1.81985	5.076173	8.56E-06	0.000773	NA	NA	NA
c16333_g1_i3	-1.81985	5.076173	8.56E-06	7.73E-04	NA	NA	NA
c16333_g1_i4	-1.81985	5.076173	8.56E-06	7.73E-04	NA	NA	NA
c20243_g1_i1	-1.81822	6.975337	1.02E-06	0.000143	NA	NA	NA
c23034_g1_i1	-1.81433	2.316653	7.19E-05	0.004106	NA	NA	NA
c13123_g1_i1	-1.81278	6.523635	2.60E-05	0.00186	NA	NA	NA
c14178_g1_i1	-1.80952	4.254723	7.39E-05	0.004184	NA	NA	NA
c12235_g1_i1	-1.80816	5.049167	2.57E-06	2.85E-04	RecName: Full=Chaperone protein DnaJ [Chlorobium phaeobacteroides DSM 266]	UniRef90_K5VFK5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VFK5_PHACS	NA
c5504_g1_i1	-1.8081	2.743633	0.000891	0.027319	NA	UniRef90_A0A0C3NZP9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NZP9_PHLGI	GO:0016021|GO:0055085
c5504_g1_i2	-1.8081	2.743633	8.91E-04	0.027319	NA	NA	GO:0016021|GO:0055085

c12443_g2_i1	-1.80644	6.861585	1.89E-05	0.001441	NA	NA	NA
c12443_g2_i2	-1.80644	6.861585	1.89E-05	0.001441	RecName: Full=DNA repair protein REV1; AltName: Full=Alpha integrin-binding protein 80; Short=AIBP80; AltName: Full=Rev1-like terminal deoxycytidyl transferase [Homo sapiens]	UniRef90_K5W5G9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5G9_PHACS	NA
c16803_g2_i1	-1.80514	3.453276	0.000914	0.027897	NA	NA	NA
c15168_g2_i1	-1.80452	2.665495	6.34E-05	0.003734	RecName: Full=Lipase 3; AltName: Full=Cholesterol esterase; Flags: Precursor [Candida rugosa]	NA	NA
c17507_g2_i1	-1.80447	5.74281	1.16E-06	0.000156	NA	NA	NA
c17507_g2_i2	-1.80447	5.74281	1.16E-06	1.56E-04	NA	NA	NA
c17507_g2_i3	-1.80447	5.74281	1.16E-06	1.56E-04	NA	UniRef90_K5WJH4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJH4_PHACS	NA
c17507_g2_i4	-1.80447	5.74281	1.16E-06	1.56E-04	NA	NA	GO:0035091
c368_g1_i1	-1.79927	6.087046	0.000195	0.008566	NA	UniRef90_K5WU77 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WU77_PHACS	NA
c368_g1_i2	-1.79927	6.087046	1.95E-04	0.008566	NA	NA	NA
c16621_g2_i1	-1.79811	4.78922	3.44E-05	0.002298	NA	NA	NA
c16621_g2_i2	-1.79811	4.78922	3.44E-05	0.002298	NA	NA	NA
c17716_g1_i1	-1.7981	10.72007	3.34E-04	1.28E-02	NA	NA	NA
c1056_g1_i1	-1.797	2.08898	0.000521	0.018104	NA	NA	NA
c16759_g2_i1	-1.79657	3.470643	2.67E-05	0.001895	RecName: Full=Glutathione S-transferase omega-like 2; AltName: Full=Glutathione-dependent dehydroascorbate reductase [Schizosaccharomyces pombe 972h-]	NA	NA
c16759_g2_i2	-1.79657	3.470643	2.67E-05	0.001895	NA	NA	NA
c4924_g1_i1	-1.79316	9.178061	4.83E-07	7.86E-05	RecName: Full=Thioredoxin; Short=Trx; AltName: Allergen=Cop c 2 [Coprinus comatus]	UniRef90_K5VYM7 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYM7_PHACS	GO:0016209|GO:0016491|GO:0045454|GO:0055114
c8609_g1_i1	-1.79003	5.688556	5.21E-04	1.81E-02	NA	NA	NA
c8609_g1_i2	-1.79003	5.688556	5.21E-04	1.81E-02	NA	NA	NA
c26196_g1_i1	-1.78852	2.750482	8.69E-04	0.026833	NA	NA	NA
c26732_g1_i1	-1.78749	2.471392	0.000716	0.022958	NA	NA	NA

c6785_g1_i1	-1.7873	7.479647	0.000336	0.012854	NA	NA	NA
c6785_g1_i2	-1.7873	7.479647	3.36E-04	0.012854	NA	NA	NA
c559_g1_i1	-1.78632	4.093229	6.68E-05	3.88E-03	NA	NA	NA
c10378_g1_i1	-1.78495	2.222305	0.000177	0.007885	NA	NA	NA
c17349_g4_i1	-1.7847	4.661725	1.25E-04	0.006209	NA	NA	GO:0009058|GO:0030170
c17349_g4_i2	-1.7847	4.661725	0.000125	0.006209	RecName: Full=Aspartate aminotransferase; Short=AspAT; AltName: Full=Transaminase A [Pyrococcus abyssi GE5]	NA	GO:0009058|GO:0030170
c19802_g1_i1	-1.77954	7.790027	6.48E-06	0.000619	NA	NA	NA
c9484_g1_i1	-1.7787	2.067662	0.001073	0.031527	NA	NA	NA
c9484_g1_i2	-1.7787	2.067662	0.001073	0.031527	NA	NA	NA
c12000_g2_i1	-1.77507	2.625527	0.000155	0.007192	NA	NA	NA
c14200_g2_i1	-1.77499	5.832349	4.85E-05	0.003021	NA	NA	NA
c14200_g2_i2	-1.77499	5.832349	4.85E-05	0.003021	NA	NA	NA
c16146_g1_i1	-1.76947	3.074074	0.000106	0.005555	NA	NA	NA
c16146_g1_i2	-1.76947	3.074074	1.06E-04	0.005555	NA	NA	NA
c16146_g1_i3	-1.76947	3.074074	0.000106	0.005555	NA	NA	NA
c16146_g1_i4	-1.76947	3.074074	1.06E-04	0.005555	NA	NA	NA
c15657_g3_i1	-1.76927	1.988931	0.001651	0.042542	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus parasiticus]	NA	NA
c17466_g1_i1	-1.76538	6.759049	6.64E-04	2.18E-02	NA	NA	NA
c17466_g1_i2	-1.76538	6.759049	0.000664	0.021781	NA	NA	NA
c17466_g1_i3	-1.76538	6.759049	6.64E-04	2.18E-02	NA	NA	NA
c17466_g1_i4	-1.76538	6.759049	6.64E-04	0.021781	NA	NA	NA
c17466_g1_i5	-1.76538	6.759049	6.64E-04	0.021781	NA	NA	NA
c17466_g1_i6	-1.76538	6.759049	6.64E-04	0.021781	NA	NA	NA
c17466_g1_i7	-1.76538	6.759049	6.64E-04	0.021781	NA	NA	NA
c22034_g1_i1	-1.76261	5.839368	6.11E-05	0.003627	RecName: Full=Quinone oxidoreductase 2 [Escherichia coli K-12]	UniRef90_K5UU09 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UU09_PHACS	GO:0003854|GO:0006694|GO:0016616|GO:0055114
c14200_g1_i1	-1.76249	4.732596	0.0001	0.005301	NA	NA	GO:0009976

c8903_g2_i1	-1.76024	3.497428	1.28E-04	0.006318	NA	NA	NA
c21757_g1_i1	-1.75114	5.454573	6.61E-04	0.021742	NA	NA	NA
c17502_g2_i1	-1.74934	4.446147	1.63E-03	0.042273	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17502_g2_i2	-1.74934	4.446147	1.63E-03	0.042273	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17502_g2_i3	-1.74934	4.446147	1.63E-03	0.042273	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]	UniRef90_K5VVU1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVU1_PHACS	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c7020_g1_i1	-1.74601	2.791489	0.000249	0.010261	NA	NA	NA
c9997_g1_i1	-1.74302	2.317203	0.002067	0.049605	NA	UniRef90_K5UNL2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UNL2_PHACS	GO:0004129
c24075_g1_i1	-1.74292	1.902009	1.03E-03	3.06E-02	NA	NA	NA
c1312_g1_i1	-1.74145	2.116295	0.000787	0.024779	RecName: Full=4-O-methyl-glucuronoyl methylesterase; AltName: Full=Glucuronoyl esterase 2; Short=GE2; Flags: Precursor [Trichoderma reesei QM6a]	NA	NA
c1312_g1_i2	-1.74145	2.116295	7.87E-04	0.024779	NA	NA	NA
c24662_g1_i1	-1.74035	4.369897	0.00068	0.022073	NA	NA	NA
c4511_g1_i1	-1.73647	2.04475	0.000642	0.021242	NA	NA	NA
c25017_g1_i1	-1.7355	2.386746	2.47E-04	1.02E-02	RecName: Full=TPR repeat-containing protein C19B12.01 [Schizosaccharomyces pombe 972h-]	NA	NA
c14187_g2_i1	-1.72924	5.787833	0.000127	0.00629	RecName: Full=Cytochrome P450 72A14 [Arabidopsis thaliana]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c14187_g2_i2	-1.72924	5.787833	0.000127	0.00629	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c14687_g1_i1	-1.71796	7.138031	6.94E-05	0.00399	NA	UniRef90_A0A0C3PVF3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PVF3_PHLGI	NA
c14687_g1_i2	-1.71796	7.138031	6.94E-05	0.00399	NA	NA	NA
c14687_g1_i3	-1.71796	7.138031	6.94E-05	0.00399	NA	NA	NA
c16344_g1_i1	-1.71446	3.781308	3.22E-05	2.20E-03	NA	NA	NA
c14844_g3_i1	-1.7133	6.462359	0.000273	0.011066	RecName: Full=Probable global transcription activator SNF2L1; AltName: Full=ATP-dependent helicase SMARCA1; AltName: Full=DNA-dependent ATPase SNF2L; AltName: Full=Nucleosome-remodeling factor subunit SNF2L; AltName: Full=SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 1 [Mus musculus]	UniRef90_K5VZS7 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZS7_PHACS	NA
c9903_g1_i1	-1.70705	4.583361	1.95E-04	0.008553	NA	NA	NA
c9903_g1_i2	-1.70705	4.583361	0.000195	0.008553	NA	NA	NA
c13657_g1_i1	-1.70701	7.28368	6.29E-06	0.000606	RecName: Full=Peroxisomal 2,4-dienoyl-CoA reductase; AltName: Full=2,4-dienoyl-CoA reductase 2 [Danio rerio]	NA	GO:0008152|GO:0016491
c13657_g1_i2	-1.70701	7.28368	6.29E-06	0.000606	NA	NA	GO:0008152|GO:0016491
c13657_g1_i3	-1.70701	7.28368	6.29E-06	0.000606	NA	NA	GO:0008152|GO:0016491
c13657_g1_i4	-1.70701	7.28368	6.29E-06	0.000606	NA	NA	GO:0008152|GO:0016491
c15239_g1_i1	-1.70585	3.065621	0.001897	0.046716	NA	NA	NA
c16855_g3_i1	-1.7036	5.08374	0.000164	0.007484	RecName: Full=Cytochrome P450 67; AltName: Full=CYPLXVII; AltName: Full=Planta-induced rust protein 16, partial [Uromyces viciae-fabae]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c16855_g3_i2	-1.7036	5.08374	0.000164	0.007484	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c16759_g1_i1	-1.70188	5.153584	3.08E-06	3.33E-04	RecName: Full=Glutathione S-transferase omega-like 2; AltName: Full=Glutathione-dependent dehydroascorbate reductase [Schizosaccharomyces pombe 972h-]	NA	GO:0005515
c16759_g1_i2	-1.70188	5.153584	3.08E-06	3.33E-04	NA	NA	GO:0005515
c16759_g1_i3	-1.70188	5.153584	3.08E-06	0.000333	NA	NA	GO:0005515
c12540_g1_i1	-1.69804	4.635548	7.12E-06	0.000665	NA	NA	NA

c12345_g1_i1	-1.6933	3.221515	3.35E-05	0.002268	NA	NA	NA
c15654_g1_i1	-1.69224	3.166642	0.000236	0.009881	NA	NA	NA
c15654_g1_i2	-1.69224	3.166642	0.000236	0.009881	NA	NA	NA
c3047_g1_i1	-1.68967	1.753761	0.001641	0.042384	NA	NA	NA
c5173_g1_i1	-1.6882	3.703562	9.57E-06	0.000854	RecName: Full=Uncharacterized MFS-type transporter EfpA; AltName: Full=Efflux protein A [Mycobacterium tuberculosis CDC1551]	UniRef90_K5W1Y1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1Y1_PHACS	GO:0016021|GO:0022857|GO:0055085
c12499_g1_i1	-1.6856	4.487137	5.95E-06	0.000578	RecName: Full=Lipase; AltName: Full=Triacylglycerol lipase; Flags: Precursor [Thermomyces lanuginosus]	UniRef90_K5V9W9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V9W9_PHACS	GO:0006629
c13456_g2_i1	-1.68467	3.751817	0.000139	0.006665	NA	NA	NA
c13456_g2_i2	-1.68467	3.751817	1.39E-04	0.006665	NA	NA	NA
c13456_g2_i3	-1.68467	3.751817	1.39E-04	0.006665	NA	NA	NA
c15992_g2_i1	-1.68393	2.733181	0.001165	0.033394	RecName: Full=Aflatoxin B1 aldehyde reductase member 4; AltName: Full=AFB1 aldehyde reductase 3; Short=AFB1-AR 3; AltName: Full=Aldoketoreductase 7-like [Homo sapiens]	NA	NA
c14187_g1_i1	-1.68174	4.567262	0.000457	0.016358	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c14397_g2_i1	-1.68062	2.982698	0.000135	0.006508	NA	NA	NA
c14397_g2_i2	-1.68062	2.982698	0.000135	0.006508	NA	NA	NA
c11481_g1_i1	-1.68013	2.730015	0.000618	0.020711	NA	NA	NA
c11481_g1_i2	-1.68013	2.730015	0.000618	0.020711	NA	NA	NA
c24836_g1_i1	-1.67738	2.796942	6.08E-05	0.003618	NA	NA	NA
c13972_g2_i1	-1.6746	4.205782	3.22E-06	0.000347	NA	NA	NA
c13972_g2_i2	-1.6746	4.205782	3.22E-06	0.000347	RecName: Full=Zinc finger transcription factor YRR1; AltName: Full=Pleiotropic drug-resistance protein 2 [Saccharomyces cerevisiae S288c]	NA	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c16855_g7_i1	-1.67352	3.691724	0.000364	0.013684	NA	NA	NA
c16855_g7_i2	-1.67352	3.691724	3.64E-04	0.013684	NA	NA	NA
c16855_g7_i3	-1.67352	3.691724	3.64E-04	0.013684	NA	NA	NA
c12007_g1_i1	-1.67093	4.882984	1.11E-05	0.00095	NA	NA	NA

c12007_g1_i2	-1.67093	4.882984	1.11E-05	0.00095	NA	NA	GO:0006400|GO:0008152|GO:0008168|GO:0008176
c12007_g1_i3	-1.67093	4.882984	1.11E-05	0.00095	NA	NA	NA
c19890_g1_i1	-1.66678	6.841776	6.38E-06	6.11E-04	NA	NA	NA
c12187_g1_i1	-1.66606	5.701242	5.89E-06	5.75E-04	RecName: Full=Heat shock protein 90 homolog [Schizosaccharomyces pombe 972h-]	UniRef90_R7S7P6 Heat shock protein 90 n=4 Tax=Polyporales RepID=R7S7P6_TRAVS	NA
c10829_g2_i1	-1.66292	2.205037	0.000745	0.023738	NA	NA	NA
c10829_g2_i2	-1.66292	2.205037	0.000745	0.023738	NA	NA	GO:0004672|GO:0005524|GO:0006468
c17507_g1_i1	-1.66278	3.393963	1.84E-04	0.00814	NA	UniRef90_K5WJH4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJH4_PHACS	NA
c19838_g1_i1	-1.66161	4.189673	1.92E-04	0.008424	NA	NA	NA
c13814_g1_i1	-1.65689	2.329116	0.000515	0.017925	NA	NA	NA
c11266_g1_i1	-1.65595	2.89037	6.77E-04	0.022	NA	NA	NA
c86_g1_i1	-1.65235	4.920449	0.00029	0.011575	NA	NA	NA
c86_g1_i2	-1.65235	4.920449	0.00029	0.011575	NA	NA	NA
c17273_g1_i1	-1.65049	4.525735	0.002013	0.048781	NA	NA	NA
c17273_g1_i2	-1.65049	4.525735	0.002013	0.048781	NA	NA	NA
c17273_g1_i3	-1.65049	4.525735	0.002013	0.048781	NA	NA	NA
c17273_g1_i4	-1.65049	4.525735	0.002013	0.048781	NA	NA	NA
c17273_g1_i5	-1.65049	4.525735	0.002013	0.048781	NA	NA	NA
c17273_g1_i6	-1.65049	4.525735	0.002013	0.048781	NA	NA	NA
c17273_g1_i7	-1.65049	4.525735	0.002013	0.048781	NA	NA	NA
c17273_g1_i8	-1.65049	4.525735	0.002013	0.048781	NA	NA	NA
c4612_g1_i1	-1.64917	4.117219	0.000226	0.009584	NA	NA	NA
c21384_g1_i1	-1.64173	2.852528	0.000214	0.009222	NA	NA	NA
c16927_g2_i1	-1.64163	3.568012	8.34E-04	0.025993	NA	NA	NA
c17125_g1_i1	-1.64061	5.418725	3.25E-04	0.01255	NA	NA	NA
c17125_g1_i2	-1.64061	5.418725	3.25E-04	1.26E-02	NA	NA	NA
c12534_g1_i1	-1.63548	2.71287	0.000324	0.012536	NA	NA	NA

c17421_g1_i1	-1.63109	3.750433	1.23E-03	3.47E-02	NA	NA	NA
c17421_g1_i2	-1.63109	3.750433	0.001229	0.034697	NA	NA	NA
c17231_g1_i1	-1.62457	1.978634	0.001694	0.043398	NA	NA	NA
c17231_g1_i2	-1.62457	1.978634	0.001694	0.043398	NA	NA	NA
c9895_g1_i1	-1.62424	2.740694	0.000242	0.010031	NA	UniRef90_A0A0C3S9Q2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S9Q2_PHLGI	NA
c12876_g1_i1	-1.62072	2.170945	0.001856	0.046129	NA	NA	NA
c16803_g1_i1	-1.61998	4.296691	0.00168	0.043086	NA	NA	NA
c16803_g1_i2	-1.61998	4.296691	0.00168	0.043086	NA	NA	NA
c16592_g2_i1	-1.61859	4.145812	0.001208	0.03418	NA	NA	NA
c16592_g2_i2	-1.61859	4.145812	0.001208	0.03418	NA	NA	NA
c16592_g2_i3	-1.61859	4.145812	1.21E-03	3.42E-02	NA	NA	NA
c9103_g2_i1	-1.61216	7.266246	6.44E-05	0.00377	NA	NA	NA
c9103_g2_i2	-1.61216	7.266246	6.44E-05	0.00377	NA	NA	NA
c10383_g1_i1	-1.60978	6.157517	9.50E-06	0.000851	NA	NA	NA
c388_g1_i1	-1.60694	2.993027	2.77E-04	1.12E-02	NA	NA	NA
c17207_g2_i1	-1.60603	5.168949	6.38E-05	0.003742	NA	NA	GO:0046872
c17207_g2_i2	-1.60603	5.168949	6.38E-05	0.003742	NA	NA	GO:0046872
c17207_g2_i3	-1.60603	5.168949	6.38E-05	0.003742	NA	NA	GO:0046872
c17207_g2_i4	-1.60603	5.168949	6.38E-05	0.003742	NA	NA	GO:0046872
c6692_g1_i1	-1.60577	8.387374	1.01E-05	0.000886	NA	NA	NA
c16756_g1_i1	-1.60273	4.502461	3.54E-04	0.013426	NA	NA	NA
c16756_g1_i2	-1.60273	4.502461	3.54E-04	0.013426	NA	NA	GO:0004871|GO:0007165|GO:0016021
c16756_g1_i3	-1.60273	4.502461	0.000354	0.013426	NA	NA	GO:0004871|GO:0007165|GO:0016021
c16756_g1_i4	-1.60273	4.502461	0.000354	0.013426	RecName: Full=Histidine protein kinase NIK1 [Candida albicans SC5314]	NA	GO:0004871|GO:0007165|GO:0016021
c15755_g2_i1	-1.6026	7.504198	3.18E-04	0.012383	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248

c15755_g2_i2	-1.6026	7.504198	0.000318	0.012383	RecName: Full=Putative amidase C869.01; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c15755_g2_i3	-1.6026	7.504198	0.000318	0.012383	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c16111_g1_i1	-1.60181	4.144055	3.50E-05	0.002329	NA	NA	NA
c16111_g1_i2	-1.60181	4.144055	3.50E-05	0.002329	NA	NA	NA
c16111_g1_i3	-1.60181	4.144055	3.50E-05	0.002329	NA	NA	NA
c16111_g1_i4	-1.60181	4.144055	3.50E-05	0.002329	NA	NA	NA
c16111_g1_i5	-1.60181	4.144055	3.50E-05	2.33E-03	NA	NA	NA
c12317_g2_i1	-1.59899	3.751415	7.84E-05	0.004345	RecName: Full=UPF0644 protein PB2B4.06 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VNE9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VNE9_PHACS	NA
c559_g2_i1	-1.59792	3.237008	0.000472	0.016811	NA	NA	NA
c12738_g1_i1	-1.59623	6.212892	0.001177	0.033618	RecName: Full=DNA polymerase kappa; AltName: Full=Meiotically up-regulated gene 40 protein [Schizosaccharomyces pombe 972h-]	UniRef90_K5W4Z4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W4Z4_PHACS	GO:0003684|GO:0003887|GO:0006281
c18584_g1_i1	-1.59264	5.184027	0.000223	0.009485	NA	NA	GO:0005515
c20269_g1_i1	-1.58924	4.608955	7.90E-05	0.004363	NA	NA	NA
c24964_g1_i1	-1.58923	5.112323	0.000129	0.00635	NA	NA	NA
c11004_g2_i1	-1.5882	1.782442	0.001661	0.042731	NA	NA	NA
c11004_g2_i2	-1.5882	1.782442	0.001661	0.042731	NA	NA	NA
c15396_g1_i1	-1.58619	2.031108	0.001	0.029917	NA	NA	NA
c3572_g1_i1	-1.58531	2.229947	1.31E-03	0.036164	NA	NA	NA
c3572_g1_i2	-1.58531	2.229947	0.001306	0.036164	NA	NA	NA
c14458_g1_i1	-1.58494	3.854324	5.77E-05	0.00349	NA	NA	NA
c14458_g1_i2	-1.58494	3.854324	5.77E-05	0.00349	RecName: Full=Ribosome biogenesis protein enp2 homolog [Schizosaccharomyces pombe 972h-]	UniRef90_K5WCQ2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCQ2_PHACS	NA

c12392_g1_i1	-1.58377	2.551859	0.00048	0.016987	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus parasiticus]	UniRef90_A0A0C3P205 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P205_PHLGI	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c3863_g1_i1	-1.58198	3.185529	0.00189	0.046639	NA	NA	NA
c3863_g1_i2	-1.58198	3.185529	0.00189	0.046639	NA	NA	NA
c14223_g3_i1	-1.57506	3.434889	0.000145	0.006852	RecName: Full=Bromodomain-containing protein 7 [Gallus gallus]	NA	GO:0005515
c16963_g1_i1	-1.57427	3.246274	2.73E-04	0.011066	NA	NA	NA
c16963_g1_i2	-1.57427	3.246274	2.73E-04	0.011066	NA	NA	NA
c16963_g1_i3	-1.57427	3.246274	0.000273	0.011066	NA	NA	NA
c9103_g3_i1	-1.57374	5.567386	1.49E-04	0.006991	NA	NA	NA
c18942_g1_i1	-1.57157	2.782227	2.37E-04	9.88E-03	NA	NA	NA
c12235_g2_i1	-1.57117	2.804651	0.000109	0.005647	NA	NA	NA
c12435_g1_i1	-1.56913	3.42763	0.000228	0.009631	NA	NA	NA
c12435_g1_i2	-1.56913	3.42763	0.000228	0.009631	NA	NA	NA
c12435_g1_i3	-1.56913	3.42763	0.000228	0.009631	NA	NA	NA
c4702_g1_i1	-1.56869	3.231652	8.11E-05	4.45E-03	NA	NA	NA
c24601_g1_i1	-1.56709	4.481909	0.00057	0.019499	NA	NA	NA
c14665_g1_i1	-1.56576	7.179821	4.85E-05	0.003021	RecName: Full=Probable aspartic-type endopeptidase CTSD; Flags: Precursor [Trichophyton verrucosum HKI 0517]	UniRef90_A0A0C3S3F0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S3F0_PHLGI	GO:0004190|GO:0006508
c14665_g1_i2	-1.56576	7.179821	4.85E-05	0.003021	NA	NA	GO:0004190|GO:0006508
c14665_g1_i3	-1.56576	7.179821	4.85E-05	0.003021	NA	NA	GO:0004190|GO:0006508
c26378_g1_i1	-1.56424	5.962392	1.64E-05	0.001301	NA	NA	NA
c12535_g2_i1	-1.56286	3.633117	3.43E-05	0.002298	NA	UniRef90_K5VHZ6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VHZ6_PHACS	NA
c15299_g1_i1	-1.55645	4.014784	2.31E-05	0.0017	RecName: Full=A/G-specific adenine DNA glycosylase; AltName: Full=MutY homolog; Short=rMYH [Rattus norvegicus]	NA	GO:0006284
c15299_g1_i2	-1.55645	4.014784	2.31E-05	0.0017	NA	NA	NA
c15299_g1_i3	-1.55645	4.014784	2.31E-05	0.0017	NA	NA	GO:0006284
c7308_g1_i1	-1.55592	2.316096	0.000495	0.017367	NA	NA	NA

c21758_g1_i1	-1.55552	5.044844	7.46E-04	0.023738	NA	NA	NA
c16425_g1_i1	-1.5523	4.073235	0.001469	0.039356	NA	NA	NA
c16425_g1_i2	-1.5523	4.073235	0.001469	0.039356	NA	NA	NA
c16425_g1_i3	-1.5523	4.073235	0.001469	0.039356	NA	UniRef90_K5W3F2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3F2_PHACS	NA
c12991_g1_i1	-1.55187	4.599532	5.80E-05	0.00349	NA	NA	NA
c12862_g3_i1	-1.55147	2.90301	0.000173	0.007753	NA	UniRef90_K5XCK0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XCK0_PHACS	NA
c12000_g1_i1	-1.54941	4.02087	0.001423	0.038565	RecName: Full=Sulfite efflux pump SSU1 [Trichophyton rubrum]	NA	GO:0016021|GO:0055085
c12890_g3_i1	-1.5472	2.569386	0.000702	0.022651	NA	NA	NA
c12187_g2_i1	-1.54318	7.316566	1.75E-05	1.37E-03	RecName: Full=Heat shock protein 90-1; Short=AtHSP90.1; AltName: Full=Heat shock protein 81-1; Short=HSP81-1; AltName: Full=Heat shock protein 83 [Arabidopsis thaliana]	UniRef90_R7S7P6 Heat shock protein 90 n=4 Tax=Polyporales RepID=R7S7P6_TRAVS	GO:0005524|GO:0006457|GO:0006950|GO:0051082
c12455_g1_i1	-1.53953	2.460815	0.00136	0.037327	NA	NA	NA
c12455_g1_i2	-1.53953	2.460815	0.00136	0.037327	NA	NA	NA
c16897_g1_i1	-1.53559	7.045866	2.04E-04	0.008914	NA	NA	GO:0018580|GO:0055114
c16897_g1_i2	-1.53559	7.045866	2.04E-04	0.008914	NA	NA	GO:0018580|GO:0055114
c16897_g1_i3	-1.53559	7.045866	0.000204	0.008914	NA	NA	GO:0018580|GO:0055114
c16897_g1_i4	-1.53559	7.045866	0.000204	0.008914	NA	NA	GO:0018580|GO:0055114
c16897_g1_i5	-1.53559	7.045866	0.000204	0.008914	RecName: Full=Probable nitronate monooxygenase; AltName: Full=Nitroalkane oxidase [Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305]	NA	GO:0018580|GO:0055114
c8903_g1_i1	-1.53373	3.086354	7.27E-05	0.004129	NA	NA	NA
c26379_g1_i1	-1.53335	7.238605	2.13E-05	0.001602	NA	NA	NA
c12317_g1_i1	-1.53283	4.593391	0.000241	0.010014	NA	UniRef90_A0A0C3RRK9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RRK9_PHLGI	NA
c17660_g1_i1	-1.53097	5.291877	9.30E-05	0.00499	NA	NA	NA
c17660_g1_i2	-1.53097	5.291877	9.30E-05	0.00499	NA	NA	NA
c17660_g1_i3	-1.53097	5.291877	9.30E-05	0.00499	NA	NA	NA

c17660_g1_i4	-1.53097	5.291877	9.30E-05	4.99E-03	NA	NA	NA
c17660_g1_i5	-1.53097	5.291877	9.30E-05	4.99E-03	NA	NA	NA
c17660_g1_i6	-1.53097	5.291877	9.30E-05	4.99E-03	RecName: Full=Xylosyltransferase oxt; AltName: Full=Peptide O-xylosyltransferase [Drosophila pseudoobscura pseudoobscura]	UniRef90_K5VKS1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VKS1_PHACS	NA
c23354_g1_i1	-1.52997	3.271386	0.000355	0.013445	NA	UniRef90_K5WLS1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLS1_PHACS	NA
c21708_g1_i1	-1.5283	2.774942	0.000182	0.008069	NA	NA	NA
c14195_g1_i1	-1.52725	3.811863	1.63E-04	0.007482	NA	NA	GO:0005515|GO:0008270|GO:0046872
c17630_g6_i1	-1.52515	6.8429	8.89E-05	0.004814	NA	NA	NA
c17630_g6_i2	-1.52515	6.8429	8.89E-05	0.004814	NA	NA	NA
c17630_g6_i3	-1.52515	6.8429	8.89E-05	0.004814	NA	NA	NA
c10170_g1_i1	-1.52391	2.377754	0.001426	0.038596	NA	NA	NA
c10170_g1_i2	-1.52391	2.377754	0.001426	0.038596	NA	NA	NA
c24963_g1_i1	-1.51848	2.578275	0.002034	0.049092	NA	NA	NA
c14813_g2_i1	-1.51262	4.211572	2.36E-04	0.009881	NA	NA	NA
c14813_g2_i2	-1.51262	4.211572	2.36E-04	0.009881	NA	NA	NA
c1440_g1_i1	-1.51128	5.54454	0.000443	0.016005	NA	NA	NA
c5193_g2_i1	-1.51078	3.213772	0.00014	0.006676	NA	NA	NA
c13623_g1_i1	-1.50767	3.464176	3.34E-04	1.28E-02	NA	NA	NA
c13623_g1_i2	-1.50767	3.464176	3.34E-04	1.28E-02	NA	NA	NA
c13513_g2_i1	-1.50504	3.677549	0.000118	0.005956	NA	NA	NA
c17142_g4_i1	-1.50331	3.963586	9.57E-04	0.028952	NA	NA	NA
c17142_g4_i2	-1.50331	3.963586	0.000957	0.028952	NA	NA	NA
c17142_g4_i3	-1.50331	3.963586	9.57E-04	0.028952	NA	NA	NA
c23358_g1_i1	-1.49973	2.222916	1.57E-03	4.10E-02	NA	NA	NA
c11190_g2_i1	-1.49914	3.500979	0.000258	0.010581	NA	NA	NA
c11190_g2_i2	-1.49914	3.500979	0.000258	0.010581	NA	NA	NA
c5146_g1_i1	-1.49901	3.383505	0.00185	0.04602	NA	NA	NA
c9410_g1_i1	-1.49575	2.442175	0.001186	0.033734	NA	NA	NA

c9410_g1_i2	-1.49575	2.442175	1.19E-03	3.37E-02	NA	NA	NA
c18181_g1_i1	-1.4947	3.201651	0.000396	0.01462	NA	NA	NA
c6692_g2_i1	-1.48759	6.085464	5.06E-05	0.003126	RecName: Full=Ornithine decarboxylase; Short=ODC [Schizosaccharomyces pombe 972h-]	NA	GO:0003824
c11439_g3_i1	-1.48416	6.990431	0.000535	0.018491	NA	NA	NA
c15659_g1_i1	-1.48309	7.432498	0.000305	0.012055	NA	NA	GO:0016614|GO:0050660|GO:0055114
c15659_g1_i2	-1.48309	7.432498	0.000305	0.012055	RecName: Full=Pyranose dehydrogenase 3; Short=PDH 3; AltName: Full=Pyranose:quinone oxidoreductase 3; Flags: Precursor [Leucoagaricus meleagris]	NA	GO:0016614|GO:0050660|GO:0055114
c12054_g1_i1	-1.48237	6.417349	0.000119	0.006022	RecName: Full=Bifunctional P-450:NADPH-P450 reductase; AltName: Full=Cytochrome P450foxy; AltName: Full=Fatty acid omega-hydroxylase; Includes: RecName: Full=Cytochrome P450 505; Includes: RecName: Full=NADPH--cytochrome P450 reductase [Fusarium oxysporum]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c16118_g1_i1	-1.48023	3.677074	0.000315	0.012335	NA	NA	NA
c16118_g1_i2	-1.48023	3.677074	3.15E-04	0.012335	NA	NA	NA
c16118_g1_i3	-1.48023	3.677074	3.15E-04	0.012335	NA	NA	NA
c16118_g1_i4	-1.48023	3.677074	0.000315	0.012335	NA	NA	NA
c15340_g2_i1	-1.48021	2.529256	7.42E-04	0.023679	NA	NA	NA
c13718_g1_i1	-1.47864	3.828229	1.26E-03	3.52E-02	NA	NA	GO:0000981|GO:0003677|GO:0005634|GO:0006351|GO:0006355|GO:0008270
c13718_g1_i2	-1.47864	3.828229	1.26E-03	0.035246	NA	NA	GO:0003677|GO:0005634|GO:0006351|GO:0008270
c17392_g3_i1	-1.47852	5.24499	0.000285	0.011437	RecName: Full=Beta-mannosidase A; AltName: Full=Mannanase A; Short=Mannase A; Flags: Precursor [Aspergillus aculeatus]	NA	NA
c13626_g1_i1	-1.4777	4.316339	2.89E-04	0.011555	NA	NA	NA
c13626_g1_i2	-1.4777	4.316339	0.000289	0.011555	RecName: Full=Aflatoxin B1 aldehyde reductase member 3; AltName: Full=AFB1 aldehyde reductase 2; Short=AFB1-AR 2 [Homo sapiens]	NA	NA

c12991_g3_i1	-1.47598	5.684183	4.30E-05	0.002735	NA	NA	NA
c18574_g1_i1	-1.47413	2.77439	1.18E-03	3.37E-02	NA	NA	NA
c13243_g2_i1	-1.47181	3.823035	0.000625	0.020868	NA	NA	NA
c12386_g1_i1	-1.46821	6.170561	1.53E-03	0.040545	NA	UniRef90_K5X1Z7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X1Z7_PHACS	NA
c12386_g1_i2	-1.46821	6.170561	0.001532	0.040545	NA	NA	NA
c10321_g2_i1	-1.46597	4.846445	0.000793	0.024932	NA	NA	NA
c10321_g2_i2	-1.46597	4.846445	7.93E-04	0.024932	NA	NA	NA
c24966_g1_i1	-1.45939	3.953209	0.000269	0.010966	NA	NA	NA
c17171_g1_i1	-1.45487	5.700004	0.001158	0.033262	RecName: Full=Vacuolar protein sorting-associated protein 13; AltName: Full=Suppression of the onset of impotence protein 1; AltName: Full=Vacuolar protein-targeting protein 2 [Saccharomyces cerevisiae S288c]	NA	NA
c12493_g1_i1	-1.44925	2.88172	7.62E-04	0.024112	NA	UniRef90_K5UUE2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UUE2_PHACS	NA
c15412_g2_i1	-1.44413	2.646094	0.000597	0.020096	RecName: Full=UPF0187 protein sll1024 [Synechocystis sp. PCC 6803 substr. Kazusa]	NA	NA
c4418_g1_i1	-1.44283	10.44444	1.84E-03	4.59E-02	NA	NA	GO:0016021|GO:0055085
c4418_g1_i2	-1.44283	10.44444	0.00184	0.045868	RecName: Full=Uncharacterized transporter C3H1.06c [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c9643_g2_i1	-1.44226	3.067379	0.001565	0.040973	NA	NA	NA
c9643_g2_i2	-1.44226	3.067379	1.56E-03	4.10E-02	NA	NA	NA
c16232_g2_i1	-1.43483	4.544642	0.000158	0.007318	NA	UniRef90_A0A060SM79 Uncharacterized protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060SM79_PYCCI	GO:0003676|GO:0004523
c16232_g2_i2	-1.43483	4.544642	0.000158	0.007318	NA	NA	NA
c13575_g1_i1	-1.43112	2.883874	1.32E-03	0.036398	NA	NA	NA
c13575_g1_i2	-1.43112	2.883874	0.001317	0.036398	NA	NA	NA
c13575_g1_i3	-1.43112	2.883874	1.32E-03	0.036398	NA	NA	NA
c13575_g1_i4	-1.43112	2.883874	0.001317	0.036398	NA	NA	NA

c14611_g3_i1	-1.42837	3.339344	0.000221	0.009421	NA	UniRef90_K5VG61 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VG61_PHACS	NA
c15869_g4_i1	-1.42804	3.9141	1.83E-03	0.045625	NA	NA	NA
c9171_g1_i1	-1.42622	4.905033	1.71E-04	7.71E-03	NA	NA	NA
c9171_g1_i2	-1.42622	4.905033	0.000171	0.007705	NA	NA	NA
c9171_g1_i3	-1.42622	4.905033	0.000171	0.007705	NA	NA	NA
c21879_g1_i1	-1.42573	4.978431	5.11E-04	0.017814	NA	NA	NA
c12879_g1_i1	-1.4256	3.34443	6.33E-04	0.020973	NA	NA	NA
c17608_g2_i1	-1.42535	5.101291	9.23E-04	0.028104	RecName: Full=Fruiting body protein SC3; AltName: Full=Hydrophobin SC3; Flags: Precursor [Schizophyllum commune]	UniRef90_UPI0004621EB0 fungal hydrophobin n=1 Tax=Trametes versicolor (strain FP-101664) RepID=UPI0004621EB0	GO:0005199|GO:0009277
c17608_g2_i2	-1.42535	5.101291	0.000923	0.028104	NA	NA	GO:0005199|GO:0009277
c17794_g1_i1	-1.4214	4.370113	0.000438	0.015878	NA	UniRef90_K5WWC3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WWC3_PHACS	NA
c16719_g1_i1	-1.42067	4.125891	0.000438	0.015878	NA	NA	NA
c16719_g1_i2	-1.42067	4.125891	0.000438	0.015878	NA	NA	NA
c16719_g1_i3	-1.42067	4.125891	0.000438	0.015878	NA	NA	NA
c8780_g1_i1	-1.41485	4.169301	1.54E-03	4.06E-02	RecName: Full=Uncharacterized protein C2A9.02 [Schizosaccharomyces pombe 972h-]	NA	GO:0003824|GO:0004616|GO:0006098|GO:0050662|GO:0055114
c702_g1_i1	-1.41253	3.515553	6.92E-04	0.022412	NA	UniRef90_A0A0C3NWU8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NWU8_PHLGI	NA
c2350_g1_i1	-1.41235	7.592542	0.00014	0.006699	NA	NA	NA
c26298_g1_i1	-1.40822	8.427996	0.000574	0.019574	RecName: Full=Probable glycosidase C21B10.07 [Schizosaccharomyces pombe 972h-]	NA	NA
c10188_g1_i1	-1.40429	5.891752	0.001732	0.043846	NA	NA	NA
c4833_g1_i1	-1.4009	7.348122	0.000176	0.007842	RecName: Full=Histone-lysine N-methyltransferase SET9; AltName: Full=SET domain protein 9 [Phaeosphaeria nodorum SN15]	UniRef90_A0A0C3SF86 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SF86_PHLGI	NA

c15580_g2_i1	-1.40067	4.040564	0.000137	0.00658	NA	NA	NA
c12052_g1_i1	-1.40023	8.161857	0.000217	0.00931	NA	NA	GO:0010181|GO:0016491|GO:0055114
c12052_g1_i2	-1.40023	8.161857	0.000217	0.00931	NA	NA	GO:0016491|GO:0055114
c12052_g1_i3	-1.40023	8.161857	0.000217	0.00931	RecName: Full=Bifunctional P-450:NADPH-P450 reductase; AltName: Full=Cytochrome P450foxy; AltName: Full=Fatty acid omega-hydroxylase; Includes: RecName: Full=Cytochrome P450 505; Includes: RecName: Full=NADPH--cytochrome P450 reductase [Fusarium oxysporum]	NA	GO:0010181|GO:0016491|GO:0055114
c12052_g1_i4	-1.40023	8.161857	0.000217	0.00931	NA	NA	GO:0010181|GO:0016491|GO:0055114
c16016_g1_i1	-1.39949	3.740719	0.000123	0.006151	NA	NA	NA
c12816_g1_i1	-1.39849	2.438891	0.001705	0.043499	NA	NA	NA
c1672_g1_i1	-1.39831	2.605726	0.001337	0.036824	NA	NA	NA
c17502_g1_i1	-1.3979	5.877126	9.51E-04	0.028841	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17502_g1_i2	-1.3979	5.877126	0.000951	0.028841	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17502_g1_i3	-1.3979	5.877126	0.000951	0.028841	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17502_g1_i4	-1.3979	5.877126	9.51E-04	2.88E-02	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17502_g1_i5	-1.3979	5.877126	9.51E-04	2.88E-02	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17502_g1_i6	-1.3979	5.877126	9.51E-04	2.88E-02	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c17502_g1_i7	-1.3979	5.877126	9.51E-04	2.88E-02	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17502_g1_i8	-1.3979	5.877126	9.51E-04	2.88E-02	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus parasiticus]	UniRef90_K5UMK4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UMK4_PHACS	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c17054_g2_i1	-1.39694	3.484454	1.57E-03	0.041152	RecName: Full=Probable drug/proton antiporter YHK8 [Saccharomyces cerevisiae S288c]	NA	GO:0016021|GO:0055085
c17054_g2_i2	-1.39694	3.484454	1.57E-03	0.041152	NA	NA	GO:0016021|GO:0055085
c16458_g1_i1	-1.39413	3.928805	7.90E-05	0.004363	NA	NA	NA
c16893_g1_i1	-1.39397	3.919732	1.18E-03	0.033685	NA	NA	NA
c16893_g1_i2	-1.39397	3.919732	1.18E-03	0.033685	NA	NA	NA
c16893_g1_i3	-1.39397	3.919732	0.001182	0.033685	NA	NA	NA
c16893_g1_i4	-1.39397	3.919732	0.001182	0.033685	NA	NA	NA
c16893_g1_i5	-1.39397	3.919732	0.001182	0.033685	NA	NA	NA
c16893_g1_i6	-1.39397	3.919732	0.001182	0.033685	NA	NA	NA
c16683_g2_i1	-1.3934	7.269975	7.43E-05	0.004195	NA	NA	GO:0005515
c16683_g2_i2	-1.3934	7.269975	7.43E-05	0.004195	NA	NA	GO:0005515
c16683_g2_i3	-1.3934	7.269975	7.43E-05	0.004195	RecName: Full=Ubiquitin; Flags: Precursor [Triticum aestivum]	NA	GO:0005515
c16683_g2_i4	-1.3934	7.269975	7.43E-05	0.004195	NA	NA	GO:0005515
c16082_g1_i1	-1.3923	4.387046	2.55E-04	0.010496	RecName: Full=Abscisic acid 8'-hydroxylase 2; Short=ABA 8'-hydroxylase 2; AltName: Full=Cytochrome P450 707A6; AltName: Full=OsABA8ox2 [Oryza sativa Indica Group]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c69_g1_i1	-1.39199	5.998405	0.000147	0.006924	RecName: Full=Heat shock protein STI1 [Saccharomyces cerevisiae S288c]	UniRef90_J4GAS7 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4GAS7_FIBRA	GO:0005515
c14420_g1_i1	-1.38761	5.924015	0.000206	0.008941	NA	NA	NA
c14420_g1_i2	-1.38761	5.924015	0.000206	0.008941	NA	NA	NA
c12054_g2_i1	-1.38194	5.976605	0.000228	0.009631	RecName: Full=Bifunctional P-450:NADPH-P450 reductase; AltName: Full=Cytochrome P450foxy; AltName: Full=Fatty acid omega-hydroxylase; Includes: RecName: Full=Cytochrome P450	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

					505; Includes: RecName: Full=NADPH--cytochrome P450 reductase [Fusarium oxysporum]		
c2892_g1_i1	-1.37772	3.766397	5.26E-04	0.018228	NA	NA	NA
c14238_g2_i1	-1.37675	3.101304	6.54E-04	0.021577	NA	NA	NA
c14238_g2_i2	-1.37675	3.101304	6.54E-04	0.021577	NA	NA	NA
c12006_g1_i1	-1.37668	5.923792	2.22E-04	0.009474	NA	NA	NA
c12006_g1_i2	-1.37668	5.923792	0.000222	0.009474	NA	NA	NA
c17345_g2_i1	-1.37503	3.799376	0.000759	0.024077	NA	NA	NA
c17345_g2_i10	-1.37503	3.799376	7.59E-04	0.024077	NA	NA	NA
c17345_g2_i2	-1.37503	3.799376	0.000759	0.024077	NA	NA	NA
c17345_g2_i3	-1.37503	3.799376	0.000759	0.024077	NA	NA	NA
c17345_g2_i4	-1.37503	3.799376	0.000759	0.024077	NA	NA	NA
c17345_g2_i5	-1.37503	3.799376	0.000759	0.024077	NA	NA	NA
c17345_g2_i6	-1.37503	3.799376	0.000759	0.024077	NA	NA	NA
c17345_g2_i7	-1.37503	3.799376	0.000759	0.024077	NA	NA	NA
c17345_g2_i8	-1.37503	3.799376	0.000759	0.024077	NA	NA	NA
c17345_g2_i9	-1.37503	3.799376	7.59E-04	0.024077	NA	NA	NA
c16683_g3_i1	-1.37218	6.091198	1.52E-04	0.007111	NA	NA	NA
c16887_g1_i1	-1.369	4.034417	2.06E-03	0.049512	NA	NA	NA
c16887_g1_i2	-1.369	4.034417	2.06E-03	0.049512	NA	NA	NA
c7429_g1_i1	-1.36534	3.182256	0.002066	0.049605	RecName: Full=PHO85 cyclin-2; AltName: Full=Cyclin HCS26 homolog; AltName: Full=G1/S-specific cyclin PCL2 [Saccharomyces cerevisiae S288c]	NA	GO:0000079|GO:0019901
c7429_g1_i2	-1.36534	3.182256	0.002066	0.049605	NA	NA	GO:0000079|GO:0019901
c11561_g1_i1	-1.36501	10.18844	0.000283	0.011376	RecName: Full=Peptidyl-prolyl cis-trans isomerase; Short=PPIase; AltName: Full=Cyclophilin; Short=CPH; AltName: Full=Cyclosporin A-binding protein; AltName: Full=Rotamase [Schizosaccharomyces pombe 972h-]	NA	GO:0000413|GO:0003755|GO:0006457
c11561_g1_i2	-1.36501	10.18844	0.000283	0.011376	NA	NA	GO:0000413|GO:0003755|GO:0006457
c16604_g2_i1	-1.36221	3.126043	0.001301	0.036076	NA	NA	NA
c16604_g2_i2	-1.36221	3.126043	1.30E-03	0.036076	NA	NA	GO:0005198

c16604_g2_i3	-1.36221	3.126043	1.30E-03	0.036076	NA	NA	NA
c16604_g2_i4	-1.36221	3.126043	0.001301	0.036076	NA	NA	NA
c24598_g1_i1	-1.35893	6.569289	6.25E-04	0.020862	NA	NA	NA
c12658_g1_i1	-1.35866	7.776003	6.32E-04	0.020973	RecName: Full=Ribosome biogenesis protein enp2 homolog [Schizosaccharomyces pombe 972h-]	UniRef90_K5WCQ2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCQ2_PHACS	GO:0005634
c13640_g1_i1	-1.35676	4.513008	0.000119	0.006022	NA	NA	NA
c17513_g1_i1	-1.35246	4.366064	5.97E-04	2.01E-02	NA	UniRef90_A0A0C3SB91 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SB91_PHLGI	NA
c17513_g1_i2	-1.35246	4.366064	5.97E-04	2.01E-02	NA	NA	NA
c17513_g1_i3	-1.35246	4.366064	5.97E-04	2.01E-02	NA	NA	NA
c14049_g1_i1	-1.35171	5.868958	3.17E-04	1.24E-02	NA	NA	NA
c14049_g1_i2	-1.35171	5.868958	0.000317	0.012362	NA	NA	NA
c24739_g1_i1	-1.34725	3.622557	5.09E-04	0.017783	NA	NA	NA
c15440_g1_i1	-1.34351	6.731251	1.14E-03	0.032972	RecName: Full=Glycerol 2-dehydrogenase (NADP(+)); AltName: Full=Galactose-inducible crystallin-like protein 1 [Saccharomyces cerevisiae S288c]	NA	NA
c13814_g2_i1	-1.34321	3.27111	0.000697	0.022523	NA	NA	NA
c13814_g2_i2	-1.34321	3.27111	0.000697	0.022523	NA	NA	NA
c22119_g1_i1	-1.34224	4.5513	2.21E-04	9.42E-03	NA	UniRef90_K5VE38 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VE38_PHACS	NA
c9799_g1_i1	-1.33529	5.95645	3.77E-04	1.41E-02	NA	NA	NA
c9799_g1_i2	-1.33529	5.95645	3.77E-04	1.41E-02	NA	UniRef90_K5W8Z2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8Z2_PHACS	NA
c13513_g1_i1	-1.33147	4.546229	0.000886	0.027204	NA	NA	NA
c10383_g2_i1	-1.33045	5.877406	0.000163	0.007484	NA	NA	NA
c10383_g2_i2	-1.33045	5.877406	0.000163	0.007484	NA	NA	NA
c15160_g1_i1	-1.32979	4.110299	1.44E-03	0.038863	RecName: Full=Probable voltage-gated potassium channel subunit beta; AltName: Full=K(+) channel subunit beta; AltName:	NA	NA

					Full=Potassium voltage beta 1; Short=KV-beta1 [Arabidopsis thaliana]		
c23397_g1_i1	-1.32824	6.260706	1.15E-03	3.31E-02	RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=PGDH [Methanothermobacter thermautotrophicus str. Delta H]	UniRef90_K5WB97 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WB97_PHACS	GO:0004616|GO:0006098|GO:0008152|GO:0016616|GO:0051287|GO:0055114
c10559_g2_i1	-1.32752	4.748147	0.000164	0.007497	RecName: Full=Purine-cytosine permease fcyB; Short=PCP fcyB; AltName: Full=Cytosine/purine transport protein fcyB; AltName: Full=Fluorocytosine resistance protein fcyB [Aspergillus nidulans FGSC A4]	NA	NA
c14851_g1_i1	-1.32522	5.408176	0.0003	0.011879	NA	NA	NA
c14851_g1_i2	-1.32522	5.408176	0.0003	0.011879	NA	NA	NA
c14851_g1_i3	-1.32522	5.408176	3.00E-04	0.011879	NA	UniRef90_K5VPY2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPY2_PHACS	NA
c22827_g1_i1	-1.32489	8.633057	1.57E-03	0.04106	NA	UniRef90_A0A0C3PA48 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PA48_PHLGI	NA
c11248_g1_i1	-1.32135	4.605352	0.001516	0.040188	RecName: Full=Uncharacterized hydrolase YugF [Bacillus subtilis subsp. subtilis str. 168]	NA	NA
c11248_g1_i2	-1.32135	4.605352	0.001516	0.040188	NA	NA	NA
c14731_g1_i1	-1.32128	7.032148	0.00041	0.015073	NA	UniRef90_K5W3K8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3K8_PHACS	NA
c14731_g1_i2	-1.32128	7.032148	0.00041	0.015073	NA	NA	NA
c14731_g1_i3	-1.32128	7.032148	0.00041	0.015073	NA	NA	NA
c15055_g1_i1	-1.32031	5.126206	5.52E-04	0.018961	RecName: Full=Uncharacterized protein YDR282C [Saccharomyces cerevisiae S288c]	NA	NA
c15055_g1_i2	-1.32031	5.126206	5.52E-04	0.018961	NA	NA	NA
c18665_g1_i1	-1.31364	5.013056	0.000714	0.022933	RecName: Full=VMS1 homolog C1827.04 [Schizosaccharomyces pombe 972h-]	NA	NA
c11779_g1_i1	-1.31148	3.746434	0.001248	0.03504	NA	NA	NA
c11779_g1_i2	-1.31148	3.746434	1.25E-03	3.50E-02	NA	NA	NA

c23387_g1_i1	-1.31061	6.717484	0.000131	0.006379	NA	NA	NA
c24224_g1_i1	-1.31042	3.346649	2.08E-03	4.99E-02	NA	NA	NA
c16340_g2_i1	-1.30932	3.455333	7.03E-04	2.27E-02	NA	NA	NA
c16340_g2_i2	-1.30932	3.455333	7.03E-04	2.27E-02	NA	NA	NA
c16340_g2_i3	-1.30932	3.455333	7.03E-04	2.27E-02	RecName: Full=Tubulin-folding cofactor D; Short=AtTFCD; AltName: Full=Protein CHAMPIGNON; AltName: Full=Protein EMBRYO DEFECTIVE 133; AltName: Full=Protein TITAN 1 [Arabidopsis thaliana]	UniRef90_K5UHS2 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UHS2_PHACS	NA
c17836_g1_i1	-1.30861	7.38286	0.000388	0.014406	NA	UniRef90_K5WJ87 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJ87_PHACS	NA
c19558_g1_i1	-1.30848	5.069224	5.83E-04	1.98E-02	NA	NA	NA
c19578_g1_i1	-1.30559	3.997376	0.000154	0.007167	NA	NA	NA
c8390_g1_i1	-1.30547	6.251464	0.001556	0.04085	NA	NA	NA
c16732_g3_i1	-1.29866	2.848852	1.76E-03	4.42E-02	NA	NA	NA
c16732_g3_i2	-1.29866	2.848852	1.76E-03	4.42E-02	NA	NA	NA
c16732_g3_i3	-1.29866	2.848852	1.76E-03	4.42E-02	NA	NA	NA
c16732_g3_i4	-1.29866	2.848852	1.76E-03	4.42E-02	NA	NA	NA
c16732_g3_i5	-1.29866	2.848852	0.001755	0.044232	NA	NA	NA
c17537_g2_i1	-1.29576	3.597244	0.001514	0.040168	NA	UniRef90_K5V3Q9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3Q9_PHACS	NA
c17537_g2_i2	-1.29576	3.597244	0.001514	0.040168	NA	NA	NA
c17498_g1_i1	-1.29503	4.080166	0.000493	0.017321	NA	NA	NA
c17498_g1_i2	-1.29503	4.080166	0.000493	0.017321	NA	NA	NA
c17498_g1_i3	-1.29503	4.080166	0.000493	0.017321	NA	NA	NA
c17498_g1_i4	-1.29503	4.080166	0.000493	0.017321	NA	NA	NA
c17498_g1_i5	-1.29503	4.080166	4.93E-04	0.017321	NA	NA	NA
c21126_g1_i1	-1.29405	7.158181	0.00031	0.012197	RecName: Full=Antizyme inhibitor 2; Short=AzI2; AltName: Full=Ornithine decarboxylase 2; Short=ODC 2; Short=xODC2; AltName: Full=Ornithine decarboxylase-like protein; Short=ODC-	NA	GO:0003824

					like protein; AltName: Full=ornithine decarboxylase paralog; Short=ODC-p [Xenopus laevis]		
c22305_g1_i1	-1.29039	3.384944	1.24E-03	3.49E-02	NA	UniRef90_K5WJG5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJG5_PHACS	NA
c17644_g3_i1	-1.28603	6.400606	0.000801	0.025136	NA	NA	GO:0016614|GO:0055114
c17644_g3_i2	-1.28603	6.400606	0.000801	0.025136	NA	NA	GO:0016614|GO:0050660|GO:0055114
c17644_g3_i3	-1.28603	6.400606	0.000801	0.025136	RecName: Full=Pyranose dehydrogenase; Short=PDH; AltName: Full=Pyranose:quinone oxidoreductase 1; Flags: Precursor [Agaricus campestris]	UniRef90_K5W1J4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1J4_PHACS	GO:0016614|GO:0050660|GO:0055114
c17644_g3_i4	-1.28603	6.400606	0.000801	0.025136	NA	NA	GO:0016614|GO:0050660|GO:0055114
c17644_g3_i5	-1.28603	6.400606	0.000801	0.025136	NA	NA	GO:0016614|GO:0050660|GO:0055114
c6460_g1_i1	-1.2825	6.496317	0.000859	0.026588	NA	NA	NA
c16578_g2_i1	-1.27894	4.488563	0.000876	0.026968	NA	NA	NA
c16578_g2_i2	-1.27894	4.488563	0.000876	0.026968	NA	NA	NA
c16578_g2_i3	-1.27894	4.488563	0.000876	0.026968	NA	NA	NA
c11439_g1_i1	-1.27504	7.044151	0.001234	0.034765	NA	NA	GO:0003824|GO:0008152
c10351_g1_i1	-1.27413	5.336921	0.00199	0.048382	RecName: Full=Alpha-protein kinase vwkA; AltName: Full=von Willebrand factor A alpha-kinase; Short=vWF kinase [Dictyostelium discoideum]	NA	NA
c14039_g1_i1	-1.27007	6.822751	2.40E-04	0.009981	NA	NA	GO:0005515
c14039_g1_i2	-1.27007	6.822751	2.40E-04	0.009981	NA	NA	GO:0005515
c14039_g1_i3	-1.27007	6.822751	2.40E-04	0.009981	RecName: Full=WD repeat-containing protein 61 [Xenopus laevis]	NA	GO:0005515
c14039_g1_i4	-1.27007	6.822751	2.40E-04	9.98E-03	NA	NA	GO:0005515
c14039_g1_i5	-1.27007	6.822751	0.00024	0.009981	NA	NA	GO:0005515
c19452_g1_i1	-1.2669	8.3334	3.17E-04	1.24E-02	RecName: Full=SPRY domain-containing protein C285.10c [Schizosaccharomyces pombe 972h-]	NA	GO:0005515

c23519_g1_i1	-1.26619	4.953863	1.54E-03	4.06E-02	NA	UniRef90_K5WCV1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCV1_PHACS	NA
c17390_g2_i1	-1.26118	3.259754	0.001468	0.039356	NA	NA	NA
c17390_g2_i2	-1.26118	3.259754	0.001468	0.039356	RecName: Full=Glutathione S-transferase 1; AltName: Full=GST-I [Schizosaccharomyces pombe 972h-]	NA	NA
c17390_g2_i3	-1.26118	3.259754	0.001468	0.039356	NA	NA	NA
c25227_g1_i1	-1.25688	4.886558	0.001884	0.046529	NA	NA	NA
c17385_g1_i1	-1.25677	3.500601	0.001541	0.040582	NA	NA	NA
c17385_g1_i2	-1.25677	3.500601	0.001541	0.040582	NA	NA	NA
c13180_g1_i1	-1.25506	6.811428	1.41E-03	0.038392	RecName: Full=Ubiquitin-like modifier hub1 [Schizosaccharomyces pombe 972h-]	NA	GO:0005515
c4823_g2_i1	-1.25248	8.430232	4.82E-04	0.017031	NA	UniRef90_K5V4H0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V4H0_PHACS	NA
c10763_g1_i1	-1.25114	4.09464	1.74E-03	0.044022	RecName: Full=3-phosphoinositide-dependent protein kinase 1; AltName: Full=Protein kinase B kinase; Short=PkB kinase [Rattus norvegicus]	NA	GO:0004672|GO:0005524|GO:0006468
c9086_g1_i1	-1.25029	3.129359	1.93E-03	0.047367	NA	NA	NA
c4834_g1_i1	-1.24416	9.255587	8.54E-04	0.026463	RecName: Full=Histone-lysine N-methyltransferase set9; AltName: Full=Lysine N-methyltransferase 5; AltName: Full=SET domain protein 9 [Schizosaccharomyces pombe 972h-]	UniRef90_K5UWX6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UWX6_PHACS	GO:0005515
c10345_g2_i1	-1.24097	3.810626	9.79E-04	0.029394	NA	NA	NA
c17369_g1_i1	-1.2384	6.095147	0.000762	0.024112	NA	NA	NA
c17369_g1_i2	-1.2384	6.095147	0.000762	0.024112	NA	NA	NA
c17369_g1_i3	-1.2384	6.095147	0.000762	0.024112	NA	NA	NA
c17369_g1_i4	-1.2384	6.095147	0.000762	0.024112	NA	NA	NA
c17369_g1_i5	-1.2384	6.095147	0.000762	0.024112	NA	NA	NA
c17369_g1_i6	-1.2384	6.095147	0.000762	0.024112	NA	NA	NA
c17369_g1_i7	-1.2384	6.095147	0.000762	0.024112	NA	NA	NA
c16793_g2_i1	-1.23479	4.81619	8.90E-04	0.027303	NA	NA	NA
c16793_g2_i2	-1.23479	4.81619	8.90E-04	0.027303	NA	NA	NA

c16793_g2_i3	-1.23479	4.81619	8.90E-04	0.027303	NA	NA	NA
c6017_g2_i1	-1.23215	6.929798	0.00036	0.013573	RecName: Full=UPF0643 protein PB2B2.08 [Schizosaccharomyces pombe 972h-]	UniRef90_K5W564 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W564_PHACS	NA
c14195_g2_i1	-1.23138	4.757693	0.001896	0.046716	NA	NA	NA
c17624_g2_i1	-1.22926	6.586006	0.000665	0.021784	NA	UniRef90_K5UL69 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UL69_PHACS	NA
c17624_g2_i2	-1.22926	6.586006	0.000665	0.021784	NA	NA	NA
c17624_g2_i3	-1.22926	6.586006	0.000665	0.021784	NA	NA	NA
c17624_g2_i4	-1.22926	6.586006	0.000665	0.021784	NA	NA	NA
c17624_g2_i5	-1.22926	6.586006	0.000665	0.021784	NA	NA	NA
c17624_g2_i6	-1.22926	6.586006	0.000665	0.021784	NA	NA	NA
c17624_g2_i7	-1.22926	6.586006	0.000665	0.021784	NA	NA	NA
c10578_g2_i1	-1.22869	6.350204	0.00054	0.018641	RecName: Full=Aspartic protease; Flags: Precursor [Xanthophyllomyces dendrorhous]	NA	GO:0004190|GO:0006508
c10366_g2_i1	-1.22459	8.097881	0.001363	0.037391	RecName: Full=Probable glycosidase CRH2; AltName: Full=Congo red hypersensitive protein 2; AltName: Full=Unknown transcript 2 protein; Flags: Precursor [Saccharomyces cerevisiae S288c]	NA	GO:0004553|GO:0005975
c10954_g3_i1	-1.21686	3.111109	0.001877	0.046421	NA	NA	NA
c13972_g1_i1	-1.21526	5.886475	0.000778	0.024537	NA	NA	GO:0003677|GO:0005634|GO:0006351|GO:0008270
c2383_g2_i1	-1.21366	6.991832	1.75E-03	4.41E-02	NA	NA	NA
c16099_g1_i1	-1.21232	5.398397	0.00165	0.042542	NA	NA	NA
c16099_g1_i2	-1.21232	5.398397	0.00165	0.042542	NA	NA	NA
c16099_g1_i3	-1.21232	5.398397	0.00165	0.042542	NA	NA	NA
c16318_g1_i1	-1.19943	5.893343	1.18E-03	0.033618	NA	NA	GO:0004672|GO:0005524|GO:0006468
c16318_g1_i2	-1.19943	5.893343	1.18E-03	0.033618	NA	NA	GO:0004672|GO:0005524|GO:0006468

c16318_g1_i3	-1.19943	5.893343	0.001178	0.033618	RecName: Full=Serine/threonine-protein kinase fray2; AltName: Full=STE20-like kinase fray2 [Dictyostelium discoideum]	UniRef90_K5XCP8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XCP8_PHACS	GO:0004672|GO:0005524|GO:0006468
c16318_g1_i4	-1.19943	5.893343	1.18E-03	0.033618	NA	NA	GO:0004672|GO:0005524|GO:0006468
c16318_g1_i5	-1.19943	5.893343	1.18E-03	0.033618	NA	NA	GO:0004672|GO:0005524|GO:0006468
c17516_g1_i1	-1.19902	4.887035	0.001709	0.043499	NA	NA	NA
c17516_g1_i2	-1.19902	4.887035	0.001709	0.043499	NA	NA	NA
c17516_g1_i3	-1.19902	4.887035	1.71E-03	0.043499	NA	NA	NA
c17516_g1_i4	-1.19902	4.887035	0.001709	0.043499	NA	NA	NA
c2383_g1_i1	-1.19871	4.187219	1.23E-03	3.47E-02	NA	NA	NA
c12420_g3_i1	-1.19863	3.513195	0.001435	0.0388	RecName: Full=Uncharacterized MFS-type transporter C1683.03c [Schizosaccharomyces pombe 972h-]	UniRef90_K5W1Y1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1Y1_PHACS	NA
c16247_g1_i1	-1.19853	4.991068	0.002087	0.049981	RecName: Full=Hsp90 co-chaperone Cdc37; AltName: Full=Cell division control protein 37; AltName: Full=Hsp90 chaperone protein kinase-targeting subunit [Schizosaccharomyces pombe 972h-]	UniRef90_K5VKN9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VKN9_PHACS	GO:0019901
c19754_g1_i1	-1.1949	4.157003	1.84E-03	0.045893	RecName: Full=Acyl-CoA dehydrogenase family member 10; Short=ACAD-10 [Mus musculus]	NA	NA
c17103_g1_i1	-1.1865	3.087421	1.68E-03	0.043084	NA	NA	NA
c2434_g1_i1	-1.18361	8.218106	0.002039	0.04917	RecName: Full=Probable indole-3-pyruvate monooxygenase YUCCA3; AltName: Full=Flavin-containing monooxygenase YUCCA3 [Arabidopsis thaliana]	NA	GO:0004499|GO:0016491|GO:0050660|GO:0050661|GO:0055114
c17007_g1_i1	-1.18344	3.587282	0.001881	0.046478	NA	NA	NA
c18603_g1_i1	-1.17634	5.772576	0.001359	0.037327	RecName: Full=Uncharacterized ABC transporter ATP-binding protein C16H5.08c [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0016887
c17414_g1_i1	-1.1632	5.179731	1.94E-03	0.04751	NA	NA	NA
c17414_g1_i2	-1.1632	5.179731	1.94E-03	0.04751	NA	NA	NA
c17414_g1_i3	-1.1632	5.179731	0.001941	0.04751	NA	NA	NA
c17414_g1_i4	-1.1632	5.179731	1.94E-03	4.75E-02	RecName: Full=Ino eighty subunit 1 [Aspergillus nidulans FGSC A4]	NA	NA

c2350_g2_i1	-1.14161	3.821807	0.001657	0.042656	NA	NA	NA
c15090_g2_i1	-1.13312	6.479523	0.001294	0.03603	NA	NA	GO:0004014|GO:0006597|GO:0008295
c15090_g2_i2	-1.13312	6.479523	0.001294	0.03603	RecName: Full=S-adenosylmethionine decarboxylase proenzyme; Short=AdoMetDC; Short=SAMDC; Contains: RecName: Full=S-adenosylmethionine decarboxylase alpha chain; Contains: RecName: Full=S-adenosylmethionine decarboxylase beta chain; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	GO:0004014|GO:0006597|GO:0008295
c4345_g1_i1	-1.13144	9.663784	1.37E-03	0.037587	NA	NA	NA
c17451_g1_i1	-1.13055	4.576357	0.001267	0.035328	NA	NA	NA
c15124_g1_i1	-1.10951	5.765137	0.001415	0.038417	NA	NA	NA
c15124_g1_i2	-1.10951	5.765137	1.42E-03	0.038417	NA	NA	NA
c15124_g1_i3	-1.10951	5.765137	0.001415	0.038417	NA	NA	NA
c15124_g1_i4	-1.10951	5.765137	1.42E-03	3.84E-02	NA	NA	NA
c4127_g1_i1	-1.10106	5.666637	0.001357	0.037305	NA	NA	NA
c4127_g1_i2	-1.10106	5.666637	1.36E-03	0.037305	NA	NA	NA
c15961_g1_i1	-1.07344	4.547347	0.001672	0.042956	RecName: Full=Cell division control protein 53; AltName: Full=Cullin-A; AltName: Full=E3 ubiquitin ligase complex SCF subunit CDC53 [Saccharomyces cerevisiae S288c]	NA	GO:0006511|GO:0031461|GO:0031625
c15961_g1_i2	-1.07344	4.547347	0.001672	0.042956	NA	NA	GO:0006511|GO:0031461|GO:0031625

Table S2 Data for *P. chrysosporium* transcripts.

id	logFC	logCPM	PValue	FDR	Swissprot	Uniref90	GO
c6426_g1_i1	8.212962	2.672911	2.81E-09	5.73E-07	NA	UniRef90_K5W115 Glycoside hydrolase family 61 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W115_PHACS	NA
c3966_g1_i1	7.601878	2.126115	7.01E-14	3.73E-11	NA	NA	NA
c3966_g1_i2	7.601878	2.126115	7.01E-14	3.73E-11	NA	NA	NA
c3966_g1_i3	7.601878	2.126115	7.01E-14	3.73E-11	NA	UniRef90_UPI000455F98D hypothetical protein CONPUDRAFT_137497 n=1 Tax=Coniophora puteana (strain RWD-64-598) RepID=UPI000455F98D	NA
c2167_g1_i1	7.259433	4.35114	2.25E-12	7.86E-10	RecName: Full=Exoglucanase 1; AltName: Full=1,4-beta-cellobiohydrolase; AltName: Full=Exocellobiohydrolase I; AltName: Full=Exoglucanase I; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_O42638 Cellulose binding protein (Fragment) n=1 Tax=Phanerochaete chrysosporium RepID=O42638_PHACH	NA
c14300_g1_i1	7.150186	4.746444	2.21E-17	2.57E-14	RecName: Full=Probable endo-beta-1,4-glucanase D; Short=Endoglucanase D; AltName: Full=Carboxymethylcellulase D; AltName: Full=Cellulase D; Flags: Precursor [Aspergillus terreus NIH2624]	NA	NA
c15257_g1_i1	7.071486	8.208553	1.97E-13	9.60E-11	RecName: Full=Cellobiose dehydrogenase; Short=CDH; AltName: Full=Cellobiose-quinone oxidoreductase; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0016614|GO:0050660|GO:0055114
c4493_g1_i1	7.050491	1.714656	0.001189	0.022682	NA	UniRef90_B8MI73 Putative uncharacterized protein n=1 Tax=Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) RepID=B8MI73_TALSN	NA

c9808_g1_i1	6.969711	9.593259	1.61E-14	1.06E-11	RecName: Full=Exoglucanase 3; AltName: Full=1,4-beta-cellobiohydrolase 3; AltName: Full=Exocellobiohydrolase 3; Flags: Precursor [Agaricus bisporus]	UniRef90_Q02321 Glucanase n=2 Tax=Phanerochaete chrysosporium RepID=Q02321_PHACH	GO:0004553|GO:0005576|GO:0005975|GO:0030245|GO:0030248
c15257_g2_i1	6.94063	6.533512	2.88E-13	1.35E-10	RecName: Full=Cellobiose dehydrogenase; Short=CDH; AltName: Full=Cellobiose-quinone oxidoreductase; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0016614|GO:0055114
c5020_g3_i1	6.822423	1.486857	1.65E-09	3.54E-07	RecName: Full=High-affinity glucose transporter ght2; AltName: Full=Hexose transporter 2 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3RU38 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RU38_PHLGI	GO:0016021|GO:0022857|GO:0055085
c5240_g1_i1	6.775648	4.399132	2.07E-22	7.23E-19	NA	UniRef90_K5WTZ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WTZ5_PHACS	GO:0005199|GO:0009277
c14846_g3_i1	6.588798	7.386647	3.67E-13	1.57E-10	RecName: Full=Exoglucanase 1; AltName: Full=1,4-beta-cellobiohydrolase; AltName: Full=Exocellobiohydrolase I; AltName: Full=Exoglucanase I; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004553|GO:0005975
c6426_g2_i1	6.566047	2.958928	1.63E-10	4.24E-08	RecName: Full=Probable endo-beta-1,4-glucanase D; Short=Endoglucanase D; AltName: Full=Carboxymethylcellulase D; AltName: Full=Cellulase D; Flags: Precursor [Aspergillus fumigatus A1163]	UniRef90_K5W115 Glycoside hydrolase family 61 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W115_PHACS	NA
c14067_g5_i1	6.394659	1.168291	2.05E-05	0.00098	RecName: Full=Acetyl-coenzyme A synthetase; AltName: Full=Acetate--CoA ligase; AltName: Full=Acyl-activating enzyme [Coprinopsis cinerea okayama7#130]	UniRef90_K5V3J7 Acetyl-coenzyme A synthetase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3J7_PHACS	GO:0003824|GO:0008152
c14846_g2_i1	6.322823	10.40369	2.49E-18	4.06E-15	RecName: Full=Exoglucanase 1; AltName: Full=1,4-beta-cellobiohydrolase; AltName: Full=Exocellobiohydrolase I; AltName:	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248

					Full=Exoglucanase I; Flags: Precursor [Phanerochaete chrysosporium]		
c14846_g2_i2	6.322823	10.40369	2.49E-18	4.06E-15	NA	NA	GO:0004553|GO:0005975
c14846_g2_i3	6.322823	10.40369	2.49E-18	4.06E-15	NA	NA	GO:0004553|GO:0005975
c13769_g2_i1	6.251581	6.417895	3.68E-17	3.90E-14	RecName: Full=Endo-1,4-beta-xylanase A; Short=Xylanase A; AltName: Full=1,4-beta-D-xylan xylanohydrolase A; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_Q9HEZ1 Endo-1,4-beta-xylanase A n=3 Tax=Phanerochaete RepID=XYNA_PHACH	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c10301_g1_i1	6.232786	2.677089	0.000475	0.011533	RecName: Full=Protein TAR1; AltName: Full=Transcript antisense to ribosomal RNA protein 1 [Saccharomyces cerevisiae S288c]	UniRef90_M3A7A3 Uncharacterized protein n=1 Tax=Pseudocercospora fijiensis (strain CIRAD86) RepID=M3A7A3_PSEFD	NA
c12070_g1_i1	6.175225	5.771051	2.71E-16	2.36E-13	NA	NA	GO:0005199|GO:0009277
c12070_g1_i2	6.175225	5.771051	2.71E-16	2.36E-13	NA	NA	GO:0005199|GO:0009277
c12070_g1_i3	6.175225	5.771051	2.71E-16	2.36E-13	NA	NA	GO:0005199|GO:0009277
c12070_g1_i4	6.175225	5.771051	2.71E-16	2.36E-13	RecName: Full=Fruiting body protein SC3; AltName: Full=Hydrophobin SC3; Flags: Precursor [Schizophyllum commune]	UniRef90_K5WUJ9 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WUJ9_PHACS	GO:0005199|GO:0009277
c12070_g1_i5	6.175225	5.771051	2.71E-16	2.36E-13	NA	NA	GO:0005199|GO:0009277
c12070_g1_i6	6.175225	5.771051	2.71E-16	2.36E-13	NA	NA	GO:0005199|GO:0009277
c8263_g1_i1	6.169547	6.390685	1.84E-17	2.34E-14	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c8263_g1_i2	6.169547	6.390685	1.84E-17	2.34E-14	RecName: Full=Exoglucanase 1; AltName: Full=1,4-beta-cellobiohydrolase; AltName: Full=Exocellobiohydrolase I; AltName: Full=Exoglucanase I; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_K5WV44 Glucanase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WV44_PHACS	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c12707_g1_i1	5.979605	5.789926	1.17E-19	2.64E-16	NA	NA	NA
c12707_g1_i2	5.979605	5.789926	1.17E-19	2.64E-16	RecName: Full=1,4-beta-D-glucan cellobiohydrolase C; AltName: Full=Beta-glucancellobiohydrolase C; AltName: Full=Exocellobiohydrolase C; AltName:	UniRef90_A0A0C3PPT0 Carbohydrate esterase family 16 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PPT0_PHLGI	GO:0004553|GO:0005576|GO:0005975|GO:0006629|GO:0016788|GO:0030248

					Full=Exoglucanase C; Flags: Precursor [Aspergillus nidulans FGSC A4]		
c12707_g1_i3	5.979605	5.789926	1.17E-19	2.64E-16	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0006629|GO:0016788|GO:0030248
c11050_g1_i1	5.897739	5.289508	3.16E-17	3.50E-14	RecName: Full=Cellobiose dehydrogenase; Short=CDH; AltName: Full=Cellobiose-quinone oxidoreductase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_Q66NB8 Cellulose binding iron reductase n=2 Tax=Phanerochaete chrysosporium RepID=Q66NB8_PHACH	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c11050_g1_i2	5.897739	5.289508	3.16E-17	3.50E-14	NA	NA	NA
c12656_g1_i1	5.848502	8.05318	5.27E-10	1.20E-07	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c12656_g1_i2	5.848502	8.05318	5.27E-10	1.20E-07	RecName: Full=Probable acetylxylan esterase A; Flags: Precursor [Aspergillus flavus NRRL3357]	UniRef90_K5VZA3 Carbohydrate esterase family 1 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZA3_PHACS	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c12656_g3_i1	5.70742	8.48396	1.84E-12	6.69E-10	RecName: Full=Probable acetylxylan esterase A; Flags: Precursor [Neosartorya fischeri NRRL 181]	UniRef90_H2ESB9 Acetyl xylan esterase n=1 Tax=Phanerochaete chrysosporium RepID=H2ESB9_PHACH	GO:0004553|GO:0005576|GO:0005975|GO:0006508|GO:0008236|GO:0030248
c18149_g1_i1	5.696408	9.761151	3.25E-13	1.45E-10	RecName: Full=Cellulose-growth-specific protein; Flags: Precursor [Agaricus bisporus]	NA	NA
c14263_g1_i1	5.616305	7.323333	5.35E-07	4.97E-05	RecName: Full=Oxidoreductase AflY; AltName: Full=Aflatoxin biosynthesis protein Y [Aspergillus parasiticus]	UniRef90_K5UHI1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UHI1_PHACS	NA
c14263_g1_i2	5.616305	7.323333	5.35E-07	4.97E-05	NA	NA	NA
c8738_g3_i1	5.374119	7.035373	1.57E-14	1.06E-11	RecName: Full=Endo-1,4-beta-xylanase B; Short=Xylanase B; AltName: Full=1,4-beta-D-xylan xylanohydrolase B; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_B7SIW1 Endo-1,4-beta-xylanase B n=3 Tax=Phanerochaete chrysosporium RepID=XYNB_PHACH	GO:0004553|GO:0005975
c9584_g1_i1	5.257536	5.492539	6.65E-14	3.69E-11	RecName: Full=Cellulose-growth-specific protein; Flags: Precursor [Agaricus bisporus]	UniRef90_A0A0C3PSY5 Carbohydrate-binding module family 1 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PSY5_PHLGI	NA

c18692_g1_i1	5.239384	0.416734	0.000316	0.008451	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase; Short=GAPDH, partial [Amanita muscaria]	NA	GO:0016620|GO:0055114
c13618_g4_i1	5.169808	1.770071	1.43E-07	1.65E-05	NA	NA	NA
c5020_g1_i1	5.142721	0.36238	0.000434	0.010766	RecName: Full=High-affinity glucose transporter ght2; AltName: Full=Hexose transporter 2 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VJA9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VJA9_PHACS	GO:0016021|GO:0022857|GO:0055085
c18150_g1_i1	5.093496	5.825168	1.92E-13	9.60E-11	RecName: Full=1,4-beta-D-glucan cellobiohydrolase xynA; AltName: Full=Beta-glucancellobiohydrolase xynA; AltName: Full=Exocellobiohydrolase xynA; AltName: Full=Exoglucanase xynA; Flags: Precursor [Talaromyces funiculosus]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c14010_g1_i1	5.075859	6.010501	3.39E-13	1.48E-10	RecName: Full=Probable mannosyl-oligosaccharide alpha-1,2-mannosidase 1B; AltName: Full=Class I alpha-mannosidase 1B; AltName: Full=Man(9)-alpha-mannosidase 1B; Flags: Precursor [Neosartorya fischeri NRRL 181]	UniRef90_K5WG90 alpha-1,2-Mannosidase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WG90_PHACS	GO:0004571|GO:0005509|GO:0016020
c3349_g1_i1	5.061224	0.321809	0.001233	0.023292	NA	UniRef90_K5WLN3 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLN3_PHACS	NA
c17864_g1_i1	5.040656	5.182128	6.18E-05	0.002305	NA	NA	NA
c12656_g2_i1	5.035304	5.818955	7.77E-14	4.04E-11	RecName: Full=Probable acetylxylan esterase A; Flags: Precursor [Aspergillus niger CBS 513.88]	UniRef90_H2ESB9 Acetyl xylan esterase n=1 Tax=Phanerochaete chrysosporium RepID=H2ESB9_PHACH	NA
c13584_g1_i1	5.033319	6.062276	8.96E-17	8.75E-14	NA	NA	GO:0004197|GO:0006508
c13584_g1_i2	5.033319	6.062276	8.96E-17	8.75E-14	RecName: Full=Metacaspase-1; Flags: Precursor [Yarrowia lipolytica CLIB122]	UniRef90_K5W2M8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2M8_PHACS	GO:0004197|GO:0006508

c17021_g1_i1	4.936202	0.257899	0.001566	0.027503	RecName: Full=DNA-directed RNA polymerase III subunit rpc1; Short=RNA polymerase III subunit C1; AltName: Full=DNA-directed RNA polymerase III subunit A [Dictyostelium discoideum]	NA	GO:0003677|GO:0003899|GO:0006351
c13886_g3_i1	4.924066	6.082384	2.16E-12	7.63E-10	RecName: Full=Sorbose reductase sou1; AltName: Full=Sorbitol utilization protein sou1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5UP13 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UP13_PHACS	GO:0008152|GO:0016491
c13438_g2_i1	4.922542	7.151938	2.87E-12	9.86E-10	RecName: Full=Endo-1,4-beta-xylanase C; Short=Xylanase C; AltName: Full=1,4-beta-D-xylan xylanohydrolase C; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_K5V2H0 Carbohydrate-binding module family 1 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V2H0_PHACS	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c8041_g1_i1	4.873625	7.146643	3.47E-14	2.07E-11	RecName: Full=Probable endo-beta-1,4-glucanase D; Short=Endoglucanase D; AltName: Full=Carboxymethylcellulase D; AltName: Full=Cellulase D; Flags: Precursor [Aspergillus terreus NIH2624]	UniRef90_A0A0C3ND31 Glycoside hydrolase family 61 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3ND31_PHLGI	NA
c9864_g1_i1	4.857874	9.069957	1.92E-17	2.34E-14	RecName: Full=Probable endo-beta-1,4-glucanase D; Short=Endoglucanase D; AltName: Full=Carboxymethylcellulase D; AltName: Full=Cellulase D; Flags: Precursor [Neosartorya fischeri NRRL 181]	UniRef90_K5X412 Glycoside hydrolase family 61 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X412_PHACS	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c15948_g1_i1	4.832681	9.984353	7.53E-13	2.92E-10	NA	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c15948_g1_i2	4.832681	9.984353	7.53E-13	2.92E-10	RecName: Full=Manganese peroxidase 1; Short=MnP-1; Short=MnP1; AltName: Full=Manganese peroxidase isozyme 1; AltName: Full=Peroxidase manganese-dependent 1; AltName: Full=Peroxidase manganese-dependent I; Flags: Precursor [Phanerochaete chrysosporium]	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114

c13856_g3_i1	4.822913	1.489836	5.97E-07	5.44E-05	RecName: Full=Fruiting body protein SC4; AltName: Full=Hydrophobin SC4; Flags: Precursor [Schizophyllum commune]	UniRef90_K5WTZ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WTZ5_PHACS	GO:0005199|GO:0009277
c4731_g1_i1	4.821132	3.41081	1.68E-05	0.000861	RecName: Full=Tryptophan 2-halogenase [Chondromyces crocatus]	UniRef90_A0A0C3S8X2 Putative halogenase n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S8X2_PHLGI	GO:0008033|GO:0016491|GO:0050660|GO:0055114
c6008_g1_i1	4.812464	0.195223	0.003251	0.04633	NA	NA	NA
c9627_g2_i1	4.811556	0.194797	0.002788	0.041596	NA	UniRef90_K5UVE9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UVE9_PHACS	NA
c6431_g1_i1	4.804537	0.190266	0.00361	0.049988	NA	UniRef90_K5VUM3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUM3_PHACS	NA
c7497_g2_i1	4.78378	4.586856	4.45E-05	0.001803	NA	UniRef90_A2V6B3 Glycopeptide n=1 Tax=Phanerochaete chrysosporium RepID=A2V6B3_PHACH	NA
c11861_g1_i1	4.780826	3.141677	1.03E-05	0.000571	NA	NA	NA
c13769_g1_i1	4.711117	9.359762	4.34E-07	4.22E-05	RecName: Full=Endo-1,4-beta-xylanase C; Short=Xylanase C; AltName: Full=1,4-beta-D-xylan xylanohydrolase C; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_B7SIW2 Endo-1,4-beta-xylanase C n=2 Tax=Phanerochaete chrysosporium RepID=XYNC_PHACH	GO:0003824|GO:0004553|GO:0005576|GO:0005975|GO:0008152|GO:0016491|GO:0030248|GO:0050662
c14829_g1_i1	4.649587	7.118063	5.64E-15	4.17E-12	RecName: Full=Probable endo-beta-1,4-glucanase D; Short=Endoglucanase D; AltName: Full=Carboxymethylcellulase D; AltName: Full=Cellulase D; Flags: Precursor [Aspergillus niger CBS 513.88]	NA	GO:0004553|GO:0005506|GO:0005576|GO:0005975|GO:0016705|GO:0020037|GO:0030248|GO:0055114
c14474_g1_i1	4.592835	6.318464	3.29E-10	7.80E-08	RecName: Full=Xyloglucanase; Short=XG; AltName: Full=Cel74a; Flags: Precursor [Trichoderma reesei QM6a]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c14474_g1_i2	4.592835	6.318464	3.29E-10	7.80E-08	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c9112_g1_i1	4.501301	11.65575	3.25E-08	4.75E-06	NA	NA	NA

c9112_g1_i2	4.501301	11.65575	3.25E-08	4.75E-06	NA	UniRef90_K5WX64 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WX64_PHACS	NA
c6145_g1_i1	4.498081	8.646496	7.21E-15	5.17E-12	RecName: Full=Endoglucanase EG-II; Short=EGLII; AltName: Full=Cellulase; AltName: Full=Endo-1,4-beta-glucanase; Flags: Precursor [Trichoderma reesei]	UniRef90_Q66NB7 Endoglucanase n=1 Tax=Phanerochaete chrysosporium RepID=Q66NB7_PHACH	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c919_g1_i1	4.495186	4.60928	3.81E-09	7.49E-07	NA	UniRef90_K5WJ66 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJ66_PHACS	NA
c9283_g1_i1	4.487527	4.753145	3.02E-18	4.60E-15	NA	NA	NA
c12373_g1_i1	4.47345	5.520945	9.85E-15	6.87E-12	RecName: Full=Uncharacterized membrane protein YFL054C [Saccharomyces cerevisiae S288c]	UniRef90_K5VYH7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYH7_PHACS	GO:0005215|GO:0006810|GO:0016020
c8694_g1_i1	4.462953	1.223991	0.001156	0.022272	RecName: Full=Sexual differentiation process protein isp4 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3PI50 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PI50_PHLGI	GO:0055085
c16108_g2_i1	4.410828	3.319183	1.56E-09	3.37E-07	NA	NA	NA
c9586_g1_i1	4.34418	5.781713	3.98E-15	3.23E-12	RecName: Full=Ferric/cupric reductase transmembrane component 1; AltName: Full=Ferric-chelate reductase 1; Flags: Precursor [Candida albicans SC5314]	UniRef90_K5X951 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X951_PHACS	GO:0016491|GO:0019049|GO:0055114
c16166_g5_i1	4.312679	5.960852	1.19E-19	2.64E-16	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]	NA	GO:0004190|GO:0006508

c13992_g1_i1	4.25285	4.789824	9.53E-22	2.91E-18	RecName: Full=Indole-3-pyruvate monooxygenase YUCCA6; AltName: Full=Flavin-containing monooxygenase YUCCA6; AltName: Full=Protein HYPERTALL1 [Arabidopsis thaliana]	UniRef90_K5WM45 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WM45_PHACS	GO:0004499|GO:0016491|GO:0050660|GO:0050661|GO:0055114
c11058_g1_i1	4.240647	4.043283	1.19E-11	3.77E-09	RecName: Full=Endoglucanase-5; AltName: Full=Cellulase V; AltName: Full=Endo-1,4-beta-glucanase V; Short=EG V; AltName: Full=Endoglucanase V; Flags: Precursor [Trichoderma reesei]	UniRef90_B3Y002 Endoglucanase V-like protein n=1 Tax=Phanerochaete chrysosporium RepID=B3Y002_PHACH	NA
c6180_g1_i1	4.222492	6.214226	2.48E-07	2.63E-05	RecName: Full=Thermolabile hemolysin; Short=TL; AltName: Full=Atypical phospholipase; AltName: Full=Lecithin-dependent hemolysin; Short=LDH; AltName: Full=Lysophospholipase; AltName: Full=Phospholipase A2; Flags: Precursor [Vibrio parahaemolyticus RIMD 2210633]	UniRef90_K5W7U7 Carbohydrate esterase family 16 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W7U7_PHACS	GO:0006629|GO:0016788
c6180_g1_i2	4.222492	6.214226	2.48E-07	2.63E-05	NA	NA	GO:0006629|GO:0016788
c9586_g2_i1	4.166287	5.476371	5.49E-13	2.27E-10	RecName: Full=Ferric reductase transmembrane component 5; AltName: Full=Ferric-chelate reductase 5; Flags: Precursor [Saccharomyces cerevisiae S288c]	UniRef90_K5X951 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X951_PHACS	GO:0016491|GO:0055114
c9609_g1_i1	4.123132	5.575407	4.78E-09	8.71E-07	RecName: Full=N,O-diacetylmuramidase; AltName: Full=Lysozyme CH [Chalara sp.]	UniRef90_A0A0C3S6S2 Glycoside hydrolase family 25 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S6S2_PHLGI	GO:0003796|GO:0009253|GO:0016998
c9584_g2_i1	4.119138	4.209185	4.39E-12	1.47E-09	RecName: Full=Cellulose-growth-specific protein; Flags: Precursor [Agaricus bisporus]	UniRef90_K5VXP2 Glycoside hydrolase family 61 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXP2_PHACS	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c8738_g1_i1	4.108572	2.360156	1.28E-06	9.96E-05	RecName: Full=Endo-1,4-beta-xylanase B; Short=Xylanase B; AltName: Full=1,4-beta-D-xylan xylanohydrolase B; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_B7SIW1 Endo-1,4-beta-xylanase B n=3 Tax=Phanerochaete chrysosporium RepID=XYNB_PHACH	NA

c10275_g1_i1	4.038558	4.835937	1.94E-10	4.84E-08	RecName: Full=Glycerol dehydrogenase; Short=GDH; Short=GLDH; Short=GlyDH [Geobacillus stearothermophilus]	UniRef90_A0A0C3RWV6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RWV6_PHLGI	GO:0016491|GO:0046872|GO:0055114
c11967_g1_i1	4.03703	1.568221	0.000361	0.009372	NA	UniRef90_K5WN63 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WN63_PHACS	NA
c17785_g1_i1	4.019758	5.680891	1.79E-05	0.000899	NA	NA	NA
c14010_g2_i1	4.005287	8.103038	4.64E-10	1.07E-07	RecName: Full=Probable mannosyl-oligosaccharide alpha-1,2-mannosidase 1B; AltName: Full=Class I alpha-mannosidase 1B; AltName: Full=Man(9)-alpha-mannosidase 1B; Flags: Precursor [Aspergillus terreus NIH2624]	UniRef90_A0A0C3SFI6 Glycoside hydrolase family 47 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SFI6_PHLGI	GO:0004571|GO:0005509|GO:0016020
c10861_g1_i1	3.954876	3.851881	2.27E-06	0.000163	NA	NA	NA
c10861_g1_i2	3.954876	3.851881	2.27E-06	0.000163	NA	NA	NA
c10861_g1_i3	3.954876	3.851881	2.27E-06	0.000163	NA	NA	NA
c17651_g1_i1	3.945249	0.869095	3.86E-05	0.001607	RecName: Full=Homeobox protein HB3, partial [Tripneustes gratilla]	NA	GO:0003677
c7497_g1_i1	3.885272	7.271912	0.000474	0.011519	NA	UniRef90_A2V6B3 Glycopeptide n=1 Tax=Phanerochaete chrysosporium RepID=A2V6B3_PHACH	NA
c10416_g1_i1	3.869341	1.423932	3.04E-05	0.001334	NA	NA	NA
c10416_g1_i2	3.869341	1.423932	3.04E-05	0.001334	NA	NA	NA
c65_g1_i1	3.866134	0.805115	0.000777	0.01664	NA	UniRef90_K5VZX4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZX4_PHACS	NA
c6281_g1_i1	3.844903	8.492101	4.01E-08	5.56E-06	RecName: Full=Endoglucanase 3; AltName: Full=Cellulase 3; AltName: Full=Endo-1,4-beta-glucanase 3; Flags: Precursor [Humicola insolens]	UniRef90_Q5W7K4 Endoglucanase n=1 Tax=Irpex lacteus RepID=Q5W7K4_IRPLA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c5687_g1_i1	3.84174	3.670638	5.38E-05	0.002069	NA	UniRef90_D0NS79 Peroxisomal 2,4-dienoyl-CoA reductase, putative n=10 Tax=Phytophthora RepID=D0NS79_PHYIT	NA
c16028_g1_i1	3.838526	2.124461	0.000163	0.005015	NA	NA	NA

c16094_g1_i1	3.82298	4.689807	8.51E-08	1.04E-05	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c13563_g1_i1	3.814747	3.32353	1.86E-10	4.74E-08	NA	UniRef90_K5VSV8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSV8_PHACS	NA
c12214_g1_i1	3.810161	5.534613	6.87E-07	6.01E-05	RecName: Full=Endo-1,4-beta-xylanase; Short=Xylanase; AltName: Full=1,4-beta-D-xylan xylanohydrolase; AltName: Full=TAXI; Flags: Precursor [Thermoascus aurantiacus]	UniRef90_K5WIK1 Beta-xylanase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WIK1_PHACS	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c7415_g1_i1	3.805016	6.230561	2.52E-11	7.50E-09	RecName: Full=Serine protease inhibitor [Lentinula edodes]	UniRef90_A0A0C3SFT8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SFT8_PHLGI	NA
c19816_g1_i1	3.803139	1.766357	6.66E-08	8.74E-06	NA	NA	NA
c16108_g1_i1	3.790106	6.744848	2.00E-12	7.19E-10	RecName: Full=Putative peroxisomal-coenzyme A synthetase [Schizosaccharomyces pombe 972h-]	NA	GO:0003824|GO:0008152
c12591_g2_i1	3.779456	1.758569	3.95E-06	0.000257	NA	NA	NA
c12591_g2_i2	3.779456	1.758569	3.95E-06	0.000257	NA	NA	NA
c14846_g4_i1	3.740355	5.496292	1.76E-15	1.48E-12	NA	NA	NA
c14846_g4_i2	3.740355	5.496292	1.76E-15	1.48E-12	NA	NA	NA
c14846_g4_i3	3.740355	5.496292	1.76E-15	1.48E-12	NA	NA	NA
c14846_g4_i4	3.740355	5.496292	1.76E-15	1.48E-12	NA	NA	NA
c13160_g2_i1	3.73543	4.072925	3.26E-13	1.45E-10	NA	NA	NA
c13160_g2_i2	3.73543	4.072925	3.26E-13	1.45E-10	NA	NA	NA
c16166_g4_i1	3.67294	8.994033	8.08E-07	6.95E-05	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName:	NA	GO:0003924|GO:0004190|GO:0005525|GO:0006508

					Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]		
c16103_g1_i1	3.652226	7.237975	3.99E-14	2.27E-11	RecName: Full=Linear gramicidin synthase subunit D; Includes: RecName: Full=ATP-dependent D-leucine adenylase; Short=D-LeuA; AltName: Full=D-leucine activase; Includes: RecName: Full=Leucine racemase [ATP-hydrolyzing]; Includes: RecName: Full=ATP-dependent tryptophan adenylase; Short=TrpA; AltName: Full=Tryptophan activase; Includes: RecName: Full=ATP-dependent glycine adenylase; Short=GlyA; AltName: Full=Glycine activase; Includes: RecName: Full=Linear gramicidin--PCP reductase [Brevibacillus parabrevis]	NA	GO:0003824|GO:0008152
c16166_g3_i1	3.612208	8.207197	1.77E-07	1.97E-05	NA	NA	GO:0004190|GO:0006508
c16166_g3_i2	3.612208	8.207197	1.77E-07	1.97E-05	NA	NA	GO:0004190|GO:0006508
c16166_g3_i3	3.612208	8.207197	1.77E-07	1.97E-05	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]	NA	GO:0004190|GO:0006508
c15859_g2_i1	3.580394	4.533577	4.54E-05	0.001833	NA	NA	NA

c13569_g4_i1	3.551616	6.616584	1.67E-12	6.19E-10	NA	UniRef90_K5VYF9 Carbohydrate-binding module family 1 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYF9_PHACS	NA
c13992_g2_i1	3.533937	2.518079	1.13E-07	1.34E-05	NA	UniRef90_K5WM45 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WM45_PHACS	NA
c9400_g4_i1	3.505557	1.151996	0.000101	0.003402	NA	UniRef90_K5WLX4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLX4_PHACS	NA
c8756_g2_i1	3.505364	4.511468	1.73E-06	0.000129	NA	UniRef90_A0A0C3PJM9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PJM9_PHLGI	NA
c3031_g1_i1	3.460641	0.576098	0.000696	0.015469	NA	NA	NA
c3031_g1_i2	3.460641	0.576098	0.000696	0.015469	NA	UniRef90_K5WJL0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJL0_PHACS	NA
c8886_g1_i1	3.45556	5.643541	2.89E-13	1.35E-10	NA	UniRef90_A0A0C3NQX2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NQX2_PHLGI	NA
c15225_g2_i1	3.444615	6.468174	3.24E-13	1.45E-10	NA	NA	NA
c15225_g2_i2	3.444615	6.468174	3.24E-13	1.45E-10	NA	NA	NA
c170_g2_i1	3.415927	1.091972	0.000104	0.003461	RecName: Full=Methylsterol monooxygenase; AltName: Full=C-4 methylsterol oxidase [Schizosaccharomyces pombe 972h-]	UniRef90_K5VIW2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VIW2_PHACS	GO:0005506|GO:0006633|GO:0016491|GO:0055114
c17694_g1_i1	3.392146	1.079133	0.000244	0.006912	NA	NA	NA
c10345_g1_i1	3.389868	6.754884	1.56E-10	4.08E-08	NA	UniRef90_S7RB38 O-methyltransferase (Fragment) n=1 Tax=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) RepID=S7RB38_GLOTA	NA
c10345_g1_i2	3.389868	6.754884	1.56E-10	4.08E-08	NA	NA	NA

c9963_g1_i1	3.383704	3.271256	2.74E-05	0.001229	RecName: Full=Intracellular endo-alpha-(1->5)-L-arabinanase; Short=ABN; AltName: Full=Endo-1,5-alpha-L-arabinanase [Geobacillus thermodenitrificans]	UniRef90_I6XPK9 Arabinan endo-1,5-alpha-L-arabinosidase n=1 Tax=Phanerochaete chrysosporium RepID=I6XPK9_PHACH	GO:0004553|GO:0005975
c9963_g1_i2	3.383704	3.271256	2.74E-05	0.001229	NA	NA	GO:0004553|GO:0005975
c14620_g2_i1	3.366597	5.348588	0.000701	0.015539	RecName: Full=Alpha-L-arabinofuranosidase A; Short=ABF A; Short=Arabinosidase A; AltName: Full=Arabinoxylan-arabinofuranohydrolase of 70 kDa; Short=AF-70; Flags: Precursor [Penicillium canescens]	NA	GO:0016798
c14620_g2_i2	3.366597	5.348588	0.000701	0.015539	NA	NA	GO:0016798
c11171_g1_i1	3.36577	0.529607	0.001698	0.029235	NA	UniRef90_K5WTU0 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WTU0_PHACS	NA
c13035_g2_i1	3.359887	3.533719	7.30E-06	0.000425	NA	NA	GO:0006629|GO:0016788
c13035_g2_i2	3.359887	3.533719	7.30E-06	0.000425	NA	NA	NA
c13035_g2_i3	3.359887	3.533719	7.30E-06	0.000425	NA	UniRef90_K5W5T3 Carbohydrate esterase family 16 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5T3_PHACS	GO:0006629|GO:0016788
c14721_g1_i1	3.355506	4.871747	5.71E-08	7.57E-06	RecName: Full=Aquaporin-3; Short=AQP-3; AltName: Full=Aquaglyceroporin-3 [Homo sapiens]	NA	GO:0005215|GO:0006810|GO:0016020
c8679_g2_i1	3.348961	2.518056	0.001032	0.020517	NA	NA	NA
c13742_g2_i1	3.343916	5.288911	5.83E-11	1.65E-08	RecName: Full=Aldehyde dehydrogenase, dimeric NADP-preferring; AltName: Full=Aldehyde dehydrogenase family 3 member A1; AltName: Full=HTC-ALDH; AltName: Full=Tumor-associated aldehyde dehydrogenase [Rattus norvegicus]	UniRef90_K5VY68 Aldehyde dehydrogenase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VY68_PHACS	GO:0008152|GO:0016491|GO:0055114
c12735_g1_i1	3.313117	6.024878	5.70E-08	7.57E-06	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248

c12735_g1_i2	3.313117	6.024878	5.70E-08	7.57E-06	RecName: Full=Probable mannan endo-1,4-beta-mannosidase F; AltName: Full=Endo-beta-1,4-mannanase F; Flags: Precursor [Aspergillus nidulans FGSC A4]	UniRef90_Q0PQY8 Man5D n=1 Tax=Phanerochaete chrysosporium RepID=Q0PQY8_PHACH	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c19170_g1_i1	3.279873	0.475129	0.001903	0.031492	NA	NA	NA
c17686_g1_i1	3.279872	0.475129	0.001902	0.031492	NA	NA	NA
c12146_g1_i1	3.263807	5.561228	4.32E-07	4.21E-05	RecName: Full=Uncharacterized membrane protein YFL054C [Saccharomyces cerevisiae S288c]	UniRef90_K5WGK0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGK0_PHACS	GO:0005215|GO:0006810|GO:0016020
c11894_g1_i1	3.215338	6.783678	4.51E-07	4.33E-05	RecName: Full=Uncharacterized N-acetyltransferase C550.08 [Schizosaccharomyces pombe 972h-]	UniRef90_K5X1B3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X1B3_PHACS	GO:0008080|GO:0016747
c5533_g1_i1	3.182655	2.523648	3.38E-05	0.001445	NA	UniRef90_A0A0C3NH58 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NH58_PHLGI	NA
c5533_g1_i2	3.182655	2.523648	3.38E-05	0.001445	NA	NA	NA
c18211_g1_i1	3.182384	4.996446	9.36E-11	2.57E-08	RecName: Full=Plasma membrane iron permease [Saccharomyces cerevisiae S288c]	NA	GO:0005381|GO:0006827|GO:0016020|GO:0033573
c10056_g1_i1	3.166198	3.897664	2.79E-10	6.75E-08	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c10056_g1_i2	3.166198	3.897664	2.79E-10	6.75E-08	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c10056_g1_i3	3.166198	3.897664	2.79E-10	6.75E-08	NA	UniRef90_K5W698 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W698_PHACS	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c4637_g1_i1	3.1657	3.910191	0.000359	0.009354	NA	UniRef90_K5V756 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V756_PHACS	NA
c15123_g4_i1	3.162504	8.612206	1.87E-08	2.91E-06	RecName: Full=Pheromone-processing carboxypeptidase kex1; AltName: Full=Carboxypeptidase D; Flags: Precursor [Pyrenophora tritici-repentis Pt-1C-BFP]	NA	GO:0004185|GO:0006508

c14227_g2_i1	3.159032	4.526438	3.88E-05	0.00161	NA	UniRef90_A0A0C3PK54 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PK54_PHLGI	NA
c13160_g3_i1	3.153443	5.070231	7.36E-13	2.90E-10	NA	NA	NA
c13160_g3_i2	3.153443	5.070231	7.36E-13	2.90E-10	NA	NA	NA
c14512_g2_i1	3.147083	6.197506	0.000183	0.005473	RecName: Full=Probable glycosidase C21B10.07 [Schizosaccharomyces pombe 972h-]	NA	GO:0004553|GO:0005975
c14512_g2_i2	3.147083	6.197506	0.000183	0.005473	NA	NA	GO:0004553|GO:0005975
c10954_g1_i1	3.134807	7.390299	6.71E-09	1.16E-06	RecName: Full=Carboxypeptidase S1 [Penicillium janthinellum]	UniRef90_K5X184 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X184_PHACS	GO:0004185|GO:0006508
c8756_g3_i1	3.127541	5.972392	2.53E-05	0.001171	NA	UniRef90_K5VMI7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VMI7_PHACS	NA
c18518_g1_i1	3.127279	1.265857	1.79E-05	0.000899	NA	NA	NA
c4908_g1_i1	3.126766	5.985299	2.25E-08	3.41E-06	NA	NA	NA
c6711_g1_i1	3.120631	8.441599	0.001098	0.0214	NA	UniRef90_K5UNU9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UNU9_PHACS	NA
c10952_g1_i1	3.10709	2.339081	1.13E-07	1.34E-05	NA	UniRef90_K5VZI8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZI8_PHACS	NA
c10952_g1_i2	3.10709	2.339081	1.13E-07	1.34E-05	NA	NA	NA
c10952_g1_i3	3.10709	2.339081	1.13E-07	1.34E-05	NA	NA	NA
c13745_g2_i1	3.092386	5.72005	3.87E-14	2.25E-11	RecName: Full=Serine/threonine-protein kinase CTR1 [Arabidopsis thaliana]	UniRef90_K5WEY5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEY5_PHACS	GO:0004672|GO:0005524|GO:0006468
c13745_g2_i2	3.092386	5.72005	3.87E-14	2.25E-11	NA	NA	GO:0004672|GO:0005524|GO:0006468
c9769_g2_i1	3.07504	3.427341	6.08E-07	5.49E-05	NA	NA	NA
c9769_g2_i2	3.07504	3.427341	6.08E-07	5.49E-05	NA	NA	NA

c11529_g1_i1	3.074718	5.903299	7.25E-13	2.90E-10	NA	NA	GO:0005975|GO:0016853
c11529_g1_i2	3.074718	5.903299	7.25E-13	2.90E-10	RecName: Full=Aldose 1-epimerase; AltName: Full=Galactose mutarotase [Sus scrofa]	UniRef90_K5WH73 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WH73_PHACS	GO:0005975|GO:0016853
c12300_g1_i1	3.050902	2.604683	7.65E-07	6.64E-05	NA	UniRef90_A0A0C3SDJ3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SDJ3_PHLGI	NA
c14471_g2_i1	3.034871	3.457932	2.00E-07	2.18E-05	RecName: Full=Uncharacterized transporter C1002.16c [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c15123_g3_i1	3.028424	5.873539	7.04E-14	3.73E-11	RecName: Full=Vitellogenic carboxypeptidase; Flags: Precursor [Aedes aegypti]	NA	GO:0004185|GO:0006508
c7013_g1_i1	3.019476	6.281165	5.62E-06	0.000347	RecName: Full=Heat shock protein 16; AltName: Full=16 kDa heat shock protein [Schizosaccharomyces pombe 972h-]	UniRef90_A0A067PGQ1 Uncharacterized protein n=1 Tax=Jaapia argillacea MUCL 33604 RepID=A0A067PGQ1_9HOMO	NA
c322_g1_i1	3.006936	2.78232	1.15E-06	9.25E-05	NA	NA	NA
c322_g1_i2	3.006936	2.78232	1.15E-06	9.25E-05	NA	NA	NA
c13207_g1_i1	2.994522	3.955061	0.000533	0.012613	RecName: Full=Osmotin-like protein; Flags: Precursor [Solanum lycopersicum]	UniRef90_K5VYQ8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYQ8_PHACS	NA
c13207_g1_i2	2.994522	3.955061	0.000533	0.012613	NA	NA	NA
c12171_g1_i1	2.991474	6.634587	1.14E-10	3.03E-08	RecName: Full=Carboxypeptidase Y; Short=CPY; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3RXC8 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RXC8_PHLGI	GO:0004185|GO:0006508
c12171_g1_i2	2.991474	6.634587	1.14E-10	3.03E-08	NA	NA	GO:0004185|GO:0006508
c12634_g1_i1	2.984796	5.506899	1.85E-05	0.000915	NA	NA	NA
c12634_g1_i2	2.984796	5.506899	1.85E-05	0.000915	NA	NA	NA
c12634_g1_i3	2.984796	5.506899	1.85E-05	0.000915	RecName: Full=Respiratory supercomplex factor 2 homolog C1565.01 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VZM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZM7_PHACS	NA
c14057_g1_i1	2.97754	6.832725	4.06E-09	7.78E-07	NA	UniRef90_K5UNU9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UNU9_PHACS	NA

c4510_g1_i1	2.972303	1.715144	8.47E-06	0.000482	NA	UniRef90_K5VNR3 Uncharacterized protein (Fragment) n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VNR3_PHACS	NA
c13089_g1_i1	2.963114	4.100413	2.83E-08	4.22E-06	NA	NA	NA
c13089_g1_i2	2.963114	4.100413	2.83E-08	4.22E-06	RecName: Full=Xylanolytic transcriptional activator xlnR; AltName: Full=Xylanase regulator [Aspergillus nidulans FGSC A4]	UniRef90_S8DRD3 Uncharacterized protein n=1 Tax=Fomitopsis pinicola (strain FP-58527) RepID=S8DRD3_FOMPI	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c4677_g1_i1	2.962467	2.833839	2.38E-05	0.001115	NA	UniRef90_R7SW61 Glycopeptide n=1 Tax=Dichomitus squalens (strain LYAD-421) RepID=R7SW61_DICSQ	NA
c4677_g1_i2	2.962467	2.833839	2.38E-05	0.001115	NA	NA	NA
c18975_g1_i1	2.948077	5.208919	1.26E-05	0.000672	RecName: Full=Ribonuclease U2; Short=RNase U2 [Ustilago sphaerogena]	NA	GO:0003723|GO:0004521
c11971_g1_i1	2.924863	2.71148	4.88E-07	4.61E-05	NA	NA	NA
c11971_g1_i2	2.924863	2.71148	4.88E-07	4.61E-05	NA	NA	NA
c11971_g1_i3	2.924863	2.71148	4.88E-07	4.61E-05	NA	NA	NA
c14135_g1_i1	2.916868	6.731409	0.000201	0.005955	NA	NA	GO:0004553|GO:0005975
c14135_g1_i2	2.916868	6.731409	0.000201	0.005955	RecName: Full=Probable mannan endo-1,4-beta-mannosidase A; AltName: Full=Endo-beta-1,4-mannanase A; Flags: Precursor [Neosartorya fischeri NRRL 181]	UniRef90_K5WNY7 Glycoside hydrolase family 5 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNY7_PHACS	GO:0004553|GO:0005975
c11432_g1_i1	2.90642	5.278786	0.000355	0.009252	RecName: Full=FAD synthase; AltName: Full=FAD pyrophosphorylase; AltName: Full=FMN adenylyltransferase; AltName: Full=Flavin adenine dinucleotide synthase; Includes: RecName: Full=Molybdenum cofactor biosynthesis protein-like region; Includes: RecName: Full=FAD synthase region [Danio rerio]	UniRef90_K5WCI9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCI9_PHACS	GO:0003824|GO:0008152
c9769_g1_i1	2.904451	1.420755	0.001863	0.031052	NA	NA	NA
c9769_g1_i2	2.904451	1.420755	0.001863	0.031052	NA	NA	NA
c14650_g2_i1	2.903245	1.124761	0.00031	0.008365	NA	NA	NA

c8756_g1_i1	2.894279	3.583079	0.000426	0.010616	NA	NA	NA
c6732_g2_i1	2.88882	0.753014	0.000908	0.018755	RecName: Full=Aspartic protease; Flags: Precursor [Xanthophyllomyces dendrorhous]	UniRef90_UPI00046229C7 acid protease n=1 Tax=Trametes versicolor (strain FP-101664) RepID=UPI00046229C7	GO:0004190|GO:0006508
c12039_g1_i1	2.88231	4.989163	4.63E-05	0.001866	RecName: Full=Ribonuclease T2; Short=RNase T2; Flags: Precursor [Aspergillus oryzae RIB40]	UniRef90_K5WBR7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WBR7_PHACS	GO:0003723|GO:0033897
c19518_g1_i1	2.873801	0.749475	0.001038	0.020586	NA	NA	NA
c5816_g1_i1	2.870673	3.983229	6.46E-08	8.53E-06	NA	NA	NA
c11792_g1_i1	2.857849	3.000024	2.63E-05	0.001194	NA	NA	NA
c11792_g1_i2	2.857849	3.000024	2.63E-05	0.001194	NA	UniRef90_K5WE49 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WE49_PHACS	NA
c6757_g1_i1	2.852565	3.504718	1.92E-05	0.00094	NA	NA	NA
c6757_g1_i2	2.852565	3.504718	1.92E-05	0.00094	NA	UniRef90_K5WR15 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WR15_PHACS	NA
c9600_g4_i1	2.846196	1.087151	0.000505	0.012114	RecName: Full=Uncharacterized protein C16H5.12c [Schizosaccharomyces pombe 972h-]	UniRef90_K5X9F6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X9F6_PHACS	NA
c9655_g1_i1	2.842663	5.329715	1.83E-06	0.000135	NA	NA	NA
c9655_g1_i2	2.842663	5.329715	1.83E-06	0.000135	NA	UniRef90_K5VRA9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRA9_PHACS	NA
c9655_g1_i3	2.842663	5.329715	1.83E-06	0.000135	NA	NA	NA
c9655_g1_i4	2.842663	5.329715	1.83E-06	0.000135	NA	NA	NA
c9655_g1_i5	2.842663	5.329715	1.83E-06	0.000135	NA	NA	NA
c9655_g1_i6	2.842663	5.329715	1.83E-06	0.000135	NA	NA	NA
c15326_g2_i1	2.824634	4.723115	0.000346	0.00907	RecName: Full=Ent-kaurene oxidase; AltName: Full=Cytochrome P450 503A1; AltName: Full=Cytochrome P450-4 [Fusarium fujikuroi]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c5901_g5_i1	2.822767	1.591779	2.11E-05	0.001007	RecName: Full=Oxygen-dependent choline dehydrogenase; Short=CDH; Short=CHD; AltName: Full=Betaine aldehyde dehydrogenase; Short=BADH [Pseudomonas syringae pv. phaseolicola 1448A]	UniRef90_A0A0C3RQY6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RQY6_PHLGI	GO:0016614|GO:0050660|GO:0055114
c15181_g1_i1	2.818973	5.45396	2.77E-11	8.15E-09	NA	NA	NA
c15181_g1_i2	2.818973	5.45396	2.77E-11	8.15E-09	NA	NA	NA
c15181_g1_i3	2.818973	5.45396	2.77E-11	8.15E-09	NA	NA	NA
c6484_g1_i1	2.813041	1.343266	0.000241	0.006855	RecName: Full=Heat shock protein 90 homolog [Candida albicans SC5314]	UniRef90_S7QG80 HSP90-domain-containing protein n=2 Tax=Agaricomycetes RepID=S7QG80_GLOTA	GO:0005524|GO:0006457|GO:0006950|GO:0051082
c9325_g1_i1	2.804514	1.777711	2.60E-05	0.001186	NA	UniRef90_K5WQ76 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQ76_PHACS	NA
c90_g1_i1	2.776872	1.323182	0.00155	0.02738	RecName: Full=Nitrate reductase [NADH]; Short=NR [Hordeum vulgare]	UniRef90_K5WGH3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGH3_PHACS	GO:0009055|GO:0055114
c18377_g1_i1	2.750156	6.318118	3.49E-07	3.50E-05	NA	NA	NA
c9112_g2_i1	2.748873	3.435834	0.000121	0.00394	NA	NA	NA
c12200_g2_i1	2.747999	2.839503	9.70E-06	0.000543	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]	UniRef90_A0A067TCJ9 Uncharacterized protein n=1 Tax=Galerina marginata CBS 339.88 RepID=A0A067TCJ9_9AGAR	GO:0004190|GO:0006508
c16239_g1_i1	2.743811	1.299122	0.002157	0.034324	NA	NA	NA
c9993_g1_i1	2.728461	7.266617	0.000131	0.004223	RecName: Full=UPF0654 protein C11D3.01c [Schizosaccharomyces pombe 972h-]	UniRef90_M2RBF5 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2RBF5_CERS8	NA

c9462_g1_i1	2.727893	2.307098	6.14E-06	0.000372	NA	UniRef90_K5WH47 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WH47_PHACS	NA
c9225_g2_i1	2.697436	4.214972	0.000578	0.013345	RecName: Full=Thaumatin-like protein 2; AltName: Full=PpAZ8; Flags: Precursor [Prunus persica]	UniRef90_K5VYQ8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYQ8_PHACS	NA
c6516_g1_i1	2.690146	4.488924	1.80E-05	0.000901	NA	UniRef90_S7PRG7 Uncharacterized protein n=1 Tax=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) RepID=S7PRG7_GLOTA	NA
c11905_g2_i1	2.687193	5.992408	6.98E-08	9.06E-06	NA	UniRef90_A0A0C3NLU2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NLU2_PHLGI	GO:0005507|GO:0009055
c7151_g1_i1	2.686897	6.923166	2.51E-10	6.18E-08	NA	NA	GO:0003824|GO:0008152
c7151_g1_i2	2.686897	6.923166	2.51E-10	6.18E-08	NA	UniRef90_A0A0C3S8W1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S8W1_PHLGI	GO:0003824|GO:0008152
c6784_g1_i1	2.685738	2.277198	1.80E-05	0.000901	NA	UniRef90_K5UQQ9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UQQ9_PHACS	NA
c8145_g1_i1	2.684415	5.497021	2.46E-08	3.70E-06	RecName: Full=Centromere protein V; Short=CENP-V; AltName: Full=Proline-rich protein 6 [Mus musculus]	UniRef90_K5WX74 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WX74_PHACS	GO:0008152|GO:0016846
c13926_g1_i1	2.683771	5.820707	8.69E-07	7.31E-05	RecName: Full=Uncharacterized ATPase YjoB [Bacillus subtilis subsp. subtilis str. 168]	UniRef90_K5VW34 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VW34_PHACS	GO:0005524
c13926_g1_i2	2.683771	5.820707	8.69E-07	7.31E-05	NA	NA	GO:0005524
c9078_g1_i1	2.68036	2.298176	2.71E-06	0.000192	NA	UniRef90_K5VZI8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZI8_PHACS	NA
c5784_g1_i1	2.676259	2.38211	4.89E-07	4.61E-05	NA	UniRef90_K5WLW9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLW9_PHACS	NA

c8646_g1_i1	2.666123	3.495361	6.13E-07	5.51E-05	NA	UniRef90_K5W024 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W024_PHACS	NA
c13569_g1_i1	2.654552	3.178802	4.92E-07	4.62E-05	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c7403_g1_i1	2.654248	6.256871	6.57E-07	5.79E-05	NA	UniRef90_A0A0C3PUQ7 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PUQ7_PHLGI	NA
c12676_g1_i1	2.650427	5.271811	0.000122	0.003966	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12676_g1_i2	2.650427	5.271811	0.000122	0.003966	RecName: Full=Cytochrome P450 3A31; AltName: Full=CYPIIIA31; AltName: Full=Cytochrome P450 SH3A-1 [Mesocricetus auratus]	UniRef90_G5EJS7 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJS7_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12676_g1_i3	2.650427	5.271811	0.000122	0.003966	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15309_g3_i1	2.642956	2.257749	6.79E-06	0.000402	RecName: Full=1,4-beta-D-glucan cellobiohydrolase xynA; AltName: Full=Beta-glucancellobiohydrolase xynA; AltName: Full=Exocellobiohydrolase xynA; AltName: Full=Exoglucanase xynA; Flags: Precursor [Talaromyces funiculosus]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c13608_g1_i1	2.634702	3.002173	4.54E-06	0.000289	NA	UniRef90_K5UPN2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UPN2_PHACS	NA
c13608_g1_i2	2.634702	3.002173	4.54E-06	0.000289	NA	NA	NA
c15299_g2_i1	2.633114	5.705564	8.15E-09	1.40E-06	NA	NA	NA
c15299_g2_i2	2.633114	5.705564	8.15E-09	1.40E-06	NA	NA	NA
c16690_g1_i1	2.631907	0.953198	0.002485	0.038269	NA	NA	GO:0005515
c13515_g1_i1	2.621699	3.68945	2.21E-08	3.39E-06	RecName: Full=Probable phosphoketolase [Schizosaccharomyces pombe 972h-]	UniRef90_K5X5E0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X5E0_PHACS	NA
c16099_g2_i1	2.612858	3.579878	2.23E-09	4.69E-07	NA	NA	NA

c15319_g1_i1	2.605893	7.123497	1.46E-08	2.36E-06	RecName: Full=Apoptosis-inducing factor homolog B [Dictyostelium discoideum]	NA	GO:0016491|GO:0050660|GO:0055114
c15319_g1_i2	2.605893	7.123497	1.46E-08	2.36E-06	NA	NA	NA
c13392_g1_i1	2.600926	4.139621	1.13E-05	0.000616	NA	NA	NA
c13392_g1_i2	2.600926	4.139621	1.13E-05	0.000616	RecName: Full=Heat shock protein 16; AltName: Full=16 kDa heat shock protein [Schizosaccharomyces pombe 972h-]	UniRef90_K5VJG7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VJG7_PHACS	NA
c9312_g2_i1	2.589648	2.572438	0.001635	0.028448	NA	NA	NA
c9312_g2_i2	2.589648	2.572438	0.001635	0.028448	NA	NA	NA
c8724_g1_i1	2.57707	1.186474	0.002026	0.032862	NA	NA	NA
c7699_g2_i1	2.575753	1.434391	0.001105	0.021497	NA	UniRef90_K5V9W4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V9W4_PHACS	NA
c9084_g1_i1	2.57452	6.462973	8.51E-08	1.04E-05	NA	UniRef90_A0A0C3S2W1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S2W1_PHLGI	NA
c14498_g1_i1	2.572259	4.068696	1.20E-06	9.59E-05	NA	NA	NA
c14498_g1_i2	2.572259	4.068696	1.20E-06	9.59E-05	NA	NA	NA
c14498_g1_i3	2.572259	4.068696	1.20E-06	9.59E-05	NA	NA	NA
c8148_g1_i1	2.56851	4.710751	1.23E-05	0.000661	NA	UniRef90_K5VHJ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VHJ5_PHACS	GO:0003885|GO:0016020|GO:0055114
c1547_g1_i1	2.566249	4.14844	6.37E-07	5.64E-05	NA	NA	NA
c11868_g2_i1	2.556729	2.316787	6.69E-06	0.000397	RecName: Full=Acyl-CoA desaturase; AltName: Full=Delta(9)-desaturase; Short=Delta-9 desaturase; AltName: Full=Fatty acid desaturase; AltName: Full=Stearoyl-CoA desaturase [Histoplasma capsulatum]	UniRef90_D4Q8S7 Delta9-fatty acid desaturase n=1 Tax=Phanerochaete chrysosporium RepID=D4Q8S7_PHACH	GO:0006629|GO:0020037
c14906_g1_i1	2.551563	5.044471	2.61E-05	0.00119	RecName: Full=UPF0364 protein C806.04c [Schizosaccharomyces pombe 972h-]	NA	NA
c14906_g1_i2	2.551563	5.044471	2.61E-05	0.00119	NA	NA	NA
c14906_g1_i3	2.551563	5.044471	2.61E-05	0.00119	NA	NA	NA

c13107_g1_i1	2.546522	4.635891	3.48E-10	8.17E-08	NA	NA	NA
c13107_g1_i2	2.546522	4.635891	3.48E-10	8.17E-08	NA	NA	NA
c13107_g1_i3	2.546522	4.635891	3.48E-10	8.17E-08	NA	NA	NA
c13107_g1_i4	2.546522	4.635891	3.48E-10	8.17E-08	NA	NA	NA
c13107_g1_i5	2.546522	4.635891	3.48E-10	8.17E-08	NA	NA	NA
c15203_g1_i1	2.545007	1.90697	9.45E-06	0.000531	RecName: Full=Protein MON2 homolog; AltName: Full=Protein SF21 [Homo sapiens]	NA	NA
c5987_g2_i1	2.541484	1.903092	2.64E-05	0.001197	NA	UniRef90_A0A0C3PBJ0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PBJ0_PHLGI	NA
c13870_g1_i1	2.538424	5.301091	4.01E-09	7.77E-07	NA	UniRef90_K5VSG7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSG7_PHACS	NA
c10351_g1_i1	2.536141	2.821493	2.77E-05	0.00124	NA	NA	NA
c10351_g1_i2	2.536141	2.821493	2.77E-05	0.00124	NA	UniRef90_K5XF19 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XF19_PHACS	NA
c13758_g1_i1	2.534779	3.031897	7.27E-08	9.35E-06	NA	UniRef90_K5VNR3 Uncharacterized protein (Fragment) n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VNR3_PHACS	NA
c15056_g1_i1	2.533787	1.161198	0.001092	0.021331	RecName: Full=Uncharacterized RNA-binding protein P16F5.06 [Schizosaccharomyces pombe 972h-]	NA	GO:0003676
c13230_g1_i1	2.532984	6.05513	5.75E-07	5.29E-05	NA	UniRef90_UPI000440F4D7 hypothetical protein STEHIDRAFT_121205 n=1 Tax=Stereum hirsutum (strain FP-91666) RepID=UPI000440F4D7	NA
c13230_g1_i2	2.532984	6.05513	5.75E-07	5.29E-05	NA	NA	NA
c13230_g1_i3	2.532984	6.05513	5.75E-07	5.29E-05	NA	NA	NA
c16094_g2_i1	2.532264	5.197583	6.66E-06	0.000397	NA	NA	NA

c16094_g2_i2	2.532264	5.197583	6.66E-06	0.000397	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c16094_g2_i3	2.532264	5.197583	6.66E-06	0.000397	NA	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c8300_g2_i1	2.519437	1.726637	0.000131	0.004214	RecName: Full=Uncharacterized PI3/PI4-kinase family protein C1F5.11c [Schizosaccharomyces pombe 972h-]	UniRef90_K5X9D8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X9D8_PHACS	NA
c5206_g1_i1	2.514264	5.724508	1.13E-05	0.000618	RecName: Full=Aldehyde dehydrogenase; Short=ALDDH; Short=ALDH [Agaricus bisporus]	UniRef90_K5VS65 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VS65_PHACS	GO:0008152|GO:0016491|GO:0055114
c5206_g2_i1	2.512786	4.169943	1.34E-05	0.000708	RecName: Full=Aldehyde dehydrogenase; Short=ALDDH; Short=ALDH [Agaricus bisporus]	UniRef90_K5VS65 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VS65_PHACS	GO:0008152|GO:0016491|GO:0055114
c15309_g2_i1	2.496647	5.049242	5.36E-07	4.97E-05	RecName: Full=Endoglucanase-7; AltName: Full=Cellulase-61B; Short=Cel61B; AltName: Full=Endo-1,4-beta-glucanase VII; Short=EGVII; AltName: Full=Endoglucanase VII; AltName: Full=Endoglucanase-61B; Flags: Precursor [Trichoderma reesei QM6a]	NA	NA
c15309_g2_i2	2.496647	5.049242	5.36E-07	4.97E-05	NA	NA	NA
c15309_g2_i3	2.496647	5.049242	5.36E-07	4.97E-05	NA	NA	NA
c15309_g2_i4	2.496647	5.049242	5.36E-07	4.97E-05	NA	NA	NA
c13618_g2_i1	2.496506	6.997317	1.02E-05	0.000566	RecName: Full=Ligninase LG6; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_K5W005 Glycoside hydrolase family 16 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W005_PHACS	GO:0004553|GO:0005975
c13618_g2_i2	2.496506	6.997317	1.02E-05	0.000566	NA	NA	NA

c13618_g2_i3	2.496506	6.997317	1.02E-05	0.000566	NA	NA	GO:0004553|GO:0005975
c13618_g2_i4	2.496506	6.997317	1.02E-05	0.000566	NA	NA	NA
c3739_g1_i1	2.494592	1.385147	0.000712	0.015698	NA	UniRef90_K5WJR0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJR0_PHACS	NA
c6015_g2_i1	2.494521	1.991036	0.003051	0.044255	NA	NA	NA
c9494_g2_i1	2.490666	3.773982	2.98E-06	0.000207	RecName: Full=Uncharacterized transcriptional regulatory protein C530.05 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VYH9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYH9_PHACS	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c14407_g1_i1	2.479691	5.054505	7.35E-08	9.39E-06	NA	NA	NA
c14407_g1_i2	2.479691	5.054505	7.35E-08	9.39E-06	NA	NA	NA
c14407_g1_i3	2.479691	5.054505	7.35E-08	9.39E-06	NA	NA	NA
c8196_g1_i1	2.479656	1.994585	2.58E-05	0.001186	NA	NA	NA
c3918_g1_i1	2.47196	3.459112	0.000409	0.010279	NA	UniRef90_K5VRP0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRP0_PHACS	NA
c13063_g1_i1	2.470437	4.646918	4.17E-09	7.88E-07	NA	UniRef90_K5VGX0 Glycoside hydrolase family 18 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VGX0_PHACS	GO:0004553|GO:0005975
c9400_g1_i1	2.464947	3.264634	3.81E-08	5.38E-06	RecName: Full=TPR and ankyrin repeat-containing protein 1; AltName: Full=Lupus brain antigen 1 homolog [Homo sapiens]	UniRef90_K5WLX4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLX4_PHACS	GO:0005524
c1784_g1_i1	2.446387	5.201875	6.40E-05	0.002376	NA	NA	NA
c11297_g2_i1	2.445653	4.714757	1.13E-06	9.15E-05	NA	UniRef90_K5VX58 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VX58_PHACS	NA
c13963_g1_i1	2.441567	3.039232	3.87E-06	0.000254	NA	UniRef90_K5W9E1 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W9E1_PHACS	NA

c5592_g1_i1	2.441073	1.513604	0.000438	0.010826	RecName: Full=DNA-directed RNA polymerase III subunit rpc1; Short=RNA polymerase III subunit C1; AltName: Full=DNA-directed RNA polymerase III largest subunit; AltName: Full=RPC158 [Schizosaccharomyces pombe 972h-]	UniRef90_K5X834 DNA-directed RNA polymerase n=2 Tax=Phanerochaetaceae RepID=K5X834_PHACS	GO:0003677|GO:0003899|GO:0006351
c10384_g1_i1	2.44081	4.883584	1.66E-05	0.000851	NA	UniRef90_K5VB42 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VB42_PHACS	NA
c10384_g1_i2	2.44081	4.883584	1.66E-05	0.000851	NA	NA	NA
c10384_g1_i3	2.44081	4.883584	1.66E-05	0.000851	NA	NA	NA
c15153_g1_i1	2.436055	5.701983	4.49E-07	4.33E-05	RecName: Full=Putative hydrolase Mb2248c; Flags: Precursor [Mycobacterium bovis AF2122/97]	NA	NA
c9412_g2_i1	2.426886	6.690944	2.57E-05	0.001186	NA	UniRef90_K5VCU0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCU0_PHACS	NA
c5344_g1_i1	2.424779	1.312046	0.000915	0.01878	NA	NA	NA
c14646_g2_i1	2.423158	1.528386	0.001174	0.022524	RecName: Full=Uncharacterized transporter C3H1.06c [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c13515_g2_i1	2.420243	6.860997	5.42E-09	9.74E-07	RecName: Full=Probable phosphoketolase [Schizosaccharomyces pombe 972h-]	UniRef90_K5X5E0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X5E0_PHACS	GO:0005975|GO:0016832
c11222_g2_i1	2.412324	2.663066	0.000733	0.015941	NA	NA	NA
c11222_g2_i2	2.412324	2.663066	0.000733	0.015941	NA	NA	NA
c11222_g2_i3	2.412324	2.663066	0.000733	0.015941	NA	NA	NA
c4612_g1_i1	2.409309	1.509045	0.000426	0.010616	NA	UniRef90_K5WJL0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJL0_PHACS	NA
c10612_g1_i1	2.404904	7.39124	2.04E-06	0.000149	RecName: Full=Trichodiene oxygenase; AltName: Full=Cytochrome P450 58 [Fusarium sporotrichioides]	UniRef90_G5EJV2 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJV2_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c10040_g1_i1	2.4027	1.656339	0.000103	0.003448	NA	UniRef90_K5VSK8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSK8_PHACS	NA
c8265_g1_i1	2.402296	1.495948	0.000381	0.009745	NA	UniRef90_K5WX35 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WX35_PHACS	NA
c14620_g1_i1	2.394686	6.549447	0.002585	0.039459	NA	NA	GO:0046373|GO:0046556
c14620_g1_i2	2.394686	6.549447	0.002585	0.039459	RecName: Full=Probable alpha-L-arabinofuranosidase A; Short=ABF A; Short=Arabinosidase A; Flags: Precursor [Aspergillus terreus NIH2624]	NA	GO:0046373|GO:0046556
c6011_g2_i1	2.394381	1.664302	0.000238	0.006814	NA	UniRef90_A0A0C3NBX4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NBX4_PHLGI	NA
c6011_g2_i2	2.394381	1.664302	0.000238	0.006814	NA	NA	NA
c6763_g1_i1	2.379883	2.789033	0.000265	0.007416	RecName: Full=Ligninase A; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_P11543 Ligninase LG5 n=1 Tax=Phanerochaete chrysosporium RepID=LIG5_PHACH	NA
c14465_g2_i1	2.3787	5.486429	4.75E-05	0.001903	RecName: Full=Glutathione-independent formaldehyde dehydrogenase; Short=FALDH; Short=FDH [Pseudomonas aeruginosa PAO1]	NA	GO:0008270|GO:0016491|GO:0055114
c11002_g1_i1	2.371066	3.708833	2.52E-05	0.00117	NA	NA	GO:0009055|GO:0055114
c11002_g1_i2	2.371066	3.708833	2.52E-05	0.00117	RecName: Full=Sulfite oxidase; AltName: Full=Moco-containing protein AtMCP; Short=At-SO; Short=AtSOX [Arabidopsis thaliana]	UniRef90_K5WGH3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGH3_PHACS	GO:0009055|GO:0016491|GO:0030151|GO:0055114
c11003_g1_i1	2.366468	6.907474	0.0003	0.00816	NA	UniRef90_K5VKV8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VKV8_PHACS	NA
c14762_g2_i1	2.364716	2.256178	0.001778	0.030269	NA	NA	NA

c12814_g2_i1	2.351793	4.198271	5.88E-05	0.00222	RecName: Full=Probable rhamnogalacturonase B; Short=RGase B; Short=RHG B; Flags: Precursor [Neosartorya fischeri NRRL 181]	UniRef90_K5VC60 Glycoside hydrolase family 28 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VC60_PHACS	NA
c12814_g2_i2	2.351793	4.198271	5.88E-05	0.00222	NA	NA	NA
c9953_g1_i1	2.34806	6.501456	0.002182	0.034632	NA	UniRef90_K5WK59 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WK59_PHACS	NA
c12844_g1_i1	2.345902	4.35135	3.98E-09	7.77E-07	RecName: Full=Protein LUTEIN DEFICIENT 5, chloroplastic; AltName: Full=Cytochrome P450 97A3; Flags: Precursor [Arabidopsis thaliana]	UniRef90_A0A0C3S4V5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S4V5_PHLGI	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15046_g1_i1	2.336945	7.21279	0.000411	0.010312	NA	NA	NA
c15046_g1_i2	2.336945	7.21279	0.000411	0.010312	RecName: Full=4-O-methyl-glucuronoyl methylesterase; AltName: Full=Glucuronoyl esterase 2; Short=GE2; Flags: Precursor [Trichoderma reesei QM6a]	NA	NA
c4515_g1_i1	2.336088	1.792728	0.000996	0.019983	NA	NA	NA
c4515_g1_i2	2.336088	1.792728	0.000996	0.019983	NA	NA	NA
c14750_g1_i1	2.334712	3.426597	0.000107	0.003543	RecName: Full=Iron transport multicopper oxidase fio1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	NA	GO:0005507|GO:0016491|GO:0055114
c14471_g1_i1	2.334489	4.770957	2.83E-05	0.001257	RecName: Full=Uncharacterized transporter C11D3.18C [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c7149_g1_i1	2.329254	1.755957	0.001054	0.020794	NA	NA	NA
c7149_g1_i2	2.329254	1.755957	0.001054	0.020794	NA	NA	NA
c14136_g1_i1	2.314698	5.800457	1.86E-07	2.06E-05	RecName: Full=von Willebrand factor A domain-containing protein DDB_G0292028 [Dictyostelium discoideum]	UniRef90_K5V3T4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3T4_PHACS	NA
c12844_g2_i1	2.307865	3.886238	1.22E-08	2.04E-06	RecName: Full=Cytochrome P450 4F8; AltName: Full=CYPIVF8 [Homo sapiens]	UniRef90_K5WLQ9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLQ9_PHACS	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c15937_g1_i1	2.303308	6.008013	0.000371	0.009521	RecName: Full=Trehalase; AltName: Full=Alpha,alpha-trehalase; AltName: Full=Alpha,alpha-trehalose glucohydrolase; Flags: Precursor [Oryctolagus cuniculus]	NA	GO:0004555|GO:0005991
c11389_g1_i1	2.303274	3.693483	3.99E-07	3.98E-05	NA	UniRef90_K5X5S7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X5S7_PHACS	NA
c13508_g3_i1	2.302151	7.867617	0.000308	0.008338	NA	NA	GO:0016491|GO:0045454|GO:0050660|GO:0055114
c13508_g3_i2	2.302151	7.867617	0.000308	0.008338	RecName: Full=Glutathione reductase; Short=GR; Short=GRase [Candida glabrata CBS 138]	UniRef90_K5WHB0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WHB0_PHACS	GO:0016491|GO:0045454|GO:0050660|GO:0055114
c13588_g3_i1	2.300221	6.210852	1.08E-07	1.29E-05	NA	UniRef90_B8PA66 Predicted protein n=2 Tax=Postia placenta (strain ATCC 44394 / Madison 698-R) RepID=B8PA66_POSPM	GO:0008168|GO:0032259
c7392_g1_i1	2.298345	6.456738	0.000748	0.016181	RecName: Full=L-amino acid amidase [Pseudomonas fluorescens SBW25]	UniRef90_K5WMK8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WMK8_PHACS	NA
c15154_g2_i1	2.297493	3.44495	2.32E-06	0.000166	NA	NA	NA
c15154_g2_i2	2.297493	3.44495	2.32E-06	0.000166	NA	NA	NA
c9497_g3_i1	2.29364	2.399651	7.48E-06	0.000435	NA	NA	NA
c9497_g3_i2	2.29364	2.399651	7.48E-06	0.000435	RecName: Full=Lactose regulatory protein LAC9 [Kluyveromyces lactis NRRL Y-1140]	UniRef90_K5WDG4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDG4_PHACS	GO:0003677|GO:0005634|GO:0006351|GO:0008270
c2976_g2_i1	2.293488	4.97304	3.57E-06	0.000239	NA	NA	NA
c5346_g1_i1	2.28811	4.698814	0.002361	0.036855	NA	NA	NA
c8093_g1_i1	2.285136	3.254391	0.000112	0.00369	RecName: Full=Probable metabolite transport protein GIT1 [Saccharomyces cerevisiae S288c]	UniRef90_K5W608 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W608_PHACS	GO:0016021|GO:0022857|GO:0055085
c6756_g1_i1	2.284104	7.213433	0.002493	0.038372	NA	NA	NA
c6756_g1_i2	2.284104	7.213433	0.002493	0.038372	NA	UniRef90_K5XD70 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XD70_PHACS	NA

c13471_g3_i1	2.278776	3.297959	1.83E-05	0.00091	RecName: Full=6-hydroxytryprostatin B O-methyltransferase; AltName: Full=Fumitremorgin biosynthesis protein D [Aspergillus fumigatus]	UniRef90_K5VNN2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VNN2_PHACS	GO:0008171
c11803_g1_i1	2.271664	5.502604	5.10E-05	0.002004	RecName: Full=Thiamine-repressible acid phosphatase pho4; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3SEZ7 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SEZ7_PHLGI	GO:0003993
c386_g1_i1	2.260278	5.255334	0.000215	0.00631	NA	UniRef90_K5UJN6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UJN6_PHACS	GO:0008080
c12200_g1_i1	2.255156	4.939653	2.62E-05	0.001193	RecName: Full=Aspergillopepsin-2; AltName: Full=Acid protease A; AltName: Full=Aspergillopepsin II; AltName: Full=Proctase A; Contains: RecName: Full=Aspergillopepsin-2 light chain; AltName: Full=Aspergillopepsin II light chain; Contains: RecName: Full=Aspergillopepsin-2 heavy chain; AltName: Full=Aspergillopepsin II heavy chain; Flags: Precursor [Aspergillus niger]	UniRef90_UPI0004621E2C aspergillopepsin n=1 Tax=Trametes versicolor (strain FP-101664) RepID=UPI0004621E2C	GO:0004190|GO:0006508
c10612_g2_i1	2.252921	5.241733	6.06E-06	0.000369	RecName: Full=Putative cytochrome P450 cyp-13B1 [Caenorhabditis elegans]	UniRef90_G5EJV2 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJV2_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c13371_g2_i1	2.244056	5.844562	7.10E-06	0.000416	NA	NA	NA
c13371_g2_i2	2.244056	5.844562	7.10E-06	0.000416	NA	NA	NA
c13371_g2_i3	2.244056	5.844562	7.10E-06	0.000416	NA	NA	NA
c12231_g2_i1	2.224671	2.93444	0.000813	0.017316	RecName: Full=Lactose permease [Kluyveromyces lactis NRRL Y-1140]	UniRef90_K5W8Q0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8Q0_PHACS	GO:0016021|GO:0022857|GO:0055085
c11548_g1_i1	2.223719	6.022347	1.93E-05	0.00094	NA	UniRef90_K5VQD3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VQD3_PHACS	NA

c15408_g3_i1	2.223519	4.807982	1.15E-05	0.000625	RecName: Full=Catalase [Methanosarcina barkeri str. Fusaro]	NA	GO:0004096|GO:0020037|GO:0055114
c15408_g3_i2	2.223519	4.807982	1.15E-05	0.000625	NA	NA	GO:0004096|GO:0020037|GO:0055114
c15408_g3_i3	2.223519	4.807982	1.15E-05	0.000625	NA	NA	GO:0004096|GO:0020037|GO:0055114
c10534_g2_i1	2.221705	2.674671	6.20E-06	0.000374	NA	NA	NA
c10534_g2_i2	2.221705	2.674671	6.20E-06	0.000374	NA	NA	NA
c14149_g2_i1	2.220485	2.418969	0.000441	0.01087	NA	UniRef90_K5UQW5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UQW5_PHACS	NA
c13471_g4_i1	2.211295	2.770576	9.67E-05	0.003309	NA	UniRef90_K5VNN2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VNN2_PHACS	NA
c13471_g4_i2	2.211295	2.770576	9.67E-05	0.003309	NA	NA	NA
c14784_g1_i1	2.209643	4.907673	7.11E-07	6.20E-05	RecName: Full=Aquaporin-1 [Saccharomyces cerevisiae EC1118]	NA	GO:0005215|GO:0006810|GO:0016020
c8323_g1_i1	2.208824	2.054599	3.89E-05	0.00161	NA	NA	NA
c8323_g1_i2	2.208824	2.054599	3.89E-05	0.00161	NA	NA	NA
c8323_g1_i3	2.208824	2.054599	3.89E-05	0.00161	NA	NA	NA
c13086_g2_i1	2.206442	2.157215	0.000136	0.004337	NA	UniRef90_K5VHK8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VHK8_PHACS	NA
c13204_g1_i1	2.199747	1.527083	0.00185	0.03098	NA	UniRef90_K5WCF3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCF3_PHACS	NA
c8241_g1_i1	2.198076	3.570971	7.05E-08	9.10E-06	NA	NA	NA
c8241_g1_i2	2.198076	3.570971	7.05E-08	9.10E-06	NA	NA	NA
c8241_g1_i3	2.198076	3.570971	7.05E-08	9.10E-06	NA	NA	NA
c16169_g3_i1	2.195962	6.640048	4.55E-05	0.001838	RecName: Full=High-affinity glucose transporter ght2; AltName: Full=Hexose	NA	GO:0016021|GO:0022857|GO:0055085

					transporter 2 [Schizosaccharomyces pombe 972h-]		
c16169_g3_i2	2.195962	6.640048	4.55E-05	0.001838	NA	NA	GO:0016021|GO:0022857|GO:0055085
c14933_g6_i1	2.191187	5.507815	1.35E-08	2.22E-06	RecName: Full=GATA zinc finger domain-containing protein 14 [Dictyostelium discoideum]	NA	GO:0003700|GO:0006355|GO:0008270|GO:0043565
c12323_g1_i1	2.187755	3.439433	4.79E-06	0.000302	NA	NA	NA
c12323_g1_i2	2.187755	3.439433	4.79E-06	0.000302	NA	UniRef90_K5WM58 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WM58_PHACS	NA
c12323_g1_i3	2.187755	3.439433	4.79E-06	0.000302	NA	NA	NA
c13422_g1_i1	2.186746	1.92299	9.98E-05	0.003379	RecName: Full=Serine/threonine-protein kinase mTOR; AltName: Full=FK506-binding protein 12-rapamycin complex-associated protein 1; AltName: Full=FKBP12-rapamycin complex-associated protein; AltName: Full=Mammalian target of rapamycin; Short=mTOR; AltName: Full=Mechanistic target of rapamycin; AltName: Full=Rapamycin target protein 1; Short=RAPT1 [Rattus norvegicus]	UniRef90_K5VYM0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYM0_PHACS	NA
c8070_g1_i1	2.174538	2.116251	0.000295	0.008062	NA	NA	NA
c8070_g1_i2	2.174538	2.116251	0.000295	0.008062	NA	UniRef90_K5UZG5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UZG5_PHACS	NA
c8070_g1_i3	2.174538	2.116251	0.000295	0.008062	NA	NA	NA
c10401_g1_i1	2.1692	5.35717	0.00018	0.005417	RecName: Full=Putative oxidoreductase bli-4, mitochondrial; AltName: Full=Blue light-induced protein 4; Flags: Precursor [Neurospora crassa OR74A]	UniRef90_K5WKD2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKD2_PHACS	GO:0008152|GO:0016491
c15791_g1_i1	2.167566	6.772201	3.98E-05	0.001639	RecName: Full=Probable beta-glucosidase I; AltName: Full=Beta-D-glucoside glucohydrolase I; AltName: Full=Cellobiase I;	NA	GO:0004553|GO:0005975

					AltName: Full=Gentiobiase I [Aspergillus clavatus NRRL 1]		
c7717_g1_i1	2.166119	1.33419	0.001346	0.02483	NA	NA	NA
c7717_g1_i2	2.166119	1.33419	0.001346	0.02483	NA	NA	NA
c14227_g1_i1	2.164549	3.877574	0.00264	0.039936	NA	UniRef90_A0A0C3PK54 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PK54_PHLGI	GO:0006629|GO:0016788
c8436_g1_i1	2.160587	2.301056	5.39E-05	0.002069	RecName: Full=HEAT repeat-containing protein 5B [Xenopus (Silurana) tropicalis]	UniRef90_K5W161 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W161_PHACS	NA
c12560_g1_i1	2.159736	3.943198	0.000157	0.004865	NA	UniRef90_K5VB42 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VB42_PHACS	NA
c9497_g1_i1	2.157874	3.618568	2.12E-06	0.000153	NA	NA	NA
c9497_g1_i2	2.157874	3.618568	2.12E-06	0.000153	NA	UniRef90_K5WDG4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDG4_PHACS	NA
c12110_g1_i1	2.157383	3.377094	7.78E-07	6.73E-05	NA	UniRef90_K5WH68 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WH68_PHACS	NA
c14972_g1_i1	2.157366	5.332469	2.95E-05	0.001303	RecName: Full=Para-nitrobenzyl esterase; AltName: Full=Intracellular esterase B; AltName: Full=PNB carboxy-esterase; Short=PNBCE [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0008152|GO:0016787
c14205_g1_i1	2.153281	6.845483	0.001945	0.031989	RecName: Full=Para-nitrobenzyl esterase; AltName: Full=Intracellular esterase B; AltName: Full=PNB carboxy-esterase; Short=PNBCE [Bacillus subtilis subsp. subtilis str. 168]	UniRef90_K5X5G6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X5G6_PHACS	GO:0008152|GO:0016787
c15262_g1_i1	2.150728	6.752141	1.98E-05	0.000959	RecName: Full=Protein argonaute-4; Short=Argonaute4; AltName: Full=Argonaute RISC catalytic component 4; AltName:	NA	GO:0005515

					Full=Eukaryotic translation initiation factor 2C 4; Short=eIF-2C 4; Short=eIF2C 4 [Xenopus laevis]		
c8249_g1_i1	2.150506	4.444354	1.52E-06	0.000115	NA	NA	GO:0016021|GO:0022857|GO:0055085
c8249_g1_i2	2.150506	4.444354	1.52E-06	0.000115	RecName: Full=Uncharacterized transporter C3H1.06c [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3RW30 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RW30_PHLGI	GO:0016021|GO:0022857|GO:0055085
c8249_g1_i3	2.150506	4.444354	1.52E-06	0.000115	NA	NA	GO:0016021|GO:0022857|GO:0055085
c14596_g6_i1	2.150238	1.493359	0.000684	0.015258	NA	NA	NA
c7889_g1_i1	2.147493	5.444969	0.000365	0.009418	RecName: Full=Tryptophan 2-halogenase [Chondromyces crocatus]	UniRef90_A0A0C3S8X2 Putative halogenase n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S8X2_PHLGI	NA
c18832_g1_i1	2.141144	1.750004	0.000182	0.005464	RecName: Full=Probable nucleoporin C890.06 [Schizosaccharomyces pombe 972h-]	NA	NA
c13479_g1_i1	2.136774	5.153491	0.000487	0.011722	RecName: Full=Tripeptidyl-peptidase SED2; AltName: Full=Sedolisin-B; Flags: Precursor [Arthroderma otae CBS 113480]	UniRef90_Q281W2 Family S53 protease n=1 Tax=Phanerochaete chrysosporium RepID=Q281W2_PHACH	GO:0004252|GO:0006508|GO:0008236
c15090_g1_i1	2.121539	7.04273	1.71E-06	0.000128	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c18255_g1_i1	2.119763	1.480576	0.001309	0.024431	NA	NA	NA
c14280_g1_i1	2.119739	5.846904	0.000293	0.008028	RecName: Full=Uncharacterized lactate 2-monooxygenase PB1A11.03 [Schizosaccharomyces pombe 972h-]	UniRef90_K5X2R1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X2R1_PHACS	GO:0003824|GO:0006537|GO:0015930|GO:0016491|GO:0016638|GO:0018580|GO:0055114

c12232_g1_i1	2.117413	8.198177	1.15E-07	1.35E-05	RecName: Full=Probable glycosidase C21B10.07 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WN06 Glycoside hydrolase family 16 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WN06_PHACS	NA
c13374_g1_i1	2.114767	6.211845	0.000325	0.008643	NA	UniRef90_A0A0C3SAP5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SAP5_PHLGI	NA
c13374_g1_i2	2.114767	6.211845	0.000325	0.008643	NA	NA	NA
c13374_g1_i3	2.114767	6.211845	0.000325	0.008643	NA	NA	NA
c14307_g2_i1	2.113656	6.231039	9.11E-05	0.003165	NA	NA	GO:0016491|GO:0055114
c14307_g2_i2	2.113656	6.231039	9.11E-05	0.003165	NA	NA	GO:0016491|GO:0055114
c14307_g2_i3	2.113656	6.231039	9.11E-05	0.003165	NA	NA	GO:0016491|GO:0055114
c14307_g2_i4	2.113656	6.231039	9.11E-05	0.003165	NA	NA	GO:0016491|GO:0055114
c14307_g2_i5	2.113656	6.231039	9.11E-05	0.003165	RecName: Full=Alpha-ketoglutarate-dependent sulfonate dioxygenase [Saccharomyces cerevisiae S288c]	NA	GO:0016491|GO:0055114
c14307_g2_i6	2.113656	6.231039	9.11E-05	0.003165	NA	NA	NA
c14307_g2_i7	2.113656	6.231039	9.11E-05	0.003165	NA	NA	GO:0016491|GO:0055114
c11916_g3_i1	2.110968	2.280076	0.000243	0.0069	NA	UniRef90_K5X176 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X176_PHACS	GO:0003968
c7697_g1_i1	2.110865	8.931807	0.000143	0.00449	NA	UniRef90_K5V3E5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3E5_PHACS	NA
c15880_g5_i1	2.109421	3.410953	1.15E-06	9.25E-05	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085

c14076_g1_i1	2.107393	1.601613	0.001196	0.022739	NA	UniRef90_M2QYE9 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2QYE9_CERS8	NA
c7365_g1_i1	2.106271	2.850393	1.09E-05	0.0006	NA	UniRef90_K5WLW9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLW9_PHACS	NA
c9079_g1_i1	2.103058	7.515028	0.001809	0.030607	NA	UniRef90_Q01772 Glyoxal oxidase n=4 Tax=Phanerochaete chrysosporium RepID=Q01772_PHACH	NA
c8280_g1_i1	2.101426	2.322542	0.001199	0.02278	NA	NA	NA
c8280_g1_i2	2.101426	2.322542	0.001199	0.02278	NA	NA	NA
c8280_g1_i3	2.101426	2.322542	0.001199	0.02278	NA	NA	NA
c3834_g1_i1	2.10114	1.280913	0.002739	0.041065	NA	UniRef90_K5VVG9 Glycosyltransferase family 8 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVG9_PHACS	NA
c11389_g2_i1	2.099105	2.001644	0.001072	0.021051	NA	UniRef90_K5X5S7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X5S7_PHACS	NA
c13662_g2_i1	2.096476	6.893841	1.83E-05	0.00091	NA	UniRef90_A0A067XG72 Glutathione transferase n=1 Tax=Phanerochaete chrysosporium RepID=A0A067XG72_PHACH	GO:0005515
c6927_g2_i1	2.093812	2.935036	3.80E-06	0.000251	RecName: Full=Beige protein homolog 1 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3SD43 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SD43_PHLGI	NA
c16119_g1_i1	2.089882	4.549562	3.15E-06	0.000217	RecName: Full=Proteasome activator complex subunit 4; AltName: Full=Proteasome activator PA200 [Xenopus laevis]	NA	NA
c14086_g1_i1	2.088061	4.501803	1.46E-05	0.000762	NA	NA	NA
c14086_g1_i2	2.088061	4.501803	1.46E-05	0.000762	NA	NA	NA
c14086_g1_i3	2.088061	4.501803	1.46E-05	0.000762	NA	UniRef90_K5VD40 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VD40_PHACS	NA
c14086_g1_i4	2.088061	4.501803	1.46E-05	0.000762	NA	NA	NA

c12231_g1_i1	2.084148	5.550788	0.000111	0.00367	RecName: Full=Lactose permease [Kluyveromyces lactis NRRL Y-1140]	UniRef90_K5W8Q0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8Q0_PHACS	GO:0016021|GO:0022857|GO:0055085
c7416_g1_i1	2.083141	4.762003	4.72E-08	6.38E-06	NA	UniRef90_A0A0C3RV13 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RV13_PHLGI	NA
c6682_g1_i1	2.081767	5.598324	0.002243	0.035287	NA	UniRef90_A0A067QNX3 Uncharacterized protein n=1 Tax=Jaapia argillacea MUCL 33604 RepID=A0A067QNX3_9HOMO	NA
c6682_g1_i2	2.081767	5.598324	0.002243	0.035287	NA	NA	NA
c11972_g1_i1	2.080141	2.339248	9.40E-05	0.003251	NA	UniRef90_K5VD20 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VD20_PHACS	NA
c15621_g2_i1	2.077335	3.456721	6.04E-07	5.49E-05	NA	NA	NA
c12461_g2_i1	2.0694	1.688506	0.002139	0.03415	NA	NA	NA
c9015_g1_i1	2.067544	2.071481	0.000204	0.006026	NA	UniRef90_K5VZJ3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZJ3_PHACS	NA
c14298_g2_i1	2.067422	2.75449	0.000129	0.004164	NA	NA	NA
c14298_g2_i2	2.067422	2.75449	0.000129	0.004164	NA	NA	NA
c4172_g1_i1	2.067025	1.598575	0.001651	0.02864	RecName: Full=ATP-binding cassette transporter abc1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VPI4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPI4_PHACS	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c7354_g1_i1	2.057406	3.524853	0.000315	0.008449	RecName: Full=Probable metabolite transport protein GIT1 [Saccharomyces cerevisiae S288c]	UniRef90_K5W608 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W608_PHACS	GO:0016021|GO:0022857|GO:0055085
c14930_g2_i1	2.050484	6.561772	8.40E-05	0.002963	RecName: Full=NAD(P) transhydrogenase, mitochondrial; AltName: Full=Nicotinamide nucleotide transhydrogenase; AltName: Full=Pyridine nucleotide transhydrogenase; Flags: Precursor [Bos taurus]	NA	GO:0008750|GO:0016021|GO:0050661|GO:0055114

c8095_g1_i1	2.048429	3.528862	5.46E-05	0.002086	NA	UniRef90_K5WD93 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WD93_PHACS	NA
c10068_g1_i1	2.041525	2.313346	0.001329	0.02459	NA	UniRef90_K5VSR1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSR1_PHACS	NA
c13273_g2_i1	2.040029	2.949565	0.000574	0.013286	RecName: Full=Cytochrome P450 67; AltName: Full=CYPLXVII; AltName: Full=Planta-induced rust protein 16, partial [Uromyces viciae-fabae]	UniRef90_G5EJL6 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJL6_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c13273_g2_i2	2.040029	2.949565	0.000574	0.013286	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12454_g1_i1	2.039429	3.885983	3.14E-05	0.001361	NA	UniRef90_K5VQD3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VQD3_PHACS	NA
c12454_g1_i2	2.039429	3.885983	3.14E-05	0.001361	NA	NA	NA
c6788_g1_i1	2.033328	1.397398	0.00269	0.040434	NA	NA	NA
c13365_g1_i1	2.0302	6.97036	1.69E-06	0.000127	RecName: Full=Sulfite oxidase, mitochondrial; Flags: Precursor [Homo sapiens]	UniRef90_K5UWL2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UWL2_PHACS	GO:0009055|GO:0016491|GO:0030151|GO:0055114
c15154_g3_i1	2.030149	2.713828	1.92E-05	0.00094	NA	NA	NA
c8227_g2_i1	2.02838	4.817194	9.59E-06	0.000538	NA	NA	GO:0000272|GO:0008810
c8227_g2_i2	2.02838	4.817194	9.59E-06	0.000538	RecName: Full=Probable xyloglucan-specific endo-beta-1,4-glucanase A; AltName: Full=Xyloglucanase A; AltName: Full=Xyloglucanendohydrolase A; Flags: Precursor [Aspergillus oryzae RIB40]	UniRef90_Q66NB6 Endoglucanase n=1 Tax=Phanerochaete chrysosporium RepID=Q66NB6_PHACH	GO:0000272|GO:0008810
c11788_g1_i1	2.024752	9.159245	0.000678	0.01516	RecName: Full=Beta-glucosidase 1B; AltName: Full=Cellobiase 1B [Phanerochaete chrysosporium]	UniRef90_Q25BW4 Beta-glucosidase 1B n=2 Tax=Phanerochaete RepID=BGL1B_PHACH	GO:0004553|GO:0005975
c13260_g1_i1	2.021903	4.920628	1.61E-07	1.82E-05	NA	UniRef90_K5WZU3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WZU3_PHACS	NA

c4959_g1_i1	2.015888	1.420128	0.001977	0.032313	NA	UniRef90_K5WNI2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNI2_PHACS	NA
c14859_g1_i1	2.014975	4.85531	5.28E-07	4.94E-05	RecName: Full=Homogentisate 1,2-dioxygenase; AltName: Full=Homogentisate oxygenase; AltName: Full=Homogentisic acid oxidase; AltName: Full=Homogentisicase [Aspergillus nidulans FGSC A4]	NA	GO:0004411|GO:0006559|GO:0006570|GO:0055114
c13911_g1_i1	2.014643	4.805727	2.90E-05	0.001284	RecName: Full=Metacaspase-1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_K5W2M8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2M8_PHACS	GO:0004197|GO:0006508
c13911_g1_i2	2.014643	4.805727	2.90E-05	0.001284	NA	NA	GO:0004197|GO:0006508
c13911_g1_i3	2.014643	4.805727	2.90E-05	0.001284	NA	NA	GO:0004197|GO:0006508
c13911_g1_i4	2.014643	4.805727	2.90E-05	0.001284	NA	NA	GO:0004197|GO:0006508
c9025_g1_i1	2.013038	5.402093	3.03E-05	0.001331	NA	UniRef90_K5WLD5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLD5_PHACS	NA
c9131_g1_i1	1.998807	1.553572	0.003236	0.046234	NA	UniRef90_K5VWM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWM7_PHACS	NA
c8678_g1_i1	1.998443	2.358455	0.000255	0.007177	NA	UniRef90_K5VW80 Protein argonaute n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VW80_PHACS	NA
c16437_g1_i1	1.995567	1.673187	0.001822	0.030774	NA	NA	NA
c13456_g3_i1	1.990856	1.523794	0.002659	0.040013	NA	NA	NA
c13456_g3_i2	1.990856	1.523794	0.002659	0.040013	NA	NA	NA
c13456_g3_i3	1.990856	1.523794	0.002659	0.040013	NA	UniRef90_K5WI42 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WI42_PHACS	NA
c10534_g3_i1	1.98953	2.268033	0.001774	0.030229	NA	NA	NA
c13933_g2_i1	1.983136	2.259609	5.84E-05	0.002213	NA	UniRef90_K5VSJ4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSJ4_PHACS	NA

c15954_g3_i1	1.978808	3.843347	0.000129	0.00418	NA	NA	NA
c4985_g1_i1	1.974558	1.87308	0.000404	0.010199	NA	UniRef90_R7S7Z7 Uncharacterized protein n=1 Tax=Trametes versicolor (strain FP-101664) RepID=R7S7Z7_TRAVS	NA
c8115_g1_i1	1.974225	2.088072	0.000285	0.007833	NA	NA	NA
c8083_g1_i1	1.973828	6.062389	9.94E-05	0.00337	NA	UniRef90_K5WD93 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WD93_PHACS	NA
c16324_g1_i1	1.97152	1.877319	0.000579	0.01336	NA	NA	NA
c14750_g2_i1	1.971265	6.586361	1.28E-05	0.000682	RecName: Full=Iron transport multicopper oxidase FET3; Flags: Precursor [Candida albicans]	NA	GO:0005507|GO:0016491|GO:0055114
c14791_g1_i1	1.970401	6.279135	2.94E-06	0.000205	RecName: Full=Brefeldin A resistance protein [Schizosaccharomyces pombe 972h-]	NA	GO:0003924|GO:0005524|GO:0005525|GO:0006810|GO:0016020|GO:0016021|GO:0016887|GO:0042626
c9667_g1_i1	1.970136	2.833003	1.86E-05	0.000915	RecName: Full=Transcription initiation factor TFIID subunit 2; AltName: Full=TBP-associated factor 150 kDa; AltName: Full=Transcription initiation factor TFIID 150 kDa subunit; Short=TAF(II)150; Short=TAFII-150; Short=TAFII150 [Danio rerio]	UniRef90_K5XEG5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XEG5_PHACS	NA
c12680_g2_i1	1.968126	5.503789	8.76E-07	7.33E-05	RecName: Full=Lysophospholipase 2; AltName: Full=Phospholipase B 2; Flags: Precursor [Candida glabrata CBS 138]	UniRef90_F8PR54 Putative uncharacterized protein n=2 Tax=Serpula lacrymans var. lacrymans RepID=F8PR54_SERL3	GO:0004620|GO:0009395
c13708_g3_i1	1.967246	3.2754	5.18E-05	0.002026	RecName: Full=Transposon Ty3-I Gag-Pol polyprotein; AltName: Full=Gag3-Pol3; AltName: Full=Transposon Ty3-2 TYA-TYB polyprotein; Contains: RecName: Full=Capsid protein; Short=CA; AltName: Full=p24; Contains: RecName: Full=Spacer peptide p3; Contains: RecName: Full=Nucleocapsid protein p11; Short=NC; Contains: RecName: Full=Ty3	UniRef90_Q45W61 Polyprotein (Fragment) n=1 Tax=Phanerochaete chrysosporium (strain RP-78 / ATCC MYA-4764 / FGSC 9002) RepID=Q45W61_PHACR	NA

					protease; Short=PR; AltName: Full=p16; Contains: RecName: Full=Spacer peptide J; Contains: RecName: Full=Reverse transcriptase/ribonuclease H; Short=RT; Short=RT-RH; AltName: Full=p55; Contains: RecName: Full=Integrase p52; Short=IN; Contains: RecName: Full=Integrase p49; Short=IN [Saccharomyces cerevisiae S288c]		
c6582_g2_i1	1.96506	6.240803	0.001005	0.020135	NA	UniRef90_K5WE36 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WE36_PHACS	NA
c13109_g1_i1	1.964929	2.832625	4.17E-05	0.001711	NA	NA	NA
c13109_g1_i2	1.964929	2.832625	4.17E-05	0.001711	NA	UniRef90_K5WHP4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WHP4_PHACS	GO:0006355
c3572_g1_i1	1.964855	3.636718	0.001617	0.028248	RecName: Full=L-amino acid amidase [Pseudomonas fluorescens SBW25]	UniRef90_K5WAH6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAH6_PHACS	NA
c10420_g1_i1	1.963353	3.502141	0.001883	0.031276	NA	UniRef90_K5WGM6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGM6_PHACS	NA
c6331_g1_i1	1.960435	2.420853	0.000232	0.00666	RecName: Full=Transcription factor Sox-14 [Danio rerio]	UniRef90_A0A0C3RST1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RST1_PHLGI	NA
c9357_g3_i1	1.957016	3.229898	1.42E-05	0.000739	NA	UniRef90_K5VBH7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VBH7_PHACS	NA
c6630_g1_i1	1.952115	2.333198	0.00015	0.004689	NA	UniRef90_K5WR68 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WR68_PHACS	NA
c9494_g1_i1	1.951286	4.390862	5.88E-05	0.00222	NA	UniRef90_K5VYH9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYH9_PHACS	NA

c13518_g3_i1	1.949466	2.306186	0.00018	0.005417	NA	UniRef90_K5WFT3 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFT3_PHACS	NA
c7403_g2_i1	1.947408	3.158322	7.14E-05	0.002578	RecName: Full=FK506-binding protein 5; AltName: Full=Peptidyl-prolyl cis-trans isomerase; Short=PPIase; AltName: Full=Rotamase [Rhizopus delemar RA 99-880]	UniRef90_K5WN55 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WN55_PHACS	NA
c16119_g4_i1	1.947167	3.916252	1.40E-06	0.000108	NA	NA	NA
c11619_g1_i1	1.946223	2.379272	5.99E-05	0.002253	RecName: Full=L-aminoadipate-semialdehyde dehydrogenase large subunit; AltName: Full=Alpha-aminoadipate reductase; Short=Alpha-AR [Ashbya gossypii ATCC 10895]	UniRef90_K5VJN5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VJN5_PHACS	GO:0003824|GO:0050662
c11315_g1_i1	1.945354	3.291092	2.49E-06	0.000177	NA	UniRef90_K5VUK8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUK8_PHACS	NA
c14418_g2_i1	1.944652	3.794268	0.000891	0.018552	NA	NA	NA
c8333_g1_i1	1.94425	4.759912	9.84E-06	0.000548	NA	NA	NA
c8333_g1_i2	1.94425	4.759912	9.84E-06	0.000548	NA	NA	NA
c14754_g1_i1	1.941523	3.381076	6.36E-05	0.002365	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus parasiticus]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c9823_g1_i1	1.94069	4.586139	0.002214	0.034979	RecName: Full=Vacuolar aspartic protease; AltName: Full=ACP; AltName: Full=Aspartate protease; Flags: Precursor [Candida albicans]	UniRef90_K5WIE5 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WIE5_PHACS	GO:0004190|GO:0006508
c14791_g2_i1	1.940089	3.869318	1.00E-06	8.17E-05	RecName: Full=Multidrug resistance protein CDR2 [Candida albicans SC5314]	NA	GO:0005524|GO:0016887

c13206_g1_i1	1.938689	5.26395	8.54E-07	7.24E-05	NA	UniRef90_UPI000441737D hypothetical protein PUNSTDRAFT_53872 n=1 Tax=Punctularia strigosozonata (strain HHB-11173) RepID=UPI000441737D	NA
c5225_g1_i1	1.937255	2.726191	0.000126	0.004082	NA	NA	NA
c5225_g1_i2	1.937255	2.726191	0.000126	0.004082	RecName: Full=Flavohemoprotein; AltName: Full=Flavohemoglobin; AltName: Full=Hemoglobin-like protein; AltName: Full=Nitric oxide dioxygenase; Short=NO oxygenase; Short=NOD [Sinorhizobium meliloti 1021]	UniRef90_UPI000455FD4D globin-like protein n=1 Tax=Coniophora puteana (strain RWD-64-598) RepID=UPI000455FD4D	GO:0005506|GO:0016491|GO:0020037|GO:0055114
c10061_g2_i1	1.934226	5.727881	9.07E-05	0.003159	NA	NA	NA
c10061_g2_i2	1.934226	5.727881	9.07E-05	0.003159	NA	UniRef90_K5UVU8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UVU8_PHACS	NA
c10061_g2_i3	1.934226	5.727881	9.07E-05	0.003159	NA	NA	NA
c15824_g2_i1	1.933621	3.811367	0.000663	0.014911	NA	NA	NA
c15812_g1_i1	1.93133	4.992446	1.52E-07	1.74E-05	RecName: Full=Uncharacterized helicase C694.02 [Schizosaccharomyces pombe 972h-]	NA	GO:0003676|GO:0003677|GO:0005524|GO:0016787
c13109_g2_i1	1.928218	1.875879	0.003553	0.049389	RecName: Full=Cyanobacterial phytochrome B [Nostoc sp. PCC 7120]	UniRef90_K5WHP4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WHP4_PHACS	NA
c13109_g2_i2	1.928218	1.875879	0.003553	0.049389	NA	NA	NA
c651_g1_i1	1.927954	2.460025	0.000115	0.003789	NA	UniRef90_K5WM41 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WM41_PHACS	NA
c12135_g1_i1	1.922991	6.532151	0.000165	0.005036	RecName: Full=Polyamine aminopropyltransferase; AltName: Full=Putrescine aminopropyltransferase; Short=PAPT; AltName: Full=Spermidine synthase; Short=SPDS; Short=SPDSY [Vibrio vulnificus YJ016]	UniRef90_K5W5Z3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5Z3_PHACS	GO:0003824
c12135_g1_i2	1.922991	6.532151	0.000165	0.005036	NA	NA	GO:0003824

c14815_g2_i1	1.922373	3.722511	1.55E-06	0.000117	RecName: Full=Artemisinic aldehyde Delta(11(13)) reductase [Artemisia annua]	NA	GO:0010181|GO:0016491|GO:0055114
c15090_g2_i1	1.9217	6.249997	4.45E-06	0.000285	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c3801_g1_i1	1.91854	3.026327	1.65E-05	0.000847	RecName: Full=TPR and ankyrin repeat-containing protein 1; AltName: Full=Lupus brain antigen 1 homolog [Homo sapiens]	UniRef90_K5W937 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W937_PHACS	GO:0005524|GO:0016787
c13652_g1_i1	1.914849	6.601234	0.000395	0.009994	RecName: Full=Protein rds1 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3PTP2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PTP2_PHLGI	NA
c18272_g1_i1	1.911309	4.43061	0.002803	0.041689	RecName: Full=4-hydroxybenzoate polyprenyltransferase, mitochondrial; AltName: Full=Coenzyme Q biosynthesis protein 2; AltName: Full=Para-hydroxybenzoate--polyprenyltransferase; Short=PHB:polyprenyltransferase; Flags: Precursor [Drosophila pseudoobscura pseudoobscura]	NA	GO:0004659|GO:0016021
c14179_g5_i1	1.906866	6.911544	0.000143	0.00449	RecName: Full=Protein argonaute 1B; Short=OsAGO1b [Oryza sativa Japonica Group]	UniRef90_K5UMY8 Protein argonaute n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UMY8_PHACS	GO:0005515
c18798_g1_i1	1.904066	2.113713	0.00094	0.019131	RecName: Full=Rho-type GTPase-activating protein 1 [Schizosaccharomyces pombe 972h-]	NA	NA
c12756_g3_i1	1.903918	2.514259	9.05E-05	0.003159	RecName: Full=TPR and ankyrin repeat-containing protein 1; AltName: Full=Lupus brain antigen 1 [Mus musculus]	UniRef90_K5WLW9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLW9_PHACS	GO:0005524

c13596_g1_i1	1.899892	4.6064	2.00E-06	0.000146	RecName: Full=Uncharacterized protein RSN1; AltName: Full=Rescuer of SRO7 at high Nacl protein 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5WI99 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WI99_PHACS	NA
c12560_g3_i1	1.893597	4.071915	7.77E-05	0.002767	NA	UniRef90_K5VB42 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VB42_PHACS	NA
c13204_g3_i1	1.890497	4.880496	1.26E-06	9.87E-05	RecName: Full=UPF0187 protein sll1024 [Synechocystis sp. PCC 6803 substr. Kazusa]	UniRef90_K5WCF3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCF3_PHACS	NA
c10726_g1_i1	1.884732	3.926524	2.68E-05	0.001207	RecName: Full=Zinc finger protein zas1 [Schizosaccharomyces pombe 972h-]	UniRef90_S7RBA2 Uncharacterized protein n=1 Tax=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) RepID=S7RBA2_GLOTA	NA
c10730_g1_i1	1.883566	3.272328	1.76E-05	0.000895	RecName: Full=Aldos-2-ulose dehydratase; AltName: Full=D-arabino-hex-2-ulose dehydratase; AltName: Full=Pyranosone dehydratase [Phanerochaete chrysosporium]	UniRef90_P84193 Aldos-2-ulose dehydratase n=2 Tax=Phanerochaete chrysosporium RepID=AUD_PHACH	NA
c13270_g2_i1	1.882529	4.195294	0.000105	0.003492	RecName: Full=Outer spore wall protein RRT8; AltName: Full=Regulator of rDNA transcription protein 8 [Saccharomyces cerevisiae S288c]	UniRef90_K5WKA2 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKA2_PHACS	NA
c3817_g1_i1	1.876497	2.197223	0.002957	0.043331	NA	UniRef90_A0A0C3NTN0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NTN0_PHLGI	NA
c11859_g1_i1	1.876407	6.976324	0.00061	0.013915	NA	NA	NA
c11859_g1_i2	1.876407	6.976324	0.00061	0.013915	NA	NA	NA
c11859_g1_i3	1.876407	6.976324	0.00061	0.013915	NA	NA	NA
c11859_g1_i4	1.876407	6.976324	0.00061	0.013915	NA	UniRef90_K5V6N4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V6N4_PHACS	NA
c2945_g2_i1	1.873994	3.07277	6.97E-06	0.00041	NA	UniRef90_K5W937 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W937_PHACS	NA

c8394_g2_i1	1.873074	1.81147	0.001162	0.022364	NA	NA	NA
c14978_g3_i1	1.869104	6.467072	5.54E-06	0.000343	RecName: Full=Alcohol dehydrogenase 3; AltName: Full=Alcohol dehydrogenase III; Short=ADH III [Aspergillus nidulans FGSC A4]	NA	GO:0008270|GO:0016491|GO:0055114
c14978_g3_i2	1.869104	6.467072	5.54E-06	0.000343	NA	NA	GO:0008270|GO:0016491|GO:0055114
c12641_g2_i1	1.866979	6.602963	0.000218	0.006365	RecName: Full=Putative serine protease K12H4.7; Flags: Precursor [Caenorhabditis elegans]	UniRef90_K5WBM1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WBM1_PHACS	GO:0006508|GO:0008236
c446_g1_i1	1.86685	1.906802	0.001453	0.026108	NA	UniRef90_K5W114 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W114_PHACS	NA
c13601_g1_i1	1.86668	6.67029	0.000373	0.009564	RecName: Full=ATP-citrate synthase; AltName: Full=ATP-citrate (pro-S-)-lyase; AltName: Full=Citrate cleavage enzyme [Bos taurus]	UniRef90_K5V2S1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V2S1_PHACS	GO:0048037
c12325_g1_i1	1.864138	3.449583	4.89E-05	0.001941	NA	UniRef90_K5VZI8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZI8_PHACS	NA
c10183_g1_i1	1.86215	3.771016	0.001354	0.024921	RecName: Full=Phospholipase D1; Short=PLD 1; AltName: Full=Choline phosphatase 1; AltName: Full=Phosphatidylcholine-hydrolyzing phospholipase D1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5UQ58 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UQ58_PHACS	GO:0035091
c12416_g1_i1	1.861758	3.302121	9.68E-05	0.003309	RecName: Full=Uncharacterized ABC transporter ATP-binding protein/permease YOL075C [Saccharomyces cerevisiae S288c]	UniRef90_K5WD65 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WD65_PHACS	GO:0005524|GO:0016020|GO:0016887
c4564_g1_i1	1.861628	7.188	0.001598	0.027961	NA	UniRef90_K5W331 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W331_PHACS	NA
c15253_g3_i1	1.855725	3.58489	0.000134	0.004271	NA	NA	GO:0004185|GO:0006508
c15253_g3_i2	1.855725	3.58489	0.000134	0.004271	NA	NA	NA

c15253_g3_i3	1.855725	3.58489	0.000134	0.004271	RecName: Full=Carboxypeptidase cpdS; Flags: Precursor [Aspergillus phoenicis]	NA	NA
c15253_g3_i4	1.855725	3.58489	0.000134	0.004271	NA	NA	NA
c14415_g1_i1	1.854988	5.892617	1.14E-05	0.000622	NA	NA	NA
c14415_g1_i2	1.854988	5.892617	1.14E-05	0.000622	NA	NA	NA
c8048_g2_i1	1.854929	2.099241	0.00045	0.011055	NA	UniRef90_K5VTJ0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VTJ0_PHACS	NA
c9697_g1_i1	1.849788	4.047142	0.001873	0.031141	NA	NA	NA
c9697_g1_i2	1.849788	4.047142	0.001873	0.031141	NA	NA	NA
c7689_g1_i1	1.849642	1.445007	0.002146	0.034246	NA	NA	NA
c7689_g1_i2	1.849642	1.445007	0.002146	0.034246	NA	NA	NA
c7689_g1_i3	1.849642	1.445007	0.002146	0.034246	NA	NA	NA
c11835_g2_i1	1.848356	9.339094	1.21E-05	0.00065	RecName: Full=Inorganic phosphate transporter PHO84 [Saccharomyces cerevisiae S288c]	UniRef90_K5W3G7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3G7_PHACS	GO:0016021|GO:0022857|GO:0055085
c14530_g1_i1	1.847725	1.693004	0.001417	0.025716	NA	NA	NA
c12260_g2_i1	1.847583	1.787936	0.001698	0.029235	RecName: Full=RNA-dependent RNA polymerase 1; Short=AtRDRP1; AltName: Full=RNA-directed RNA polymerase 1 [Arabidopsis thaliana]	UniRef90_K5WXV9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WXV9_PHACS	GO:0003968
c6560_g1_i1	1.845521	2.584132	0.000731	0.015938	NA	UniRef90_A0A0C3PEK6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PEK6_PHLGI	NA
c6674_g1_i1	1.845474	3.829155	0.000301	0.00818	NA	NA	NA
c6674_g1_i2	1.845474	3.829155	0.000301	0.00818	NA	NA	NA
c11671_g1_i1	1.840369	5.986154	0.002052	0.033115	NA	UniRef90_A0A0C3PUK8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PUK8_PHLGI	NA
c16880_g1_i1	1.836105	2.168777	0.0006	0.013709	RecName: Full=E3 ubiquitin-protein ligase ptr1; AltName: Full=Poly(A)+ RNA transport protein 1 [Schizosaccharomyces pombe 972h-]	NA	NA

c10165_g1_i1	1.834541	8.062987	0.000209	0.006159	NA	UniRef90_S7PUP6 Uncharacterized protein n=1 Tax=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) RepID=S7PUP6_GLOTA	NA
c12678_g1_i1	1.833754	4.148434	3.19E-06	0.000219	NA	UniRef90_A0A0C3S769 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S769_PHLGI	NA
c14295_g3_i1	1.832363	3.192249	0.000151	0.004699	RecName: Full=TPR and ankyrin repeat-containing protein 1; AltName: Full=Lupus brain antigen 1 [Mus musculus]	UniRef90_K5XBQ0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XBQ0_PHACS	GO:0005524|GO:0016787
c10711_g1_i1	1.830446	3.175792	2.63E-05	0.001194	RecName: Full=E3 ubiquitin-protein ligase ptr1; AltName: Full=Poly(A)+ RNA transport protein 1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5W668 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W668_PHACS	NA
c8995_g1_i1	1.829925	2.585591	4.96E-05	0.001957	RecName: Full=Ent-kaurene oxidase; AltName: Full=Cytochrome P450 503A1; AltName: Full=Cytochrome P450-4 [Fusarium fujikuroi]	UniRef90_G5EJP9 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJP9_PHACH	NA
c15290_g2_i1	1.825988	2.613622	0.002039	0.032989	RecName: Full=Nitrate reductase [NAD(P)H]; Short=NR [Betula pendula]	NA	GO:0009055|GO:0055114
c15621_g1_i1	1.823128	2.322544	0.00033	0.008726	RecName: Full=ATP-binding cassette transporter abc1 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c6770_g1_i1	1.818793	6.545755	0.00058	0.013362	NA	UniRef90_K5WGE0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGE0_PHACS	NA
c14184_g2_i1	1.818594	5.31027	2.07E-06	0.000151	NA	NA	NA
c11999_g3_i1	1.81601	3.941243	0.000245	0.006939	NA	UniRef90_K5UPN2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UPN2_PHACS	NA
c11999_g3_i2	1.81601	3.941243	0.000245	0.006939	NA	NA	NA
c16013_g1_i1	1.812101	6.638381	1.41E-05	0.000738	NA	NA	NA
c16013_g1_i2	1.812101	6.638381	1.41E-05	0.000738	NA	NA	NA
c16013_g1_i3	1.812101	6.638381	1.41E-05	0.000738	NA	NA	NA

c16013_g1_i4	1.812101	6.638381	1.41E-05	0.000738	NA	NA	NA
c16013_g1_i5	1.812101	6.638381	1.41E-05	0.000738	NA	NA	NA
c13112_g2_i1	1.811333	6.4038	0.001709	0.029332	RecName: Full=Beta-hexosaminidase 2; AltName: Full=Beta-GlcNAcase 2; AltName: Full=Beta-N-acetylhexosaminidase 2; AltName: Full=Beta-hexosaminidase 3; Short=AtHEX3; AltName: Full=N-acetyl-beta-glucosaminidase 2; Flags: Precursor [Arabidopsis thaliana]	UniRef90_A0A0C3PD03 Glycoside hydrolase family 20 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PD03_PHLGI	GO:0004553|GO:0005975
c15679_g1_i1	1.810109	6.437657	0.001908	0.03153	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus parasiticus]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12522_g4_i1	1.808291	4.296142	4.44E-05	0.001802	RecName: Full=4-hydroxybenzoate octaprenyltransferase; AltName: Full=4-HB polyprenyltransferase [Pseudoalteromonas haloplanktis TAC125]	UniRef90_K5VVU9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVU9_PHACS	GO:0004659|GO:0016021
c11996_g1_i1	1.807276	4.194272	0.001404	0.025621	NA	NA	NA
c18795_g1_i1	1.807145	7.999529	0.000751	0.016214	RecName: Full=White colony protein WHS11 [Candida albicans WO-1]	NA	GO:0006950
c5418_g2_i1	1.804133	4.43245	2.53E-05	0.001171	NA	UniRef90_K5W5B5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5B5_PHACS	NA
c15482_g1_i1	1.802204	4.931269	0.000519	0.012334	NA	NA	NA
c15482_g1_i2	1.802204	4.931269	0.000519	0.012334	NA	NA	NA
c15482_g1_i3	1.802204	4.931269	0.000519	0.012334	NA	NA	NA
c14838_g1_i1	1.801897	7.22233	0.001316	0.024471	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	NA	GO:0004190|GO:0006508
c8046_g1_i1	1.793145	3.780355	7.85E-06	0.000453	NA	UniRef90_K5VXL6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXL6_PHACS	NA

c8046_g1_i2	1.793145	3.780355	7.85E-06	0.000453	NA	NA	NA
c14739_g1_i1	1.791151	5.43369	0.001291	0.024167	RecName: Full=Uncharacterized ATPase YjoB [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0005524
c3905_g1_i1	1.789052	1.662028	0.00132	0.024504	NA	UniRef90_K5UWH7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UWH7_PHACS	NA
c13518_g2_i1	1.786571	3.176893	8.09E-05	0.002866	NA	UniRef90_K5WFT3 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFT3_PHACS	NA
c15458_g1_i1	1.785526	4.540644	2.44E-05	0.001136	NA	NA	NA
c15458_g1_i2	1.785526	4.540644	2.44E-05	0.001136	NA	NA	NA
c11555_g1_i1	1.781204	3.321351	0.000229	0.006612	NA	NA	NA
c11555_g1_i2	1.781204	3.321351	0.000229	0.006612	NA	UniRef90_UPI000441737D hypothetical protein PUNSTDRAFT_53872 n=1 Tax=Punctularia strigosozonata (strain HHB-11173) RepID=UPI000441737D	NA
c8546_g1_i1	1.780945	2.756344	0.000241	0.006855	NA	UniRef90_K5W3J1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3J1_PHACS	NA
c13596_g2_i1	1.780483	4.768186	8.06E-06	0.000464	RecName: Full=Uncharacterized protein RSN1; AltName: Full=Rescuer of SRO7 at high Nacl protein 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5WI99 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WI99_PHACS	GO:0016020
c11157_g1_i1	1.776894	4.014685	6.48E-05	0.002395	RecName: Full=Homeobox protein 10; Short=DdHbx-10 [Dictyostelium discoideum]	UniRef90_K5V5G5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V5G5_PHACS	GO:0003677
c9605_g1_i1	1.776459	1.939465	0.002161	0.034371	NA	UniRef90_K5W7E9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W7E9_PHACS	GO:0005515
c9605_g1_i2	1.776459	1.939465	0.002161	0.034371	NA	NA	GO:0005515
c10630_g1_i1	1.770822	2.75411	0.000336	0.008835	RecName: Full=Putative ATP-dependent RNA helicase C550.03c [Schizosaccharomyces pombe 972h-]	UniRef90_K5XEF0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XEF0_PHACS	GO:0003676|GO:0005524

c4996_g1_i1	1.76738	1.868383	0.002758	0.041256	NA	UniRef90_K5W554 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W554_PHACS	NA
c6600_g1_i1	1.766054	5.548883	0.003378	0.047673	NA	UniRef90_K5VCP3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCP3_PHACS	NA
c6600_g1_i2	1.766054	5.548883	0.003378	0.047673	NA	NA	NA
c13816_g1_i1	1.765042	4.113372	0.000134	0.004271	RecName: Full=Tripeptidyl aminopeptidase; Short=Tap; Flags: Precursor [Streptomyces lividans]	UniRef90_K5VW85 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VW85_PHACS	NA
c12499_g1_i1	1.763823	1.939812	0.000485	0.011697	RecName: Full=Aldo-keto reductase yakc [Schizosaccharomyces pombe 972h-]	UniRef90_K5VRE6 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRE6_PHACS	NA
c15980_g2_i1	1.763576	4.818465	1.42E-06	0.000109	RecName: Full=ATP-binding cassette transporter abc2; Short=ABC transporter abc2; AltName: Full=ATP-energized glutathione S-conjugate pump abc2; AltName: Full=Glutathione S-conjugate-transporting ATPase abc2 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c5418_g1_i1	1.75732	4.435954	2.86E-05	0.001268	RecName: Full=2-hydroxy-6-oxo-2,4-heptadienoate hydrolase; Short=HOHH [Pseudomonas putida F1]	UniRef90_K5W5B5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5B5_PHACS	NA
c9400_g3_i1	1.755422	5.142857	9.47E-07	7.81E-05	NA	UniRef90_K5WLX4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLX4_PHACS	NA
c15791_g2_i1	1.753495	3.947524	0.001074	0.021061	RecName: Full=Probable beta-glucosidase H; AltName: Full=Beta-D-glucoside glucohydrolase H; AltName: Full=Cellobiase H; AltName: Full=Gentiobiase H [Neosartorya fischeri NRRL 181]	NA	NA
c14984_g2_i1	1.751089	3.092507	5.87E-05	0.00222	NA	NA	NA

c11096_g1_i1	1.749241	3.107833	8.91E-05	0.003115	RecName: Full=Fumitremorgin C synthase; AltName: Full=Fumitremorgin biosynthesis protein E [Aspergillus fumigatus Af293]	UniRef90_G5EJT2 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJT2_PHACH	NA
c10588_g1_i1	1.747931	6.433432	0.001264	0.023741	NA	NA	NA
c10588_g1_i2	1.747931	6.433432	0.001264	0.023741	RecName: Full=Uncharacterized hemerythrin-like protein C869.06c [Schizosaccharomyces pombe 972h-]	UniRef90_A0A060SMV1 Uncharacterized protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060SMV1_PYCCI	NA
c14301_g1_i1	1.744804	5.401098	1.48E-05	0.000767	RecName: Full=Uncharacterized MFS-type transporter PB1E7.08c [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0022857|GO:0055085
c16235_g1_i1	1.743665	1.740883	0.003251	0.04633	NA	NA	NA
c2945_g1_i1	1.743148	2.112018	0.001262	0.02372	RecName: Full=TPR and ankyrin repeat-containing protein 1; AltName: Full=Lupus brain antigen 1 homolog [Homo sapiens]	UniRef90_K5UYY2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UYY2_PHACS	NA
c14615_g1_i1	1.738187	4.515741	2.68E-05	0.001207	NA	NA	NA
c15342_g1_i1	1.737118	5.587582	0.003039	0.044167	NA	NA	NA
c15342_g1_i2	1.737118	5.587582	0.003039	0.044167	NA	NA	NA
c15342_g1_i3	1.737118	5.587582	0.003039	0.044167	NA	NA	NA
c15342_g1_i4	1.737118	5.587582	0.003039	0.044167	NA	NA	NA
c11738_g1_i1	1.733244	6.643741	0.002431	0.037612	RecName: Full=Oxidoreductase AflY; AltName: Full=Aflatoxin biosynthesis protein Y [Aspergillus parasiticus]	UniRef90_K5WLS1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLS1_PHACS	NA
c9063_g1_i1	1.732856	2.886615	6.69E-05	0.002448	RecName: Full=Carboxypeptidase Y homolog A; Flags: Precursor [Paracoccidioides brasiliensis Pb18]	UniRef90_K5VYK6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYK6_PHACS	GO:0004185|GO:0006508
c15454_g1_i1	1.732499	5.571861	0.00044	0.01087	RecName: Full=Uncharacterized protein C17G6.02c [Schizosaccharomyces pombe 972h-]	NA	GO:0006950|GO:0016021
c8701_g2_i1	1.729914	7.765607	0.002523	0.038669	NA	UniRef90_K5WCI5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCI5_PHACS	NA

c14659_g2_i1	1.725075	5.134733	9.13E-07	7.56E-05	RecName: Full=Putative uncharacterized protein At4g01020, chloroplastic; Flags: Precursor [Arabidopsis thaliana]	NA	GO:0046872
c9077_g1_i1	1.719849	3.201309	0.001168	0.022448	NA	UniRef90_K5WD38 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WD38_PHACS	NA
c15998_g1_i1	1.717388	6.345913	3.18E-05	0.001373	RecName: Full=Aminopeptidase 1; AltName: Full=Aminopeptidase I [Schizosaccharomyces pombe 972h-]	NA	GO:0008237|GO:0008270
c15273_g1_i1	1.712544	5.349344	0.002409	0.037356	RecName: Full=ATP-binding cassette sub-family G member 8; AltName: Full=Sterolin-2 [Rattus norvegicus]	NA	GO:0005524|GO:0016020|GO:0016887
c15273_g1_i2	1.712544	5.349344	0.002409	0.037356	NA	NA	GO:0005524|GO:0016887
c10485_g1_i1	1.712053	4.200798	0.001317	0.024471	NA	UniRef90_K5W111 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W111_PHACS	NA
c10485_g1_i2	1.712053	4.200798	0.001317	0.024471	NA	NA	NA
c15151_g2_i1	1.711382	2.759101	0.000163	0.00501	NA	NA	NA
c15880_g4_i1	1.708413	3.247384	8.30E-05	0.002933	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c12349_g1_i1	1.70725	2.423633	0.000483	0.011668	NA	UniRef90_K5W8U5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8U5_PHACS	NA
c11730_g2_i1	1.706545	4.947077	0.000209	0.006176	NA	UniRef90_S8FGL2 Uncharacterized protein n=1 Tax=Fomitopsis pinicola (strain FP-58527) RepID=S8FGL2_FOMPI	NA
c11730_g2_i2	1.706545	4.947077	0.000209	0.006176	NA	NA	NA
c12558_g3_i1	1.704991	3.056753	0.001476	0.026379	NA	NA	NA

c12558_g3_i2	1.704991	3.056753	0.001476	0.026379	NA	UniRef90_A0A0C3S5W8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S5W8_PHLGI	NA
c14239_g1_i1	1.702312	5.326325	0.00198	0.032313	NA	NA	GO:0004553|GO:0005975
c14239_g1_i2	1.702312	5.326325	0.00198	0.032313	NA	NA	GO:0004553|GO:0005975
c14239_g1_i3	1.702312	5.326325	0.00198	0.032313	NA	NA	GO:0004553|GO:0005975
c14239_g1_i4	1.702312	5.326325	0.00198	0.032313	RecName: Full=Endo-1,4-beta-xylanase; Short=Xylanase; Flags: Precursor [Agaricus bisporus]	UniRef90_A0A060SIX2 Beta-xylanase n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060SIX2_PYCCI	GO:0004553|GO:0005975
c14239_g1_i5	1.702312	5.326325	0.00198	0.032313	NA	NA	GO:0004553|GO:0005975
c11481_g1_i1	1.699561	3.706619	0.000456	0.011146	NA	UniRef90_K5W2P1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2P1_PHACS	NA
c13796_g1_i1	1.699031	5.392306	0.000362	0.009376	NA	UniRef90_K5UJ57 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UJ57_PHACS	NA
c13796_g1_i2	1.699031	5.392306	0.000362	0.009376	NA	NA	NA
c13796_g1_i3	1.699031	5.392306	0.000362	0.009376	NA	NA	NA
c11261_g1_i1	1.698583	4.710175	1.48E-06	0.000113	RecName: Full=Uncharacterized protein C11G11.07 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3P3K1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P3K1_PHLGI	GO:0006886|GO:0008536
c13738_g1_i1	1.696514	4.344412	0.00109	0.021303	NA	NA	GO:0008080
c13738_g1_i2	1.696514	4.344412	0.00109	0.021303	NA	UniRef90_K5VSQ6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSQ6_PHACS	GO:0008080
c10016_g1_i1	1.696477	2.60486	0.001016	0.020254	NA	UniRef90_K5WLW5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLW5_PHACS	NA
c10016_g1_i2	1.696477	2.60486	0.001016	0.020254	NA	NA	NA
c9326_g1_i1	1.696308	8.64842	0.000804	0.01715	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	UniRef90_K5XFK3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XFK3_PHACS	GO:0004190|GO:0006508

c12788_g2_i1	1.695432	2.080265	0.0014	0.025619	NA	UniRef90_K5VGZ8 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VGZ8_PHACS	NA
c14824_g2_i1	1.69495	6.59819	3.79E-05	0.001591	NA	NA	NA
c14824_g2_i2	1.69495	6.59819	3.79E-05	0.001591	NA	NA	NA
c14824_g2_i3	1.69495	6.59819	3.79E-05	0.001591	RecName: Full=Aldo-keto reductase yakc [Schizosaccharomyces pombe 972h-]	NA	NA
c2872_g1_i1	1.693835	4.681141	6.57E-05	0.002426	RecName: Full=Global transcription regulator sge1 [Fusarium fujikuroi IMI 58289]	UniRef90_K5VJC3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VJC3_PHACS	NA
c410_g1_i1	1.692035	2.639702	0.001361	0.025033	NA	NA	NA
c410_g1_i2	1.692035	2.639702	0.001361	0.025033	NA	NA	NA
c3540_g1_i1	1.689914	3.54303	1.77E-05	0.000895	NA	UniRef90_K5W518 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W518_PHACS	NA
c12752_g1_i1	1.687183	4.357073	0.000468	0.011384	NA	NA	NA
c12752_g1_i2	1.687183	4.357073	0.000468	0.011384	NA	NA	NA
c12752_g1_i3	1.687183	4.357073	0.000468	0.011384	NA	UniRef90_A0A0C3S7F4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S7F4_PHLGI	NA
c8544_g1_i1	1.68701	7.560237	0.000436	0.010784	NA	UniRef90_K5UNU9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UNU9_PHACS	NA
c13738_g3_i1	1.680887	5.0024	1.34E-05	0.000707	NA	NA	GO:0016491|GO:0016706|GO:0055114
c13738_g3_i2	1.680887	5.0024	1.34E-05	0.000707	NA	UniRef90_K5VEY5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VEY5_PHACS	GO:0016491|GO:0016706|GO:0055114
c13738_g3_i3	1.680887	5.0024	1.34E-05	0.000707	NA	NA	GO:0016491|GO:0016706|GO:0055114
c13738_g3_i4	1.680887	5.0024	1.34E-05	0.000707	NA	NA	GO:0016491|GO:0016706|GO:0055114

c4480_g1_i1	1.673811	2.707499	0.000204	0.006027	NA	UniRef90_K5W4B6 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W4B6_PHACS	NA
c14418_g1_i1	1.669895	7.269279	0.002066	0.033289	RecName: Full=Probable vacuolar protease A; AltName: Full=Aspartic endopeptidase PEP2; AltName: Full=Aspartic protease PEP2; Flags: Precursor [Trichophyton verrucosum HKI 0517]	NA	GO:0004190|GO:0006508
c13528_g1_i1	1.668671	4.364497	0.000933	0.019067	NA	NA	NA
c13528_g1_i2	1.668671	4.364497	0.000933	0.019067	NA	NA	NA
c10258_g1_i1	1.663975	2.422301	0.002321	0.036338	RecName: Full=Protein CbbX [Rhodobacter sphaeroides]	UniRef90_K5XC85 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XC85_PHACS	GO:0005524
c16127_g1_i1	1.660491	6.645902	2.05E-05	0.000979	RecName: Full=NFX1-type zinc finger-containing protein 1 [Homo sapiens]	NA	NA
c9185_g1_i1	1.659776	2.412375	0.000677	0.015155	NA	UniRef90_K5WJR0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJR0_PHACS	NA
c9257_g1_i1	1.656654	3.961728	5.27E-05	0.002046	RecName: Full=Acetamidase [Aspergillus oryzae RIB40]	UniRef90_K5VTR9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VTR9_PHACS	GO:0016884
c8641_g3_i1	1.656078	2.117816	0.001519	0.02702	RecName: Full=Protein pyrABCN; Includes: RecName: Full=Glutamine-dependent carbamoyl-phosphate; Includes: RecName: Full=Aspartate carbamoyltransferase [Aspergillus nidulans FGSC A4]	UniRef90_A0A0C3RU48 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RU48_PHLGI	GO:0005524|GO:0008716
c11096_g3_i1	1.65593	4.371879	2.81E-05	0.001253	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]	UniRef90_G5EJT2 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJT2_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c8574_g1_i1	1.650909	3.191305	0.000661	0.01488	NA	UniRef90_A0A0C3SDS4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SDS4_PHLGI	NA
c8574_g1_i2	1.650909	3.191305	0.000661	0.01488	NA	NA	NA
c11424_g2_i1	1.646476	3.88616	0.000315	0.008449	RecName: Full=Uncharacterized protein MT2089 [Mycobacterium tuberculosis CDC1551]	UniRef90_K5WNY9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNY9_PHACS	NA
c4266_g2_i1	1.645233	2.659714	0.00121	0.022949	NA	UniRef90_M2R874 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2R874_CERS8	NA
c12729_g1_i1	1.644436	3.789928	0.001035	0.020547	NA	NA	NA
c12729_g1_i2	1.644436	3.789928	0.001035	0.020547	NA	NA	NA
c12729_g1_i3	1.644436	3.789928	0.001035	0.020547	NA	UniRef90_A0A0C3NP25 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NP25_PHLGI	NA
c12729_g1_i4	1.644436	3.789928	0.001035	0.020547	NA	NA	NA
c12729_g1_i5	1.644436	3.789928	0.001035	0.020547	NA	NA	NA
c13838_g3_i1	1.643116	4.787619	6.36E-06	0.000382	RecName: Full=Transcription initiation factor TFIID subunit 2; AltName: Full=TBP-associated factor 2 [Schizosaccharomyces pombe 972h-]	UniRef90_K5XEG5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XEG5_PHACS	GO:0008237|GO:0008270
c9497_g4_i1	1.641566	3.770462	0.000125	0.004078	NA	UniRef90_K5WDG4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDG4_PHACS	NA
c15269_g1_i1	1.64108	4.265249	5.20E-06	0.000326	NA	NA	GO:0005515
c15269_g1_i2	1.64108	4.265249	5.20E-06	0.000326	RecName: Full=Protein HIR1 [Cryptococcus neoformans var. neoformans B-3501A]	NA	GO:0005515
c8772_g1_i1	1.640709	2.642244	0.00285	0.042113	NA	UniRef90_K5VVX4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVX4_PHACS	NA
c11244_g1_i1	1.640428	4.309638	0.002623	0.03981	RecName: Full=External NADH-ubiquinone oxidoreductase 2, mitochondrial; AltName:	UniRef90_K5W804 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W804_PHACS	GO:0016491|GO:0055114

					Full=External NADH dehydrogenase 2; Flags: Precursor [Saccharomyces cerevisiae S288c]		
c15225_g1_i1	1.63948	3.467843	0.000518	0.012323	NA	NA	NA
c10609_g1_i1	1.637867	5.526942	0.000231	0.00663	RecName: Full=Conidiation-specific protein 6 [Neurospora crassa OR74A]	UniRef90_K5W543 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W543_PHACS	NA
c4049_g1_i1	1.635943	2.468004	0.001554	0.027402	RecName: Full=Elongator complex protein 2; AltName: Full=Gamma-toxin target 2 [Saccharomyces cerevisiae S288c]	UniRef90_S8FX70 Uncharacterized protein n=1 Tax=Fomitopsis pinicola (strain FP-58527) RepID=S8FX70_FOMPI	GO:0005515
c13161_g1_i1	1.631707	5.169469	3.22E-06	0.00022	RecName: Full=26S proteasome non-ATPase regulatory subunit 1 homolog A; AltName: Full=26S proteasome regulatory subunit RPN2a; Short=AtRPN2a; AltName: Full=26S proteasome regulatory subunit S1 homolog A [Arabidopsis thaliana]	UniRef90_K5XDW6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XDW6_PHACS	NA
c16870_g1_i1	1.630166	5.668421	0.001563	0.027494	NA	NA	NA
c3834_g2_i1	1.629482	2.753514	0.000386	0.009822	NA	NA	NA
c14633_g1_i1	1.626124	4.914443	0.000269	0.007481	RecName: Full=Elongation factor 2; Short=EF-2 [Komagataella pastoris]	NA	GO:0003924|GO:0005525
c9383_g1_i1	1.62603	4.824228	3.40E-06	0.000229	NA	UniRef90_K5WI51 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WI51_PHACS	NA
c12534_g1_i1	1.623156	4.147144	0.00033	0.008738	NA	UniRef90_K5VPN6 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPN6_PHACS	NA
c8555_g2_i1	1.621978	2.008383	0.001347	0.02483	NA	NA	NA
c15869_g1_i1	1.620762	3.485775	2.79E-05	0.001247	RecName: Full=Choline dehydrogenase, mitochondrial; Short=CDH; Short=CHD; Flags: Precursor [Homo sapiens]	NA	GO:0016614|GO:0050660|GO:0055114
c8031_g1_i1	1.619975	3.499562	0.000225	0.006525	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c8031_g1_i2	1.619975	3.499562	0.000225	0.006525	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]	UniRef90_G5EJW0 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJW0_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15324_g2_i1	1.617292	4.957927	0.001627	0.028341	RecName: Full=Peroxide stress-activated histidine kinase mak3; AltName: Full=His-Asp phosphorelay kinase phk2; AltName: Full=Mcs4-associated kinase 3 [Schizosaccharomyces pombe 972h-]	NA	NA
c7472_g1_i1	1.617284	4.778091	9.07E-06	0.000513	NA	UniRef90_K5WAB4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAB4_PHACS	NA
c13866_g1_i1	1.61244	3.601747	0.001835	0.030891	NA	NA	NA
c13866_g1_i2	1.61244	3.601747	0.001835	0.030891	NA	UniRef90_K5WBU2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WBU2_PHACS	NA
c8759_g1_i1	1.610562	2.083683	0.000942	0.019154	NA	UniRef90_K5VPB5 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPB5_PHACS	GO:0000781|GO:0005697|GO:0007004|GO:0042162|GO:0051973
c14791_g3_i1	1.609242	5.213909	4.10E-05	0.001687	RecName: Full=Brefeldin A resistance protein [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016020|GO:0016021|GO:0042626
c8531_g1_i1	1.608146	3.704954	0.002183	0.034634	NA	NA	NA
c7102_g1_i1	1.604313	4.634647	0.000133	0.004261	NA	UniRef90_A0A0C3PTL0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PTL0_PHLGI	NA
c7102_g1_i2	1.604313	4.634647	0.000133	0.004261	NA	NA	NA
c11476_g1_i1	1.598854	4.720299	5.78E-05	0.002196	NA	NA	NA
c11476_g1_i2	1.598854	4.720299	5.78E-05	0.002196	NA	NA	NA

c10045_g1_i1	1.597887	2.687497	0.001315	0.024471	RecName: Full=Uncharacterized oxidoreductase C162.03 [Schizosaccharomyces pombe 972h-]	UniRef90_K5UQC9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UQC9_PHACS	GO:0003824|GO:0008152|GO:0016491|GO:0050662
c10045_g1_i2	1.597887	2.687497	0.001315	0.024471	NA	NA	NA
c15478_g2_i1	1.592727	3.677945	7.79E-05	0.002769	RecName: Full=Nuclear pore complex protein Nup214; AltName: Full=214 kDa nucleoporin; AltName: Full=Nucleoporin Nup214; AltName: Full=Protein CAN [Homo sapiens]	NA	NA
c11972_g2_i1	1.590165	4.17306	2.59E-05	0.001186	RecName: Full=Proteasome activator complex subunit 4A; AltName: Full=Proteasome activator PA200-A [Danio rerio]	UniRef90_K5VD20 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VD20_PHACS	NA
c13888_g1_i1	1.589757	5.352477	0.000664	0.014924	NA	NA	GO:0046872
c13888_g1_i2	1.589757	5.352477	0.000664	0.014924	NA	NA	GO:0046872
c13888_g1_i3	1.589757	5.352477	0.000664	0.014924	NA	NA	GO:0046872
c13888_g1_i4	1.589757	5.352477	0.000664	0.014924	NA	NA	GO:0046872
c13888_g1_i5	1.589757	5.352477	0.000664	0.014924	NA	NA	GO:0046872
c13888_g1_i6	1.589757	5.352477	0.000664	0.014924	NA	NA	GO:0046872
c13888_g1_i7	1.589757	5.352477	0.000664	0.014924	NA	UniRef90_K5VRP6 Glycoside hydrolase family 79 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRP6_PHACS	GO:0046872
c12647_g1_i1	1.589415	2.465279	0.001473	0.026344	NA	NA	GO:0008152|GO:0016491|GO:0055114
c12647_g1_i2	1.589415	2.465279	0.001473	0.026344	RecName: Full=Aldehyde dehydrogenase; Short=ALDDH; Short=ALDH [Agaricus bisporus]	UniRef90_A0A0C3SCG1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SCG1_PHLGI	GO:0008152|GO:0016491|GO:0055114
c14230_g1_i1	1.585588	4.320818	0.000828	0.017512	NA	NA	NA
c14230_g1_i2	1.585588	4.320818	0.000828	0.017512	NA	NA	NA
c14230_g1_i3	1.585588	4.320818	0.000828	0.017512	NA	NA	NA
c14230_g1_i4	1.585588	4.320818	0.000828	0.017512	NA	NA	NA
c14230_g1_i5	1.585588	4.320818	0.000828	0.017512	NA	NA	NA

c13532_g1_i1	1.582717	4.944835	0.000592	0.013597	RecName: Full=Zinc-type alcohol dehydrogenase-like protein C2E1P3.01 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VAK6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VAK6_PHACS	GO:0008270|GO:0016491|GO:0055114
c10921_g1_i1	1.582561	4.748225	0.000516	0.012278	RecName: Full=Pyranose 2-oxidase; Short=P2O; Short=P2Ox; Short=POD; Short=POx; Short=PROD; Short=Pyranose oxidase; AltName: Full=FAD-oxidoreductase; AltName: Full=Glucose 2-oxidase; AltName: Full=Pyranose:oxygen 2-oxidoreductase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_Q6QWR1 Pyranose 2-oxidase n=1 Tax=Phanerochaete chrysosporium RepID=P2OX_PHACH	GO:0016614|GO:0055114
c11004_g1_i1	1.580666	6.041642	0.002008	0.032618	RecName: Full=Zinc-type alcohol dehydrogenase-like protein C1198.01 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V6U5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V6U5_PHACS	GO:0008270|GO:0016491|GO:0055114
c14461_g3_i1	1.577205	3.312197	5.33E-05	0.002057	NA	NA	NA
c13140_g2_i1	1.576826	3.610621	0.002649	0.039981	NA	NA	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c13140_g2_i2	1.576826	3.610621	0.002649	0.039981	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V311 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V311_PHACS	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c9965_g1_i1	1.574703	2.453051	0.002988	0.043593	NA	NA	NA
c12680_g1_i1	1.57382	3.167506	0.0004	0.010096	NA	UniRef90_K5VAV5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VAV5_PHACS	NA
c12356_g1_i1	1.568947	5.157307	0.001353	0.024921	NA	NA	NA
c12356_g1_i2	1.568947	5.157307	0.001353	0.024921	NA	NA	NA
c12356_g1_i3	1.568947	5.157307	0.001353	0.024921	NA	UniRef90_K5X3G4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X3G4_PHACS	NA

c9871_g2_i1	1.567942	3.797218	8.06E-05	0.002861	NA	UniRef90_K5XCE9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XCE9_PHACS	NA
c9871_g2_i2	1.567942	3.797218	8.06E-05	0.002861	NA	NA	NA
c9871_g2_i3	1.567942	3.797218	8.06E-05	0.002861	NA	NA	NA
c9871_g2_i4	1.567942	3.797218	8.06E-05	0.002861	NA	NA	NA
c9074_g2_i1	1.566944	3.935308	0.000101	0.003406	RecName: Full=THO complex subunit 2; Short=Tho2 [Callithrix jacchus]	UniRef90_K5V975 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V975_PHACS	NA
c10036_g1_i1	1.561871	2.401429	0.001374	0.025233	NA	NA	NA
c13536_g1_i1	1.56181	5.304853	0.000255	0.007187	RecName: Full=Pyranose 2-oxidase; Short=P2O; Short=P2Ox; Short=POD; Short=POx; Short=PROD; Short=Pyranose oxidase; AltName: Full=FAD-oxidoreductase; AltName: Full=Glucose 2-oxidase; AltName: Full=Pyranose:oxygen 2-oxidoreductase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_Q6QWR1 Pyranose 2-oxidase n=1 Tax=Phanerochaete chrysosporium RepID=P2OX_PHACH	NA
c9131_g3_i1	1.561164	3.487535	0.00066	0.01488	RecName: Full=Probable indole-3-pyruvate monooxygenase YUCCA8; AltName: Full=Flavin-containing monooxygenase YUCCA8 [Arabidopsis thaliana]	UniRef90_K5VWM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWM7_PHACS	GO:0004499|GO:0016491|GO:0050660|GO:0050661|GO:0055114
c2815_g1_i1	1.560403	3.668814	0.000108	0.003586	RecName: Full=Retinal dehydrogenase 1; Short=RALDH 1; Short=RalDH1; AltName: Full=ALDH-E1; AltName: Full=ALHDII; AltName: Full=Aldehyde dehydrogenase family 1 member A1; AltName: Full=Aldehyde dehydrogenase, cytosolic [Gallus gallus]	UniRef90_K5WYS2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYS2_PHACS	GO:0008152|GO:0016491|GO:0055114
c14818_g2_i1	1.557225	5.684061	0.000734	0.01596	NA	NA	NA
c14818_g2_i2	1.557225	5.684061	0.000734	0.01596	NA	NA	NA
c15044_g2_i1	1.555602	5.488591	9.65E-05	0.003308	RecName: Full=Probable transporter MCH2 [Saccharomyces cerevisiae S288c]	NA	GO:0016021|GO:0055085
c15044_g2_i2	1.555602	5.488591	9.65E-05	0.003308	NA	NA	GO:0016021|GO:0055085

c9428_g1_i1	1.55165	2.915723	0.000386	0.009822	NA	UniRef90_M2RMI3 Histidine kinase n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2RMI3_CERS8	NA
c8083_g2_i1	1.550888	5.524733	0.001636	0.028448	NA	UniRef90_K5WD93 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WD93_PHACS	NA
c9803_g1_i1	1.550399	2.773741	0.000902	0.018681	RecName: Full=DNA-binding protein SMUBP-2; AltName: Full=ATP-dependent helicase IGHMBP2; AltName: Full=Immunoglobulin mu-binding protein 2; AltName: Full=Insulin II gene enhancer-binding protein; AltName: Full=RIPE3B-binding complex 3B2 p110 subunit; Short=RIP-1 [Mesocricetus auratus]	UniRef90_K5UR85 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UR85_PHACS	GO:0005524
c15193_g1_i1	1.549702	3.969364	0.000294	0.008049	NA	NA	NA
c10615_g2_i1	1.549543	3.566851	0.000258	0.007245	NA	NA	NA
c10615_g2_i2	1.549543	3.566851	0.000258	0.007245	RecName: Full=Cell division cycle-related protein res2/pct1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V9V9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V9V9_PHACS	NA
c14818_g1_i1	1.547436	5.124104	0.000214	0.006281	RecName: Full=Uncharacterized protein YEL023C [Saccharomyces cerevisiae S288c]	NA	NA
c14659_g1_i1	1.546484	4.886179	1.50E-05	0.000778	RecName: Full=Zinc finger CCCH domain-containing protein 37; Short=AtC3H37; AltName: Full=ENHANCER OF AG-4 protein 1 [Arabidopsis thaliana]	NA	GO:0046872
c6155_g1_i1	1.544298	2.755591	0.000862	0.018078	NA	NA	NA
c6155_g1_i2	1.544298	2.755591	0.000862	0.018078	NA	NA	NA
c6155_g1_i3	1.544298	2.755591	0.000862	0.018078	NA	NA	NA
c15060_g1_i1	1.54216	4.191036	6.32E-05	0.002352	NA	NA	NA
c15060_g1_i2	1.54216	4.191036	6.32E-05	0.002352	NA	NA	NA
c15784_g1_i1	1.541874	4.33178	4.81E-05	0.00192	NA	NA	NA
c15784_g1_i2	1.541874	4.33178	4.81E-05	0.00192	NA	NA	NA

c12194_g1_i1	1.537858	2.518692	0.00198	0.032313	NA	UniRef90_K5WAB6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAB6_PHACS	NA
c8419_g2_i1	1.537378	2.986678	0.000913	0.018761	RecName: Full=Steroid 17-alpha-hydroxylase/17,20 lyase; AltName: Full=17-alpha-hydroxyprogesterone aldolase; AltName: Full=CYPXVII; AltName: Full=Cytochrome P450 17A1; AltName: Full=Cytochrome P450-C17; Short=Cytochrome P450c17 [Cavia porcellus]	UniRef90_K5V0F3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V0F3_PHACS	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c18328_g1_i1	1.536141	2.239658	0.002002	0.032558	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase; Short=GAPDH [Lentinula edodes]	NA	GO:0016620|GO:0055114
c7404_g1_i1	1.535432	2.973969	0.000275	0.007609	RecName: Full=Nucleoporin nup184; AltName: Full=Nuclear pore protein nup184 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WL59 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WL59_PHACS	NA
c16090_g1_i1	1.534704	7.989102	0.000142	0.004469	NA	NA	GO:0003678|GO:0005524
c16090_g1_i2	1.534704	7.989102	0.000142	0.004469	NA	NA	GO:0003678|GO:0005524
c16090_g1_i3	1.534704	7.989102	0.000142	0.004469	NA	NA	GO:0003678|GO:0005524
c16090_g1_i4	1.534704	7.989102	0.000142	0.004469	NA	NA	NA
c16090_g1_i5	1.534704	7.989102	0.000142	0.004469	NA	NA	GO:0003678|GO:0005524
c16090_g1_i6	1.534704	7.989102	0.000142	0.004469	NA	NA	GO:0003678|GO:0005524
c16090_g1_i7	1.534704	7.989102	0.000142	0.004469	RecName: Full=RuvB-like helicase 2 [Ustilago maydis 521]	NA	GO:0003678|GO:0005524
c16090_g1_i8	1.534704	7.989102	0.000142	0.004469	NA	NA	GO:0003678|GO:0005524
c16090_g1_i9	1.534704	7.989102	0.000142	0.004469	NA	NA	NA
c10252_g1_i1	1.534621	2.850558	0.001882	0.031276	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]	UniRef90_G5EJT3 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJT3_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c10826_g1_i1	1.534206	2.915821	0.001166	0.022435	NA	UniRef90_K5VP41 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VP41_PHACS	NA
c10826_g1_i2	1.534206	2.915821	0.001166	0.022435	NA	NA	NA
c13086_g1_i1	1.533425	3.507779	0.000449	0.011046	RecName: Full=Thioredoxin; Short=Trx [Mycoplasma gallisepticum str. R(low)]	UniRef90_K5VHK8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VHK8_PHACS	GO:0045454
c11096_g2_i1	1.532726	2.381753	0.001189	0.022682	RecName: Full=Isoleucine N-monooxygenase 1; AltName: Full=Cytochrome P450 79D3 [Lotus japonicus]	UniRef90_G5EJT2 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJT2_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c13414_g1_i1	1.532263	5.237624	0.000179	0.005393	NA	UniRef90_K5WAP3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAP3_PHACS	NA
c9135_g1_i1	1.5315	1.966893	0.003053	0.044255	NA	NA	NA
c11424_g6_i1	1.530768	3.714802	0.000448	0.01104	RecName: Full=Uncharacterized protein MT2089 [Mycobacterium tuberculosis CDC1551]	UniRef90_K5WNY9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNY9_PHACS	GO:0046677
c2970_g1_i1	1.528193	3.109243	0.000838	0.01767	NA	NA	GO:0005515
c2970_g1_i2	1.528193	3.109243	0.000838	0.01767	NA	UniRef90_K5XAK6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XAK6_PHACS	GO:0005515
c12889_g2_i1	1.52616	2.59051	0.001649	0.028638	RecName: Full=Formin-F; AltName: Full=Diaphanous-related formin dia1 [Dictyostelium discoideum]	UniRef90_K5WIR6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WIR6_PHACS	GO:0003779|GO:0016043|GO:0017048|GO:0030036
c11651_g1_i1	1.524397	2.824105	0.001196	0.022739	NA	UniRef90_K5VE51 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VE51_PHACS	NA
c11651_g1_i2	1.524397	2.824105	0.001196	0.022739	NA	NA	NA
c330_g1_i1	1.524149	2.855738	0.000467	0.011383	RecName: Full=Caffeine resistance protein 5 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WBN2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WBN2_PHACS	GO:0016021|GO:0055085

c7627_g2_i1	1.524134	5.185788	1.80E-05	0.000901	RecName: Full=DNA repair protein RAD16; AltName: Full=ATP-dependent helicase RAD16 [Saccharomyces cerevisiae S288c]	UniRef90_K5X9G9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X9G9_PHACS	GO:0003676|GO:0003677|GO:0005524|GO:0016787|GO:0046872
c8357_g1_i1	1.522843	6.377634	0.000173	0.005243	NA	UniRef90_K5WCJ4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCJ4_PHACS	NA
c16014_g1_i1	1.522218	5.432931	5.32E-05	0.002057	RecName: Full=Activator of stress genes protein 1 [Candida albicans SC5314]	NA	GO:0000981|GO:0003677|GO:0005634|GO:0006351|GO:0006355|GO:0008270
c7627_g3_i1	1.52101	3.422869	0.000924	0.018937	NA	NA	NA
c16101_g2_i1	1.518579	5.722005	3.08E-05	0.001345	RecName: Full=26S proteasome regulatory subunit rpn1; AltName: Full=19S regulatory cap region of 26S protease subunit 2; AltName: Full=Proteasome non-ATPase subunit mts4 [Schizosaccharomyces pombe 972h-]	NA	NA
c11728_g1_i1	1.513099	3.418069	0.000933	0.019067	NA	UniRef90_K5VUH1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUH1_PHACS	NA
c8485_g3_i1	1.512555	3.66794	0.000103	0.003446	RecName: Full=Myosin heavy chain IB; AltName: Full=Myosin heavy chain IL [Acanthamoeba castellanii]	UniRef90_K5VKI5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VKI5_PHACS	GO:0005515
c2866_g1_i1	1.5117	3.094625	0.000339	0.008902	NA	UniRef90_A0A0C3S9I9 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S9I9_PHLGI	NA
c15329_g1_i1	1.509243	4.800923	2.00E-05	0.000964	RecName: Full=THO complex subunit 2; Short=Tho2 [Rhinolophus ferrumequinum]	NA	NA
c12641_g1_i1	1.509164	4.485382	0.001848	0.03098	NA	UniRef90_K5WBM1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WBM1_PHACS	NA
c15420_g1_i1	1.508238	8.1009	0.002101	0.033721	RecName: Full=Stabilin-2; AltName: Full=Fasciclin, EGF-like, laminin-type EGF-like and link domain-containing scavenger receptor 2; Short=FEEL-2; AltName:	NA	NA

					Full=Hyaluronan receptor for endocytosis; Contains: RecName: Full=175 kDa stabilin-2; AltName: Full=175 kDa hyaluronan receptor for endocytosis; Flags: Precursor, partial [Rattus norvegicus]		
c13745_g1_i1	1.500866	4.08227	3.68E-05	0.001558	NA	UniRef90_K5V5B9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V5B9_PHACS	NA
c8308_g1_i1	1.500823	4.296833	0.000228	0.006597	NA	UniRef90_K5XBQ0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XBQ0_PHACS	NA
c11449_g3_i1	1.50038	5.849078	9.91E-05	0.003363	RecName: Full=Probable serine-O-acetyltransferase cys2 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3PXG3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PXG3_PHLGI	NA
c15503_g1_i1	1.500056	6.636035	0.000736	0.015963	RecName: Full=Thiamine pathway transporter THI73 [Saccharomyces cerevisiae S288c]	NA	GO:0016021|GO:0055085
c14489_g1_i1	1.497502	3.896905	4.68E-05	0.001881	NA	NA	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c14489_g1_i2	1.497502	3.896905	4.68E-05	0.001881	RecName: Full=ATP-dependent bile acid permease [Saccharomyces cerevisiae S288c]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0042626|GO:0055085
c1801_g1_i1	1.495973	2.462329	0.002053	0.033115	RecName: Full=HEAT repeat-containing protein 5B [Homo sapiens]	UniRef90_K5W161 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W161_PHACS	NA
c12619_g2_i1	1.494234	4.315223	0.001121	0.021712	NA	UniRef90_K5X176 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X176_PHACS	GO:0003968
c8485_g2_i1	1.493188	2.568603	0.000981	0.019753	NA	UniRef90_K5VKI5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VKI5_PHACS	NA

c12238_g2_i1	1.487523	5.238251	4.00E-05	0.001648	RecName: Full=K(+)/H(+) antiporter 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5VYX8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYX8_PHACS	GO:0006812|GO:0015299|GO:0016021|GO:0055085
c14650_g3_i1	1.483384	2.573433	0.002645	0.039981	NA	NA	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c9730_g1_i1	1.48102	2.07577	0.003177	0.045595	NA	UniRef90_K5WLD1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLD1_PHACS	NA
c15828_g1_i1	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i10	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i2	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i3	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i4	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i5	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i6	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i7	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i8	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c15828_g1_i9	1.479673	3.868027	0.002901	0.04281	NA	NA	NA
c12509_g1_i1	1.478471	3.907515	0.000619	0.014077	NA	UniRef90_K5WZK5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WZK5_PHACS	NA
c12509_g1_i2	1.478471	3.907515	0.000619	0.014077	NA	NA	NA
c12194_g2_i1	1.47645	3.167576	0.000488	0.01173	NA	UniRef90_K5V105 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V105_PHACS	NA
c11449_g2_i1	1.475253	4.173672	9.49E-05	0.003267	RecName: Full=Probable serine-O-acetyltransferase cys2 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3PXG3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PXG3_PHLGI	NA
c11449_g2_i2	1.475253	4.173672	9.49E-05	0.003267	NA	NA	NA
c12522_g2_i1	1.472965	6.230946	0.000277	0.007659	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c12522_g2_i2	1.472965	6.230946	0.000277	0.007659	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12522_g2_i3	1.472965	6.230946	0.000277	0.007659	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12522_g2_i4	1.472965	6.230946	0.000277	0.007659	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12522_g2_i5	1.472965	6.230946	0.000277	0.007659	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12522_g2_i6	1.472965	6.230946	0.000277	0.007659	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12522_g2_i7	1.472965	6.230946	0.000277	0.007659	RecName: Full=Cytochrome P450 67; AltName: Full=CYPLXVII; AltName: Full=Planta-induced rust protein 16, partial [Uromyces viciae-fabae]	UniRef90_K5X8G2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X8G2_PHACS	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12522_g2_i8	1.472965	6.230946	0.000277	0.007659	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c16026_g4_i1	1.470694	6.237887	0.000228	0.006599	RecName: Full=Dicer-like protein 2-1; Includes: RecName: Full=Endoribonuclease dcl2-1; Includes: RecName: Full=ATP-dependent helicase dcl2-1 [Aspergillus niger CBS 513.88]	NA	GO:0003723|GO:0004525|GO:0006396|GO:0016891
c4132_g1_i1	1.470428	2.80092	0.000884	0.018468	NA	UniRef90_K5WE10 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WE10_PHACS	NA
c11423_g2_i1	1.468771	3.707592	0.003136	0.045267	NA	NA	NA
c11423_g2_i2	1.468771	3.707592	0.003136	0.045267	NA	UniRef90_K5X1H9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X1H9_PHACS	NA
c11423_g2_i3	1.468771	3.707592	0.003136	0.045267	NA	NA	NA
c12127_g1_i1	1.468532	4.675774	0.000385	0.009822	NA	NA	NA
c12127_g1_i2	1.468532	4.675774	0.000385	0.009822	NA	NA	NA
c12127_g1_i3	1.468532	4.675774	0.000385	0.009822	NA	NA	NA
c12127_g1_i4	1.468532	4.675774	0.000385	0.009822	NA	NA	NA

c11708_g1_i1	1.468059	4.86245	0.001004	0.020132	RecName: Full=Aryl-alcohol dehydrogenase [NADP(+)]; Short=AAD [Phanerochaete chrysosporium]	UniRef90_K5W6R1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6R1_PHACS	NA
c11708_g1_i2	1.468059	4.86245	0.001004	0.020132	NA	NA	NA
c14459_g1_i1	1.466841	3.797481	0.002121	0.033957	NA	NA	GO:0008270|GO:0016491|GO:0055114
c14459_g1_i2	1.466841	3.797481	0.002121	0.033957	RecName: Full=(R,R)-butanediol dehydrogenase; AltName: Full=Acetoin reductase/2,3-butanediol dehydrogenase; Short=AR/BDH [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0008270|GO:0016491|GO:0055114
c11801_g2_i1	1.464152	4.644452	4.94E-05	0.00195	NA	NA	NA
c11801_g2_i2	1.464152	4.644452	4.94E-05	0.00195	NA	UniRef90_K5VPL9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPL9_PHACS	NA
c8891_g2_i1	1.463292	2.509362	0.003295	0.046818	NA	UniRef90_K5W3K6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3K6_PHACS	NA
c15448_g1_i1	1.460037	2.268792	0.002948	0.043242	RecName: Full=Condensin complex subunit 1; AltName: Full=XCAP-D2 homolog [Saccharomyces cerevisiae S288c]	NA	NA
c6104_g1_i1	1.458701	3.814648	0.000291	0.007982	RecName: Full=1-phosphatidylinositol 3-phosphate 5-kinase FAB1; Short=Phosphatidylinositol 3-phosphate 5-kinase; AltName: Full=Type III PIP kinase; Short=PIPkin-III [Saccharomyces cerevisiae S288c]	UniRef90_K5WQE6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQE6_PHACS	GO:0005524|GO:0044267
c13257_g2_i1	1.458538	4.781381	2.25E-05	0.001064	RecName: Full=Ankyrin-1; Short=ANK-1; AltName: Full=Ankyrin-R; AltName: Full=Erythrocyte ankyrin [Homo sapiens]	UniRef90_A0A0C3PX59 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PX59_PHLGI	GO:0005515
c15994_g2_i1	1.457093	5.918717	0.00027	0.007509	NA	NA	GO:0007165
c15994_g2_i2	1.457093	5.918717	0.00027	0.007509	NA	NA	GO:0007165

c3119_g1_i1	1.456495	2.796306	0.001463	0.026226	NA	UniRef90_K5WAB4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAB4_PHACS	NA
c19429_g1_i1	1.45643	4.184996	0.000396	0.010011	RecName: Full=Putative fungistatic metabolite [Chaetomium globosum CBS 148.51]	NA	NA
c11609_g1_i1	1.456428	2.442633	0.00167	0.028876	RecName: Full=Riboflavin transporter MCH5 [Saccharomyces cerevisiae S288c]	UniRef90_K5X0W9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X0W9_PHACS	GO:0016021|GO:0055085
c8481_g1_i1	1.454688	5.100345	6.04E-05	0.002264	RecName: Full=Acetamidase [Aspergillus oryzae RIB40]	UniRef90_A0A0C3PRR9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PRR9_PHLGI	GO:0016884
c13849_g2_i1	1.451909	5.554278	0.00262	0.03981	NA	UniRef90_A0A0C3NZF0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NZF0_PHLGI	NA
c14179_g1_i1	1.447702	3.683179	0.000306	0.008274	NA	UniRef90_K5VW80 Protein argonaute n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VW80_PHACS	NA
c14641_g2_i1	1.446106	3.408404	0.000418	0.010481	NA	NA	NA
c14815_g3_i1	1.445934	4.587731	6.44E-05	0.002385	RecName: Full=NADPH dehydrogenase 3; AltName: Full=Old yellow enzyme 3 [Saccharomyces cerevisiae S288c]	NA	GO:0010181|GO:0016491|GO:0055114
c14349_g1_i1	1.440498	5.485048	0.000231	0.00663	NA	NA	NA
c14349_g1_i2	1.440498	5.485048	0.000231	0.00663	NA	NA	NA
c14698_g4_i1	1.436797	4.134385	7.17E-05	0.002585	NA	NA	NA
c14698_g4_i2	1.436797	4.134385	7.17E-05	0.002585	NA	NA	NA
c15621_g4_i1	1.436764	2.663775	0.001183	0.022642	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085

c6331_g2_i1	1.435036	3.064159	0.002852	0.042114	NA	UniRef90_K5WM41 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WM41_PHACS	NA
c10515_g1_i1	1.434051	4.263347	0.003548	0.049389	NA	UniRef90_K5W3E3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3E3_PHACS	NA
c14793_g1_i1	1.430537	8.412166	0.000385	0.009822	RecName: Full=Sulfite reductase [NADPH] subunit beta [Schizosaccharomyces pombe 972h-]	NA	GO:0010181|GO:0016491|GO:0020037|GO:0051536|GO:0055114
c13415_g2_i1	1.430125	4.58624	4.74E-05	0.001898	RecName: Full=5'-3' exoribonuclease 1; AltName: Full=Exonuclease 2; AltName: Full=Exonuclease II; Short=Exo II; AltName: Full=p140 [Schizosaccharomyces pombe 972h-]	UniRef90_J4G5W3 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4G5W3_FIBRA	GO:0003676|GO:0004527
c16067_g1_i1	1.427671	6.916641	0.001414	0.025716	RecName: Full=Xyloglucanase; Short=XG; AltName: Full=Cel74a; Flags: Precursor [Trichoderma reesei QM6a]	NA	GO:0020037
c16067_g1_i2	1.427671	6.916641	0.001414	0.025716	NA	NA	NA
c16067_g1_i3	1.427671	6.916641	0.001414	0.025716	NA	NA	NA
c16067_g1_i4	1.427671	6.916641	0.001414	0.025716	NA	NA	NA
c15260_g1_i1	1.42556	4.922367	3.32E-05	0.001429	RecName: Full=Chromatin modification-related protein EAF1; AltName: Full=ESA1-associated factor 1; AltName: Full=Vacuolar import and degradation protein 21 [Ustilago maydis 521]	NA	NA
c10300_g1_i1	1.424252	3.834546	0.000224	0.006505	RecName: Full=Uncharacterized protein C211.03 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VVQ9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVQ9_PHACS	GO:0005086|GO:0032012
c16061_g1_i1	1.422135	6.93324	0.002152	0.034269	RecName: Full=Uncharacterized WD repeat-containing protein alr3466 [Nostoc sp. PCC 7120]	NA	GO:0005515

c15730_g2_i1	1.419656	6.927632	0.000535	0.012635	RecName: Full=ZZ-type zinc finger-containing protein P35G2.11c [Schizosaccharomyces pombe 972h-]	NA	GO:0008270
c15503_g2_i1	1.418737	3.81693	0.002626	0.039821	RecName: Full=Uncharacterized transporter PB1C11.03 [Schizosaccharomyces pombe 972h-]	NA	NA
c15503_g2_i2	1.418737	3.81693	0.002626	0.039821	NA	NA	NA
c8046_g2_i1	1.418348	4.682335	6.31E-05	0.002351	NA	UniRef90_K5WM42 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WM42_PHACS	GO:0004672|GO:0005524|GO:0006468
c8046_g2_i2	1.418348	4.682335	6.31E-05	0.002351	NA	NA	GO:0004672|GO:0005524|GO:0006468
c14340_g1_i1	1.418232	5.681386	0.000798	0.017051	NA	NA	GO:0004553|GO:0005975
c14340_g1_i2	1.418232	5.681386	0.000798	0.017051	NA	NA	NA
c14340_g1_i3	1.418232	5.681386	0.000798	0.017051	NA	NA	GO:0004553|GO:0005975
c14340_g1_i4	1.418232	5.681386	0.000798	0.017051	NA	NA	GO:0004553|GO:0005975
c14340_g1_i5	1.418232	5.681386	0.000798	0.017051	NA	NA	GO:0004553|GO:0005975
c14340_g1_i6	1.418232	5.681386	0.000798	0.017051	NA	NA	GO:0004553|GO:0005975
c14340_g1_i7	1.418232	5.681386	0.000798	0.017051	NA	NA	GO:0004553|GO:0005975
c14340_g1_i8	1.418232	5.681386	0.000798	0.017051	NA	NA	NA
c9497_g2_i1	1.418186	4.013682	0.0003	0.008164	NA	UniRef90_K5WDG4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDG4_PHACS	NA
c15908_g1_i1	1.413129	2.74862	0.001805	0.030572	NA	NA	NA
c15908_g1_i2	1.413129	2.74862	0.001805	0.030572	NA	NA	NA
c15697_g1_i1	1.410375	5.109009	0.00011	0.003643	NA	NA	NA
c15697_g1_i2	1.410375	5.109009	0.00011	0.003643	NA	NA	NA
c15697_g1_i3	1.410375	5.109009	0.00011	0.003643	NA	NA	NA
c16045_g1_i1	1.40951	4.971809	0.000165	0.005036	RecName: Full=Vacuolar membrane protease; AltName: Full=FXNA-related family protease 1 [Schizophyllum commune H4-8]	NA	GO:0008152|GO:0016787
c15231_g1_i1	1.40923	7.18145	0.000315	0.008449	NA	NA	GO:0003723

c15231_g1_i2	1.40923	7.18145	0.000315	0.008449	RecName: Full=Meiotically up-regulated gene 60 protein [Schizosaccharomyces pombe 972h-]	NA	GO:0003723
c7016_g1_i1	1.407032	2.711247	0.001763	0.030071	RecName: Full=Uncharacterized transporter C460.05 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WWQ6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WWQ6_PHACS	GO:0016021|GO:0055085
c10884_g1_i1	1.404105	7.219265	0.001542	0.027278	NA	UniRef90_K5UW40 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UW40_PHACS	NA
c16036_g1_i1	1.403402	5.363689	0.001925	0.031687	RecName: Full=Cell division cycle protein 123 [Schizosaccharomyces pombe 972h-]	NA	NA
c8544_g2_i1	1.400709	3.368866	0.000668	0.015012	NA	NA	NA
c8575_g2_i1	1.400298	3.896617	0.000429	0.010687	RecName: Full=5-methylthioadenosine/S-adenosylhomocysteine deaminase; Short=MTA/SAH deaminase [Thermococcus kodakarensis KOD1]	UniRef90_A0A0C3PVK0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PVK0_PHLGI	GO:0016787
c8575_g2_i2	1.400298	3.896617	0.000429	0.010687	NA	NA	GO:0016787
c11646_g1_i1	1.399829	4.911212	0.000138	0.004384	NA	NA	GO:0003677|GO:0005524
c11646_g1_i2	1.399829	4.911212	0.000138	0.004384	RecName: Full=ATP-dependent helicase fft2; AltName: Full=Fun thirty-related protein 2 [Schizosaccharomyces pombe 972h-]	UniRef90_J4H3P1 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4H3P1_FIBRA	GO:0003677|GO:0005524
c15416_g2_i1	1.392803	2.502977	0.001755	0.029975	NA	NA	NA
c12300_g2_i1	1.392695	8.357195	0.000544	0.012777	RecName: Full=Transcriptional activator protein acu-15; AltName: Full=Acetate utilization protein 15 [Neurospora crassa OR74A]	UniRef90_K5VZC5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZC5_PHACS	GO:0000981|GO:0003677|GO:0005634|GO:0006351|GO:0006355|GO:0008270
c12300_g2_i2	1.392695	8.357195	0.000544	0.012777	NA	NA	GO:0000981|GO:0003677|GO:0005634|GO:0006351|GO:0006355|GO:0008270
c15895_g4_i1	1.391169	2.867898	0.003354	0.047441	RecName: Full=Calcium-channel protein cch1 [Schizosaccharomyces pombe 972h-]	NA	GO:0005216|GO:0006811|GO:0016020|GO:0055085
c15895_g4_i2	1.391169	2.867898	0.003354	0.047441	NA	NA	GO:0005216|GO:0006811|GO:0016020|GO:0055085

c16124_g1_i1	1.386385	7.190037	0.001089	0.021298	RecName: Full=NFX1-type zinc finger-containing protein 1 [Mus musculus]	NA	GO:0005524
c11835_g1_i1	1.385699	7.692092	0.000539	0.012695	RecName: Full=Inorganic phosphate transporter PHO84 [Saccharomyces cerevisiae S288c]	UniRef90_A0A0C3S079 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S079_PHLGI	NA
c12751_g1_i1	1.384874	4.632676	0.000452	0.011095	RecName: Full=N-acyl homoserine lactonase AttM; Short=AHL-lactonase AttM [Azorhizobium caulinodans ORS 571]	UniRef90_K5W3N9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3N9_PHACS	NA
c12751_g1_i2	1.384874	4.632676	0.000452	0.011095	NA	NA	NA
c13688_g1_i1	1.381309	4.557572	0.000707	0.015623	NA	UniRef90_A0A0C3SB59 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SB59_PHLGI	NA
c14295_g1_i1	1.378462	5.161442	0.000266	0.007428	NA	NA	NA
c14295_g1_i2	1.378462	5.161442	0.000266	0.007428	NA	UniRef90_K5XBQ0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XBQ0_PHACS	NA
c10816_g2_i1	1.374043	3.060914	0.002401	0.037274	RecName: Full=Oligopeptide transporter 6; Short=AtOPT6 [Arabidopsis thaliana]	UniRef90_M9PA79 Oligopeptide transporter 7 n=1 Tax=Phanerochaete chrysosporium RepID=M9PA79_PHACH	GO:0055085
c12647_g3_i1	1.373364	7.198625	0.000557	0.012989	RecName: Full=Aldehyde dehydrogenase; Short=ALDDH; Short=ALDH [Agaricus bisporus]	UniRef90_K5WYS2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYS2_PHACS	GO:0008152|GO:0016491|GO:0055114
c16192_g1_i1	1.37178	5.927773	0.001406	0.025621	NA	NA	NA
c16192_g1_i2	1.37178	5.927773	0.001406	0.025621	NA	NA	NA
c16192_g1_i3	1.37178	5.927773	0.001406	0.025621	NA	NA	GO:0004672|GO:0005524|GO:0006468
c16192_g1_i4	1.37178	5.927773	0.001406	0.025621	NA	NA	NA
c16192_g1_i5	1.37178	5.927773	0.001406	0.025621	NA	NA	GO:0004672|GO:0005524|GO:0006468
c16192_g1_i6	1.37178	5.927773	0.001406	0.025621	NA	NA	GO:0004672|GO:0005524|GO:0006468
c16192_g1_i7	1.37178	5.927773	0.001406	0.025621	NA	NA	GO:0004672|GO:0005524|GO:0006468

c15050_g1_i1	1.37025	3.80595	0.000483	0.011668	RecName: Full=Aldo-keto reductase yakc [Schizosaccharomyces pombe 972h-]	NA	NA
c15050_g1_i2	1.37025	3.80595	0.000483	0.011668	NA	NA	NA
c15050_g1_i3	1.37025	3.80595	0.000483	0.011668	NA	NA	NA
c15410_g3_i1	1.364458	4.522351	0.00043	0.010702	NA	NA	NA
c15410_g3_i2	1.364458	4.522351	0.00043	0.010702	RecName: Full=von Willebrand factor A domain-containing protein 5A; AltName: Full=Loss of heterozygosity 11 chromosomal region 2 gene A protein homolog [Mus musculus]	NA	NA
c13933_g1_i1	1.364011	4.138167	0.00023	0.00663	NA	NA	GO:0005515
c13933_g1_i2	1.364011	4.138167	0.00023	0.00663	RecName: Full=Histone-lysine N-methyltransferase ASHR1; AltName: Full=ASH1-related protein 1; AltName: Full=Protein SET DOMAIN GROUP 37 [Arabidopsis thaliana]	UniRef90_K5VEG0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VEG0_PHACS	GO:0005515
c12703_g1_i1	1.363148	3.475416	0.000329	0.008726	NA	UniRef90_K5VIL3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VIL3_PHACS	NA
c12663_g1_i1	1.361198	6.911754	0.003552	0.049389	RecName: Full=Uncharacterized protein YcbX [Escherichia coli K-12]	UniRef90_K5XEJ8 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XEJ8_PHACS	GO:0003824|GO:0030151|GO:0030170
c5263_g1_i1	1.355577	2.835397	0.002092	0.033604	RecName: Full=Uncharacterized transcriptional regulatory protein C1F7.11c [Schizosaccharomyces pombe 972h-]	UniRef90_K5WDG4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDG4_PHACS	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c9251_g2_i1	1.352594	4.050522	0.000923	0.018936	NA	NA	NA
c9251_g2_i2	1.352594	4.050522	0.000923	0.018936	NA	NA	NA
c10625_g1_i1	1.352178	6.978546	0.002834	0.042004	NA	NA	NA
c10625_g1_i2	1.352178	6.978546	0.002834	0.042004	NA	UniRef90_K5WK68 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WK68_PHACS	NA
c14918_g1_i1	1.352053	6.925819	0.000912	0.018761	NA	NA	NA
c14304_g1_i1	1.348398	3.520525	0.000722	0.015831	NA	NA	NA

c14748_g4_i1	1.346142	2.661308	0.003476	0.04863	RecName: Full=Probable ATP-dependent permease; Flags: Precursor [Saccharomyces cerevisiae S288c]	NA	GO:0005524|GO:0016887
c11716_g2_i1	1.345993	4.692185	0.000323	0.008604	NA	NA	NA
c11716_g2_i2	1.345993	4.692185	0.000323	0.008604	RecName: Full=Uncharacterized protein RSN1; AltName: Full=Rescuer of SRO7 at high Nacl protein 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5X3J8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X3J8_PHACS	GO:0016020
c11716_g2_i3	1.345993	4.692185	0.000323	0.008604	NA	NA	NA
c1519_g1_i1	1.345347	2.258055	0.003564	0.049488	NA	UniRef90_K5X4J9 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X4J9_PHACS	NA
c15616_g1_i1	1.344253	2.664811	0.003608	0.049988	RecName: Full=3-phytase B; AltName: Full=3 phytase B; AltName: Full=Myo-inositol hexakisphosphate phosphohydrolase B; AltName: Full=Myo-inositol-hexaphosphate 3-phosphohydrolase B; Flags: Precursor [Aspergillus nidulans FGSC A4]	NA	GO:0003993
c8930_g1_i1	1.341809	3.770248	0.000907	0.018755	NA	NA	NA
c11315_g2_i1	1.341199	2.62349	0.002261	0.035491	NA	UniRef90_K5VUK8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUK8_PHACS	NA
c16123_g1_i1	1.340335	5.627417	0.00051	0.012214	NA	NA	NA
c16123_g1_i2	1.340335	5.627417	0.00051	0.012214	NA	NA	NA
c16123_g1_i3	1.340335	5.627417	0.00051	0.012214	NA	NA	NA
c14450_g2_i1	1.337655	4.091974	0.000955	0.019343	RecName: Full=Pre-mRNA-splicing factor SYF1 [Cryptococcus neoformans var. neoformans B-3501A]	NA	NA
c16985_g1_i1	1.335917	4.075919	0.000333	0.008787	NA	NA	NA
c7156_g1_i1	1.334972	4.088337	0.000305	0.00827	RecName: Full=Protein dopey-1 [Homo sapiens]	UniRef90_K5WBW7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WBW7_PHACS	NA

c13446_g1_i1	1.333962	3.819077	0.001825	0.030786	NA	UniRef90_K5VBQ0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VBQ0_PHACS	NA
c19407_g1_i1	1.333633	2.8114	0.002014	0.032685	NA	NA	NA
c12579_g1_i1	1.333186	9.105452	0.00069	0.015335	RecName: Full=Lysosomal acid phosphatase; Short=LAP; Flags: Precursor [Mus musculus]	UniRef90_A0A0C3S0X3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S0X3_PHLGI	GO:0003993
c15540_g1_i1	1.332685	5.538372	0.003032	0.044083	NA	NA	NA
c15540_g1_i2	1.332685	5.538372	0.003032	0.044083	RecName: Full=Glutamate decarboxylase 5; Short=GAD 5 [Arabidopsis thaliana]	NA	GO:0008152|GO:0016831|GO:0019752|GO:0030170
c15540_g1_i3	1.332685	5.538372	0.003032	0.044083	NA	NA	GO:0016831|GO:0019752|GO:0030170
c11424_g4_i1	1.329474	4.496576	0.002384	0.037096	RecName: Full=Uncharacterized protein MT2089 [Mycobacterium tuberculosis CDC1551]	UniRef90_K5WNY9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNY9_PHACS	GO:0046677
c13296_g1_i1	1.328934	8.100341	0.000544	0.012777	NA	UniRef90_K5WJM6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJM6_PHACS	NA
c9074_g1_i1	1.328479	3.806532	0.000506	0.01214	RecName: Full=THO complex subunit 2 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V975 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V975_PHACS	NA
c10834_g2_i1	1.326209	7.891077	0.002601	0.039663	RecName: Full=Glutathione S-transferase D7; Short=DmGST26 [Drosophila melanogaster]	UniRef90_M2RSA2 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2RSA2_CERS8	GO:0005515
c10797_g1_i1	1.325217	3.310259	0.000828	0.017512	NA	NA	NA
c10797_g1_i2	1.325217	3.310259	0.000828	0.017512	NA	UniRef90_K5WLE2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLE2_PHACS	NA
c10797_g1_i3	1.325217	3.310259	0.000828	0.017512	NA	NA	NA
c5048_g1_i1	1.320036	5.239724	0.000133	0.004261	NA	UniRef90_K5XBN7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XBN7_PHACS	NA

c12198_g4_i1	1.318508	5.074703	0.001567	0.027507	RecName: Full=Poly [ADP-ribose] polymerase 4; Short=PARP-4; AltName: Full=193 kDa vault protein; AltName: Full=ADP-ribosyltransferase diphtheria toxin-like 4; Short=ARTD4; AltName: Full=PARP-related/IalphaI-related H5/proline-rich; Short=PH5P; AltName: Full=Vault poly(ADP-ribose) polymerase; Short=VPARP [Homo sapiens]	UniRef90_K5V3T4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3T4_PHACS	NA
c14136_g3_i1	1.317149	6.634276	0.002654	0.03999	NA	UniRef90_K5V3T4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3T4_PHACS	NA
c11449_g1_i1	1.317143	3.901074	0.000833	0.017591	RecName: Full=Probable serine-O-acetyltransferase cys2 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A067NN39 Uncharacterized protein n=1 Tax=Pleurotus ostreatus PC15 RepID=A0A067NN39_PLEOS	NA
c14748_g3_i1	1.316922	3.429296	0.001442	0.025985	NA	NA	NA
c14748_g3_i2	1.316922	3.429296	0.001442	0.025985	RecName: Full=Probable ATP-dependent permease; Flags: Precursor [Saccharomyces cerevisiae S288c]	NA	GO:0005524|GO:0016887
c13575_g2_i1	1.315125	3.863498	0.000319	0.008531	NA	NA	NA
c13575_g2_i2	1.315125	3.863498	0.000319	0.008531	NA	NA	NA
c13575_g2_i3	1.315125	3.863498	0.000319	0.008531	NA	UniRef90_K5WLV5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLV5_PHACS	NA
c15165_g1_i1	1.314681	5.492835	0.000394	0.009968	NA	NA	NA
c15165_g1_i2	1.314681	5.492835	0.000394	0.009968	NA	NA	NA
c15165_g1_i3	1.314681	5.492835	0.000394	0.009968	NA	NA	NA
c15165_g1_i4	1.314681	5.492835	0.000394	0.009968	NA	NA	NA
c11896_g1_i1	1.314499	3.71435	0.001435	0.025894	NA	UniRef90_A0A0C3NGU1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NGU1_PHLGI	GO:0003676

c14099_g1_i1	1.313558	5.227767	0.000884	0.018468	RecName: Full=Heavy metal tolerance protein; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_K5WU82 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WU82_PHACS	NA
c16119_g2_i1	1.306773	5.124721	0.000433	0.010747	RecName: Full=Proteasome activator complex subunit 4; AltName: Full=Proteasome activator PA200; AltName: Full=Protein TEMO [Mus musculus]	NA	NA
c15295_g2_i1	1.303323	5.409059	0.00021	0.006183	RecName: Full=Probable metabolite transport protein YBR241C [Saccharomyces cerevisiae S288c]	NA	GO:0005506|GO:0016021|GO:0016705|GO:0020037|GO:0022857|GO:0055085|GO:0055114
c15295_g2_i2	1.303323	5.409059	0.00021	0.006183	NA	NA	GO:0005506|GO:0016021|GO:0016705|GO:0020037|GO:0022857|GO:0055085|GO:0055114
c15295_g2_i3	1.303323	5.409059	0.00021	0.006183	NA	NA	GO:0016021|GO:0022857|GO:0055085
c14398_g1_i1	1.303093	5.238416	0.000898	0.018646	NA	NA	GO:0004190|GO:0006508
c11807_g2_i1	1.30136	3.534301	0.000939	0.019131	NA	UniRef90_K5W3J1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3J1_PHACS	NA
c11879_g1_i1	1.301064	4.199905	0.000454	0.011136	NA	UniRef90_A0A0C3PSI5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PSI5_PHLGI	NA
c15742_g1_i1	1.296999	5.384798	0.000259	0.007265	RecName: Full=Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial; AltName: Full=Dehydrogenase E1 and transketolase domain-containing protein 1; Flags: Precursor [Xenopus laevis]	NA	GO:0008152|GO:0016624
c15399_g1_i1	1.29668	6.303163	0.00057	0.013198	RecName: Full=Protein rad9; AltName: Full=SCC2 homolog [Coprinopsis cinerea okayama7#130]	NA	NA

c13305_g1_i1	1.296286	3.846702	0.000898	0.018646	RecName: Full=Cell morphogenesis protein PAG1; AltName: Full=Protein TAO3 [Saccharomyces cerevisiae S288c]	UniRef90_K5V308 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V308_PHACS	NA
c14246_g1_i1	1.295129	4.308259	0.002033	0.032912	RecName: Full=N-lysine methyltransferase SMYD2; AltName: Full=Histone methyltransferase SMYD2; AltName: Full=SET and MYND domain-containing protein 2 [Gallus gallus]	UniRef90_K5VZB3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZB3_PHACS	GO:0005515
c14246_g1_i2	1.295129	4.308259	0.002033	0.032912	NA	NA	GO:0005515
c14246_g1_i3	1.295129	4.308259	0.002033	0.032912	NA	NA	GO:0005515
c14327_g1_i1	1.292537	3.482071	0.001406	0.025621	NA	NA	GO:0005524|GO:0016887
c14327_g1_i2	1.292537	3.482071	0.001406	0.025621	RecName: Full=ATP-binding cassette sub-family G member 8; AltName: Full=Sterolin-2 [Rattus norvegicus]	NA	GO:0005524|GO:0016020|GO:0016887
c12461_g1_i1	1.292235	4.815066	0.001544	0.027287	NA	UniRef90_K5VWV5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWV5_PHACS	GO:0005515
c14415_g2_i1	1.291584	5.791405	0.00068	0.015179	NA	NA	NA
c14832_g2_i1	1.288996	3.561017	0.001684	0.02903	RecName: Full=Pre-mRNA-splicing factor ATP-dependent RNA helicase prp16 [Schizosaccharomyces pombe 972h-]	NA	NA
c14832_g2_i2	1.288996	3.561017	0.001684	0.02903	NA	NA	NA
c7831_g1_i1	1.281796	4.795143	0.000243	0.0069	NA	NA	GO:0003824|GO:0003854|GO:0006694|GO:0016616|GO:0050662|GO:0055114
c7831_g1_i2	1.281796	4.795143	0.000243	0.0069	RecName: Full=GDP-mannose 3,5-epimerase; Short=GDP-Man 3,5-epimerase [Arabidopsis thaliana]	UniRef90_K5V9M4 Glycosyltransferase family 2 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V9M4_PHACS	GO:0003824|GO:0003854|GO:0006694|GO:0016616|GO:0050662|GO:0055114
c7831_g1_i3	1.281796	4.795143	0.000243	0.0069	NA	NA	GO:0003824|GO:0003854|GO:0006694|GO:0016616|GO:0050662|GO:0055114

c7831_g1_i4	1.281796	4.795143	0.000243	0.0069	NA	NA	GO:0003824|GO:0003854|GO:0006694|GO:0016616|GO:0050662|GO:0055114
c7831_g1_i5	1.281796	4.795143	0.000243	0.0069	NA	NA	GO:0003824|GO:0003854|GO:0006694|GO:0016616|GO:0050662|GO:0055114
c13964_g2_i1	1.277593	3.779743	0.001139	0.02201	RecName: Full=DNA-directed RNA polymerase III subunit rpc1; Short=RNA polymerase III subunit C1; AltName: Full=DNA-directed RNA polymerase III largest subunit; AltName: Full=RPC158 [Schizosaccharomyces pombe 972h-]	UniRef90_K5X834 DNA-directed RNA polymerase n=2 Tax=Phanerochaetaceae RepID=K5X834_PHACS	GO:0003677|GO:0003899|GO:0006351
c16089_g2_i1	1.275352	6.009309	0.000827	0.017512	NA	NA	NA
c18280_g1_i1	1.272096	5.454391	0.001996	0.032533	NA	NA	GO:0008080
c15167_g1_i1	1.270208	8.090637	0.002465	0.037997	RecName: Full=Protein FDD123; AltName: Full=CvHSP30/1 [Trametes versicolor]	NA	GO:0016020
c13654_g1_i1	1.269799	3.756191	0.001913	0.031565	RecName: Full=Cytochrome P450 714A1; AltName: Full=EUI-like P450 A1 [Arabidopsis thaliana]	UniRef90_K5WA52 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WA52_PHACS	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c6272_g2_i1	1.268873	4.323102	0.00127	0.023813	NA	NA	NA
c6272_g2_i2	1.268873	4.323102	0.00127	0.023813	NA	UniRef90_K5W6Q7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6Q7_PHACS	NA
c6272_g2_i3	1.268873	4.323102	0.00127	0.023813	NA	NA	NA
c15350_g1_i1	1.258234	4.4052	0.001086	0.021274	NA	NA	NA
c9357_g1_i1	1.256373	5.146653	0.003443	0.048301	NA	UniRef90_K5VBH7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VBH7_PHACS	NA
c15628_g1_i1	1.255922	7.555431	0.001914	0.031565	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15628_g1_i2	1.255922	7.555431	0.001914	0.031565	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase;	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

					AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]		
c6943_g1_i1	1.254692	4.446384	0.001135	0.021951	RecName: Full=Beige protein homolog 1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5UTE7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UTE7_PHACS	NA
c15082_g1_i1	1.252646	6.196058	0.001011	0.020187	NA	NA	NA
c7749_g1_i1	1.250659	4.819857	0.000439	0.010851	NA	UniRef90_K5UZP4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UZP4_PHACS	NA
c15929_g1_i1	1.249999	4.436784	0.002505	0.03849	RecName: Full=DNA excision repair protein ERCC-6-like 2 [Bos taurus]	NA	GO:0003677|GO:0005524
c5071_g1_i1	1.249267	4.935765	0.000285	0.007833	NA	UniRef90_K5X9H4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X9H4_PHACS	GO:0003723|GO:0005515|GO:0016070
c15614_g1_i1	1.248187	4.163291	0.000987	0.019838	NA	NA	NA
c15614_g1_i2	1.248187	4.163291	0.000987	0.019838	NA	NA	NA
c9081_g1_i1	1.247461	4.204463	0.00043	0.010702	RecName: Full=Probable importin c550.11 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VZL4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZL4_PHACS	GO:0006886|GO:0008536
c15215_g3_i1	1.247403	4.463286	0.00065	0.014684	RecName: Full=Dolichyl-phosphate-mannose--protein mannosyltransferase 1; Short=Protein mannosyltransferase 1 [Candida albicans SC5314]	NA	GO:0000030|GO:0006493|GO:0016020
c4146_g1_i1	1.244728	5.461284	0.00264	0.039936	NA	UniRef90_K5VXL6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXL6_PHACS	GO:0004672|GO:0005524|GO:0006468
c15344_g1_i1	1.243067	4.371653	0.000477	0.011559	RecName: Full=Probable cytosolic iron-sulfur protein assembly protein Ciao1 [Aedes aegypti]	NA	GO:0005515
c14641_g1_i1	1.242587	4.770816	0.000653	0.014727	NA	NA	NA
c14554_g1_i1	1.240268	4.77164	0.000405	0.010202	RecName: Full=WD repeat-containing protein mip1 [Schizosaccharomyces pombe 972h-]	NA	NA
c13814_g1_i1	1.239043	3.961587	0.002329	0.036416	NA	NA	NA

c13814_g1_i2	1.239043	3.961587	0.002329	0.036416	NA	UniRef90_K5X5N2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X5N2_PHACS	NA
c13195_g1_i1	1.236114	6.251097	0.002963	0.043368	RecName: Full=Protein argonaute-2; Short=Argonaute2; AltName: Full=Argonaute RISC catalytic component 2; AltName: Full=Eukaryotic translation initiation factor 2C 2; Short=eIF-2C 2; Short=eIF2C 2; AltName: Full=Protein slicer, partial [Oryctolagus cuniculus]	UniRef90_K5V8R3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V8R3_PHACS	NA
c15919_g1_i1	1.234058	5.632979	0.000757	0.016312	RecName: Full=Probable alpha-galactosidase B; AltName: Full=Melibiase B; Flags: Precursor [Penicillium simplicissimum]	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c15919_g1_i2	1.234058	5.632979	0.000757	0.016312	NA	NA	GO:0004553|GO:0005576|GO:0005975|GO:0030248
c14539_g1_i1	1.231093	3.80024	0.003397	0.047886	RecName: Full=Cytochrome P450 67; AltName: Full=CYPLXVII; AltName: Full=Planta-induced rust protein 16, partial [Uromyces viciae-fabae]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c13400_g1_i1	1.229296	4.794808	0.000636	0.014415	NA	UniRef90_K5VZF5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZF5_PHACS	GO:0046872
c14933_g5_i1	1.227306	4.449995	0.000859	0.018022	NA	NA	NA
c14530_g4_i1	1.226221	4.314323	0.000567	0.01315	RecName: Full=Transcriptional regulatory protein SIN3 [Saccharomyces cerevisiae S288c]	NA	GO:0005634|GO:0006355
c12430_g2_i1	1.223615	3.756363	0.001184	0.022643	NA	NA	NA
c11636_g1_i1	1.222779	3.324027	0.001555	0.027406	RecName: Full=Transcription factor tau subunit sfc4; AltName: Full=TFIIIC subunit sfc4; AltName: Full=Transcription factor C subunit 4 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VYV4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYV4_PHACS	GO:0005515
c14872_g1_i1	1.220717	4.803454	0.001208	0.022939	RecName: Full=Uncharacterized transporter C1529.01 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0022857|GO:0055085

c14872_g1_i2	1.220717	4.803454	0.001208	0.022939	NA	NA	GO:0016021|GO:0022857|GO:0055085
c15570_g1_i1	1.219749	4.627204	0.00134	0.024761	NA	NA	NA
c15891_g1_i1	1.218972	4.400548	0.001055	0.020796	NA	NA	GO:0003856|GO:0009073
c15891_g1_i2	1.218972	4.400548	0.001055	0.020796	NA	NA	GO:0003856|GO:0009073
c15891_g1_i3	1.218972	4.400548	0.001055	0.020796	NA	NA	GO:0003856|GO:0009073
c15891_g1_i4	1.218972	4.400548	0.001055	0.020796	RecName: Full=2-epi-5-epi-valiolone synthase; AltName: Full=Sedoheptulose 7-phosphate cyclase [Actinoplanes sp. SE50/110]	NA	GO:0003856|GO:0009073
c12680_g3_i1	1.21312	7.519223	0.002523	0.038669	RecName: Full=Lysophospholipase 3; AltName: Full=Phospholipase B 3; Flags: Precursor [Aspergillus fumigatus A1163]	UniRef90_A0A0C3S6E2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S6E2_PHLGI	GO:0004620|GO:0009395
c13935_g2_i1	1.210637	6.426398	0.001718	0.02947	RecName: Full=Putative helicase MOV-10 [Gallus gallus]	UniRef90_K5VY63 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VY63_PHACS	NA
c14962_g1_i1	1.206134	4.914469	0.00083	0.017534	NA	NA	NA
c14962_g1_i2	1.206134	4.914469	0.00083	0.017534	NA	NA	NA
c8585_g1_i1	1.205425	4.094571	0.002535	0.038828	NA	UniRef90_K5W6Q6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6Q6_PHACS	NA
c8092_g2_i1	1.204004	4.034358	0.001274	0.023868	RecName: Full=Zinc transporter 7; Short=ZnT-7; AltName: Full=Solute carrier family 30 member 7 [Danio rerio]	UniRef90_K5VUC9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUC9_PHACS	GO:0006812|GO:0008324|GO:0016021|GO:0055085
c14832_g4_i1	1.203439	4.182073	0.000753	0.016243	NA	NA	GO:0003676|GO:0005524
c14832_g4_i2	1.203439	4.182073	0.000753	0.016243	RecName: Full=Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16; AltName: Full=ATP-dependent RNA helicase DHX38; AltName: Full=DEAH box protein 38 [Bos taurus]	NA	GO:0003676|GO:0005524
c13639_g1_i1	1.200985	3.891021	0.003407	0.047994	RecName: Full=Neurofibromin; AltName: Full=Neurofibromatosis-related protein NF-1 [Mus musculus]	UniRef90_K5W7R3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W7R3_PHACS	GO:0005096|GO:0005622|GO:0051056
c13639_g1_i2	1.200985	3.891021	0.003407	0.047994	NA	NA	NA

c15784_g3_i1	1.200731	5.498802	0.001537	0.02723	NA	NA	NA
c15784_g3_i2	1.200731	5.498802	0.001537	0.02723	NA	NA	NA
c15784_g3_i3	1.200731	5.498802	0.001537	0.02723	NA	NA	NA
c15784_g3_i4	1.200731	5.498802	0.001537	0.02723	NA	NA	NA
c15011_g1_i1	1.200262	6.379674	0.003422	0.048119	NA	NA	GO:0004672|GO:0005524|GO:0006468
c15011_g1_i2	1.200262	6.379674	0.003422	0.048119	NA	NA	GO:0004672|GO:0005524|GO:0006468
c10975_g1_i1	1.199308	3.917613	0.001588	0.027834	NA	UniRef90_A0A0C3S1A2 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S1A2_PHLGI	NA
c13045_g2_i1	1.199084	6.301842	0.002822	0.041911	RecName: Full=Eukaryotic translation initiation factor 5B; Short=eIF-5B; AltName: Full=Translation initiation factor IF-2 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3NLC9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NLC9_PHLGI	GO:0003924|GO:0005525
c15259_g2_i1	1.196706	5.944494	0.00244	0.037681	RecName: Full=Probable sulfate permease C3H7.02 [Schizosaccharomyces pombe 972h-]	NA	GO:0008272|GO:0015116|GO:0016021
c15511_g2_i1	1.195991	3.913859	0.000911	0.018761	NA	NA	NA
c15511_g2_i2	1.195991	3.913859	0.000911	0.018761	NA	NA	NA
c15780_g2_i1	1.188919	3.873334	0.001855	0.031019	NA	NA	NA
c15780_g2_i2	1.188919	3.873334	0.001855	0.031019	NA	NA	NA
c15780_g2_i3	1.188919	3.873334	0.001855	0.031019	NA	NA	NA
c15780_g2_i4	1.188919	3.873334	0.001855	0.031019	RecName: Full=Tripeptidyl aminopeptidase; Short=Tap; Flags: Precursor [Streptomyces lividans]	NA	NA
c15780_g2_i5	1.188919	3.873334	0.001855	0.031019	NA	NA	NA
c15097_g1_i1	1.187335	4.855399	0.000493	0.011837	RecName: Full=General negative regulator of transcription subunit 1 [Schizosaccharomyces pombe 972h-]	NA	NA
c14952_g2_i1	1.183951	6.370008	0.001621	0.028285	RecName: Full=Pre-mRNA-splicing factor brr2; AltName: Full=Pre-mRNA-splicing factor spp41; AltName: Full=Pre-mRNA-splicing	NA	GO:0003676|GO:0003677|GO:0005524|GO:0016787

					helicase BRR2 [Schizosaccharomyces pombe 972h-]		
c13645_g1_i1	1.179067	4.738252	0.001785	0.030353	NA	NA	NA
c13645_g1_i2	1.179067	4.738252	0.001785	0.030353	NA	NA	NA
c13645_g1_i3	1.179067	4.738252	0.001785	0.030353	NA	NA	NA
c13645_g1_i4	1.179067	4.738252	0.001785	0.030353	NA	UniRef90_K5VIX5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VIX5_PHACS	NA
c15664_g3_i1	1.177928	4.223685	0.001556	0.027414	RecName: Full=Putative GTPase-activating protein AN11010 [Aspergillus nidulans FGSC A4]	NA	GO:0005097|GO:0032313
c15899_g1_i1	1.175457	4.712692	0.000893	0.018592	RecName: Full=Insulin-degrading enzyme; AltName: Full=Insulin protease; Short=Insulinase; AltName: Full=Insulysin [Rattus norvegicus]	NA	NA
c15899_g1_i2	1.175457	4.712692	0.000893	0.018592	NA	NA	NA
c11221_g1_i1	1.175231	5.67682	0.002239	0.03526	RecName: Full=Serine/threonine-protein phosphatase 2B catalytic subunit [Schizosaccharomyces pombe 972h-]	UniRef90_K5VCV5 Serine/threonine-protein phosphatase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCV5_PHACS	GO:0016787
c11221_g1_i2	1.175231	5.67682	0.002239	0.03526	NA	NA	GO:0016787
c15114_g2_i1	1.174933	5.028322	0.000722	0.015831	NA	NA	NA
c15114_g2_i2	1.174933	5.028322	0.000722	0.015831	NA	NA	NA
c15114_g2_i3	1.174933	5.028322	0.000722	0.015831	RecName: Full=Probable alpha-fucosidase A; AltName: Full=Alpha-L-fucoside fucohydrolase A; Flags: Precursor [Aspergillus niger CBS 513.88]	NA	NA
c15114_g2_i4	1.174933	5.028322	0.000722	0.015831	NA	NA	NA
c13522_g2_i1	1.173759	4.863391	0.000784	0.01678	NA	UniRef90_K5VV46 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VV46_PHACS	NA

c12502_g2_i1	1.173657	6.606986	0.002511	0.038555	NA	NA	GO:0000981|GO:0003677|GO:0005634|GO:0006351|GO:0006355|GO:0008270
c12502_g2_i2	1.173657	6.606986	0.002511	0.038555	RecName: Full=Protein priB [Lentinula edodes]	UniRef90_K5VUP4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUP4_PHACS	GO:0000981|GO:0003677|GO:0005634|GO:0006351|GO:0006355|GO:0008270
c12502_g2_i3	1.173657	6.606986	0.002511	0.038555	NA	NA	GO:0000981|GO:0003677|GO:0005634|GO:0006351|GO:0006355|GO:0008270
c15769_g2_i1	1.173377	4.218285	0.003237	0.046234	RecName: Full=Regulator of V-ATPase in vacuolar membrane protein 1; AltName: Full=RAVE complex subunit rav1 [Schizosaccharomyces pombe 972h-]	NA	NA
c9932_g1_i1	1.171542	3.308604	0.002982	0.043535	NA	UniRef90_K5V849 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V849_PHACS	NA
c15572_g3_i1	1.168178	4.937863	0.001562	0.027494	RecName: Full=Histone-lysine N-methyltransferase, H3 lysine-4 specific; AltName: Full=COMPASS component set1; AltName: Full=Lysine N-methyltransferase 2; AltName: Full=SET domain-containing protein 1; AltName: Full=Set1 complex component set1; Short=Set1C component set1; AltName: Full=Spset1 [Schizosaccharomyces pombe 972h-]	NA	GO:0003676
c3579_g1_i1	1.167695	3.781092	0.001912	0.031565	NA	UniRef90_K5V8F9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V8F9_PHACS	GO:0003723|GO:0005515
c14179_g4_i1	1.166678	6.886521	0.001978	0.032313	NA	NA	GO:0005515
c14179_g4_i2	1.166678	6.886521	0.001978	0.032313	RecName: Full=Protein argonaute 1B; Short=OsAGO1b [Oryza sativa Japonica Group]	UniRef90_K5VW80 Protein argonaute n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VW80_PHACS	GO:0005515
c14179_g4_i3	1.166678	6.886521	0.001978	0.032313	NA	NA	GO:0005515

c14179_g4_i4	1.166678	6.886521	0.001978	0.032313	NA	NA	GO:0005515
c14179_g4_i5	1.166678	6.886521	0.001978	0.032313	NA	NA	GO:0005515
c14894_g1_i1	1.164117	4.092086	0.001957	0.032052	NA	NA	GO:0004672|GO:0005524|GO:0006468
c14970_g1_i1	1.161949	5.102172	0.002804	0.041689	NA	NA	GO:0008152|GO:0016846
c14970_g1_i2	1.161949	5.102172	0.002804	0.041689	RecName: Full=Centromere protein V; Short=CENP-V; AltName: Full=Proline-rich protein 6 [Mus musculus]	NA	GO:0008152|GO:0016846
c16060_g1_i1	1.160959	6.265944	0.001739	0.029792	NA	NA	NA
c16060_g1_i2	1.160959	6.265944	0.001739	0.029792	NA	NA	NA
c16060_g1_i3	1.160959	6.265944	0.001739	0.029792	NA	NA	NA
c8956_g1_i1	1.160732	4.139099	0.001951	0.032024	NA	UniRef90_K5XA19 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XA19_PHACS	NA
c7818_g3_i1	1.160704	6.564812	0.002109	0.033822	NA	UniRef90_K5VAP9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VAP9_PHACS	NA
c5463_g1_i1	1.159978	4.678914	0.003014	0.043899	NA	NA	NA
c5463_g1_i2	1.159978	4.678914	0.003014	0.043899	NA	UniRef90_M2Q5G4 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2Q5G4_CERS8	NA
c5463_g1_i3	1.159978	4.678914	0.003014	0.043899	NA	NA	NA
c13522_g1_i1	1.154433	5.243717	0.001043	0.020641	RecName: Full=Autoinducer 2 sensor kinase/phosphatase LuxQ [Vibrio parahaemolyticus RIMD 2210633]	UniRef90_K5VV46 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VV46_PHACS	GO:0000155|GO:0000160|GO:0007165|GO:0016020
c13522_g1_i2	1.154433	5.243717	0.001043	0.020641	NA	NA	GO:0000160
c14166_g5_i1	1.153003	4.900595	0.001421	0.025716	RecName: Full=Coatomer subunit alpha-2; AltName: Full=Alpha-coat protein 2; Short=Alpha-COP 2 [Arabidopsis thaliana]	UniRef90_K5WFM2 Coatomer subunit alpha n=2 Tax=Phanerochaetaceae RepID=K5WFM2_PHACS	GO:0005515
c9748_g3_i1	1.152382	3.90373	0.001454	0.026108	NA	NA	GO:0000439|GO:0004003|GO:0005634|GO:0006289

c9748_g3_i2	1.152382	3.90373	0.001454	0.026108	RecName: Full=RNA polymerase II transcription factor B subunit 2; AltName: Full=RNA polymerase II transcription factor B 52 kDa subunit; AltName: Full=RNA polymerase II transcription factor B p52 subunit [Yarrowia lipolytica CLIB122]	UniRef90_K5W1U7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1U7_PHACS	GO:0000439|GO:0004003|GO:0005634|GO:0006289
c15812_g2_i1	1.152194	5.042214	0.000804	0.01715	NA	NA	NA
c15812_g2_i2	1.152194	5.042214	0.000804	0.01715	RecName: Full=Uncharacterized helicase C694.02 [Schizosaccharomyces pombe 972h-]	NA	NA
c15668_g1_i1	1.149859	3.808214	0.002233	0.035188	RecName: Full=Chitin synthase 8; AltName: Full=Chitin-UDP acetyl-glucosaminyl transferase 8; AltName: Full=Myosin chitin synthase 1 [Ustilago maydis 521]	NA	GO:0003774|GO:0005524|GO:0016459
c14489_g2_i1	1.147233	5.45066	0.001228	0.023233	RecName: Full=ATP-dependent bile acid permease [Saccharomyces cerevisiae S288c]	NA	GO:0005524|GO:0006810|GO:0016021|GO:0016887|GO:0042626|GO:0055085
c7749_g2_i1	1.146697	4.798661	0.001109	0.021543	NA	UniRef90_K5UZP4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UZP4_PHACS	NA
c7749_g2_i2	1.146697	4.798661	0.001109	0.021543	NA	NA	NA
c15997_g2_i1	1.142551	4.496535	0.001835	0.030891	RecName: Full=H(+)/Cl(-) exchange transporter 3; AltName: Full=Chloride channel protein 3; Short=ClC-3; AltName: Full=Chloride transporter ClC-3 [Mus musculus]	NA	GO:0005247|GO:0006821|GO:0016020|GO:0055085
c15997_g2_i2	1.142551	4.496535	0.001835	0.030891	NA	NA	GO:0005247|GO:0006821|GO:0016020|GO:0055085
c11411_g1_i1	1.13405	3.863899	0.001742	0.029829	RecName: Full=UDP-galactose transporter; AltName: Full=Golgi UDP-Gal transporter [Schizosaccharomyces pombe 972h-]	UniRef90_K5W7V2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W7V2_PHACS	GO:0000139|GO:0005351|GO:0008643|GO:0016021
c10464_g1_i1	1.13349	3.300797	0.00349	0.048802	NA	NA	NA

c13435_g1_i1	1.133177	4.599593	0.001924	0.031687	RecName: Full=Vacuolar protein-sorting protein BRO1; AltName: Full=BRO domain-containing protein 1 [Cryptococcus neoformans var. neoformans JEC21]	UniRef90_K5X3D3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X3D3_PHACS	GO:0005515
c14900_g1_i1	1.12777	4.517232	0.001472	0.026344	NA	NA	NA
c9702_g1_i1	1.12761	4.559185	0.001851	0.03098	NA	UniRef90_K5WB38 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WB38_PHACS	NA
c15835_g2_i1	1.126467	3.904801	0.002583	0.039459	NA	NA	NA
c15835_g2_i2	1.126467	3.904801	0.002583	0.039459	NA	NA	NA
c13621_g1_i1	1.124924	4.68972	0.001225	0.023194	RecName: Full=Putative transcriptional regulatory protein YJL206C [Saccharomyces cerevisiae S288c]	UniRef90_K5WH87 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WH87_PHACS	GO:0003677|GO:0005634|GO:0006351|GO:0008270
c14670_g2_i1	1.124486	5.746717	0.002816	0.041836	NA	NA	NA
c15908_g3_i1	1.122647	4.967738	0.001851	0.03098	NA	NA	NA
c15908_g3_i2	1.122647	4.967738	0.001851	0.03098	NA	NA	NA
c15908_g3_i3	1.122647	4.967738	0.001851	0.03098	NA	NA	NA
c10135_g1_i1	1.122328	4.210427	0.002256	0.035445	NA	NA	NA
c10135_g1_i2	1.122328	4.210427	0.002256	0.035445	NA	UniRef90_K5WLV5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLV5_PHACS	NA
c981_g1_i1	1.119724	4.485004	0.002372	0.03697	NA	UniRef90_K5WCD0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCD0_PHACS	NA
c16187_g1_i1	1.11703	6.298046	0.003421	0.048119	NA	NA	GO:0005524|GO:0005975|GO:0006810|GO:0016021|GO:0016853|GO:0016887|GO:0042626|GO:0055085
c16187_g1_i2	1.11703	6.298046	0.003421	0.048119	NA	NA	GO:0005524|GO:0016887
c16187_g1_i3	1.11703	6.298046	0.003421	0.048119	NA	NA	NA
c16187_g1_i4	1.11703	6.298046	0.003421	0.048119	RecName: Full=ATP-binding cassette transporter abc4; Short=ABC transporter abc4; AltName: Full=ATP-energized glutathione S-	NA	GO:0005524|GO:0005975|GO:0006810|GO:0016021|GO:001

					conjugate pump abc4; AltName: Full=Glutathione S-conjugate-transporting ATPase abc4 [Schizosaccharomyces pombe 972h-]		6853|GO:0016887|GO:0042626|GO:0055085
c8654_g2_i1	1.116428	5.354572	0.001846	0.03098	NA	UniRef90_K5WB03 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WB03_PHACS	NA
c8654_g2_i2	1.116428	5.354572	0.001846	0.03098	NA	NA	NA
c13331_g1_i1	1.112394	3.447347	0.002803	0.041689	RecName: Full=Condensin complex subunit 2; AltName: Full=Barren homolog; AltName: Full=CAPH homolog; AltName: Full=p105 [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3PPE6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PPE6_PHLGI	GO:0000796|GO:0007076
c13161_g2_i1	1.111542	6.304226	0.002425	0.03758	RecName: Full=26S proteasome non-ATPase regulatory subunit 1 homolog A; AltName: Full=26S proteasome regulatory subunit RPN2a; Short=AtRPN2a; AltName: Full=26S proteasome regulatory subunit S1 homolog A [Arabidopsis thaliana]	UniRef90_K5XDW6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XDW6_PHACS	NA
c8334_g2_i1	1.105446	4.955832	0.001867	0.031093	RecName: Full=Vacuolar protein sorting-associated protein 35; AltName: Full=Maternal-embryonic 3; AltName: Full=Vesicle protein sorting 35 [Mus musculus]	UniRef90_A0A0C3S2U2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S2U2_PHLGI	GO:0015031|GO:0030904|GO:0042147
c9388_g1_i1	1.105196	4.626324	0.001534	0.027216	NA	UniRef90_A0A0C3S3L1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S3L1_PHLGI	NA
c12728_g1_i1	1.104033	4.545569	0.001795	0.030489	RecName: Full=Probable cation-transporting ATPase C1672.11c [Schizosaccharomyces pombe 972h-]	UniRef90_K5W5A5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5A5_PHACS	GO:0000166|GO:0006812|GO:0016021|GO:0016887|GO:0046872
c15777_g1_i1	1.100789	4.087662	0.002652	0.039989	NA	NA	NA
c15777_g1_i2	1.100789	4.087662	0.002652	0.039989	NA	NA	NA
c15777_g1_i3	1.100789	4.087662	0.002652	0.039989	NA	NA	NA
c15777_g1_i4	1.100789	4.087662	0.002652	0.039989	NA	NA	NA
c15777_g1_i5	1.100789	4.087662	0.002652	0.039989	NA	NA	NA

c13524_g1_i1	1.100535	4.186329	0.00215	0.034269	NA	UniRef90_K5W8R6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8R6_PHACS	NA
c15041_g2_i1	1.098785	4.193697	0.002624	0.03981	RecName: Full=Ubiquitin-like-specific protease 2 [Schizosaccharomyces pombe 972h-]	NA	GO:0006508|GO:0008234
c12583_g1_i1	1.09782	5.260567	0.001527	0.027117	RecName: Full=Cohesin subunit rad21; AltName: Full=Double-strand-break repair protein rad21; AltName: Full=SCC1 homolog [Schizosaccharomyces pombe 972h-]	UniRef90_K5VCW0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCW0_PHACS	GO:0000228|GO:0005515
c15177_g1_i1	1.097515	6.455501	0.003504	0.048961	NA	NA	NA
c15177_g1_i2	1.097515	6.455501	0.003504	0.048961	NA	NA	NA
c15177_g1_i3	1.097515	6.455501	0.003504	0.048961	NA	NA	NA
c15177_g1_i4	1.097515	6.455501	0.003504	0.048961	NA	NA	NA
c15177_g1_i5	1.097515	6.455501	0.003504	0.048961	NA	NA	NA
c15177_g1_i6	1.097515	6.455501	0.003504	0.048961	NA	NA	NA
c12252_g1_i1	1.094038	6.014705	0.003261	0.046443	RecName: Full=Actin cytoskeleton-regulatory complex protein pan1 [Aspergillus clavatus NRRL 1]	UniRef90_K5X024 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X024_PHACS	NA
c14000_g1_i1	1.091032	4.627965	0.001905	0.031516	RecName: Full=Xenotropic and polytropic retrovirus receptor 1 homolog [Xenopus laevis]	UniRef90_K5WFY7 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFY7_PHACS	GO:0016021
c14000_g1_i2	1.091032	4.627965	0.001905	0.031516	NA	NA	GO:0016021
c15900_g2_i1	1.087628	5.243754	0.003222	0.04611	RecName: Full=Transcription-associated protein 1; AltName: Full=p400 kDa component of SAGA [Saccharomyces cerevisiae S288c]	NA	GO:0005515
c15561_g2_i1	1.085413	4.465788	0.001746	0.02987	RecName: Full=Transcription termination factor 2; AltName: Full=RNA polymerase II termination factor; AltName: Full=Transcription release factor 2 [Mus musculus]	NA	GO:0003677|GO:0005524
c15932_g1_i1	1.083888	4.873971	0.001383	0.025359	NA	NA	GO:0005515

c14304_g2_i1	1.08321	4.376615	0.002497	0.038382	NA	NA	NA
c14304_g2_i2	1.08321	4.376615	0.002497	0.038382	RecName: Full=Altered inheritance of mitochondria protein 9, mitochondrial; AltName: Full=Found in mitochondrial proteome protein 29; Flags: Precursor [Debaryomyces hansenii CBS767]	NA	NA
c14509_g2_i1	1.08313	4.693818	0.002003	0.032558	RecName: Full=Exportin-1; AltName: Full=Caffeine resistance protein 2; AltName: Full=Chromosome region maintenance protein 1 [Schizosaccharomyces pombe 972h-]	NA	GO:0006886|GO:0008536
c16010_g2_i1	1.076456	6.209388	0.003548	0.049389	NA	NA	NA
c16129_g2_i1	1.071452	5.169542	0.001527	0.027117	RecName: Full=Nucleoprotein TPR; AltName: Full=Megator; AltName: Full=NPC-associated intranuclear protein; AltName: Full=Translocated promoter region protein [Homo sapiens]	NA	GO:0005643|GO:0006606
c9758_g2_i1	1.071128	4.566844	0.002787	0.041596	RecName: Full=ATP-dependent helicase fft2; AltName: Full=Fun thirty-related protein 2 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WVE7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WVE7_PHACS	GO:0003677|GO:0005524
c14174_g1_i1	1.064633	4.760398	0.003066	0.044418	NA	UniRef90_K5V0E1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V0E1_PHACS	NA
c14174_g1_i2	1.064633	4.760398	0.003066	0.044418	NA	NA	NA
c15131_g1_i1	1.051641	4.994626	0.00245	0.037802	NA	NA	NA
c15668_g2_i1	1.041516	4.590379	0.002649	0.039981	RecName: Full=Chitin synthase 8; AltName: Full=Chitin-UDP acetyl-glucosaminyl transferase 8; AltName: Full=Myosin chitin synthase 1 [Ustilago maydis 521]	NA	GO:0003774|GO:0005524|GO:0016459
c11879_g2_i1	1.039173	4.932074	0.002831	0.041983	NA	UniRef90_UPI00044144FE hypothetical protein DICSQDRAFT_103796 n=1 Tax=Dichomitus squalens (strain LYAD-421) RepID=UPI00044144FE	NA

c15805_g1_i1	1.03526	5.103995	0.002774	0.041466	RecName: Full=Uncharacterized WD repeat-containing protein C343.04c [Schizosaccharomyces pombe 972h-]	NA	GO:0005515
c14075_g1_i1	1.032037	5.14973	0.00285	0.042113	NA	NA	NA
c14075_g1_i2	1.032037	5.14973	0.00285	0.042113	NA	NA	NA
c14075_g1_i3	1.032037	5.14973	0.00285	0.042113	NA	NA	NA
c14075_g1_i4	1.032037	5.14973	0.00285	0.042113	RecName: Full=Probable mitochondrial 2-oxodicarboxylate carrier [Schizosaccharomyces pombe 972h-]	UniRef90_K5W196 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W196_PHACS	NA
c11567_g1_i1	1.031272	4.697865	0.002631	0.039859	NA	UniRef90_K5W8F1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8F1_PHACS	NA
c11755_g1_i1	1.022922	4.641599	0.002846	0.042113	NA	UniRef90_K5W6Q6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6Q6_PHACS	NA
c10615_g1_i1	1.018897	5.201282	0.003527	0.049224	RecName: Full=Cell division cycle-related protein res2/pct1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V9V9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V9V9_PHACS	GO:0005515
c10615_g1_i2	1.018897	5.201282	0.003527	0.049224	NA	NA	GO:0005515
c10004_g3_i1	-1.42181	5.534491	0.001892	0.031393	RecName: Full=D-lactate dehydrogenase [cytochrome] 1, mitochondrial; AltName: Full=D-lactate ferricytochrome C oxidoreductase; Short=D-LCR; Flags: Precursor [Saccharomyces cerevisiae S288c]	UniRef90_A0A0C3PSH9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PSH9_PHLGI	GO:0003824|GO:0050660
c10007_g1_i1	-1.98241	10.97111	9.79E-06	0.000547	RecName: Full=Respiratory supercomplex factor 2, mitochondrial; AltName: Full=Altered inheritance of mitochondria protein 38 [Saccharomyces cerevisiae S288c]	UniRef90_K5WJ87 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJ87_PHACS	NA
c10037_g1_i1	-1.88414	9.112288	0.002028	0.032866	RecName: Full=Regulatory protein abaA [Aspergillus nidulans FGSC A4]	UniRef90_K5W343 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W343_PHACS	GO:0003700|GO:0005634|GO:0006355
c10090_g1_i1	-1.3761	3.906289	0.000525	0.012448	NA	NA	NA

c10122_g2_i1	-1.26301	4.046622	0.002659	0.040013	NA	UniRef90_A0A0C3NNB3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NNB3_PHLGI	NA
c10129_g1_i1	-1.6592	6.867414	0.000189	0.005638	RecName: Full=Diphosphomevalonate decarboxylase; AltName: Full=Mevalonate pyrophosphate decarboxylase; AltName: Full=Mevalonate-5-diphosphate decarboxylase; Short=MDDase [Debaryomyces hansenii CBS767]	UniRef90_M2R667 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2R667_CERS8	GO:0005524
c10129_g1_i2	-1.6592	6.867414	0.000189	0.005638	NA	NA	GO:0005524
c10129_g2_i1	-1.45653	3.710162	0.000562	0.013086	RecName: Full=Diphosphomevalonate decarboxylase; AltName: Full=Mevalonate (diphospho)decarboxylase; Short=MDDase; AltName: Full=Mevalonate pyrophosphate decarboxylase [Dictyostelium discoideum]	UniRef90_S8EHV4 Uncharacterized protein n=1 Tax=Fomitopsis pinicola (strain FP-58527) RepID=S8EHV4_FOMPI	NA
c10143_g1_i1	-1.28749	3.48251	0.002978	0.043509	NA	UniRef90_K5W7R1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W7R1_PHACS	NA
c10151_g1_i1	-1.63139	4.003875	0.001999	0.032553	NA	NA	NA
c10222_g2_i1	-1.52721	4.217963	0.00014	0.004437	NA	UniRef90_A0A0C3RRK9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RRK9_PHLGI	NA
c10225_g1_i1	-1.25476	3.455268	0.001851	0.03098	RecName: Full=Uncharacterized protein YDL144C [Saccharomyces cerevisiae S288c]	UniRef90_K5WMR5 2-dehydropantoate 2-reductase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WMR5_PHACS	GO:0008677|GO:0055114
c10228_g5_i1	-2.56152	3.598888	3.57E-05	0.001515	NA	NA	NA
c10236_g1_i1	-2.1955	6.754214	8.48E-07	7.24E-05	NA	UniRef90_K5VZ28 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZ28_PHACS	NA
c10237_g1_i1	-1.86393	6.320722	0.000168	0.005108	NA	UniRef90_K5VZU2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZU2_PHACS	GO:0016021

c10244_g1_i1	-1.84368	7.295968	5.52E-05	0.002105	RecName: Full=Aspartic protease pep1; AltName: Full=Penicillopepsin pep1; Flags: Precursor [Penicillium rubens Wisconsin 54-1255]	UniRef90_K5VAM8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VAM8_PHACS	GO:0004190|GO:0006508
c10244_g2_i1	-2.23861	7.261268	4.62E-07	4.39E-05	RecName: Full=Endothiapepsin; AltName: Full=Aspartate protease; Flags: Precursor [Cryphonectria parasitica]	UniRef90_K5VAM8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VAM8_PHACS	GO:0004190|GO:0006508
c10246_g1_i1	-1.70918	3.997532	0.000725	0.015863	NA	UniRef90_K5VMI2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VMI2_PHACS	NA
c10263_g1_i1	-2.24978	5.877093	8.51E-08	1.04E-05	NA	NA	NA
c10263_g1_i2	-2.24978	5.877093	8.51E-08	1.04E-05	NA	UniRef90_K5WRB2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WRB2_PHACS	NA
c10284_g1_i1	-1.83958	3.972297	2.59E-06	0.000184	NA	NA	NA
c10286_g1_i1	-1.44082	5.225528	0.000581	0.013379	NA	UniRef90_K5VPM8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPM8_PHACS	NA
c10286_g1_i2	-1.44082	5.225528	0.000581	0.013379	NA	NA	NA
c10286_g2_i1	-1.27764	6.750159	0.002455	0.037854	NA	NA	GO:0005515
c10286_g2_i2	-1.27764	6.750159	0.002455	0.037854	RecName: Full=Glutathione S-transferase omega-1; Short=GSTO-1; AltName: Full=Glutathione S-transferase omega 1-1; Short=GSTO 1-1; AltName: Full=Glutathione-dependent dehydroascorbate reductase; AltName: Full=Monomethylarsonic acid reductase; Short=MMA(V) reductase; AltName: Full=S-(Phenacyl)glutathione reductase; Short=SPG-R [Sus scrofa]	UniRef90_K5VPM8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPM8_PHACS	GO:0005515
c10305_g1_i1	-1.72184	8.216051	0.000717	0.015767	NA	NA	NA
c10305_g1_i2	-1.72184	8.216051	0.000717	0.015767	NA	UniRef90_K5WGJ9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGJ9_PHACS	NA

c10305_g2_i1	-1.51198	8.681612	0.002209	0.034945	NA	UniRef90_K5WGJ9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGJ9_PHACS	NA
c10307_g2_i1	-1.46162	5.575372	5.14E-05	0.002016	NA	UniRef90_K5WCU0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCU0_PHACS	GO:0046872
c10307_g2_i2	-1.46162	5.575372	5.14E-05	0.002016	NA	NA	GO:0046872
c10307_g2_i3	-1.46162	5.575372	5.14E-05	0.002016	NA	NA	GO:0046872
c10307_g3_i1	-1.43752	4.675982	3.13E-05	0.001357	NA	UniRef90_K5WCU0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCU0_PHACS	NA
c10313_g1_i1	-1.21315	4.152554	0.003273	0.046557	NA	NA	NA
c10313_g1_i2	-1.21315	4.152554	0.003273	0.046557	NA	NA	NA
c1033_g1_i1	-1.92307	2.006719	0.002562	0.039206	NA	UniRef90_K5XA71 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XA71_PHACS	NA
c10343_g1_i1	-2.17712	2.065169	0.000386	0.009822	NA	NA	GO:0003824|GO:0006813|GO:0016491|GO:0055114
c10343_g1_i2	-2.17712	2.065169	0.000386	0.009822	NA	UniRef90_K5W8X4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8X4_PHACS	NA
c10343_g2_i1	-2.00613	3.524352	5.20E-05	0.002028	RecName: Full=Pentachlorophenol 4-monooxygenase; AltName: Full=Pentachlorophenol hydroxylase [Sphingobium chlorophenolicum]	UniRef90_K5W8X4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8X4_PHACS	NA
c10352_g1_i1	-3.51058	3.729884	6.52E-13	2.65E-10	NA	UniRef90_K5WDM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDM7_PHACS	NA
c10352_g1_i2	-3.51058	3.729884	6.52E-13	2.65E-10	NA	NA	NA
c10352_g2_i1	-2.08756	3.366146	9.05E-07	7.51E-05	NA	UniRef90_K5WDM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDM7_PHACS	NA

c10352_g3_i1	-2.82458	4.03445	4.14E-08	5.67E-06	NA	UniRef90_K5WDM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDM7_PHACS	NA
c10371_g2_i1	-8.79671	8.742112	2.60E-28	2.12E-24	RecName: Full=Uncharacterized protein YcaC [Escherichia coli K-12]	UniRef90_K5VIG9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VIG9_PHACS	GO:0003824|GO:0008152
c10371_g3_i1	-9.49502	7.985338	4.28E-35	1.05E-30	RecName: Full=Uncharacterized protein YcaC [Escherichia coli K-12]	UniRef90_K5VIG9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VIG9_PHACS	GO:0003824|GO:0008152
c10378_g1_i1	-2.19244	6.14297	3.50E-05	0.001491	NA	NA	NA
c10378_g2_i1	-2.27392	5.727939	2.33E-05	0.001098	NA	NA	NA
c10379_g1_i1	-1.57799	5.993999	5.40E-05	0.002071	NA	UniRef90_A0A0C3NM31 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NM31_PHLGI	NA
c10400_g1_i1	-1.70857	8.221131	0.000131	0.00421	NA	UniRef90_K5X3K3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X3K3_PHACS	NA
c10400_g1_i2	-1.70857	8.221131	0.000131	0.00421	NA	NA	NA
c10437_g1_i1	-2.24032	3.644619	2.79E-06	0.000196	RecName: Full=FAD-linked sulfhydryl oxidase ALR; AltName: Full=Augmenter of liver regeneration [Mus musculus]	UniRef90_K5UKL2 Sulfhydryl oxidase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UKL2_PHACS	GO:0016972|GO:0055114
c10437_g1_i2	-2.24032	3.644619	2.79E-06	0.000196	NA	NA	NA
c10489_g1_i1	-3.12308	1.748242	2.81E-07	2.91E-05	NA	UniRef90_K5V6F1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V6F1_PHACS	NA
c10531_g1_i1	-2.42035	3.528096	1.81E-07	2.01E-05	NA	NA	NA
c10567_g2_i1	-2.80084	4.623482	2.82E-09	5.73E-07	RecName: Full=Putative sterigmatocystin biosynthesis peroxidase stcC; Flags: Precursor [Aspergillus nidulans FGSC A4]	UniRef90_A0A0C3RWQ1 Heme-thiolate peroxidase n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RWQ1_PHLGI	GO:0004601
c10570_g1_i1	-1.73456	7.922288	3.38E-05	0.001445	NA	UniRef90_A0A0C3PD06 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PD06_PHLGI	NA
c10590_g1_i1	-2.03622	1.784315	0.000984	0.019797	NA	NA	NA

c10590_g2_i1	-1.47073	5.40309	4.70E-05	0.001885	RecName: Full=Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase; AltName: Full=Asparagine-linked glycosylation protein 6; AltName: Full=Dol-P-Man-dependent alpha(1-3)-mannosyltransferase; AltName: Full=Dolichyl-P-Man:Man(5)GlcNAc(2)-PP-dolichyl mannosyltransferase [Phaeosphaeria nodorum SN15]	UniRef90_K5W6V0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6V0_PHACS	NA
c10623_g1_i1	-1.9061	2.852921	0.000337	0.008859	RecName: Full=Uncharacterized ATP-dependent helicase C17A2.12 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VN01 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VN01_PHACS	NA
c10623_g2_i1	-1.98285	5.86069	0.00016	0.00493	RecName: Full=Versiconal hemiacetal acetate reductase; AltName: Full=VHA reductase [Aspergillus parasiticus]	UniRef90_K5VN01 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VN01_PHACS	NA
c10634_g1_i1	-2.02287	7.891589	7.54E-05	0.002701	RecName: Full=Putative voltage-gated potassium channel subunit beta; AltName: Full=K(+) channel subunit beta [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3S6V3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S6V3_PHLGI	NA
c10634_g2_i1	-2.19836	8.688132	3.27E-05	0.00141	RecName: Full=Putative voltage-gated potassium channel subunit beta; AltName: Full=K(+) channel subunit beta [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3S6V3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S6V3_PHLGI	NA
c10641_g1_i1	-1.28328	7.188247	0.002777	0.041484	NA	UniRef90_K5WB59 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WB59_PHACS	NA
c10658_g1_i1	-1.23369	8.040858	0.002757	0.041256	RecName: Full=Transcription activator of gluconeogenesis ERT1 [Postia placenta Mad-698-R]	UniRef90_K5UWS6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UWS6_PHACS	NA
c10715_g1_i1	-2.24429	3.722096	1.45E-08	2.36E-06	NA	NA	NA
c10715_g1_i2	-2.24429	3.722096	1.45E-08	2.36E-06	NA	NA	NA
c10715_g2_i1	-2.01256	2.260569	0.000145	0.004549	NA	NA	NA
c10715_g2_i2	-2.01256	2.260569	0.000145	0.004549	NA	NA	NA

c10736_g1_i1	-1.18588	4.751397	0.001229	0.023233	NA	UniRef90_A0A0C3S2M9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S2M9_PHLGI	NA
c10740_g2_i1	-1.30828	4.073474	0.002793	0.041627	NA	NA	NA
c10741_g1_i1	-1.8086	7.173294	3.46E-05	0.001478	NA	NA	GO:0008152|GO:0016787
c10741_g1_i2	-1.8086	7.173294	3.46E-05	0.001478	RecName: Full=N-carbamoyl-L-amino acid hydrolase; AltName: Full=L-carbamoylase [Geobacillus stearothermophilus]	UniRef90_K5VWV3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWV3_PHACS	GO:0008152|GO:0016787
c10741_g1_i3	-1.8086	7.173294	3.46E-05	0.001478	NA	NA	GO:0008152|GO:0016787
c10741_g1_i4	-1.8086	7.173294	3.46E-05	0.001478	NA	NA	NA
c10762_g1_i1	-1.35715	5.098033	0.002573	0.039334	NA	NA	NA
c10762_g1_i2	-1.35715	5.098033	0.002573	0.039334	NA	NA	NA
c10762_g1_i3	-1.35715	5.098033	0.002573	0.039334	NA	NA	NA
c10792_g1_i1	-1.41411	3.920641	0.000546	0.012806	NA	NA	NA
c10792_g1_i2	-1.41411	3.920641	0.000546	0.012806	NA	NA	NA
c10804_g1_i1	-1.84787	9.506503	5.32E-05	0.002057	NA	NA	NA
c10804_g1_i2	-1.84787	9.506503	5.32E-05	0.002057	NA	NA	NA
c10804_g1_i3	-1.84787	9.506503	5.32E-05	0.002057	NA	UniRef90_A0A0C3S0I9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S0I9_PHLGI	NA
c10804_g1_i4	-1.84787	9.506503	5.32E-05	0.002057	NA	NA	NA
c10817_g1_i1	-1.66908	3.893001	7.22E-05	0.002598	NA	NA	NA
c10817_g1_i2	-1.66908	3.893001	7.22E-05	0.002598	RecName: Full=YTH domain-containing protein 2 [Pongo abelii]	UniRef90_K5VXL5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXL5_PHACS	NA
c10817_g2_i1	-1.13168	4.917195	0.003463	0.048529	RecName: Full=Zinc finger CCCH domain-containing protein 45; Short=OsC3H45 [Oryza sativa Japonica Group]	UniRef90_K5VXL5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXL5_PHACS	GO:0003676
c10830_g3_i1	-2.57291	2.162987	7.65E-06	0.000444	NA	UniRef90_K5WJE1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJE1_PHACS	NA
c10914_g1_i1	-2.25992	3.721894	2.97E-06	0.000207	NA	NA	NA

c10914_g1_i2	-2.25992	3.721894	2.97E-06	0.000207	RecName: Full=Probable quinone oxidoreductase; AltName: Full=NADPH:quinone reductase [Schizosaccharomyces pombe 972h-]	UniRef90_K5VEW6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VEW6_PHACS	NA
c10914_g2_i1	-1.61462	4.98827	2.57E-05	0.001186	RecName: Full=Quinone oxidoreductase; AltName: Full=NADPH:quinone reductase [Pseudomonas aeruginosa PAO1]	UniRef90_K5VEW6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VEW6_PHACS	GO:0008270|GO:0016491|GO:0055114
c10914_g2_i2	-1.61462	4.98827	2.57E-05	0.001186	NA	NA	GO:0008270|GO:0016491|GO:0055114
c10927_g2_i1	-2.59608	4.329335	5.39E-08	7.24E-06	NA	UniRef90_K5W774 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W774_PHACS	NA
c10943_g2_i1	-2.57898	2.840278	5.19E-05	0.002026	NA	NA	NA
c10949_g2_i1	-2.86176	3.10011	1.86E-09	3.94E-07	RecName: Full=P-type cation-transporting ATPase; AltName: Full=Cadmium resistance protein 2; AltName: Full=Cadmium-translocating P-type ATPase; AltName: Full=Cd(2+)-exporting ATPase [Saccharomyces cerevisiae S288c]	UniRef90_K5VU34 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VU34_PHACS	GO:0000166|GO:0030001|GO:0046872
c10950_g1_i1	-1.73831	2.652714	0.000959	0.01938	RecName: Full=E3 ubiquitin-protein ligase TRIM38; AltName: Full=Tripartite motif-containing protein 38 [Bos taurus]	UniRef90_K5ULP8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5ULP8_PHACS	GO:0005515|GO:0008270|GO:0046872
c10995_g1_i1	-2.07418	9.720338	5.00E-06	0.000314	NA	NA	NA
c10995_g1_i2	-2.07418	9.720338	5.00E-06	0.000314	RecName: Full=Ripening-related protein grip22; Flags: Precursor [Vitis vinifera]	UniRef90_K5WY06 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WY06_PHACS	NA
c11025_g1_i1	-1.57663	7.009435	0.001385	0.025382	NA	NA	GO:0004725|GO:0006470|GO:0008138
c11025_g1_i2	-1.57663	7.009435	0.001385	0.025382	NA	NA	NA
c11025_g1_i3	-1.57663	7.009435	0.001385	0.025382	RecName: Full=Dual specificity protein phosphatase [Chlamydomonas moewusii]	UniRef90_K5W5Q4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5Q4_PHACS	GO:0004725|GO:0006470|GO:0008138

c11034_g1_i1	-1.39867	3.71381	0.001402	0.025621	NA	UniRef90_K5VZK4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZK4_PHACS	NA
c11034_g1_i2	-1.39867	3.71381	0.001402	0.025621	NA	NA	NA
c11039_g1_i1	-2.39175	3.540416	6.14E-05	0.002298	RecName: Full=Synaptic vesicle membrane protein VAT-1 homolog-like [Mus musculus]	UniRef90_K5VU64 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VU64_PHACS	GO:0016491|GO:0055114
c11056_g3_i1	-2.36297	2.399281	0.00157	0.027534	RecName: Full=Ligninase B; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_P06181 Ligninase H8 n=7 Tax=Phanerochaete RepID=LIG8_PHACH	NA
c11076_g1_i1	-1.75944	4.785026	5.77E-05	0.002196	NA	NA	NA
c11076_g1_i2	-1.75944	4.785026	5.77E-05	0.002196	NA	NA	NA
c11080_g1_i1	-2.39222	5.434436	9.55E-10	2.10E-07	NA	UniRef90_K5WRB2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WRB2_PHACS	NA
c11080_g1_i2	-2.39222	5.434436	9.55E-10	2.10E-07	NA	NA	NA
c11094_g1_i1	-1.89764	2.813351	0.000598	0.013672	RecName: Full=Guanine nucleotide-binding protein alpha-4 subunit [Ustilago maydis 521]	UniRef90_A0A0C3S4G9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S4G9_PHLGI	GO:0003924|GO:0004871|GO:0005525|GO:0007186|GO:0019001|GO:0031683
c11103_g1_i1	-1.84713	8.349738	6.98E-05	0.002532	NA	UniRef90_K5WFQ6 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFQ6_PHACS	NA
c11106_g1_i1	-1.74826	7.594811	0.00014	0.004434	RecName: Full=Uncharacterized protein in dcmA 3'region	UniRef90_K5W4M4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W4M4_PHACS	NA
c11119_g1_i1	-2.23593	1.589444	0.000869	0.018186	NA	NA	NA
c11119_g1_i2	-2.23593	1.589444	0.000869	0.018186	NA	UniRef90_R7SS05 Ricin B-like lectin n=1 Tax=Dichomitus squalens (strain LYAD-421) RepID=R7SS05_DICSQ	GO:0009405
c11121_g1_i1	-1.50276	6.744161	0.000375	0.009588	NA	UniRef90_K5UVN5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UVN5_PHACS	NA

c11122_g5_i1	-1.2604	3.142353	0.001951	0.032024	RecName: Full=Release factor glutamine methyltransferase; Short=RF MTase; AltName: Full=N5-glutamine methyltransferase PrmC; AltName: Full=Protein-(glutamine-N5) MTase PrmC; AltName: Full=Protein-glutamine N-methyltransferase PrmC [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	UniRef90_K5W5T1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5T1_PHACS	NA
c11128_g1_i1	-1.20873	4.016506	0.001806	0.030572	NA	NA	NA
c11128_g1_i2	-1.20873	4.016506	0.001806	0.030572	NA	NA	NA
c1113_g1_i1	-2.95862	1.64086	1.11E-06	9.05E-05	NA	UniRef90_K5VAU8 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VAU8_PHACS	NA
c11151_g1_i1	-2.16494	5.335488	1.99E-07	2.18E-05	NA	UniRef90_A0A0C3NKX4 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NKX4_PHLGI	NA
c11177_g1_i1	-2.09252	5.596626	5.85E-06	0.000359	RecName: Full=Putative quercetin 2,3-dioxygenase sll1773; Short=Putative quercetinase; AltName: Full=Pirin-like protein sll1773 [Synechocystis sp. PCC 6803 substr. Kazusa]	UniRef90_K5WIK9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WIK9_PHACS	NA
c11177_g1_i2	-2.09252	5.596626	5.85E-06	0.000359	NA	NA	NA
c11189_g2_i1	-1.21234	5.229663	0.001435	0.025894	NA	NA	NA
c11189_g3_i1	-1.59131	6.513753	0.000163	0.005013	NA	UniRef90_K5WL48 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WL48_PHACS	NA
c11205_g1_i1	-1.0332	5.611464	0.003551	0.049389	NA	NA	GO:0006950
c11205_g1_i2	-1.0332	5.611464	0.003551	0.049389	RecName: Full=Uncharacterized protein C1711.08 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WX27 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WX27_PHACS	GO:0006950
c11210_g2_i1	-1.13152	4.830333	0.001022	0.020343	NA	UniRef90_A0A0C3S7C2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S7C2_PHLGI	NA

c11216_g1_i1	-1.35466	8.429674	0.003171	0.045582	NA	NA	NA
c11216_g1_i2	-1.35466	8.429674	0.003171	0.045582	NA	UniRef90_K5WCB9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCB9_PHACS	NA
c11225_g1_i1	-2.63086	2.735059	8.11E-08	1.02E-05	NA	NA	NA
c11225_g1_i2	-2.63086	2.735059	8.11E-08	1.02E-05	NA	NA	NA
c11225_g1_i3	-2.63086	2.735059	8.11E-08	1.02E-05	NA	NA	NA
c11225_g1_i4	-2.63086	2.735059	8.11E-08	1.02E-05	NA	NA	NA
c11225_g1_i5	-2.63086	2.735059	8.11E-08	1.02E-05	NA	NA	NA
c11227_g1_i1	-1.86573	4.577045	3.89E-05	0.00161	NA	UniRef90_K5WG67 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WG67_PHACS	NA
c11227_g2_i1	-1.86646	5.005504	1.40E-05	0.000736	NA	UniRef90_K5WG67 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WG67_PHACS	NA
c11245_g1_i1	-1.10499	5.246443	0.001662	0.028787	NA	NA	NA
c11245_g1_i2	-1.10499	5.246443	0.001662	0.028787	RecName: Full=Iron-sulfur cluster assembly 2 homolog, mitochondrial; AltName: Full=Iron-sulfur assembly protein isca2; Flags: Precursor [Dictyostelium discoideum]	UniRef90_K5W376 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W376_PHACS	NA
c11264_g1_i1	-1.88378	8.758212	0.000365	0.009418	NA	NA	GO:0003824|GO:0016491|GO:0018580|GO:0055114
c11264_g1_i2	-1.88378	8.758212	0.000365	0.009418	RecName: Full=Nitronate monooxygenase; AltName: Full=2-nitropropane dioxygenase; Short=2-NPD; AltName: Full=Nitroalkane oxidase; Flags: Precursor [Neurospora crassa OR74A]	UniRef90_K5WCY7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCY7_PHACS	GO:0003824|GO:0016491|GO:0018580|GO:0055114
c11316_g1_i1	-2.1655	2.91511	1.87E-05	0.00092	RecName: Full=Protein priA; Flags: Precursor [Lentinula edodes]	UniRef90_K5W2A0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2A0_PHACS	NA
c11319_g1_i1	-1.32738	4.699667	0.000187	0.005589	NA	NA	NA

c11319_g1_i2	-1.32738	4.699667	0.000187	0.005589	NA	UniRef90_K5V2K4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V2K4_PHACS	NA
c11319_g1_i3	-1.32738	4.699667	0.000187	0.005589	NA	NA	NA
c11328_g3_i1	-1.14179	4.497786	0.003072	0.044475	RecName: Full=Putative fungistatic metabolite [Chaetomium globosum CBS 148.51]	UniRef90_K5VVS7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVS7_PHACS	NA
c11340_g1_i1	-1.64809	5.723007	0.0001	0.003386	RecName: Full=CinA-like protein [Sulfurihydrogenibium sp. YO3AOP1]	UniRef90_K5V0R6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V0R6_PHACS	NA
c11340_g1_i2	-1.64809	5.723007	0.0001	0.003386	NA	NA	NA
c11353_g1_i1	-1.88966	6.127134	9.44E-05	0.00326	NA	NA	NA
c11355_g1_i1	-1.83494	5.263038	0.001327	0.024578	NA	UniRef90_UPI00046230C6 hypothetical protein TRAVEDRAFT_126209 n=1 Tax=Trametes versicolor (strain FP-101664) RepID=UPI00046230C6	NA
c11355_g1_i2	-1.83494	5.263038	0.001327	0.024578	NA	NA	NA
c11361_g2_i1	-1.96718	4.12908	1.99E-05	0.000959	NA	UniRef90_K5VTC6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VTC6_PHACS	NA
c11367_g1_i1	-1.32618	6.697086	0.000943	0.01917	NA	UniRef90_A0A0C3NUB5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NUB5_PHLGI	NA
c11379_g1_i1	-1.39523	4.678908	0.00032	0.008542	NA	UniRef90_A0A0C3RZX1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RZX1_PHLGI	GO:0016491|GO:0055114
c11379_g1_i2	-1.39523	4.678908	0.00032	0.008542	NA	NA	GO:0016491|GO:0055114
c11381_g1_i1	-3.00849	4.280193	8.37E-08	1.04E-05	NA	NA	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c11381_g1_i2	-3.00849	4.280193	8.37E-08	1.04E-05	NA	UniRef90_K5WIJ2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WIJ2_PHACS	NA
c11381_g1_i3	-3.00849	4.280193	8.37E-08	1.04E-05	NA	NA	NA

c11381_g2_i1	-2.35313	2.011091	0.000736	0.015963	NA	UniRef90_K5WIJ2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WIJ2_PHACS	GO:0003677|GO:0005634|GO:0006351|GO:0008270
c11381_g2_i2	-2.35313	2.011091	0.000736	0.015963	NA	NA	GO:0003677|GO:0005634|GO:0006351|GO:0008270
c11382_g1_i1	-2.68971	5.111856	0.00014	0.004437	RecName: Full=Tripeptidyl-peptidase sed2; AltName: Full=Sedolisin-B; Flags: Precursor [Aspergillus fumigatus Af293]	UniRef90_A0A0C3S0L2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S0L2_PHLGI	GO:0004252|GO:0006508
c11382_g2_i1	-2.34079	6.261804	0.000166	0.005074	NA	NA	GO:0008236
c11382_g2_i2	-2.34079	6.261804	0.000166	0.005074	RecName: Full=Tripeptidyl-peptidase SED2; AltName: Full=Sedolisin-B; Flags: Precursor [Arthroderma otae CBS 113480]	UniRef90_K5W588 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W588_PHACS	GO:0004252|GO:0006508|GO:0008236
c11398_g1_i1	-1.60048	10.56472	0.001147	0.022129	RecName: Full=ATPase 11, plasma membrane-type; AltName: Full=Proton pump 11 [Arabidopsis thaliana]	UniRef90_A0A0C3RPV4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RPV4_PHLGI	NA
c11398_g1_i2	-1.60048	10.56472	0.001147	0.022129	NA	NA	NA
c11405_g1_i1	-1.33101	7.908983	0.002791	0.041627	NA	NA	NA
c11405_g1_i2	-1.33101	7.908983	0.002791	0.041627	NA	NA	NA
c11405_g1_i3	-1.33101	7.908983	0.002791	0.041627	NA	NA	NA
c11405_g1_i4	-1.33101	7.908983	0.002791	0.041627	NA	NA	NA
c11461_g1_i1	-2.42526	6.366474	4.21E-06	0.000271	NA	NA	NA
c11505_g1_i1	-2.85971	6.493215	1.41E-07	1.63E-05	NA	NA	NA
c11505_g1_i2	-2.85971	6.493215	1.41E-07	1.63E-05	RecName: Full=Uncharacterized 21.2 kDa protein [Botrytis cinerea]	UniRef90_A0A0C3SDY6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SDY6_PHLGI	NA
c11518_g1_i1	-1.90498	8.031784	9.27E-06	0.000523	NA	NA	GO:0004602|GO:0006979|GO:0016209|GO:0016491|GO:0055114
c11518_g1_i2	-1.90498	8.031784	9.27E-06	0.000523	RecName: Full=Glutathione peroxidase 2 [Saccharomyces cerevisiae S288c]	UniRef90_K5X689 Glutathione peroxidase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X689_PHACS	GO:0004602|GO:0006979|GO:0016209|GO:0016491|GO:0055114

c11538_g1_i1	-1.27965	4.195643	0.000864	0.018114	RecName: Full=C-8 sterol isomerase; AltName: Full=Delta-8--delta-7 sterol isomerase [Magnaporthe oryzae 70-15]	UniRef90_K5WE32 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WE32_PHACS	NA
c11569_g1_i1	-1.53996	6.570302	0.000101	0.003402	NA	NA	NA
c11569_g2_i1	-1.29803	7.161651	0.001565	0.027503	NA	NA	NA
c11569_g2_i2	-1.29803	7.161651	0.001565	0.027503	NA	UniRef90_K5W0U6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W0U6_PHACS	NA
c11572_g1_i1	-2.15533	7.238583	1.96E-05	0.00095	NA	NA	NA
c11572_g2_i1	-1.62113	5.912364	0.00028	0.007728	NA	UniRef90_K5WFU1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFU1_PHACS	NA
c11572_g3_i1	-1.48018	7.225257	0.000912	0.018761	RecName: Full=Repressor ROX1; AltName: Full=Heme-dependent repression factor; AltName: Full=Hypoxic function repressor [Saccharomyces cerevisiae S288c]	UniRef90_K5WFU1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFU1_PHACS	NA
c11584_g1_i1	-2.52823	8.223349	6.74E-08	8.80E-06	NA	UniRef90_K5X5U8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X5U8_PHACS	GO:0015035
c11584_g2_i1	-1.70179	8.013314	6.02E-05	0.00226	RecName: Full=Protein sfk1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5W2X3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2X3_PHACS	GO:0015035
c11587_g1_i1	-1.43339	5.965053	0.000199	0.005903	NA	UniRef90_K5WEX5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEX5_PHACS	NA
c11626_g1_i1	-1.25741	7.96072	0.000985	0.019805	NA	NA	NA
c11626_g1_i2	-1.25741	7.96072	0.000985	0.019805	RecName: Full=Putative sterigmatocystin biosynthesis peroxidase stcC; Flags: Precursor [Aspergillus nidulans FGSC A4]	UniRef90_K5V3F8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V3F8_PHACS	GO:0004601
c1162_g1_i1	-2.50743	2.910874	1.66E-06	0.000125	RecName: Full=22.0 kDa heat shock protein; Short=AtHsp22.0; Flags: Precursor [Arabidopsis thaliana]	UniRef90_M2QM04 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2QM04_CERS8	NA

c11635_g1_i1	-1.69998	5.481667	6.95E-06	0.00041	RecName: Full=Uncharacterized zinc-type alcohol dehydrogenase-like protein YogA [Bacillus subtilis subsp. subtilis str. 168]	UniRef90_K5UYA9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UYA9_PHACS	GO:0008270|GO:0016491|GO:0055114
c11635_g1_i2	-1.69998	5.481667	6.95E-06	0.00041	NA	NA	GO:0008270|GO:0016491|GO:0055114
c11635_g2_i1	-1.79046	2.64442	0.000114	0.003765	NA	UniRef90_K5UYA9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UYA9_PHACS	NA
c11643_g1_i1	-1.48758	7.673636	0.001066	0.020973	RecName: Full=Carboxypeptidase S; AltName: Full=GLY-X carboxypeptidase; AltName: Full=YSCS [Saccharomyces cerevisiae S288c]	UniRef90_K5VT85 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VT85_PHACS	GO:0008152|GO:0016787
c11664_g2_i1	-1.32506	5.428518	0.000768	0.016452	NA	NA	GO:0000413|GO:0003755|GO:0006457
c11664_g2_i2	-1.32506	5.428518	0.000768	0.016452	RecName: Full=Peptidyl-prolyl cis-trans isomerase A; Short=PPIase A; AltName: Full=Cyclophilin ScCypA; AltName: Full=Cyclophilin homolog; AltName: Full=Rotamase A [Streptomyces anulatus]	UniRef90_K5WDP7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDP7_PHACS	GO:0000413|GO:0003755|GO:0006457
c11664_g2_i3	-1.32506	5.428518	0.000768	0.016452	NA	NA	GO:0000413|GO:0003755|GO:0006457
c11664_g2_i4	-1.32506	5.428518	0.000768	0.016452	NA	NA	GO:0000413|GO:0003755|GO:0006457
c11667_g1_i1	-1.24085	3.918621	0.001253	0.023578	NA	UniRef90_G5EJU5 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJU5_PHACH	NA
c11673_g1_i1	-1.59071	5.596875	7.48E-05	0.002684	NA	NA	NA
c11673_g1_i2	-1.59071	5.596875	7.48E-05	0.002684	NA	NA	NA
c11673_g1_i3	-1.59071	5.596875	7.48E-05	0.002684	NA	NA	NA
c11673_g1_i4	-1.59071	5.596875	7.48E-05	0.002684	NA	NA	NA
c11673_g1_i5	-1.59071	5.596875	7.48E-05	0.002684	NA	UniRef90_K5VXL5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXL5_PHACS	NA

c11713_g1_i1	-1.25661	7.442527	0.003158	0.04553	RecName: Full=D-galacturonate reductase; AltName: Full=D-galacturonic acid reductase [Trichoderma reesei]	UniRef90_A0A0C3S751 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S751_PHLGI	NA
c11717_g1_i1	-1.98754	8.754063	5.98E-05	0.002253	NA	UniRef90_A0A0C3S008 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S008_PHLGI	NA
c11726_g1_i1	-1.84787	9.281547	0.00022	0.006434	RecName: Full=Alternative oxidase, mitochondrial; Flags: Precursor [Cryptococcus neoformans var. grubii H99]	UniRef90_K5WH20 Alternative oxidase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WH20_PHACS	GO:0009916|GO:0055114
c11746_g1_i1	-1.35104	6.90126	0.001095	0.021368	RecName: Full=Acyl-coenzyme A thioesterase 8; Short=Acyl-CoA thioesterase 8; AltName: Full=Choloyl-coenzyme A thioesterase; AltName: Full=Peroxisomal acyl-CoA thioesterase 2; Short=PTE-2; AltName: Full=Peroxisomal acyl-coenzyme A thioester hydrolase 1; Short=PTE-1; AltName: Full=Peroxisomal long-chain acyl-CoA thioesterase 1 [Rattus norvegicus]	UniRef90_K5WAB8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAB8_PHACS	NA
c11747_g1_i1	-2.31712	6.62	1.39E-06	0.000107	RecName: Full=Isonitrile hydratase; AltName: Full=Cyclohexyl-isocyanide hydratase [Pseudomonas putida]	UniRef90_K5VRW8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRW8_PHACS	NA
c11779_g1_i1	-1.96084	7.528293	3.34E-06	0.000226	NA	NA	NA
c11779_g1_i2	-1.96084	7.528293	3.34E-06	0.000226	NA	UniRef90_K5UUN6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UUN6_PHACS	NA
c11779_g1_i3	-1.96084	7.528293	3.34E-06	0.000226	NA	NA	NA
c11790_g2_i1	-3.83289	4.106314	1.48E-16	1.34E-13	RecName: Full=Malate synthase, glyoxysomal; AltName: Full=Acetate utilization protein 9 [Neurospora crassa OR74A]	UniRef90_A0A060SX45 Uncharacterized protein n=3 Tax=Polyporales RepID=A0A060SX45_PYCCI	GO:0004474|GO:0006097
c11790_g3_i1	-5.63435	3.992338	3.27E-18	4.69E-15	RecName: Full=Malate synthase 1, glyoxysomal [Saccharomyces cerevisiae S288c]	UniRef90_A0A0C3S5Z8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S5Z8_PHLGI	GO:0004474|GO:0006097

c11790_g4_i1	-1.36433	8.199754	0.002977	0.043509	RecName: Full=Malate synthase, glyoxysomal [Aspergillus nidulans FGSC A4]	UniRef90_K5VRR7 Malate synthase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRR7_PHACS	GO:0004474|GO:0006097
c11809_g1_i1	-1.34912	3.205673	0.001503	0.026795	NA	NA	NA
c11809_g1_i2	-1.34912	3.205673	0.001503	0.026795	NA	UniRef90_A0A0C2T0V9 Uncharacterized protein n=1 Tax=Amanita muscaria Koide BX008 RepID=A0A0C2T0V9_AMAMU	NA
c11809_g1_i3	-1.34912	3.205673	0.001503	0.026795	NA	NA	NA
c11809_g1_i4	-1.34912	3.205673	0.001503	0.026795	NA	NA	NA
c11809_g2_i1	-1.43718	4.17364	0.001377	0.025268	NA	UniRef90_A0A0C3P9R0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P9R0_PHLGI	NA
c11809_g2_i2	-1.43718	4.17364	0.001377	0.025268	NA	NA	NA
c11833_g1_i1	-2.00566	8.26643	3.77E-05	0.001586	NA	UniRef90_K5W628 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W628_PHACS	NA
c11837_g1_i1	-1.53915	5.021158	8.79E-05	0.003085	NA	NA	NA
c11837_g1_i2	-1.53915	5.021158	8.79E-05	0.003085	NA	NA	NA
c11862_g1_i1	-1.28803	4.544813	0.003215	0.04606	NA	UniRef90_K5XAR0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XAR0_PHACS	NA
c11864_g2_i1	-1.34876	4.517678	0.000587	0.013502	NA	NA	GO:0004659|GO:0016021
c11864_g2_i2	-1.34876	4.517678	0.000587	0.013502	RecName: Full=4-hydroxybenzoate polyprenyltransferase, mitochondrial; AltName: Full=Coenzyme Q biosynthesis protein 2; AltName: Full=Para-hydroxybenzoate--polyprenyltransferase; Short=PHB:polyprenyltransferase; Flags: Precursor [Drosophila pseudoobscura pseudoobscura]	UniRef90_K5WJ58 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJ58_PHACS	GO:0004659|GO:0016021
c11864_g3_i1	-1.47906	4.01657	0.000231	0.00663	RecName: Full=4-hydroxybenzoate polyprenyltransferase, mitochondrial; AltName: Full=Para-hydroxybenzoate--	UniRef90_A0A0C3S7U4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S7U4_PHLGI	NA

					polyprenyltransferase; Short=PHB:polyprenyltransferase; Flags: Precursor [Caenorhabditis elegans]		
c11864_g6_i1	-4.31245	1.907403	5.75E-10	1.30E-07	NA	NA	NA
c11868_g1_i1	-1.21403	3.10317	0.003007	0.043829	RecName: Full=Acyl-CoA desaturase; AltName: Full=Delta(9)-desaturase; Short=Delta-9 desaturase; AltName: Full=Fatty acid desaturase; AltName: Full=Stearoyl-CoA desaturase [Histoplasma capsulatum]	UniRef90_D4Q8S7 Delta9-fatty acid desaturase n=1 Tax=Phanerochaete chrysosporium RepID=D4Q8S7_PHACH	GO:0006629
c11872_g1_i1	-1.69282	2.596069	0.0018	0.030531	NA	UniRef90_K5WFG9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WFG9_PHACS	NA
c11881_g1_i1	-2.1898	4.727846	3.97E-06	0.000258	RecName: Full=Uncharacterized beta-glucan synthesis-associated protein C23H3.11c [Schizosaccharomyces pombe 972h-]	UniRef90_K5XDN4 Glycoside hydrolase family 16 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XDN4_PHACS	NA
c11881_g2_i1	-2.18589	1.967925	6.88E-05	0.002502	NA	UniRef90_UPI00046213DA glycoside hydrolase family 16 protein n=1 Tax=Trametes versicolor (strain FP-101664) RepID=UPI00046213DA	NA
c11902_g1_i1	-1.44139	7.41623	0.000617	0.014045	NA	UniRef90_K5W5T4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5T4_PHACS	NA
c11910_g1_i1	-1.42442	3.154764	0.002632	0.039859	NA	UniRef90_K5UTG6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UTG6_PHACS	NA
c11910_g1_i2	-1.42442	3.154764	0.002632	0.039859	NA	NA	NA
c11910_g1_i3	-1.42442	3.154764	0.002632	0.039859	NA	NA	NA
c11910_g1_i4	-1.42442	3.154764	0.002632	0.039859	NA	NA	NA
c11922_g1_i1	-1.81818	9.155384	0.001347	0.02483	RecName: Full=Glutathione S-transferase 2; AltName: Full=GST-II [Schizosaccharomyces pombe 972h-]	UniRef90_K5WTL8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WTL8_PHACS	GO:0005515
c11923_g1_i1	-1.70908	7.711829	0.001105	0.021497	NA	NA	NA

c11937_g1_i1	-1.49849	7.599264	0.000849	0.017839	NA	UniRef90_A0A0C3SFA1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SFA1_PHLGI	NA
c11958_g1_i1	-1.3791	6.712502	0.000706	0.01562	NA	NA	NA
c11958_g1_i2	-1.3791	6.712502	0.000706	0.01562	NA	UniRef90_K5WVW2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WVW2_PHACS	GO:0003700|GO:0006355|GO:0043565
c11962_g1_i1	-1.32954	5.574593	0.001454	0.026108	RecName: Full=N-alpha-acetyltransferase 30; AltName: Full=N-terminal acetyltransferase C complex catalytic subunit mak3 homolog; AltName: Full=NatC catalytic subunit [Schizosaccharomyces pombe 972h-]	UniRef90_K5URW0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5URW0_PHACS	GO:0008080|GO:0016747
c11962_g1_i2	-1.32954	5.574593	0.001454	0.026108	NA	NA	GO:0008080|GO:0016747
c11969_g1_i1	-3.01894	4.11881	7.96E-07	6.87E-05	NA	UniRef90_K5X9S1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X9S1_PHACS	NA
c11969_g2_i1	-2.06496	4.559712	0.000274	0.007603	NA	UniRef90_K5X9S1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X9S1_PHACS	NA
c11970_g1_i1	-1.38962	3.043516	0.003174	0.045582	NA	NA	NA
c12023_g1_i1	-2.36251	7.87185	3.94E-08	5.49E-06	RecName: Full=Riboflavin transporter MCH5 [Saccharomyces cerevisiae S288c]	UniRef90_K5WXA5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WXA5_PHACS	GO:0016021|GO:0055085
c12030_g1_i1	-1.28256	5.379676	0.001852	0.03098	NA	NA	NA
c12030_g1_i2	-1.28256	5.379676	0.001852	0.03098	NA	UniRef90_K5WJ17 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WJ17_PHACS	NA
c12033_g1_i1	-1.39071	6.871304	0.000635	0.014406	NA	NA	NA
c12033_g1_i2	-1.39071	6.871304	0.000635	0.014406	RecName: Full=Mitochondrial oxaloacetate transport protein [Schizosaccharomyces pombe 972h-]	UniRef90_K5WQ45 Uncharacterized protein n=2 Tax=Phanerochaetaceae RepID=K5WQ45_PHACS	NA

c12079_g1_i1	-2.19411	9.224326	5.36E-05	0.002067	RecName: Full=Putative NADPH dehydrogenase C23G7.10c; AltName: Full=Old yellow enzyme homolog 3 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V5X6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V5X6_PHACS	GO:0010181|GO:0016491|GO:0055114
c12079_g2_i1	-2.43036	8.158302	1.61E-05	0.000833	RecName: Full=Putative NADPH dehydrogenase C23G7.10c; AltName: Full=Old yellow enzyme homolog 3 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V5X6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V5X6_PHACS	GO:0010181|GO:0016491|GO:0055114
c12112_g1_i1	-2.18778	4.853722	2.10E-06	0.000152	NA	NA	NA
c12112_g1_i2	-2.18778	4.853722	2.10E-06	0.000152	NA	NA	NA
c12115_g1_i1	-1.58623	6.120921	0.000177	0.005352	NA	NA	NA
c12115_g1_i2	-1.58623	6.120921	0.000177	0.005352	NA	UniRef90_K5VLN5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VLN5_PHACS	NA
c12115_g2_i1	-1.5841	4.023422	0.000215	0.00631	NA	NA	NA
c12154_g1_i1	-2.1822	11.84148	0.002323	0.036346	RecName: Full=Glucose transport transcription regulator RGT1; AltName: Full=Restores glucose transport protein 1 [Lachancea thermotolerans CBS 6340]	UniRef90_K5XAH8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XAH8_PHACS	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c12161_g2_i1	-2.74442	2.600163	2.87E-05	0.00127	NA	UniRef90_A0A0C3PGX4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PGX4_PHLGI	NA
c12164_g1_i1	-1.37435	6.953071	0.001857	0.031021	NA	NA	GO:0005779|GO:0016559
c12164_g1_i2	-1.37435	6.953071	0.001857	0.031021	RecName: Full=Peroxisomal membrane protein PMP30A; AltName: Full=Peroxin-11A; AltName: Full=Peroxisomal membrane protein PMP31 [Candida boidinii]	UniRef90_K5WAH7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAH7_PHACS	GO:0005779|GO:0016559
c12164_g1_i3	-1.37435	6.953071	0.001857	0.031021	NA	NA	GO:0005779|GO:0016559
c12168_g1_i1	-1.20909	5.882624	0.001779	0.030269	NA	UniRef90_K5X581 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X581_PHACS	NA

c12173_g1_i1	-1.08462	5.591771	0.002316	0.036295	RecName: Full=Peptidyl-prolyl cis-trans isomerase D; Short=PPIase D; AltName: Full=Rotamase D [Amanita muscaria]	UniRef90_K5WE68 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WE68_PHACS	GO:0000413|GO:0003755|GO:0006457
c12190_g1_i1	-1.54299	3.960847	0.000374	0.00957	NA	NA	NA
c12190_g1_i2	-1.54299	3.960847	0.000374	0.00957	NA	NA	NA
c12190_g1_i3	-1.54299	3.960847	0.000374	0.00957	NA	NA	NA
c12210_g1_i1	-4.1841	4.694523	4.29E-06	0.000275	RecName: Full=Bifunctional epoxide hydrolase 2; Includes: RecName: Full=Cytosolic epoxide hydrolase 2; Short=CEH; AltName: Full=Epoxide hydratase; AltName: Full=Soluble epoxide hydrolase; Short=SEH; Includes: RecName: Full=Lipid-phosphate phosphatase [Mus musculus]	UniRef90_K5W403 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W403_PHACS	NA
c12222_g1_i1	-1.46566	4.318285	0.000279	0.007702	NA	NA	NA
c12222_g1_i2	-1.46566	4.318285	0.000279	0.007702	NA	NA	NA
c12222_g2_i1	-1.69186	4.31597	7.46E-05	0.002681	NA	NA	NA
c12222_g2_i2	-1.69186	4.31597	7.46E-05	0.002681	NA	NA	NA
c12222_g2_i3	-1.69186	4.31597	7.46E-05	0.002681	NA	NA	NA
c12309_g1_i1	-2.03692	6.961408	0.00056	0.013058	RecName: Full=Polyamine oxidase; Flags: Precursor [Zea mays]	UniRef90_A0A0C3NVL8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NVL8_PHLGI	GO:0016491|GO:0055114
c12309_g2_i1	-2.07084	4.099112	3.82E-05	0.001594	NA	UniRef90_K5VM77 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VM77_PHACS	GO:0016491|GO:0055114
c12316_g1_i1	-1.73291	7.012362	1.10E-05	0.000605	NA	NA	NA
c12316_g1_i2	-1.73291	7.012362	1.10E-05	0.000605	NA	NA	NA
c12377_g1_i1	-1.74922	4.891112	2.59E-05	0.001186	NA	UniRef90_K5VRS8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRS8_PHACS	NA
c12377_g1_i2	-1.74922	4.891112	2.59E-05	0.001186	NA	NA	NA
c12377_g1_i3	-1.74922	4.891112	2.59E-05	0.001186	NA	NA	NA
c12380_g1_i1	-1.063	4.358822	0.003165	0.045563	NA	NA	GO:0005509

c12380_g1_i2	-1.063	4.358822	0.003165	0.045563	RecName: Full=Myosin regulatory light chain 2, smooth muscle minor isoform; Short=MLC-2; AltName: Full=DTNB; AltName: Full=G1; AltName: Full=Isoform L20-B1 [Gallus gallus]	UniRef90_A0A0C3SFB4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SFB4_PHLGI	GO:0005509
c12385_g1_i1	-1.61297	5.518357	0.000179	0.0054	NA	UniRef90_A0A067SAC0 Uncharacterized protein n=1 Tax=Galerina marginata CBS 339.88 RepID=A0A067SAC0_9AGAR	NA
c12385_g1_i2	-1.61297	5.518357	0.000179	0.0054	NA	NA	NA
c12401_g1_i1	-1.38192	5.747647	0.001152	0.022208	RecName: Full=Lactam utilization protein lamB [Aspergillus nidulans FGSC A4]	UniRef90_UPI00046230B7 lactam utilization protein lamb n=1 Tax=Trametes versicolor (strain FP-101664) RepID=UPI00046230B7	NA
c12405_g1_i1	-1.28908	6.962613	0.00332	0.047066	NA	NA	GO:0016021
c12405_g1_i2	-1.28908	6.962613	0.00332	0.047066	RecName: Full=Uncharacterized TLC domain-containing protein C17A2.02c [Schizosaccharomyces pombe 972h-]	UniRef90_K5UY74 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UY74_PHACS	GO:0016021
c12409_g2_i1	-1.12099	4.958401	0.003027	0.044043	NA	NA	NA
c12409_g2_i2	-1.12099	4.958401	0.003027	0.044043	NA	UniRef90_K5V9Q9 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V9Q9_PHACS	NA
c12409_g2_i3	-1.12099	4.958401	0.003027	0.044043	NA	NA	NA
c12439_g1_i1	-3.134	4.178191	7.85E-06	0.000453	RecName: Full=Bifunctional epoxide hydrolase 2; Includes: RecName: Full=Cytosolic epoxide hydrolase 2; Short=CEH; AltName: Full=Epoxide hydratase; AltName: Full=Soluble epoxide hydrolase; Short=SEH; Includes: RecName: Full=Lipid-phosphate phosphatase [Rattus norvegicus]	UniRef90_K5WTB3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WTB3_PHACS	NA
c12439_g1_i2	-3.134	4.178191	7.85E-06	0.000453	NA	NA	NA
c12444_g1_i1	-2.87444	4.666017	8.72E-07	7.31E-05	NA	NA	NA
c12444_g1_i2	-2.87444	4.666017	8.72E-07	7.31E-05	NA	NA	NA

c12444_g1_i3	-2.87444	4.666017	8.72E-07	7.31E-05	NA	UniRef90_K5VMM1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VMM1_PHACS	NA
c12444_g1_i4	-2.87444	4.666017	8.72E-07	7.31E-05	NA	NA	NA
c12444_g1_i5	-2.87444	4.666017	8.72E-07	7.31E-05	NA	NA	NA
c12447_g2_i1	-1.54703	8.70384	0.002041	0.032991	NA	UniRef90_K5W2L9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2L9_PHACS	NA
c12447_g3_i1	-1.75385	6.099617	0.000957	0.019379	NA	UniRef90_K5W2L9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2L9_PHACS	NA
c12458_g2_i1	-1.65554	7.594732	9.54E-05	0.003277	NA	UniRef90_K5VZG6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZG6_PHACS	NA
c12483_g1_i1	-2.26859	7.653752	0.000109	0.003615	RecName: Full=Cytochrome b5 [Candida tropicalis]	UniRef90_K5WEN8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEN8_PHACS	GO:0003995|GO:0008152|GO:0016627|GO:0020037|GO:0050660|GO:0055114
c12483_g2_i1	-2.22827	7.640716	5.37E-05	0.002069	RecName: Full=Isovaleryl-CoA dehydrogenase, mitochondrial; Short=IVD; Flags: Precursor [Pongo abelii]	UniRef90_K5WEN8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEN8_PHACS	GO:0003995|GO:0016627|GO:0055114
c12557_g1_i1	-2.702	7.707252	1.25E-06	9.79E-05	RecName: Full=Apoptosis-inducing factor homolog B [Dictyostelium discoideum]	UniRef90_K5WF02 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WF02_PHACS	GO:0016491|GO:0050660|GO:0055114
c12594_g1_i1	-1.90062	7.223409	6.66E-05	0.002448	NA	UniRef90_K5W2N9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2N9_PHACS	NA
c12612_g1_i1	-1.57515	6.347964	6.68E-05	0.002448	NA	NA	NA
c12612_g1_i2	-1.57515	6.347964	6.68E-05	0.002448	RecName: Full=Ribonucleases P/MRP protein subunit pop3; AltName: Full=RNA-processing protein pop3 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WEW0 Uncharacterized protein (Fragment) n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEW0_PHACS	NA

c12713_g1_i1	-1.23083	7.240512	0.002439	0.037681	RecName: Full=Lon protease homolog 2, peroxisomal [Yarrowia lipolytica CLIB122]	UniRef90_K5WQT3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQT3_PHACS	GO:0004176|GO:0004252|GO:0005524|GO:0006508|GO:0016887
c12726_g1_i1	-1.82257	2.57434	0.000154	0.004785	NA	NA	NA
c12763_g4_i1	-1.34889	5.760076	0.002209	0.034945	RecName: Full=F-box/LRR-repeat protein 7; AltName: Full=F-box and leucine-rich repeat protein 7 [Mus musculus]	UniRef90_K5W726 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W726_PHACS	GO:0005515
c12763_g4_i2	-1.34889	5.760076	0.002209	0.034945	NA	NA	NA
c12766_g1_i1	-1.68666	3.693755	0.00096	0.019383	NA	NA	NA
c12766_g1_i2	-1.68666	3.693755	0.00096	0.019383	NA	UniRef90_K5VQY5 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VQY5_PHACS	GO:0005525
c12766_g1_i3	-1.68666	3.693755	0.00096	0.019383	NA	NA	NA
c12790_g1_i1	-4.26619	2.661518	1.36E-06	0.000106	RecName: Full=NADPH-dependent aldehyde reductase ARI1 [Saccharomyces cerevisiae S288c]	UniRef90_K5WQA8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQA8_PHACS	NA
c12790_g2_i1	-4.01741	4.351949	4.05E-08	5.59E-06	RecName: Full=Putative uncharacterized oxidoreductase C513.07 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WQA8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQA8_PHACS	GO:0003824|GO:0003854|GO:0006694|GO:0008152|GO:0016491|GO:0016616|GO:0050662|GO:0055114
c12790_g3_i1	-3.19136	6.956623	3.80E-11	1.09E-08	RecName: Full=NADPH-dependent methylglyoxal reductase GRE2; AltName: Full=3-methylbutanal reductase; AltName: Full=Genes de respuesta a estres protein 2; AltName: Full=Isovaleraldehyde reductase [Saccharomyces cerevisiae S288c]	UniRef90_K5X254 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X254_PHACS	GO:0003824|GO:0003854|GO:0006694|GO:0016616|GO:0050662|GO:0055114
c12800_g1_i1	-1.72638	6.013475	0.000144	0.004511	NA	UniRef90_K5VT30 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VT30_PHACS	NA
c12805_g1_i1	-1.35787	4.876668	0.001861	0.031037	NA	NA	NA

c12805_g1_i2	-1.35787	4.876668	0.001861	0.031037	RecName: Full=Putative epoxide hydrolase; AltName: Full=Epoxide hydratase; Flags: Precursor [Stigmatella aurantiaca DW4/3-1]	UniRef90_K5UHX8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UHX8_PHACS	NA
c12805_g2_i1	-1.65449	2.750302	0.000328	0.008726	RecName: Full=Putative epoxide hydrolase; AltName: Full=Epoxide hydratase; Flags: Precursor [Stigmatella aurantiaca DW4/3-1]	UniRef90_K5UHX8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UHX8_PHACS	NA
c12816_g1_i1	-2.46436	5.102301	3.50E-08	4.99E-06	NA	UniRef90_A0A067ML79 Uncharacterized protein n=1 Tax=Botryobasidium botryosum FD-172 SS1 RepID=A0A067ML79_9HOMO	NA
c12816_g1_i2	-2.46436	5.102301	3.50E-08	4.99E-06	NA	NA	NA
c12816_g1_i3	-2.46436	5.102301	3.50E-08	4.99E-06	NA	NA	NA
c12847_g1_i1	-1.84867	8.088959	9.08E-06	0.000513	NA	NA	NA
c12847_g1_i2	-1.84867	8.088959	9.08E-06	0.000513	NA	NA	GO:0016021|GO:0022857|GO:0055085
c12847_g1_i3	-1.84867	8.088959	9.08E-06	0.000513	RecName: Full=Uncharacterized transporter C3H1.06c [Schizosaccharomyces pombe 972h-]	UniRef90_K5W905 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W905_PHACS	GO:0016021|GO:0055085
c12848_g2_i1	-4.03014	0.715595	9.53E-05	0.003277	NA	NA	NA
c12854_g1_i1	-2.14991	7.311845	1.84E-05	0.000912	RecName: Full=Uncharacterized protein YBR096W [Saccharomyces cerevisiae S288c]	UniRef90_K5W1E2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1E2_PHACS	NA
c12854_g1_i2	-2.14991	7.311845	1.84E-05	0.000912	NA	NA	NA
c12887_g1_i1	-2.43603	6.143032	6.48E-06	0.000389	RecName: Full=Cytochrome P450 67; AltName: Full=CYPLXVII; AltName: Full=Planta-induced rust protein 16, partial [Uromyces viciae-fabae]	UniRef90_Q2VR01 High nitrogen upregulated cytochrome P450 monooxygenase 1 n=1 Tax=Phanerochaete chrysosporium RepID=Q2VR01_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12887_g2_i1	-3.58204	4.821175	2.20E-08	3.39E-06	RecName: Full=Tryprostatin B 6-hydroxylase; AltName: Full=Fumitremorgin biosynthesis protein C [Neosartorya fischeri NRRL 181]	UniRef90_Q2VR01 High nitrogen upregulated cytochrome P450 monooxygenase 1 n=1 Tax=Phanerochaete chrysosporium RepID=Q2VR01_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c12926_g1_i1	-1.21927	6.40708	0.001211	0.022961	NA	UniRef90_A0A060SNZ4 Uncharacterized protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060SNZ4_PYCCI	NA

c12947_g1_i1	-1.40181	7.698467	0.001844	0.03098	RecName: Full=Aspartate--tRNA ligase, cytoplasmic; AltName: Full=Aspartyl-tRNA synthetase; Short=AspRS; AltName: Full=Cell proliferation-inducing gene 40 protein [Homo sapiens]	UniRef90_K5VZ77 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZ77_PHACS	GO:0000166|GO:0004812|GO:0005524|GO:0006418
c12950_g1_i1	-1.49913	3.188886	0.001631	0.028405	NA	NA	NA
c12957_g1_i1	-2.48733	11.64801	8.85E-08	1.08E-05	RecName: Full=Protein FDD123; AltName: Full=CvHSP30/1 [Trametes versicolor]	UniRef90_K5UZK2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UZK2_PHACS	GO:0016020
c12979_g1_i1	-3.35419	10.29199	1.06E-11	3.41E-09	NA	UniRef90_K5VXJ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXJ5_PHACS	NA
c12979_g2_i1	-3.61854	9.91591	4.67E-12	1.54E-09	NA	UniRef90_K5VXJ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXJ5_PHACS	NA
c12998_g2_i1	-2.0686	8.178835	7.60E-05	0.002715	NA	UniRef90_K5VYE7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VYE7_PHACS	NA
c13018_g1_i1	-2.01219	6.319846	1.22E-06	9.66E-05	RecName: Full=Uncharacterized WD repeat-containing protein C126.01c [Schizosaccharomyces pombe 972h-]	UniRef90_A0A060S8T6 Uncharacterized protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060S8T6_PYCCI	GO:0005515|GO:0018580|GO:0055114
c13018_g2_i1	-1.73432	6.350392	0.001798	0.030515	RecName: Full=Putative monooxygenase Rv1533 [Mycobacterium tuberculosis H37Rv]	UniRef90_K5WYP1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYP1_PHACS	GO:0018580|GO:0055114
c13019_g1_i1	-1.80124	3.583997	3.44E-06	0.000231	NA	UniRef90_K5WSY2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WSY2_PHACS	NA
c13019_g1_i2	-1.80124	3.583997	3.44E-06	0.000231	NA	NA	NA
c13020_g1_i1	-2.03002	4.080546	0.000945	0.01917	NA	UniRef90_K5V427 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V427_PHACS	GO:0005515

c13020_g2_i1	-2.09498	5.077353	0.000514	0.012249	NA	UniRef90_K5V427 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V427_PHACS	NA
c13060_g1_i1	-1.11934	5.302358	0.001596	0.027947	RecName: Full=External alternative NAD(P)H-ubiquinone oxidoreductase B1, mitochondrial; AltName: Full=External alternative NADH dehydrogenase NDB1; AltName: Full=NADH:ubiquinone reductase (non-electrogenic) NDB1; Flags: Precursor [Solanum tuberosum]	UniRef90_K5W804 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W804_PHACS	GO:0005509
c13068_g1_i1	-1.79176	8.754396	6.61E-05	0.002437	NA	NA	NA
c13068_g1_i2	-1.79176	8.754396	6.61E-05	0.002437	RecName: Full=Perilipin-2; AltName: Full=Adipophilin; AltName: Full=Adipose differentiation-related protein; Short=ADRP [Mus musculus]	UniRef90_K5W2Q7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2Q7_PHACS	NA
c13097_g1_i1	-1.46752	7.713662	0.002954	0.04331	RecName: Full=Putative aryl-alcohol dehydrogenase C977.14c [Schizosaccharomyces pombe 972h-]	UniRef90_K5VWF0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWF0_PHACS	NA
c13105_g1_i1	-1.98848	2.521654	8.71E-05	0.003059	NA	NA	NA
c13105_g1_i2	-1.98848	2.521654	8.71E-05	0.003059	NA	NA	NA
c13105_g1_i3	-1.98848	2.521654	8.71E-05	0.003059	NA	NA	NA
c13105_g1_i4	-1.98848	2.521654	8.71E-05	0.003059	NA	NA	NA
c13105_g1_i5	-1.98848	2.521654	8.71E-05	0.003059	NA	NA	NA
c13110_g2_i1	-2.36567	5.334962	1.05E-08	1.77E-06	NA	UniRef90_A0A0C3SAQ2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SAQ2_PHLGI	NA
c13110_g3_i1	-2.41665	5.781079	3.76E-08	5.33E-06	RecName: Full=Putative fungistatic metabolite [Chaetomium globosum CBS 148.51]	UniRef90_K5W1G4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1G4_PHACS	NA
c13110_g4_i1	-4.01867	3.65376	2.78E-09	5.73E-07	NA	UniRef90_A0A0C3SAQ2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SAQ2_PHLGI	NA

c13127_g1_i1	-1.68315	9.349037	0.000265	0.007416	RecName: Full=Ribulose-phosphate 3-epimerase; AltName: Full=Pentose-5-phosphate 3-epimerase; Short=PPE; AltName: Full=RPE [Candida glabrata CBS 138]	UniRef90_UPI0004413375 Ribulose-phosphate 3-epimerase n=2 Tax=Polyporales RepID=UPI0004413375	GO:0004129|GO:0005743|GO:0005751|GO:0005975|GO:0016857
c13134_g2_i1	-1.48028	1.907582	0.00309	0.044685	NA	NA	NA
c1313_g1_i1	-1.79683	4.842051	4.20E-05	0.001719	NA	NA	NA
c1313_g1_i2	-1.79683	4.842051	4.20E-05	0.001719	NA	NA	NA
c13150_g1_i1	-1.3752	11.53643	0.001113	0.021589	NA	UniRef90_K5WNV9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNV9_PHACS	NA
c13150_g2_i1	-1.70407	8.543994	4.19E-05	0.001718	NA	NA	NA
c13163_g1_i1	-1.48776	4.73429	0.000758	0.016312	NA	NA	NA
c13163_g1_i2	-1.48776	4.73429	0.000758	0.016312	NA	NA	NA
c13175_g1_i1	-1.71358	4.164132	3.97E-05	0.001638	NA	NA	GO:0016491|GO:0055114
c13175_g1_i2	-1.71358	4.164132	3.97E-05	0.001638	RecName: Full=Ferric reductase transmembrane component 3; AltName: Full=Ferric-chelate reductase 3; Flags: Precursor [Saccharomyces cerevisiae S288c]	UniRef90_K5WEH9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEH9_PHACS	NA
c13175_g1_i3	-1.71358	4.164132	3.97E-05	0.001638	NA	NA	GO:0016491|GO:0055114
c13179_g1_i1	-3.79701	5.878647	8.75E-17	8.75E-14	NA	UniRef90_K5WL10 Glycoside hydrolase family 79 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WL10_PHACS	NA
c13179_g2_i1	-3.27984	6.170118	7.32E-11	2.06E-08	NA	UniRef90_K5WL10 Glycoside hydrolase family 79 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WL10_PHACS	NA
c13179_g3_i1	-3.34801	5.399242	4.94E-15	3.76E-12	NA	UniRef90_K5WL10 Glycoside hydrolase family 79 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WL10_PHACS	NA

c13206_g4_i1	-1.46533	4.157676	0.00054	0.012717	RecName: Full=Beta-mannosidase A; AltName: Full=Mannanase A; Short=Mannase A; Flags: Precursor [Aspergillus terreus NIH2624]	UniRef90_K5W7F1 Glycoside hydrolase family 2 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W7F1_PHACS	NA
c13217_g1_i1	-1.65886	7.072731	0.00061	0.013911	RecName: Full=Citrate synthase [Dictyostelium discoideum]	UniRef90_K5X696 Citrate synthase (unknown stereospecificity) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X696_PHACS	GO:0044262|GO:0046912
c13259_g1_i1	-2.03567	4.477837	2.77E-07	2.88E-05	NA	UniRef90_K5WQC4 Glycosyltransferase family 69 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQC4_PHACS	NA
c13259_g2_i1	-2.04624	4.292725	1.11E-07	1.32E-05	NA	UniRef90_K5WQC4 Glycosyltransferase family 69 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQC4_PHACS	NA
c13259_g3_i1	-1.85003	3.131138	0.000138	0.004399	NA	NA	NA
c13259_g3_i2	-1.85003	3.131138	0.000138	0.004399	NA	UniRef90_S8FCW3 Uncharacterized protein n=1 Tax=Fomitopsis pinicola (strain FP-58527) RepID=S8FCW3_FOMPI	NA
c13264_g1_i1	-2.13515	5.952013	5.46E-06	0.00034	RecName: Full=Uncharacterized WD repeat-containing protein C25H1.08c [Schizosaccharomyces pombe 972h-]	UniRef90_K5WGW4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGW4_PHACS	GO:0005515
c13302_g1_i1	-1.45391	7.141008	0.001317	0.024471	NA	NA	NA
c13302_g1_i2	-1.45391	7.141008	0.001317	0.024471	RecName: Full=Uncharacterized protein C17A5.05c [Schizosaccharomyces pombe 972h-]	UniRef90_K5UP44 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UP44_PHACS	NA
c13303_g2_i1	-1.4239	3.616252	0.000631	0.014332	NA	UniRef90_K5VKF4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VKF4_PHACS	NA
c13332_g2_i1	-1.45645	3.568069	0.000161	0.004966	NA	NA	NA
c13332_g2_i2	-1.45645	3.568069	0.000161	0.004966	NA	NA	NA

c13361_g3_i1	-1.10405	4.293931	0.003335	0.047253	RecName: Full=Alcohol dehydrogenase 1; AltName: Full=Alcohol dehydrogenase I; Short=ADH I [Zymomonas mobilis subsp. mobilis ZM4 = ATCC 31821]	UniRef90_C9W365 Alcohol dehydogenase n=1 Tax=Phanerochaete chrysosporium RepID=C9W365_PHACH	GO:0008270|GO:0016491|GO:0055114
c13366_g1_i1	-2.20034	5.141813	5.98E-06	0.000367	RecName: Full=Chitinase 4 [Candida albicans SC5314]	UniRef90_A0A0C3NM81 Glycoside hydrolase family 18 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NM81_PHLGI	GO:0004553|GO:0005975|GO:0035091
c13366_g2_i1	-2.92394	2.800462	1.92E-06	0.000141	RecName: Full=Chitinase A1; Flags: Precursor [Bacillus circulans]	UniRef90_A0A0C3NM81 Glycoside hydrolase family 18 protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NM81_PHLGI	GO:0004553|GO:0005975
c13366_g2_i2	-2.92394	2.800462	1.92E-06	0.000141	NA	NA	GO:0004553|GO:0005975
c13395_g1_i1	-1.8075	2.228281	0.000767	0.016452	NA	NA	NA
c13399_g1_i1	-1.45178	4.138431	0.000671	0.015033	NA	UniRef90_K5VTC6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VTC6_PHACS	NA
c13404_g1_i1	-1.31337	5.397476	0.001047	0.0207	NA	UniRef90_A0A0C3NQ67 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NQ67_PHLGI	NA
c13459_g4_i1	-1.44855	5.053949	3.01E-05	0.001327	RecName: Full=Oligo-1,6-glucosidase; AltName: Full=Dextrin 6-alpha-D-glucanohydrolase; AltName: Full=Oligosaccharide alpha-1,6-glucosidase; AltName: Full=Sucrase-isomaltase; Short=Isomaltase [Geobacillus thermoglucosidasius]	UniRef90_K5WNG8 Glycoside hydrolase family 13 protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNG8_PHACS	NA
c13470_g1_i1	-2.05353	3.737351	0.000824	0.017498	NA	UniRef90_A0A0C3PPJ1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PPJ1_PHLGI	GO:0005515
c13492_g1_i1	-1.39901	4.556322	0.000103	0.003446	RecName: Full=Zinc-type alcohol dehydrogenase-like protein C2E1P3.01 [Schizosaccharomyces pombe 972h-]	UniRef90_K5V784 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V784_PHACS	GO:0016491|GO:0055114
c13492_g1_i2	-1.39901	4.556322	0.000103	0.003446	NA	NA	GO:0008270|GO:0016491|GO:0055114

c13497_g1_i1	-2.07258	4.21739	0.000102	0.003435	RecName: Full=Alpha-methylacyl-CoA racemase; AltName: Full=2-methylacyl-CoA racemase [Mus musculus]	UniRef90_K5VY83 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VY83_PHACS	NA
c13497_g2_i1	-1.96336	4.417928	0.001505	0.026813	RecName: Full=Alpha-methylacyl-CoA racemase; AltName: Full=2-methylacyl-CoA racemase [Homo sapiens]	UniRef90_K5VY83 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VY83_PHACS	GO:0003824
c13497_g2_i2	-1.96336	4.417928	0.001505	0.026813	NA	NA	GO:0003824
c13497_g2_i3	-1.96336	4.417928	0.001505	0.026813	NA	NA	GO:0003824
c13497_g2_i4	-1.96336	4.417928	0.001505	0.026813	NA	NA	GO:0003824
c13497_g2_i5	-1.96336	4.417928	0.001505	0.026813	NA	NA	GO:0003824
c13497_g2_i6	-1.96336	4.417928	0.001505	0.026813	NA	NA	GO:0003824
c13497_g2_i7	-1.96336	4.417928	0.001505	0.026813	NA	NA	GO:0003824
c13497_g2_i8	-1.96336	4.417928	0.001505	0.026813	NA	NA	GO:0003824
c13497_g3_i1	-2.51713	1.760098	9.85E-05	0.003355	NA	UniRef90_K5VY83 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VY83_PHACS	NA
c13521_g1_i1	-1.75251	7.170943	4.84E-05	0.001926	NA	NA	NA
c13521_g1_i2	-1.75251	7.170943	4.84E-05	0.001926	RecName: Full=Uncharacterized GTP-binding protein YjiA [Escherichia coli K-12]	UniRef90_K5WEZ0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEZ0_PHACS	NA
c13521_g1_i3	-1.75251	7.170943	4.84E-05	0.001926	NA	NA	NA
c13521_g1_i4	-1.75251	7.170943	4.84E-05	0.001926	NA	NA	NA
c13577_g1_i1	-4.2056	4.602791	4.10E-15	3.23E-12	RecName: Full=Enoyl reductase LovC [Aspergillus terreus]	UniRef90_K5WGV0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGV0_PHACS	GO:0008270|GO:0016491|GO:0055114
c13597_g1_i1	-1.57223	3.659722	6.72E-05	0.002455	NA	UniRef90_UPI000455E762 hypothetical protein CONPUDRAFT_69099 n=1 Tax=Coniophora puteana (strain RWD-64-598) RepID=UPI000455E762	NA
c13597_g1_i2	-1.57223	3.659722	6.72E-05	0.002455	NA	NA	NA
c13598_g1_i1	-2.18475	10.39607	6.15E-06	0.000372	NA	UniRef90_K5WUR8 Carbohydrate-binding module family 12 protein n=1	GO:0004553|GO:0005576|GO:0005975|GO:0030246

						Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WUR8_PHACS	
c13618_g7_i1	-2.25797	2.892191	0.002369	0.036953	NA	NA	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c13618_g7_i2	-2.25797	2.892191	0.002369	0.036953	RecName: Full=Ligninase LG5; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_Q9UW80 Lignin peroxidase n=1 Tax=Phanerochaete chrysosporium RepID=Q9UW80_PHACH	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c13665_g1_i1	-2.53548	4.890831	4.21E-07	4.16E-05	NA	NA	NA
c13665_g1_i2	-2.53548	4.890831	4.21E-07	4.16E-05	NA	NA	NA
c13665_g1_i3	-2.53548	4.890831	4.21E-07	4.16E-05	NA	NA	NA
c13665_g1_i4	-2.53548	4.890831	4.21E-07	4.16E-05	NA	UniRef90_A0A067SQW0 Uncharacterized protein n=1 Tax=Galerina marginata CBS 339.88 RepID=A0A067SQW0_9AGAR	NA
c13665_g1_i5	-2.53548	4.890831	4.21E-07	4.16E-05	NA	NA	NA
c13667_g2_i1	-1.58522	3.604939	0.000458	0.01118	RecName: Full=Bifunctional epoxide hydrolase 2; Includes: RecName: Full=Cytosolic epoxide hydrolase 2; Short=CEH; AltName: Full=Epoxide hydratase; AltName: Full=Soluble epoxide hydrolase; Short=SEH; Includes: RecName: Full=Lipid-phosphate phosphatase [Sus scrofa]	UniRef90_K5VL46 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VL46_PHACS	NA
c13720_g1_i1	-1.71115	4.403479	1.26E-05	0.000671	RecName: Full=Purine-cytosine permease fcyB; Short=PCP fcyB; AltName: Full=Cytosine/purine transport protein fcyB; AltName: Full=Fluorocytosine resistance protein fcyB [Aspergillus nidulans FGSC A4]	UniRef90_K5WBT1 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WBT1_PHACS	NA
c13720_g1_i2	-1.71115	4.403479	1.26E-05	0.000671	NA	NA	NA
c13720_g2_i1	-1.37684	5.571896	0.001182	0.022635	RecName: Full=Purine-cytosine permease FCY2; Short=PCP FCY2; AltName: Full=Cytosine/purine transport protein FCY2; AltName: Full=Fluorocytosine resistance protein 2 [Saccharomyces cerevisiae S288c]	UniRef90_K5WBT1 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WBT1_PHACS	GO:0015205|GO:0015851|GO:0016020

c13723_g1_i1	-1.69835	7.843686	0.000475	0.011534	RecName: Full=Uncharacterized MFS-type transporter C409.08 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VDZ9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VDZ9_PHACS	GO:0016021|GO:0055085
c13731_g1_i1	-1.7298	7.095168	6.81E-05	0.002481	NA	NA	NA
c13731_g1_i2	-1.7298	7.095168	6.81E-05	0.002481	RecName: Full=Acyl-coenzyme A thioesterase 9, mitochondrial; Short=Acyl-CoA thioesterase 9; AltName: Full=Acyl-CoA thioester hydrolase 9; Flags: Precursor [Bos taurus]	UniRef90_K5W128 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W128_PHACS	NA
c13745_g3_i1	-1.26272	5.884703	0.000724	0.015846	NA	UniRef90_K5V5B9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V5B9_PHACS	NA
c13747_g2_i1	-1.54596	6.323708	0.00223	0.035164	RecName: Full=Amino-acid permease BAT1; AltName: Full=Bidirectional amino acid transporter 1; AltName: Full=GABA permease; Short=AtGABP [Arabidopsis thaliana]	UniRef90_K5W831 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W831_PHACS	GO:0003333|GO:0015171|GO:0016020
c13747_g3_i1	-1.72655	6.257322	0.000465	0.011357	RecName: Full=Uncharacterized amino-acid permease C15C4.04c [Schizosaccharomyces pombe 972h-]	UniRef90_K5W831 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W831_PHACS	GO:0003333|GO:0006810|GO:0015171|GO:0016020|GO:0055085
c13749_g1_i1	-1.19562	4.700134	0.002054	0.033115	NA	NA	NA
c13749_g1_i2	-1.19562	4.700134	0.002054	0.033115	RecName: Full=Solute carrier family 25 member 38 homolog [Laccaria bicolor S238N-H82]	UniRef90_A0A0C3FHZ7 Uncharacterized protein n=1 Tax=Piloderma croceum F 1598 RepID=A0A0C3FHZ7_9HOMO	NA
c13763_g1_i1	-1.42332	4.799569	0.002849	0.042113	NA	NA	NA
c13763_g1_i2	-1.42332	4.799569	0.002849	0.042113	RecName: Full=Pentachlorophenol 4-monooxygenase; AltName: Full=Pentachlorophenol hydroxylase [Sphingobium chlorophenolicum]	UniRef90_K5WK99 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WK99_PHACS	NA
c13763_g2_i1	-1.99871	4.588401	3.29E-05	0.001418	NA	UniRef90_K5WK99 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WK99_PHACS	NA
c1376_g1_i1	-2.91239	0.566128	0.003024	0.044018	NA	NA	NA
c13773_g1_i1	-4.01267	0.705569	0.000944	0.01917	NA	NA	NA

c13780_g1_i1	-1.67573	2.994039	0.000251	0.007095	NA	UniRef90_A0A0C3S3W8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S3W8_PHLGI	NA
c13780_g1_i2	-1.67573	2.994039	0.000251	0.007095	NA	NA	NA
c13780_g2_i1	-3.17413	2.618323	2.07E-07	2.26E-05	NA	NA	NA
c13780_g2_i2	-3.17413	2.618323	2.07E-07	2.26E-05	NA	UniRef90_K5UQ30 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UQ30_PHACS	NA
c13780_g3_i1	-2.47984	4.307668	3.07E-06	0.000212	RecName: Full=Uncharacterized MFS-type transporter C409.08 [Schizosaccharomyces pombe 972h-]	UniRef90_K5UQ30 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UQ30_PHACS	GO:0016021|GO:0022857|GO:0055085
c13794_g1_i1	-1.47598	4.922977	0.000683	0.015237	RecName: Full=L-serine dehydratase/L-threonine deaminase; Short=SDH; AltName: Full=L-serine deaminase; AltName: Full=L-threonine dehydratase; Short=TDH [Homo sapiens]	UniRef90_K5WYY9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYY9_PHACS	NA
c13801_g2_i1	-3.89476	11.5297	2.29E-06	0.000164	RecName: Full=Ligninase LG5; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_P11543 Ligninase LG5 n=1 Tax=Phanerochaete chrysosporium RepID=LIG5_PHACH	GO:0004601|GO:0006979|GO:0020037|GO:0055114
c1380_g1_i1	-3.12127	2.39255	9.75E-08	1.17E-05	RecName: Full=Isocitrate lyase; Short=ICL; Short=Isocitrase; Short=Isocitratase [Coprinopsis cinerea okayama7#130]	UniRef90_A0A067QGD2 Uncharacterized protein n=1 Tax=Jaapia argillacea MUCL 33604 RepID=A0A067QGD2_9HOMO	GO:0004451|GO:0019752
c13811_g1_i1	-1.72653	7.966762	0.001007	0.020149	NA	NA	NA
c13811_g1_i2	-1.72653	7.966762	0.001007	0.020149	NA	UniRef90_A0A0C3PIY2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PIY2_PHLGI	NA
c13817_g2_i1	-1.95578	6.901203	3.36E-05	0.001442	NA	UniRef90_K5VTZ2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VTZ2_PHACS	NA
c1385_g1_i1	-2.25896	3.750694	2.68E-08	4.02E-06	NA	NA	NA

c13887_g2_i1	-1.22009	8.064424	0.001834	0.030891	RecName: Full=Probable helicase mot1; AltName: Full=Modifier of transcription 1; AltName: Full=TBP-associated factor mot1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5W9R0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W9R0_PHACS	GO:0003677|GO:0005524
c13903_g1_i1	-1.97797	7.402429	8.35E-06	0.000476	NA	NA	GO:0005515|GO:0008270|GO:0046872
c13903_g1_i2	-1.97797	7.402429	8.35E-06	0.000476	NA	UniRef90_K5VZ28 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZ28_PHACS	GO:0005515|GO:0008270|GO:0046872
c13903_g2_i1	-1.57171	4.265178	7.67E-05	0.002739	NA	NA	NA
c1390_g1_i1	-1.20077	5.879584	0.001825	0.030786	NA	NA	NA
c13921_g2_i1	-1.3026	5.178449	0.001901	0.031492	NA	UniRef90_A0A0C3S2K6 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S2K6_PHLGI	NA
c1392_g1_i1	-2.17399	0.930429	0.003583	0.049722	NA	NA	NA
c13943_g2_i1	-1.53337	3.88288	0.002134	0.03409	NA	NA	NA
c13943_g2_i2	-1.53337	3.88288	0.002134	0.03409	NA	UniRef90_K5VX88 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VX88_PHACS	NA
c13943_g2_i3	-1.53337	3.88288	0.002134	0.03409	NA	NA	NA
c13943_g2_i4	-1.53337	3.88288	0.002134	0.03409	NA	NA	NA
c13943_g2_i5	-1.53337	3.88288	0.002134	0.03409	NA	NA	NA
c13961_g1_i1	-1.6494	4.918253	1.34E-05	0.000707	NA	NA	GO:0016021|GO:0055085
c13961_g1_i2	-1.6494	4.918253	1.34E-05	0.000707	RecName: Full=Caffeine resistance protein 5 [Schizosaccharomyces pombe 972h-]	UniRef90_K5X3H5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X3H5_PHACS	GO:0016021|GO:0055085
c13961_g1_i3	-1.6494	4.918253	1.34E-05	0.000707	NA	NA	GO:0016021|GO:0055085
c13961_g3_i1	-1.39683	3.428688	0.000711	0.015696	RecName: Full=Cycloheximide resistance protein [Candida maltosa]	UniRef90_K5VXF1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VXF1_PHACS	NA
c13961_g3_i2	-1.39683	3.428688	0.000711	0.015696	NA	NA	NA

c13963_g2_i1	-1.05321	4.562086	0.003267	0.046508	NA	UniRef90_A0A0C3PES5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PES5_PHLGI	NA
c13970_g1_i1	-2.04555	5.579666	1.66E-07	1.87E-05	RecName: Full=Beta-hexosaminidase 2; AltName: Full=Beta-GlcNAcase 2; AltName: Full=Beta-N-acetylhexosaminidase 2; AltName: Full=Beta-hexosaminidase 3; Short=AtHEX3; AltName: Full=N-acetyl-beta-glucosaminidase 2; Flags: Precursor [Arabidopsis thaliana]	UniRef90_K5WX86 Beta-hexosaminidase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WX86_PHACS	GO:0004553|GO:0005975
c13983_g1_i1	-3.33384	6.689216	4.45E-09	8.22E-07	RecName: Full=Protein priA; Flags: Precursor [Lentinula edodes]	UniRef90_K5VEP6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VEP6_PHACS	NA
c14001_g1_i1	-1.92815	5.704256	4.53E-07	4.34E-05	NA	UniRef90_K5WCL6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCL6_PHACS	NA
c14001_g2_i1	-2.02222	8.691059	1.22E-06	9.63E-05	NA	UniRef90_K5WCL6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCL6_PHACS	NA
c14001_g2_i2	-2.02222	8.691059	1.22E-06	9.63E-05	NA	NA	NA
c14007_g1_i1	-1.25815	6.056076	0.002069	0.033318	NA	UniRef90_K5WNW1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNW1_PHACS	NA
c14007_g1_i2	-1.25815	6.056076	0.002069	0.033318	NA	NA	NA
c14007_g1_i3	-1.25815	6.056076	0.002069	0.033318	NA	NA	NA
c14019_g1_i1	-1.64564	3.817141	0.000109	0.003612	NA	UniRef90_K5WMP8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WMP8_PHACS	NA
c14019_g1_i2	-1.64564	3.817141	0.000109	0.003612	NA	NA	NA
c14019_g1_i3	-1.64564	3.817141	0.000109	0.003612	NA	NA	NA
c14104_g3_i1	-1.39607	3.075816	0.003049	0.044255	NA	NA	GO:0005515

c14104_g3_i2	-1.39607	3.075816	0.003049	0.044255	RecName: Full=Glutathione S-transferase 1; AltName: Full=GST-I [Schizosaccharomyces pombe 972h-]	UniRef90_K5VZ09 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZ09_PHACS	GO:0005515
c14133_g1_i1	-1.55358	4.515844	7.59E-05	0.002715	NA	NA	NA
c14133_g1_i2	-1.55358	4.515844	7.59E-05	0.002715	NA	NA	NA
c14133_g1_i3	-1.55358	4.515844	7.59E-05	0.002715	NA	NA	NA
c14133_g1_i4	-1.55358	4.515844	7.59E-05	0.002715	NA	NA	NA
c14133_g1_i5	-1.55358	4.515844	7.59E-05	0.002715	NA	UniRef90_K5WQR6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQR6_PHACS	NA
c14141_g1_i1	-1.49214	4.721047	0.000758	0.016312	NA	NA	GO:0005515
c14141_g1_i2	-1.49214	4.721047	0.000758	0.016312	RecName: Full=Probable glutathione S-transferase; AltName: Full=Auxin-induced protein PCNT107 [Nicotiana tabacum]	UniRef90_K5UTW3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UTW3_PHACS	NA
c14172_g1_i1	-1.17774	8.907408	0.002225	0.035116	RecName: Full=Extracellular metalloproteinase MEP; AltName: Full=Elastinolytic metalloproteinase MEP; AltName: Full=Fungalysin MEP; Flags: Precursor [Leptosphaeria maculans JN3]	UniRef90_K5VWH1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VWH1_PHACS	GO:0004222|GO:0005615|GO:0008270
c14197_g1_i1	-1.84697	5.56936	0.001477	0.026379	NA	UniRef90_K5V5Q2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V5Q2_PHACS	NA
c14203_g2_i1	-3.07287	6.675843	5.40E-07	4.99E-05	RecName: Full=Protein priA; Flags: Precursor [Lentinula edodes]	UniRef90_K5XDD5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XDD5_PHACS	NA
c14209_g1_i1	-1.25027	5.676079	0.003369	0.047616	RecName: Full=Manganese transporter pdt1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WR84 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WR84_PHACS	GO:0005215|GO:0006810|GO:0016020
c14209_g1_i2	-1.25027	5.676079	0.003369	0.047616	NA	NA	GO:0005215|GO:0006810|GO:0016020
c14217_g1_i1	-2.77347	6.10768	5.52E-09	9.83E-07	RecName: Full=TBC domain-containing protein C4G8.04 [Schizosaccharomyces pombe 972h-]	UniRef90_K5X4W7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X4W7_PHACS	GO:0005097|GO:0032313

c14228_g1_i1	-1.42843	4.757871	0.001422	0.025716	NA	NA	NA
c14228_g1_i2	-1.42843	4.757871	0.001422	0.025716	NA	NA	NA
c14326_g1_i1	-1.42883	4.214667	6.68E-05	0.002448	NA	NA	NA
c14346_g2_i1	-3.5818	3.433579	4.29E-07	4.21E-05	RecName: Full=Fruiting body protein SC3; AltName: Full=Hydrophobin SC3; Flags: Precursor [Schizophyllum commune]	NA	GO:0005199|GO:0009277
c14357_g1_i1	-1.72073	2.122726	0.000593	0.013597	NA	NA	NA
c1435_g1_i1	-2.10781	2.443266	1.08E-05	0.000593	NA	NA	NA
c1435_g1_i2	-2.10781	2.443266	1.08E-05	0.000593	NA	NA	NA
c14361_g1_i1	-3.44607	5.311712	2.96E-14	1.81E-11	NA	NA	NA
c14361_g1_i2	-3.44607	5.311712	2.96E-14	1.81E-11	NA	NA	NA
c14363_g2_i1	-1.29411	6.079156	0.001643	0.028546	NA	NA	NA
c14363_g3_i1	-1.35906	3.882837	0.000688	0.015325	NA	NA	NA
c14373_g3_i1	-1.52085	5.036894	0.003243	0.046267	RecName: Full=Enoyl reductase LovC [Aspergillus terreus]	NA	GO:0008270|GO:0016491|GO:0055114
c14384_g2_i1	-1.325	4.039427	0.000409	0.010279	RecName: Full=Mitochondrial dicarboxylate transporter; AltName: Full=DTP; AltName: Full=Dicarboxylate carrier 1 [Saccharomyces cerevisiae S288c]	NA	NA
c14414_g1_i1	-1.1193	4.456311	0.00167	0.028876	NA	NA	NA
c14436_g1_i1	-2.5495	9.071694	2.22E-07	2.40E-05	NA	NA	NA
c14436_g2_i1	-2.13143	9.406569	5.85E-06	0.000359	RecName: Full=Uncharacterized membrane protein C3B8.06 [Schizosaccharomyces pombe 972h-]	NA	NA
c14441_g1_i1	-1.62579	6.106497	7.72E-05	0.002752	RecName: Full=Uncharacterized transporter mfs2 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0055085
c14453_g1_i1	-2.22189	4.282772	0.000129	0.004164	RecName: Full=Probable indole-3-pyruvate monooxygenase YUCCA5; AltName: Full=Flavin-containing monooxygenase YUCCA5; AltName: Full=Protein SUPPRESSOR OF ER 1 [Arabidopsis thaliana]	NA	GO:0004499|GO:0050660|GO:0050661|GO:0055114
c14457_g1_i1	-1.4064	4.899731	0.001806	0.030572	NA	NA	NA

c14457_g1_i2	-1.4064	4.899731	0.001806	0.030572	NA	NA	NA
c14457_g1_i3	-1.4064	4.899731	0.001806	0.030572	NA	NA	NA
c14457_g1_i4	-1.4064	4.899731	0.001806	0.030572	NA	NA	NA
c14457_g1_i5	-1.4064	4.899731	0.001806	0.030572	NA	NA	NA
c14457_g1_i6	-1.4064	4.899731	0.001806	0.030572	NA	NA	NA
c14465_g1_i1	-2.75353	1.332064	0.00187	0.031116	NA	NA	NA
c14487_g1_i1	-2.29602	9.137369	1.93E-05	0.00094	RecName: Full=Ubiquitin-conjugating enzyme E2 1; AltName: Full=Ubiquitin carrier protein; AltName: Full=Ubiquitin-conjugating enzyme E2-24 kDa; AltName: Full=Ubiquitin-protein ligase [Saccharomyces cerevisiae S288c]	NA	GO:0004190|GO:0006508|GO:0016881
c14515_g10_i1	-1.39934	3.93266	0.003289	0.046767	NA	NA	NA
c14526_g1_i1	-1.69585	6.01158	8.67E-05	0.003049	NA	NA	NA
c14526_g1_i2	-1.69585	6.01158	8.67E-05	0.003049	NA	NA	NA
c14526_g1_i3	-1.69585	6.01158	8.67E-05	0.003049	NA	NA	NA
c14549_g1_i1	-1.25768	3.308669	0.003162	0.045543	NA	NA	NA
c14549_g1_i2	-1.25768	3.308669	0.003162	0.045543	NA	NA	NA
c14549_g1_i3	-1.25768	3.308669	0.003162	0.045543	NA	NA	NA
c14549_g1_i4	-1.25768	3.308669	0.003162	0.045543	NA	NA	NA
c14555_g1_i1	-1.49499	9.739281	0.000364	0.009418	RecName: Full=Serine palmitoyltransferase 2; Short=SPT 2; AltName: Full=Long chain base biosynthesis protein 2 [Saccharomyces cerevisiae S288c]	NA	GO:0009058|GO:0030170
c14577_g2_i1	-1.21791	6.880151	0.001267	0.023766	NA	NA	NA
c14582_g1_i1	-1.34126	4.940871	0.00074	0.016036	NA	NA	NA
c14582_g1_i2	-1.34126	4.940871	0.00074	0.016036	NA	NA	GO:0005199|GO:0008152|GO:0009277|GO:0016846
c14582_g1_i3	-1.34126	4.940871	0.00074	0.016036	NA	NA	GO:0005199|GO:0008152|GO:0009277|GO:0016846
c14596_g5_i1	-2.36203	3.485077	3.83E-06	0.000252	NA	NA	NA
c14601_g2_i1	-1.14235	5.194792	0.002298	0.036032	NA	NA	NA

c14618_g1_i1	-2.56037	4.10552	5.31E-09	9.60E-07	NA	NA	NA
c14618_g1_i2	-2.56037	4.10552	5.31E-09	9.60E-07	NA	NA	NA
c14618_g1_i3	-2.56037	4.10552	5.31E-09	9.60E-07	NA	NA	NA
c14618_g1_i4	-2.56037	4.10552	5.31E-09	9.60E-07	NA	NA	NA
c14643_g3_i1	-2.35194	9.292819	2.03E-05	0.000974	RecName: Full=Uncharacterized MFS-type transporter C409.08 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0022857|GO:0055085
c14653_g2_i1	-1.20407	5.631739	0.000959	0.01938	RecName: Full=Transcription factor tau subunit sfc6; AltName: Full=TFIIIC subunit sfc6; AltName: Full=Transcription factor C subunit 6 [Schizosaccharomyces pombe 972h-]	NA	GO:0005515
c14689_g2_i1	-1.46319	5.70219	0.000371	0.009521	NA	NA	NA
c14689_g2_i2	-1.46319	5.70219	0.000371	0.009521	NA	NA	NA
c14689_g2_i3	-1.46319	5.70219	0.000371	0.009521	NA	NA	NA
c14689_g2_i4	-1.46319	5.70219	0.000371	0.009521	NA	NA	NA
c14689_g2_i5	-1.46319	5.70219	0.000371	0.009521	NA	NA	NA
c14700_g1_i1	-1.50171	3.471676	0.000202	0.005981	NA	NA	NA
c14700_g2_i1	-1.44821	6.573436	0.000563	0.0131	NA	NA	NA
c14709_g1_i1	-1.9447	4.644903	8.65E-05	0.003047	NA	NA	NA
c14709_g2_i1	-1.42585	7.273812	0.002518	0.038636	RecName: Full=AB hydrolase superfamily protein C4A8.06c [Schizosaccharomyces pombe 972h-]	NA	GO:0008152|GO:0016787
c14713_g1_i1	-1.25369	7.007849	0.001033	0.020517	NA	NA	NA
c14716_g1_i1	-1.72644	5.414226	8.29E-05	0.002933	RecName: Full=Uncharacterized protein YEL023C [Saccharomyces cerevisiae S288c]	NA	NA
c14716_g1_i2	-1.72644	5.414226	8.29E-05	0.002933	NA	NA	NA
c14716_g3_i1	-1.91303	3.98075	4.91E-05	0.001944	NA	NA	NA
c14749_g3_i1	-1.59616	5.336138	2.58E-05	0.001186	NA	NA	NA
c14760_g2_i1	-1.0943	5.293079	0.003424	0.048119	RecName: Full=Molybdenum cofactor sulfurase; Short=MCS; Short=MOS; Short=MoCo sulfurase; AltName:	NA	GO:0008152

					Full=Molybdenum cofactor sulfurtransferase [Bos taurus]		
c14821_g2_i1	-2.0242	9.771681	0.001193	0.022723	RecName: Full=Probable serine/threonine-protein kinase vps15; AltName: Full=Phosphoinositide 3-kinase regulatory subunit 4; AltName: Full=Vacuolar protein sorting protein 15 [Dictyostelium discoideum]	NA	GO:0005515
c14821_g2_i2	-2.0242	9.771681	0.001193	0.022723	NA	NA	GO:0005515
c14826_g1_i1	-2.23826	8.967264	3.27E-06	0.000222	RecName: Full=Methylisocitrate lyase, mitochondrial; AltName: Full=2-methylisocitrate lyase, mitochondrial; Flags: Precursor [Aspergillus nidulans FGSC A4]	NA	GO:0004451|GO:0019752
c14867_g1_i1	-1.42586	5.660955	0.000817	0.017394	NA	NA	NA
c14867_g1_i2	-1.42586	5.660955	0.000817	0.017394	NA	NA	NA
c14867_g1_i3	-1.42586	5.660955	0.000817	0.017394	NA	NA	NA
c1487_g1_i1	-2.21999	3.869758	6.05E-06	0.000369	NA	UniRef90_K5UK38 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UK38_PHACS	NA
c14905_g1_i1	-2.2929	4.472916	2.63E-09	5.49E-07	RecName: Full=High affinity potassium transporter [Schwanniomyces occidentalis]	NA	GO:0015079|GO:0016020|GO:0071805
c14921_g1_i1	-1.337	5.787389	0.000722	0.015831	RecName: Full=Uncharacterized protein YNL144C [Saccharomyces cerevisiae S288c]	NA	NA
c14930_g3_i1	-2.55308	5.705892	4.77E-05	0.001908	RecName: Full=L-threo-3-deoxy-hexylosonate aldolase; AltName: Full=L-threo-3-deoxy-hexulosonate aldolase [Aspergillus niger]	NA	GO:0008152|GO:0016829
c14935_g1_i1	-1.21358	3.841648	0.001679	0.028985	RecName: Full=Trans-cinnamate 4-monooxygenase; AltName: Full=Cinnamic acid 4-hydroxylase; Short=C4H; Short=CA4H; AltName: Full=Cytochrome P450 73; AltName: Full=Cytochrome P450C4H [Vigna radiata var. radiata]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c14995_g1_i1	-1.96055	10.32401	0.000561	0.013062	NA	NA	NA

c14995_g1_i2	-1.96055	10.32401	0.000561	0.013062	NA	NA	GO:0005215|GO:0006810|GO:0016020
c14995_g1_i3	-1.96055	10.32401	0.000561	0.013062	NA	NA	GO:0005215|GO:0006810|GO:0016020
c15010_g1_i1	-2.82421	1.530871	1.68E-05	0.000861	NA	NA	NA
c15010_g1_i2	-2.82421	1.530871	1.68E-05	0.000861	NA	NA	NA
c15010_g2_i1	-2.69734	3.568841	0.000887	0.0185	NA	NA	GO:0016491|GO:0055114
c15010_g2_i2	-2.69734	3.568841	0.000887	0.0185	NA	NA	GO:0016491|GO:0055114
c15010_g2_i3	-2.69734	3.568841	0.000887	0.0185	RecName: Full=Enoyl reductase LovC [Aspergillus terreus]	NA	GO:0016491|GO:0055114
c15010_g2_i4	-2.69734	3.568841	0.000887	0.0185	NA	NA	GO:0008270|GO:0016491|GO:0055114
c15015_g1_i1	-1.51357	5.618981	0.000313	0.008435	RecName: Full=Uncharacterized glycosidase Rv0584; Flags: Precursor [Mycobacterium tuberculosis H37Rv]	NA	NA
c15020_g1_i1	-1.26263	4.895982	0.001457	0.026141	NA	NA	NA
c15020_g1_i2	-1.26263	4.895982	0.001457	0.026141	NA	NA	NA
c15020_g1_i3	-1.26263	4.895982	0.001457	0.026141	NA	NA	NA
c15064_g1_i1	-1.22506	4.705886	0.001062	0.02091	NA	NA	NA
c15064_g1_i2	-1.22506	4.705886	0.001062	0.02091	NA	NA	NA
c15073_g1_i1	-3.1474	5.442755	3.91E-12	1.33E-09	RecName: Full=FKBP12-associated protein 1 homolog [Schizosaccharomyces pombe 972h-]	NA	NA
c15073_g2_i1	-2.51199	6.467525	9.13E-09	1.55E-06	RecName: Full=FKBP12-associated protein 1 homolog [Schizosaccharomyces pombe 972h-]	NA	GO:0003700|GO:0005634|GO:0006355|GO:0008270
c15073_g3_i1	-3.0267	5.430429	2.59E-10	6.32E-08	NA	NA	GO:0003676
c15073_g4_i1	-2.14149	5.30687	2.92E-07	3.00E-05	RecName: Full=FKBP12-associated protein 1 homolog [Schizosaccharomyces pombe 972h-]	NA	NA
c15087_g2_i1	-1.5566	3.045342	0.000841	0.017718	NA	NA	NA
c15106_g2_i1	-1.10417	4.873839	0.00262	0.03981	NA	NA	GO:0016491
c15106_g2_i2	-1.10417	4.873839	0.00262	0.03981	NA	NA	GO:0016491|GO:0020037
c15106_g2_i3	-1.10417	4.873839	0.00262	0.03981	NA	NA	GO:0016491
c15106_g2_i4	-1.10417	4.873839	0.00262	0.03981	NA	NA	GO:0016491|GO:0020037

c15106_g2_i5	-1.10417	4.873839	0.00262	0.03981	NA	NA	GO:0016491|GO:0020037
c15106_g2_i6	-1.10417	4.873839	0.00262	0.03981	RecName: Full=(S)-mandelate dehydrogenase, mitochondrial; AltName: Full=Flavocytochrome b; AltName: Full=L(+)-mandelate dehydrogenase; Short=L-MDH; Flags: Precursor [Rhodotorula graminis]	NA	GO:0016491|GO:0020037
c15106_g2_i7	-1.10417	4.873839	0.00262	0.03981	NA	NA	GO:0016491|GO:0020037
c15106_g2_i8	-1.10417	4.873839	0.00262	0.03981	NA	NA	GO:0016491|GO:0020037
c15109_g1_i1	-1.45531	2.531476	0.0009	0.018646	NA	NA	NA
c15111_g1_i1	-1.38811	5.893759	0.000718	0.015767	NA	NA	NA
c15111_g1_i2	-1.38811	5.893759	0.000718	0.015767	NA	NA	NA
c15111_g1_i3	-1.38811	5.893759	0.000718	0.015767	NA	NA	NA
c15111_g1_i4	-1.38811	5.893759	0.000718	0.015767	NA	NA	NA
c15171_g1_i1	-3.6513	8.790459	1.67E-11	5.02E-09	NA	NA	NA
c15219_g1_i1	-1.95641	5.485899	4.51E-06	0.000288	RecName: Full=Cytochrome P450 3A6; AltName: Full=CYPIIIA6; AltName: Full=Cytochrome P450-3C [Oryctolagus cuniculus]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15219_g1_i2	-1.95641	5.485899	4.51E-06	0.000288	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15221_g2_i1	-1.56006	5.673408	3.77E-05	0.001586	RecName: Full=Uncharacterized acyltransferase CST26; AltName: Full=Chromosome stability protein 26 [Saccharomyces cerevisiae S288c]	NA	GO:0008152|GO:0016746
c15221_g3_i1	-1.381	3.268436	0.002131	0.034082	NA	NA	NA
c15230_g1_i1	-1.32301	5.03532	0.000509	0.0122	NA	NA	NA
c15230_g1_i2	-1.32301	5.03532	0.000509	0.0122	NA	NA	NA
c15230_g1_i3	-1.32301	5.03532	0.000509	0.0122	NA	NA	NA
c15230_g1_i4	-1.32301	5.03532	0.000509	0.0122	NA	NA	NA
c15230_g1_i5	-1.32301	5.03532	0.000509	0.0122	NA	NA	NA
c15243_g1_i1	-1.02431	5.156534	0.002923	0.043017	NA	NA	NA
c15243_g1_i2	-1.02431	5.156534	0.002923	0.043017	NA	NA	GO:0005515

c15245_g4_i1	-5.04827	0.232937	0.000732	0.015938	NA	NA	NA
c15254_g1_i1	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15254_g1_i2	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15254_g1_i3	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15254_g1_i4	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15254_g1_i5	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15254_g1_i6	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15254_g1_i7	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15254_g1_i8	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15254_g1_i9	-2.27102	5.342839	3.00E-08	4.44E-06	NA	NA	NA
c15271_g2_i1	-2.36537	3.626707	1.74E-06	0.000129	NA	NA	NA
c15271_g2_i2	-2.36537	3.626707	1.74E-06	0.000129	NA	NA	NA
c15271_g2_i3	-2.36537	3.626707	1.74E-06	0.000129	NA	NA	NA
c15271_g2_i4	-2.36537	3.626707	1.74E-06	0.000129	NA	NA	NA
c15271_g4_i1	-5.49237	0.469813	0.002427	0.037587	NA	NA	NA
c15271_g5_i1	-4.54471	3.471202	1.65E-08	2.63E-06	NA	NA	NA
c15272_g3_i1	-1.27375	3.63699	0.002269	0.035599	NA	NA	NA
c15272_g3_i2	-1.27375	3.63699	0.002269	0.035599	NA	NA	NA
c15272_g3_i3	-1.27375	3.63699	0.002269	0.035599	NA	NA	NA
c15334_g1_i1	-1.89456	6.013128	0.000145	0.004559	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus parasiticus]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15336_g1_i1	-2.17182	4.33977	3.37E-07	3.41E-05	NA	NA	NA
c15336_g2_i1	-1.45774	7.891302	0.000827	0.017512	NA	NA	NA
c15337_g1_i1	-2.92321	9.310026	3.15E-11	9.15E-09	RecName: Full=Uncharacterized transporter C1529.01 [Schizosaccharomyces pombe 972h-]	NA	GO:0016021|GO:0022857|GO:0055085
c15337_g1_i2	-2.92321	9.310026	3.15E-11	9.15E-09	NA	NA	GO:0016021|GO:0022857|GO:0055085
c15349_g2_i1	-1.70523	2.28924	0.00039	0.009908	NA	NA	NA

c15379_g1_i1	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i10	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i11	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i2	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i3	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i4	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i5	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i6	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i7	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i8	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g1_i9	-1.8859	7.728376	3.56E-05	0.001515	NA	NA	NA
c15379_g2_i1	-2.78483	5.554574	6.35E-09	1.12E-06	NA	NA	NA
c15418_g2_i1	-1.27517	6.325022	0.001861	0.031037	RecName: Full=Putative oxidoreductase YteT; Flags: Precursor [Bacillus subtilis subsp. subtilis str. 168]	NA	GO:0008152|GO:0016491|GO:0055114
c15512_g4_i1	-1.63067	4.755266	3.82E-05	0.001594	RecName: Full=Ribosome biogenesis protein ERB1; AltName: Full=Eukaryotic ribosome biogenesis protein 1 [Coprinopsis cinerea okayama7#130]	NA	GO:0005515
c15512_g4_i2	-1.63067	4.755266	3.82E-05	0.001594	NA	NA	GO:0005515
c15519_g1_i1	-1.52473	5.467335	0.000329	0.008726	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase; AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus flavus NRRL3357]	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c15519_g1_i2	-1.52473	5.467335	0.000329	0.008726	NA	NA	NA
c15519_g1_i3	-1.52473	5.467335	0.000329	0.008726	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114

c15538_g1_i1	-1.20638	7.846988	0.002931	0.043099	RecName: Full=Peroxisomal hydratase-dehydrogenase-epimerase; Short=HDE; AltName: Full=Multifunctional beta-oxidation protein; Short=MFP; Includes: RecName: Full=2-enoyl-CoA hydratase; Includes: RecName: Full=(3R)-3-hydroxyacyl-CoA dehydrogenase [Neurospora crassa OR74A]	NA	GO:0008152|GO:0016491
c15538_g1_i2	-1.20638	7.846988	0.002931	0.043099	NA	NA	NA
c15553_g3_i1	-1.66136	8.460679	0.000366	0.009418	RecName: Full=Putative SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 3-like 2; Short=SMARCA3-like protein 2 [Arabidopsis thaliana]	NA	GO:0003677|GO:0005524
c15553_g4_i1	-1.40671	3.736367	0.000548	0.012832	NA	NA	NA
c15553_g4_i2	-1.40671	3.736367	0.000548	0.012832	NA	NA	NA
c15591_g1_i1	-1.53721	5.331427	9.46E-05	0.003263	NA	NA	NA
c15610_g2_i1	-1.52442	7.153981	0.000329	0.008726	NA	NA	NA
c15610_g2_i2	-1.52442	7.153981	0.000329	0.008726	NA	NA	NA
c15615_g3_i1	-1.18335	6.951886	0.002171	0.034487	NA	NA	GO:0005515
c15615_g4_i1	-2.04409	6.467049	3.21E-07	3.27E-05	NA	NA	NA
c15641_g1_i1	-1.58592	6.585442	0.000821	0.017458	NA	NA	NA
c15654_g2_i1	-1.59508	4.929363	1.86E-05	0.000915	NA	NA	GO:0005515
c15691_g1_i1	-2.57812	5.910017	4.39E-05	0.001788	RecName: Full=Bifunctional P-450:NADPH-P450 reductase; AltName: Full=Cytochrome P450foxy; AltName: Full=Fatty acid omega-hydroxylase; Includes: RecName: Full=Cytochrome P450 505; Includes: RecName: Full=NADPH--cytochrome P450 reductase [Fusarium oxysporum]	NA	GO:0010181|GO:0016491|GO:0055114
c15691_g2_i1	-1.99468	4.19496	0.001419	0.025716	RecName: Full=Bifunctional P-450:NADPH-P450 reductase; AltName: Full=Cytochrome P450foxy; AltName: Full=Fatty acid omega-hydroxylase; Includes: RecName:	NA	GO:0016491|GO:0055114

					Full=Cytochrome P450 505; Includes: RecName: Full=NADPH--cytochrome P450 reductase [Fusarium oxysporum]		
c15726_g3_i1	-1.2529	7.287141	0.002907	0.042881	NA	NA	NA
c15741_g1_i1	-1.39649	3.129338	0.001836	0.030892	NA	NA	NA
c15741_g1_i2	-1.39649	3.129338	0.001836	0.030892	NA	NA	NA
c15749_g2_i1	-1.35599	3.747771	0.001293	0.024191	NA	NA	NA
c15785_g1_i1	-1.73998	5.01548	1.75E-06	0.00013	RecName: Full=Protein transport protein sec22 [Schizosaccharomyces pombe 972h-]	NA	NA
c15788_g1_i1	-2.53601	4.870971	6.17E-07	5.52E-05	NA	NA	NA
c15788_g1_i2	-2.53601	4.870971	6.17E-07	5.52E-05	NA	NA	NA
c15837_g2_i1	-1.35838	3.311972	0.003234	0.046234	NA	NA	NA
c15837_g2_i2	-1.35838	3.311972	0.003234	0.046234	NA	NA	NA
c15837_g2_i3	-1.35838	3.311972	0.003234	0.046234	RecName: Full=DNA repair protein SWI5 homolog; AltName: Full=Protein SAE3 homolog [Xenopus (Silurana) tropicalis]	NA	NA
c15837_g2_i4	-1.35838	3.311972	0.003234	0.046234	NA	NA	NA
c15837_g2_i5	-1.35838	3.311972	0.003234	0.046234	NA	NA	NA
c15837_g2_i6	-1.35838	3.311972	0.003234	0.046234	NA	NA	NA
c15885_g1_i1	-1.21372	5.155082	0.003472	0.048605	NA	NA	NA
c15885_g1_i2	-1.21372	5.155082	0.003472	0.048605	NA	NA	NA
c15885_g1_i3	-1.21372	5.155082	0.003472	0.048605	NA	NA	NA
c15898_g2_i1	-1.55959	5.545871	0.000164	0.005026	RecName: Full=Lactose permease [Kluyveromyces lactis NRRL Y-1140]	NA	GO:0016021|GO:0022857|GO:0055085
c1598_g1_i1	-2.29503	0.792682	0.002341	0.036592	NA	UniRef90_A0A0C3PUS9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PUS9_PHLGI	GO:0005375|GO:0016021|GO:0035434
c16050_g1_i1	-2.49516	6.105552	1.26E-07	1.47E-05	NA	NA	NA
c16050_g1_i2	-2.49516	6.105552	1.26E-07	1.47E-05	NA	NA	NA
c16050_g1_i3	-2.49516	6.105552	1.26E-07	1.47E-05	NA	NA	NA
c16050_g1_i4	-2.49516	6.105552	1.26E-07	1.47E-05	NA	NA	NA
c16050_g1_i5	-2.49516	6.105552	1.26E-07	1.47E-05	NA	NA	NA

c16050_g1_i6	-2.49516	6.105552	1.26E-07	1.47E-05	NA	NA	NA
c16050_g1_i7	-2.49516	6.105552	1.26E-07	1.47E-05	NA	NA	NA
c16111_g1_i1	-2.01632	7.960534	0.00105	0.020739	NA	NA	NA
c16111_g1_i2	-2.01632	7.960534	0.00105	0.020739	NA	NA	NA
c16130_g2_i1	-1.14262	6.88675	0.003116	0.045032	NA	NA	NA
c16130_g2_i2	-1.14262	6.88675	0.003116	0.045032	NA	NA	NA
c16178_g4_i1	-3.77436	1.780721	3.12E-05	0.001357	NA	NA	NA
c16178_g7_i1	-3.82379	3.057734	1.56E-12	5.87E-10	NA	NA	NA
c16198_g1_i1	-2.43073	2.759301	4.05E-07	4.02E-05	NA	NA	NA
c16245_g1_i1	-2.43887	2.435255	9.71E-05	0.003314	NA	NA	NA
c16260_g1_i1	-2.47562	3.364205	1.78E-08	2.81E-06	RecName: Full=Sulfate adenylyltransferase; AltName: Full=ATP-sulfurylase; AltName: Full=Sulfate adenylate transferase; Short=SAT [Aspergillus niger]	NA	GO:0000103|GO:0004020|GO:0005524
c16288_g1_i1	-2.57569	1.162009	0.000934	0.019069	RecName: Full=Isocitrate lyase; Short=ICL; Short=Isocitrase; Short=Isocitratase [Coprinopsis cinerea okayama7#130]	NA	GO:0004451|GO:0019752
c16294_g1_i1	-2.37665	1.660319	0.000393	0.009968	NA	NA	NA
c16354_g1_i1	-2.67616	6.7515	0.000267	0.007437	NA	NA	NA
c16367_g1_i1	-2.58362	2.417508	5.22E-05	0.002034	NA	NA	NA
c16384_g1_i1	-4.17846	0.81011	2.42E-05	0.001131	RecName: Full=Uncharacterized protein C1711.08 [Schizosaccharomyces pombe 972h-]	NA	GO:0001671|GO:0051087
c16463_g1_i1	-2.98972	2.112518	4.62E-06	0.000292	NA	NA	NA
c16521_g1_i1	-4.90966	0.160647	0.001321	0.024504	NA	NA	NA
c16549_g1_i1	-3.8024	0.576069	0.000788	0.016853	NA	NA	NA
c16589_g1_i1	-2.45429	1.103152	0.001539	0.027249	NA	NA	NA
c16625_g1_i1	-2.91547	0.564633	0.003507	0.048973	NA	NA	NA
c16801_g1_i1	-2.52627	1.13554	0.001243	0.023455	NA	NA	NA
c16803_g1_i1	-3.60388	3.017113	1.29E-08	2.14E-06	NA	NA	NA
c16831_g1_i1	-4.3352	4.215615	6.11E-21	1.66E-17	NA	NA	NA
c16836_g1_i1	-1.5539	2.390867	0.002379	0.037046	RecName: Full=Retrovirus-related Pol polyprotein from transposon TNT 1-94;	NA	GO:0015074

					Includes: RecName: Full=Protease; Includes: RecName: Full=Reverse transcriptase; Includes: RecName: Full=Endonuclease [Nicotiana tabacum]		
c16878_g1_i1	-2.60927	5.614651	5.76E-07	5.29E-05	NA	NA	NA
c16889_g1_i1	-2.90201	2.201661	8.97E-07	7.48E-05	NA	NA	NA
c16917_g1_i1	-3.32528	1.896338	8.13E-08	1.02E-05	NA	NA	NA
c16918_g1_i1	-3.00937	0.617213	0.001765	0.030086	NA	NA	NA
c16967_g1_i1	-2.19251	1.438965	0.00091	0.018761	RecName: Full=Diacetyl reductase [(S)-acetoin forming]; AltName: Full=Acetoin(diacetyl) reductase; Short=AR; AltName: Full=Meso-2,3-butanediol dehydrogenase [Staphylococcus epidermidis RP62A]	NA	NA
c16999_g1_i1	-1.8312	1.324039	0.003467	0.048554	NA	NA	NA
c17185_g1_i1	-3.45779	2.349413	8.62E-07	7.28E-05	RecName: Full=Heat shock protein 16; AltName: Full=16 kDa heat shock protein [Schizosaccharomyces pombe 972h-]	NA	NA
c17189_g1_i1	-3.95839	0.680789	0.000191	0.005696	RecName: Full=Uncharacterized lactate 2-monooxygenase PB1A11.03 [Schizosaccharomyces pombe 972h-]	NA	GO:0016491
c17222_g1_i1	-5.46288	0.461376	0.001249	0.023528	NA	NA	NA
c17240_g1_i1	-5.09269	1.47568	1.33E-08	2.19E-06	RecName: Full=Heat shock protein 104; AltName: Full=Protein aggregation-remodeling factor hsp104 [Schizosaccharomyces pombe 972h-]	NA	GO:0019538
c17241_g1_i1	-4.94428	1.999928	4.52E-10	1.05E-07	RecName: Full=Heat shock protein hsp98; AltName: Full=Protein aggregation-remodeling factor hsp98 [Neurospora crassa OR74A]	NA	GO:0019538
c17276_g1_i1	-3.86413	0.616168	0.000221	0.006458	NA	NA	NA
c17302_g1_i1	-5.47845	0.46531	0.000164	0.005026	RecName: Full=Probable phosphoketolase [Schizosaccharomyces pombe 972h-]	NA	GO:0005975|GO:0016832
c17385_g1_i1	-4.21605	0.835667	0.000141	0.004459	NA	NA	NA
c17434_g1_i1	-1.4839	11.10249	0.000148	0.004628	NA	NA	NA

c17440_g1_i1	-2.9731	2.11957	1.21E-06	9.62E-05	NA	NA	NA
c17450_g1_i1	-5.1184	1.484174	3.24E-06	0.000221	NA	NA	NA
c17454_g1_i1	-3.27367	2.79825	8.86E-08	1.08E-05	NA	NA	NA
c17493_g1_i1	-3.6731	3.055358	1.58E-11	4.83E-09	NA	NA	NA
c17539_g1_i1	-4.68915	1.782133	8.70E-11	2.41E-08	NA	NA	NA
c1759_g2_i1	-3.16408	0.717108	0.000701	0.015539	NA	NA	NA
c17636_g1_i1	-2.59118	0.704016	0.001331	0.024618	NA	NA	NA
c17736_g1_i1	-2.75195	1.08367	0.001405	0.025621	RecName: Full=Meiotic recombination protein rec12 [Schizosaccharomyces pombe 972h-]	NA	NA
c17787_g1_i1	-2.81296	2.726041	4.27E-09	8.01E-07	NA	NA	NA
c17836_g1_i1	-2.76745	1.310744	0.000245	0.006937	NA	NA	NA
c17854_g1_i1	-2.13238	1.361417	0.002923	0.043017	RecName: Full=Retrovirus-related Pol polyprotein from transposon TNT 1-94; Includes: RecName: Full=Protease; Includes: RecName: Full=Reverse transcriptase; Includes: RecName: Full=Endonuclease [Nicotiana tabacum]	NA	NA
c17869_g1_i1	-1.79302	6.344882	0.001181	0.022625	NA	NA	NA
c17953_g1_i1	-5.73813	0.621985	1.18E-05	0.000639	RecName: Full=Probable phosphoketolase [Schizosaccharomyces pombe 972h-]	NA	GO:0005975|GO:0016832
c18074_g1_i1	-3.76752	0.569766	0.00097	0.019574	NA	NA	NA
c18084_g1_i1	-3.37697	0.346198	0.002735	0.041037	NA	NA	NA
c18106_g1_i1	-2.45578	1.086367	0.002933	0.04311	NA	NA	NA
c18110_g1_i1	-2.37664	1.8883	0.000728	0.015889	NA	NA	NA
c18126_g1_i1	-2.91138	2.048873	1.20E-07	1.40E-05	NA	NA	NA
c18187_g1_i1	-1.52077	9.605641	0.000104	0.003461	NA	NA	NA
c18206_g1_i1	-2.39778	3.544209	1.73E-05	0.000881	NA	NA	NA
c18256_g1_i1	-2.05681	3.34852	0.00023	0.00663	NA	NA	NA
c18305_g1_i1	-2.00863	2.992007	0.000152	0.00472	NA	NA	NA
c18318_g1_i1	-2.17302	1.677631	0.000596	0.013655	NA	NA	NA

c18329_g1_i1	-2.18005	1.416057	0.000576	0.013325	RecName: Full=Uncharacterized WD repeat-containing protein all2124 [Nostoc sp. PCC 7120]	NA	GO:0005515
c18348_g1_i1	-3.72742	1.467796	1.33E-05	0.000707	NA	NA	NA
c18399_g1_i1	-3.32107	1.17673	6.66E-05	0.002448	NA	NA	NA
c18401_g1_i1	-5.16925	0.29453	0.000423	0.010557	NA	NA	NA
c18402_g1_i1	-2.34852	1.023452	0.001674	0.028917	NA	NA	NA
c18429_g1_i1	-5.47946	0.465423	9.08E-05	0.003159	NA	NA	NA
c18431_g1_i1	-2.58554	0.965677	0.00106	0.020882	RecName: Full=Ubiquitin-conjugating enzyme E2 4; AltName: Full=Ubiquitin carrier protein 4; AltName: Full=Ubiquitin-protein ligase 4 [Schizosaccharomyces pombe 972h-]	NA	GO:0016881
c18493_g1_i1	-5.05082	0.233055	0.001072	0.021051	NA	NA	NA
c18577_g1_i1	-1.32979	2.728793	0.002613	0.03978	NA	NA	NA
c185_g1_i1	-2.0491	1.02908	0.003423	0.048119	NA	NA	NA
c18766_g1_i1	-1.94752	3.414355	3.02E-05	0.001327	NA	NA	NA
c18796_g1_i1	-3.15328	1.555695	1.62E-05	0.000834	RecName: Full=Filamentous growth regulator 27 [Candida albicans SC5314]	NA	GO:0000981|GO:0005634|GO:0006355|GO:0008270
c18802_g1_i1	-1.25826	2.776642	0.003387	0.047761	NA	NA	NA
c18846_g1_i1	-2.54375	4.069758	6.68E-09	1.16E-06	NA	NA	NA
c18906_g1_i1	-1.18417	4.355154	0.001422	0.025716	NA	NA	NA
c18910_g1_i1	-1.91822	2.930346	0.0028	0.041689	NA	NA	NA
c18926_g1_i1	-2.83267	1.135145	0.0009	0.018646	NA	NA	NA
c18964_g1_i1	-3.85987	1.161869	0.000888	0.018516	NA	NA	NA
c19057_g1_i1	-4.91444	0.164802	0.00361	0.049988	NA	NA	NA
c19117_g1_i1	-3.59414	0.463336	0.001553	0.027402	NA	NA	NA
c19139_g1_i1	-2.14836	1.401699	0.000514	0.012249	NA	NA	NA
c19214_g1_i1	-6.33705	1.025135	4.30E-07	4.21E-05	RecName: Full=Spore protein SP21 [Stigmatella aurantiaca DW4/3-1]	NA	NA
c19290_g1_i1	-5.39458	0.418215	0.000186	0.005562	RecName: Full=Aldehyde reductase 1; Short=ALR 1; AltName: Full=Alcohol dehydrogenase [NADP(+)]; AltName:	NA	NA

					Full=Aldehyde reductase I [Sporidiobolus salmonicolor]		
c19344_g1_i1	-2.75411	14.00374	1.09E-10	2.93E-08	NA	NA	NA
c19346_g1_i1	-2.38547	11.058	4.73E-08	6.38E-06	RecName: Full=Regulator of rDNA transcription protein 15 [Saccharomyces cerevisiae S288c]	NA	NA
c19362_g1_i1	-5.55212	0.515483	0.003089	0.044685	NA	NA	NA
c19372_g1_i1	-2.78337	1.088226	0.001918	0.031615	NA	NA	NA
c19388_g1_i1	-1.61597	4.383634	0.000945	0.01917	NA	NA	NA
c19458_g1_i1	-3.69383	0.526139	0.001754	0.029975	RecName: Full=Probable phosphoketolase [Schizosaccharomyces pombe 972h-]	NA	NA
c19459_g1_i1	-1.45224	6.864722	0.00017	0.005153	NA	NA	NA
c19502_g1_i1	-2.52488	0.668128	0.002573	0.039334	NA	NA	NA
c19529_g1_i1	-5.14539	0.283397	0.001722	0.029517	RecName: Full=ATP synthase subunit a; AltName: Full=F-ATPase protein 6; Flags: Precursor (mitochondrion) [Ustilago maydis 521]	NA	GO:0015078|GO:0015986|GO:0045263
c19530_g1_i1	-5.65814	0.572658	3.72E-05	0.001572	RecName: Full=ATP synthase subunit a; AltName: Full=F-ATPase protein 6; Flags: Precursor (mitochondrion) [Ustilago maydis 521]	NA	GO:0015078|GO:0015986|GO:0045263
c1956_g1_i1	-3.7288	5.56549	1.29E-11	4.05E-09	NA	NA	NA
c19585_g1_i1	-5.47593	1.784187	2.93E-10	7.02E-08	NA	NA	NA
c19626_g1_i1	-5.14211	0.283163	0.002091	0.033601	NA	NA	NA
c19668_g1_i1	-1.39371	6.446029	0.000348	0.009118	NA	NA	NA
c19732_g1_i1	-4.76197	0.093224	0.003461	0.048523	RecName: Full=Uncharacterized lactate 2-monooxygenase PB1A11.03 [Schizosaccharomyces pombe 972h-]	NA	GO:0006537|GO:0015930|GO:0016491|GO:0016638|GO:0055114
c1977_g1_i1	-4.76706	0.096819	0.002684	0.040369	RecName: Full=Ubiquitin-conjugating enzyme E2-16 kDa; AltName: Full=Colletotrichum hard-surface-induced protein 1; AltName: Full=Ubiquitin carrier protein; AltName:	UniRef90_R8BUH7 Putative ubiquitin-conjugating enzyme e2-16 kDa protein n=3 Tax=leotiomyceta RepID=R8BUH7_TOGMI	GO:0016881

					Full=Ubiquitin-protein ligase [Colletotrichum gloeosporioides]		
c2019_g1_i1	-4.25301	4.06894	5.67E-12	1.85E-09	NA	UniRef90_S7PTH2 HSP20-like chaperone n=1 Tax=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) RepID=S7PTH2_GLOTA	NA
c2019_g2_i1	-6.43751	2.621911	1.95E-13	9.60E-11	RecName: Full=Small heat shock protein C2 [Rickettsia felis URRWXCal2]	UniRef90_S7QMH6 HSP20-like chaperone n=1 Tax=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) RepID=S7QMH6_GLOTA	NA
c2057_g1_i1	-5.03407	0.225545	0.002074	0.033371	NA	NA	NA
c2080_g1_i1	-2.26545	6.035492	7.60E-08	9.61E-06	NA	NA	NA
c2159_g1_i1	-1.98231	1.41196	0.003546	0.049389	RecName: Full=Ent-kaurene oxidase; AltName: Full=Cytochrome P450 503A1; AltName: Full=Cytochrome P450-4 [Fusarium proliferatum]	UniRef90_Q587P2 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=Q587P2_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c2211_g1_i1	-5.05894	0.236817	0.00126	0.023703	RecName: Full=Cytochrome b; AltName: Full=Complex III subunit 3; AltName: Full=Complex III subunit III; AltName: Full=Cytochrome b-c1 complex subunit 3; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome b subunit (mitochondrion) [Schizophyllum commune]	UniRef90_A0A0C3S0Z5 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S0Z5_PHLGI	GO:0009055|GO:0016020|GO:0016491
c2212_g1_i1	-3.00081	0.626943	0.003303	0.046904	NA	UniRef90_K5UVV6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UVV6_PHACS	NA
c2263_g1_i1	-2.33681	1.22002	0.00042	0.010509	NA	UniRef90_A0A0C3SD89 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SD89_PHLGI	NA
c2339_g1_i1	-6.12595	0.869306	1.00E-05	0.000557	NA	NA	NA
c2347_g1_i1	-4.53457	1.660463	2.95E-09	5.95E-07	NA	UniRef90_A0A0C3P032 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P032_PHLGI	GO:0005975|GO:0016832

c2399_g1_i1	-2.52022	0.910101	0.00139	0.025457	NA	NA	NA
c241_g1_i1	-1.09491	6.817589	0.003431	0.048186	RecName: Full=ATP synthase subunit J, mitochondrial [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3NB88 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NB88_PHLGI	GO:0015078|GO:0015986|GO:0045263
c2609_g1_i1	-2.30705	1.361365	0.000298	0.00813	NA	NA	NA
c2609_g2_i1	-3.15746	1.792048	6.20E-07	5.52E-05	NA	UniRef90_R7S5J5 DUF1929-domain-containing protein n=1 Tax=Punctularia strigosozonata (strain HHB-11173) RepID=R7S5J5_PUNST	NA
c2613_g2_i1	-2.01902	1.864249	0.003564	0.049488	RecName: Full=Thaumatin-like protein 1; Flags: Precursor [Pyrus pyrifolia]	UniRef90_A0A0C3NZF0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NZF0_PHLGI	NA
c2724_g2_i1	-2.17142	1.891001	9.77E-05	0.003332	NA	UniRef90_K5V182 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V182_PHACS	NA
c2890_g1_i1	-2.72062	1.282983	0.000149	0.004643	RecName: Full=Protein P80; AltName: Full=Endosomal membrane protein; Flags: Precursor [Dictyostelium discoideum]	UniRef90_K5WRA5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WRA5_PHACS	GO:0005375|GO:0016021|GO:0035434
c2900_g1_i1	-2.08174	1.198953	0.001446	0.026035	NA	NA	NA
c2907_g1_i1	-1.44914	4.838662	0.000138	0.004384	RecName: Full=4-coumarate--CoA ligase; Short=4CL; AltName: Full=4-coumaroyl-CoA synthase [Pinus taeda]	UniRef90_K5UU00 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UU00_PHACS	GO:0003824|GO:0008152
c2910_g1_i1	-4.77541	7.382794	1.04E-25	5.06E-22	NA	UniRef90_J4H587 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4H587_FIBRA	NA
c2910_g2_i1	-4.84053	8.056424	4.25E-27	2.60E-23	NA	UniRef90_L8WI23 Uncharacterized protein n=1 Tax=Thanatephorus cucumeris (strain AG1-IA) RepID=L8WI23_THACA	NA
c2912_g2_i1	-1.35675	10.10289	0.000456	0.011146	NA	UniRef90_A0A098INF1 Uncharacterized protein n=2 Tax=Xanthomonas citri pv. citri RepID=A0A098INF1_XANCI	NA
c2932_g1_i1	-3.17662	5.058315	4.55E-09	8.36E-07	NA	NA	NA
c2932_g2_i1	-3.14458	5.254628	3.91E-06	0.000255	NA	NA	NA
c2936_g1_i1	-3.52575	5.229627	4.96E-13	2.09E-10	NA	NA	NA

c2936_g2_i1	-2.5521	4.521232	1.51E-06	0.000115	NA	NA	NA
c2949_g1_i1	-1.57488	4.368163	0.00037	0.009511	NA	NA	NA
c3082_g1_i1	-2.35117	1.044079	0.002082	0.033485	NA	NA	NA
c31_g1_i1	-1.18485	4.191143	0.001894	0.031404	NA	UniRef90_K5V7H2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V7H2_PHACS	NA
c3361_g1_i1	-4.05954	0.73726	0.000483	0.011668	NA	NA	NA
c3361_g1_i2	-4.05954	0.73726	0.000483	0.011668	NA	NA	NA
c3403_g1_i1	-3.10378	1.749226	1.17E-06	9.36E-05	NA	NA	NA
c3556_g1_i1	-5.27448	0.349931	0.000393	0.009968	NA	NA	NA
c3597_g1_i1	-2.63532	1.581478	0.000119	0.003892	NA	UniRef90_A0A0C3S8L4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S8L4_PHLGI	NA
c3664_g1_i1	-2.70498	2.200747	0.000894	0.018595	NA	UniRef90_K5VU64 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VU64_PHACS	NA
c3791_g1_i1	-2.25374	2.637941	0.000349	0.009118	NA	NA	NA
c3795_g1_i1	-2.24628	1.452885	0.00224	0.035261	NA	NA	NA
c37_g1_i1	-1.54732	6.04414	5.16E-05	0.002021	RecName: Full=NifU-like protein 5, mitochondrial; Short=AtNfu-I; Short=AtNfu5; Flags: Precursor [Arabidopsis thaliana]	UniRef90_A0A0C3RTK8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RTK8_PHLGI	GO:0005506|GO:0016226|GO:0051536
c37_g1_i2	-1.54732	6.04414	5.16E-05	0.002021	NA	NA	GO:0005506|GO:0016226|GO:0051536
c3824_g1_i1	-2.01298	1.787092	0.000716	0.015753	RecName: Full=Uncharacterized transporter C36.02c [Schizosaccharomyces pombe 972h-]	UniRef90_M2RHQ6 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2RHQ6_CERS8	NA
c3833_g1_i1	-2.34909	1.035048	0.000709	0.015673	NA	NA	NA
c3877_g1_i1	-1.73308	2.200969	0.000908	0.018755	NA	UniRef90_A0A0C3P2A5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P2A5_PHLGI	NA
c3878_g1_i1	-2.82886	1.846857	2.37E-05	0.001115	NA	NA	NA
c3881_g1_i1	-2.14821	5.488647	1.68E-08	2.67E-06	NA	NA	NA

c3881_g1_i2	-2.14821	5.488647	1.68E-08	2.67E-06	NA	UniRef90_B0DY77 Predicted protein n=1 Tax=Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) RepID=B0DY77_LACBS	NA
c3962_g1_i1	-3.37362	2.315945	1.51E-08	2.42E-06	RecName: Full=AN1-type zinc finger protein TMC1; AltName: Full=Trivalent metalloid-sensitive Cuz1-related protein 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5W8H6 Uncharacterized protein n=2 Tax=Phanerochaetaceae RepID=K5W8H6_PHACS	GO:0008270
c3968_g1_i1	-1.60919	4.711385	4.07E-06	0.000264	NA	UniRef90_K5WG16 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WG16_PHACS	NA
c3985_g1_i1	-4.55605	1.062758	6.51E-06	0.000389	RecName: Full=Uncharacterized membrane protein YFL054C [Saccharomyces cerevisiae S288c]	UniRef90_K5WMV9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WMV9_PHACS	GO:0005215|GO:0006810|GO:0016020
c4092_g2_i1	-4.94246	2.441357	2.02E-14	1.26E-11	NA	UniRef90_S7PTE9 Uncharacterized protein n=1 Tax=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) RepID=S7PTE9_GLOTA	NA
c4112_g1_i1	-1.99171	7.987216	1.18E-05	0.000637	RecName: Full=Disulfide-bond oxidoreductase YfcG; AltName: Full=GSH-dependent disulfide-bond oxidoreductase YfcG; AltName: Full=GST N1-1; AltName: Full=GST-like protein YfcG; AltName: Full=Organic hydroperoxidase [Escherichia coli K-12]	UniRef90_I7A570 Glutathione transferase Ure2p1 (Fragment) n=1 Tax=Phanerochaete chrysosporium RepID=I7A570_PHACH	GO:0005515
c4112_g2_i1	-2.56017	4.144904	2.63E-07	2.74E-05	NA	UniRef90_I7A570 Glutathione transferase Ure2p1 (Fragment) n=1 Tax=Phanerochaete chrysosporium RepID=I7A570_PHACH	NA
c4115_g1_i1	-1.85906	2.828218	0.000277	0.007659	NA	NA	NA
c4139_g1_i1	-2.46514	1.099927	0.000413	0.01037	NA	NA	NA
c4139_g1_i2	-2.46514	1.099927	0.000413	0.01037	NA	NA	NA
c4210_g1_i1	-3.46787	2.023816	3.18E-09	6.37E-07	RecName: Full=Probable intron-encoded endonuclease aI7; Contains: RecName: Full=Truncated non-functional cytochrome oxidase 1; Contains: RecName: Full=Intron-	UniRef90_L8B980 Cytochrome c oxidase subunit 1 n=5 Tax=Agaricomycetes incertae sedis RepID=L8B980_PHLRA	GO:0004129|GO:0005506|GO:0009055|GO:0009060|GO:0016021|GO:0020037|GO:0055114

					encoded endonuclease aI7; Flags: Precursor (mitochondrion) [Ustilago maydis 521]		
c4232_g1_i1	-1.39022	5.198938	0.001117	0.021651	NA	UniRef90_K5VSR9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSR9_PHACS	NA
c4298_g1_i1	-1.11823	6.236803	0.002909	0.042884	RecName: Full=Probable peptide methionine sulfoxide reductase; Short=Protein-methionine-S-oxide reductase; AltName: Full=Peptide-methionine (S)-S-oxide reductase; Short=Peptide Met(O) reductase [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3S738 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S738_PHLGI	GO:0008113|GO:0055114
c4298_g1_i2	-1.11823	6.236803	0.002909	0.042884	NA	NA	GO:0008113|GO:0055114
c4307_g1_i1	-1.28977	2.820193	0.003347	0.047387	NA	UniRef90_A0A0C3S4V1 Glycoside hydrolase family 61 protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S4V1_PHLGI	NA
c4308_g1_i1	-1.77692	8.629231	3.81E-05	0.001594	NA	NA	NA
c4370_g1_i1	-1.23196	9.877626	0.003045	0.044221	RecName: Full=PHO85 cyclin-9 [Saccharomyces cerevisiae S288c]	UniRef90_K5WWY7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WWY7_PHACS	GO:0000079|GO:0019901
c4403_g1_i1	-3.31561	0.802159	0.000293	0.008028	RecName: Full=DnaJ homolog subfamily B member 4 [Mus musculus]	UniRef90_A0A0C3SEX1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SEX1_PHLGI	NA
c4448_g1_i1	-1.37518	6.969291	0.000275	0.007619	RecName: Full=Cytochrome P450 61; AltName: Full=C-22 sterol desaturase [Schizosaccharomyces pombe 972h-]	UniRef90_G5EJV0 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJV0_PHACH	NA
c4448_g2_i1	-1.15989	6.59258	0.001702	0.029239	RecName: Full=Cytochrome P450 61; AltName: Full=C-22 sterol desaturase [Schizosaccharomyces pombe 972h-]	UniRef90_G5EJV0 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJV0_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c4494_g1_i1	-3.02499	0.623038	0.002437	0.03767	RecName: Full=Chaperone protein ClpB [Gloeobacter violaceus PCC 7421]	UniRef90_A0A066WGP6 Uncharacterized protein (Fragment) n=1 Tax=Rhizoctonia solani AG-8 WAC10335 RepID=A0A066WGP6_9HOMO	NA

c4494_g2_i1	-4.55733	1.671136	2.58E-07	2.71E-05	NA	NA	NA
c4494_g3_i1	-3.60396	1.661203	3.11E-07	3.19E-05	RecName: Full=Heat shock protein hsp98; AltName: Full=Protein aggregation-remodeling factor hsp98 [Neurospora crassa OR74A]	UniRef90_K5WPA0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WPA0_PHACS	GO:0005524
c4494_g4_i1	-3.90711	2.168298	8.51E-07	7.24E-05	RecName: Full=Chaperone protein ClpB1; AltName: Full=ATP-dependent Clp protease ATP-binding subunit ClpB homolog 1; AltName: Full=Casein lytic proteinase B1; AltName: Full=Heat shock protein 101 [Arabidopsis thaliana]	UniRef90_A0A0C3SDL6 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SDL6_PHLGI	NA
c4494_g5_i1	-3.19944	1.611674	1.84E-05	0.000912	RecName: Full=Heat shock protein 104; AltName: Full=Protein aggregation-remodeling factor hsp104 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WPA0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WPA0_PHACS	GO:0005524
c4498_g1_i1	-3.63297	1.002861	3.06E-05	0.001338	NA	NA	NA
c4530_g1_i1	-2.34809	12.65192	2.21E-07	2.40E-05	NA	NA	NA
c4533_g1_i1	-1.80777	2.699074	0.000643	0.01455	NA	NA	NA
c4537_g1_i1	-2.47565	3.46055	1.59E-07	1.81E-05	NA	NA	NA
c4537_g1_i2	-2.47565	3.46055	1.59E-07	1.81E-05	NA	NA	NA
c4558_g1_i1	-1.33962	8.712775	0.001312	0.024466	RecName: Full=GTP-binding protein rho1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_B0DYK0 Predicted protein n=37 Tax=Agaricomycotina RepID=B0DYK0_LACBS	GO:0005525|GO:0007264
c4599_g1_i1	-1.56507	4.046942	0.002216	0.034996	NA	UniRef90_K5UPM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UPM7_PHACS	NA
c4600_g1_i1	-1.8713	3.568086	0.001509	0.026861	NA	NA	NA
c4604_g1_i1	-1.96977	1.918226	0.000153	0.004761	NA	NA	NA
c4604_g1_i2	-1.96977	1.918226	0.000153	0.004761	RecName: Full=Putative acyl-coenzyme A synthetase [Aspergillus nidulans FGSC A4]	UniRef90_K5WCS6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCS6_PHACS	NA
c4670_g1_i1	-1.76039	2.904188	0.002134	0.03409	NA	NA	NA

c4735_g1_i1	-4.53837	7.73351	3.33E-08	4.84E-06	RecName: Full=Ligninase LG5; AltName: Full=Diarylpropane peroxidase; AltName: Full=Lignin peroxidase; Flags: Precursor [Phanerochaete chrysosporium]	UniRef90_P11543 Ligninase LG5 n=1 Tax=Phanerochaete chrysosporium RepID=LIG5_PHACH	NA
c475_g1_i1	-4.12767	0.781703	0.00026	0.00729	NA	UniRef90_M2R3D8 Uncharacterized protein n=1 Tax=Ceriporiopsis subvermispora (strain B) RepID=M2R3D8_CERS8	NA
c4862_g1_i1	-1.4254	5.435207	0.001953	0.032024	RecName: Full=Protein arginine N-methyltransferase 8-B; AltName: Full=Heterogeneous nuclear ribonucleoprotein methyltransferase-like protein 4; AltName: Full=zfL3 [Danio rerio]	UniRef90_A0A0C3SC07 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SC07_PHLGI	GO:0004719|GO:0005737|GO:0006464|GO:0006479|GO:0008152|GO:0008168|GO:0008276|GO:0008610
c4875_g1_i1	-1.42797	8.505037	0.000555	0.012972	NA	UniRef90_K5WNM2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNM2_PHACS	NA
c4883_g1_i1	-1.24879	3.831724	0.002402	0.037274	NA	UniRef90_K5UVQ8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UVQ8_PHACS	GO:0006812|GO:0008324|GO:0016021|GO:0055085
c4943_g1_i1	-2.93526	3.802323	1.48E-09	3.23E-07	NA	UniRef90_A0A067SQW0 Uncharacterized protein n=1 Tax=Galerina marginata CBS 339.88 RepID=A0A067SQW0_9AGAR	NA
c4960_g2_i1	-2.31837	7.058537	3.41E-06	0.000229	NA	NA	NA
c4989_g2_i1	-2.30309	1.181348	0.001606	0.028084	NA	NA	NA
c5011_g1_i1	-1.53843	2.715606	0.001953	0.032024	NA	NA	NA
c5049_g1_i1	-1.38476	4.886655	0.000454	0.011137	NA	NA	NA
c5069_g1_i1	-1.63852	2.020384	0.002623	0.03981	NA	NA	NA
c5081_g1_i1	-1.6082	5.43785	3.59E-05	0.001522	NA	NA	NA
c5157_g1_i1	-3.27484	1.858509	1.97E-05	0.000953	NA	NA	NA
c5169_g1_i1	-2.55403	2.246172	3.45E-07	3.49E-05	NA	NA	NA
c5187_g1_i1	-1.16746	4.358442	0.001304	0.024355	RecName: Full=Cysteine-rich protein 1; Short=CRP-1; AltName: Full=Cysteine-rich heart protein; Short=CRHP; Short=hCRHP;	UniRef90_K5W0G0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W0G0_PHACS	GO:0008270

					AltName: Full=Cysteine-rich intestinal protein; Short=CRIP [Homo sapiens]		
c5207_g1_i1	-1.96004	2.822991	0.000168	0.005109	NA	NA	NA
c5219_g1_i1	-3.49057	1.282634	0.000421	0.010527	NA	NA	NA
c5231_g1_i1	-3.69213	9.108393	8.97E-19	1.68E-15	RecName: Full=Uncharacterized protein TC_0114	UniRef90_L8B9G8 Uncharacterized protein n=1 Tax=Phlebia radiata RepID=L8B9G8_PHLRA	NA
c5231_g2_i1	-3.54836	5.432078	1.24E-18	2.17E-15	NA	UniRef90_C7DK00 Mitochondrial DNA (Fragment) n=1 Tax=Polyporus grammocephalus RepID=C7DK00_9APHY	NA
c5231_g3_i1	-4.48433	6.763243	3.91E-23	1.59E-19	NA	UniRef90_L8B9G2 Uncharacterized protein n=1 Tax=Phlebia radiata RepID=L8B9G2_PHLRA	NA
c5233_g1_i1	-2.51642	2.548529	1.28E-06	9.97E-05	NA	NA	NA
c5241_g1_i1	-1.62473	8.007051	0.002431	0.037612	NA	UniRef90_K5WCB7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCB7_PHACS	NA
c5268_g1_i1	-4.08114	0.750924	0.00013	0.004193	NA	NA	NA
c5375_g1_i1	-1.26402	4.423898	0.000512	0.01223	NA	NA	NA
c5386_g1_i1	-1.19497	4.023653	0.001535	0.02722	NA	UniRef90_K5W7X5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W7X5_PHACS	NA
c5422_g1_i1	-2.08337	1.67974	0.001858	0.031024	NA	NA	NA
c5425_g1_i1	-2.47106	2.139336	0.001243	0.023455	NA	NA	NA
c5438_g1_i1	-1.74337	3.353773	4.88E-05	0.001939	NA	UniRef90_K5WYH4 Citrate synthase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYH4_PHACS	NA
c544_g1_i1	-2.35496	2.212334	0.000232	0.00666	RecName: Full=Polyubiquitin; Contains: RecName: Full=Ubiquitin; Flags: Precursor, partial [Hordeum vulgare]	UniRef90_M0UCV0 Uncharacterized protein n=13 Tax=Mesangiospermae RepID=M0UCV0_MUSAM	GO:0005515
c5453_g1_i1	-1.22238	4.839497	0.002921	0.043017	NA	NA	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c5453_g1_i2	-1.22238	4.839497	0.002921	0.043017	RecName: Full=O-methylsterigmatocystin oxidoreductase; Short=OMST oxidoreductase; AltName: Full=Aflatoxin B synthase;	UniRef90_G5EJQ1 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJQ1_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114

					AltName: Full=Aflatoxin biosynthesis protein Q; AltName: Full=Cytochrome P450 64 [Aspergillus parasiticus]		
c5460_g1_i1	-2.23184	0.966723	0.003173	0.045582	RecName: Full=Heat shock protein sti1 homolog [Schizosaccharomyces pombe 972h-]	UniRef90_J4GAS7 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4GAS7_FIBRA	GO:0005515
c5526_g1_i1	-2.1004	6.103977	4.21E-05	0.001719	NA	NA	NA
c5526_g1_i2	-2.1004	6.103977	4.21E-05	0.001719	NA	NA	NA
c5526_g1_i3	-2.1004	6.103977	4.21E-05	0.001719	NA	NA	NA
c5605_g1_i1	-1.90716	2.725345	0.0013	0.024302	NA	NA	NA
c5675_g1_i1	-5.27463	3.824734	1.65E-19	3.36E-16	RecName: Full=ATP synthase subunit 9, mitochondrial; AltName: Full=Lipid-binding protein (mitochondrion) [Ustilago maydis 521]	UniRef90_S4SQ89 ATP synthase subunit 9, mitochondrial n=3 Tax=Agaricales RepID=S4SQ89_AGABB	GO:0015078|GO:0015991|GO:0033177
c5739_g1_i1	-2.43579	1.453839	0.000173	0.005243	NA	NA	NA
c5751_g2_i1	-1.32981	3.982372	0.000466	0.01136	NA	NA	NA
c5751_g2_i2	-1.32981	3.982372	0.000466	0.01136	NA	UniRef90_K5WA14 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WA14_PHACS	NA
c5793_g2_i1	-2.2336	2.172444	2.33E-05	0.001099	NA	NA	NA
c5793_g2_i2	-2.2336	2.172444	2.33E-05	0.001099	NA	NA	NA
c5793_g2_i3	-2.2336	2.172444	2.33E-05	0.001099	NA	NA	NA
c5793_g2_i4	-2.2336	2.172444	2.33E-05	0.001099	NA	NA	NA
c5855_g2_i1	-3.85776	0.619123	0.000283	0.0078	NA	NA	NA
c5895_g2_i1	-3.22094	2.303697	6.22E-07	5.52E-05	NA	NA	NA
c5985_g1_i1	-4.10911	1.341977	6.72E-06	0.000398	NA	NA	NA
c6025_g1_i1	-1.47191	6.222789	0.002614	0.03978	RecName: Full=3-ketoacyl-CoA thiolase A, peroxisomal; AltName: Full=Acetyl-CoA acyltransferase A; AltName: Full=Beta-ketothiolase A; AltName: Full=Peroxisomal 3-oxoacyl-CoA thiolase A; Flags: Precursor [Mus musculus]	UniRef90_K5VUA2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUA2_PHACS	GO:0008152|GO:0016747

c6025_g2_i1	-1.80153	7.1177	0.000935	0.019077	RecName: Full=3-ketoacyl-CoA thiolase A, peroxisomal; AltName: Full=Acetyl-CoA acyltransferase A; AltName: Full=Beta-ketothiolase A; AltName: Full=Peroxisomal 3-oxoacyl-CoA thiolase A; AltName: Full=Thiolase IA; Flags: Precursor [Candida tropicalis]	UniRef90_K5VUA2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUA2_PHACS	GO:0008152|GO:0016747
c6025_g3_i1	-1.82061	9.589791	0.000433	0.010747	RecName: Full=3-ketoacyl-CoA thiolase, peroxisomal; AltName: Full=Acetyl-CoA acyltransferase; AltName: Full=Beta-ketothiolase; AltName: Full=Peroxisomal 3-oxoacyl-CoA thiolase; Flags: Precursor [Yarrowia lipolytica CLIB122]	UniRef90_K5VUA2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUA2_PHACS	GO:0008152|GO:0016747
c6031_g1_i1	-2.77437	1.967654	6.53E-06	0.00039	NA	NA	NA
c6040_g1_i1	-1.45004	7.834056	0.001762	0.030071	RecName: Full=Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial; Short=MCAD; Flags: Precursor [Drosophila melanogaster]	UniRef90_K5W6I9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6I9_PHACS	GO:0003995|GO:0008152|GO:0008270|GO:0016627|GO:0016787|GO:0020037|GO:0050660|GO:0055114
c6056_g3_i1	-1.40328	5.331451	0.000349	0.009118	NA	UniRef90_K5VW16 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VW16_PHACS	NA
c6084_g1_i1	-1.79733	7.331492	0.000146	0.004573	RecName: Full=Mitochondrial dicarboxylate transporter; AltName: Full=DTP; AltName: Full=Dicarboxylate carrier 1 [Saccharomyces cerevisiae S288c]	UniRef90_A0A0C3S0Z1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S0Z1_PHLGI	NA
c6084_g2_i1	-1.47641	8.775638	0.002247	0.035316	RecName: Full=Mitochondrial 2-oxoglutarate/malate carrier protein; Short=OGCP; AltName: Full=Solute carrier family 25 member 11 [Mus musculus]	UniRef90_K5W1J0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1J0_PHACS	NA
c6084_g2_i2	-1.47641	8.775638	0.002247	0.035316	NA	NA	NA
c6089_g1_i1	-1.83137	10.31424	0.000669	0.015019	NA	UniRef90_K5W6K3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6K3_PHACS	NA

c6103_g1_i1	-2.35979	8.402629	5.42E-05	0.002074	NA	UniRef90_A0A0C3NTS5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NTS5_PHLGI	NA
c6103_g1_i2	-2.35979	8.402629	5.42E-05	0.002074	NA	NA	NA
c6107_g1_i1	-1.93092	2.567052	0.000533	0.012613	RecName: Full=Potassium transporter 18; AltName: Full=OsHAK18 [Oryza sativa Japonica Group]	UniRef90_K5VR52 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VR52_PHACS	GO:0015079|GO:0016020|GO:0071805
c6116_g1_i1	-1.41577	3.714035	0.000535	0.012635	NA	NA	NA
c6116_g1_i2	-1.41577	3.714035	0.000535	0.012635	NA	NA	NA
c6116_g1_i3	-1.41577	3.714035	0.000535	0.012635	NA	NA	NA
c6120_g1_i1	-1.59804	8.990859	0.00162	0.028285	NA	NA	NA
c6131_g1_i1	-1.26343	5.775936	0.002601	0.039663	NA	UniRef90_A0A0C3GH71 Uncharacterized protein n=1 Tax=Piloderma croceum F 1598 RepID=A0A0C3GH71_9HOMO	NA
c6131_g2_i1	-2.48926	3.530809	9.91E-07	8.12E-05	NA	NA	NA
c6154_g1_i1	-1.74795	1.484721	0.002395	0.037218	NA	UniRef90_K5URZ3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5URZ3_PHACS	NA
c6161_g1_i1	-4.70364	1.173594	3.84E-06	0.000252	NA	NA	NA
c6192_g1_i1	-1.37002	8.484098	0.001663	0.028797	NA	UniRef90_K5V8P8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V8P8_PHACS	NA
c6199_g1_i1	-1.1195	5.005665	0.002751	0.041203	NA	NA	NA
c6199_g1_i2	-1.1195	5.005665	0.002751	0.041203	NA	UniRef90_K5WR56 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WR56_PHACS	NA
c6242_g1_i1	-4.29348	1.480444	2.49E-07	2.64E-05	NA	NA	NA
c6242_g1_i2	-4.29348	1.480444	2.49E-07	2.64E-05	NA	NA	NA
c6266_g1_i1	-1.70182	3.806017	5.53E-06	0.000343	RecName: Full=Flavin reductase (NADPH); Short=FR; AltName: Full=Biliverdin reductase B; Short=BVR-B; AltName: Full=Biliverdin-IX beta-reductase; AltName: Full=NADPH-dependent diaphorase; AltName:	UniRef90_K5VCQ8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCQ8_PHACS	GO:0003824|GO:0050662

					Full=NADPH-flavin reductase; Short=FLR [Mus musculus]		
c6280_g1_i1	-1.27369	7.855641	0.001043	0.020641	NA	NA	GO:0005740|GO:0016021
c6280_g1_i2	-1.27369	7.855641	0.001043	0.020641	RecName: Full=Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial; Short=CybS; AltName: Full=Succinate-ubiquinone reductase membrane anchor subunit; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_K5VU00 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VU00_PHACS	GO:0005740|GO:0016021
c6280_g1_i3	-1.27369	7.855641	0.001043	0.020641	NA	NA	GO:0005740|GO:0016021
c6323_g1_i1	-1.84958	5.127233	9.62E-07	7.91E-05	RecName: Full=Copper resistance protein CRF1; AltName: Full=YlCRF1 [Yarrowia lipolytica CLIB122]	UniRef90_K5W925 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W925_PHACS	GO:0003677|GO:0003700|GO:0005507|GO:0005634|GO:0006355
c6335_g1_i1	-1.36572	7.773645	0.001127	0.021825	NA	NA	GO:0004017
c6335_g1_i2	-1.36572	7.773645	0.001127	0.021825	RecName: Full=GTP:AMP phosphotransferase, mitochondrial; AltName: Full=Adenylate kinase 3; Short=AK 3 [Saccharomyces cerevisiae S288c]	UniRef90_K5W8S5 GTP:AMP phosphotransferase, mitochondrial n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8S5_PHACS	GO:0004017
c6335_g1_i3	-1.36572	7.773645	0.001127	0.021825	NA	NA	GO:0004017
c6335_g2_i1	-1.56642	6.137654	0.000102	0.003416	NA	UniRef90_K5W8S5 GTP:AMP phosphotransferase, mitochondrial n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8S5_PHACS	NA
c6346_g1_i1	-1.84099	3.080461	8.83E-05	0.003092	NA	UniRef90_K5VCL7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCL7_PHACS	NA
c6346_g1_i2	-1.84099	3.080461	8.83E-05	0.003092	NA	NA	NA
c6346_g1_i3	-1.84099	3.080461	8.83E-05	0.003092	NA	NA	GO:0046872
c6359_g1_i1	-1.31015	4.717233	0.000601	0.013733	RecName: Full=Cysteine and glycine-rich protein 1; AltName: Full=Cysteine-rich protein 1; Short=CRP1 [Pongo abelii]	UniRef90_UPI0004416F31 hypothetical protein PUNSTDRAFT_73819 n=1 Tax=Punctularia strigosozonata (strain HHB-11173) RepID=UPI0004416F31	GO:0008270
c6359_g1_i2	-1.31015	4.717233	0.000601	0.013733	NA	NA	GO:0008270

c6359_g1_i3	-1.31015	4.717233	0.000601	0.013733	NA	NA	GO:0008270
c6364_g1_i1	-3.01223	1.467634	2.01E-05	0.000964	NA	NA	NA
c6382_g1_i1	-3.89548	4.911918	1.16E-17	1.57E-14	NA	NA	NA
c6382_g1_i2	-3.89548	4.911918	1.16E-17	1.57E-14	NA	NA	NA
c639_g1_i1	-3.11735	0.68216	0.002374	0.036988	RecName: Full=mRNA stability protein mug134; AltName: Full=Initiation of G zero protein 1 [Schizosaccharomyces pombe 972h-]	UniRef90_UPI0004414B6A Endosulfine-domain-containing protein n=1 Tax=Dichomitus squalens (strain LYAD-421) RepID=UPI0004414B6A	NA
c6425_g3_i1	-2.27094	1.829265	0.0002	0.005939	NA	NA	NA
c6440_g1_i1	-1.55536	8.582072	0.001418	0.025716	NA	UniRef90_K5VZN9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZN9_PHACS	NA
c6454_g1_i1	-1.83551	3.71948	1.12E-05	0.000611	NA	UniRef90_K5VTJ6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VTJ6_PHACS	NA
c6454_g1_i2	-1.83551	3.71948	1.12E-05	0.000611	NA	NA	NA
c6467_g1_i1	-1.77358	2.916385	0.001419	0.025716	NA	NA	GO:0003824|GO:0008152
c6467_g1_i2	-1.77358	2.916385	0.001419	0.025716	RecName: Full=Probable 4-coumarate--CoA ligase 1; Short=4CL 1; AltName: Full=4-coumaroyl-CoA synthase 1 [Dictyostelium discoideum]	UniRef90_K5WCS6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WCS6_PHACS	GO:0003824|GO:0008152
c6477_g1_i1	-1.58594	2.04633	0.001073	0.021051	NA	UniRef90_K5UVM1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UVM1_PHACS	NA
c6482_g1_i1	-2.26083	4.04419	8.77E-09	1.50E-06	NA	NA	NA
c6499_g1_i1	-1.36069	2.714356	0.003202	0.045922	NA	NA	NA
c6559_g1_i1	-1.67278	11.96981	0.000763	0.016388	NA	NA	NA
c6588_g1_i1	-2.04947	5.040278	3.22E-08	4.74E-06	NA	UniRef90_A0A0C3PQR8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PQR8_PHLGI	NA
c6588_g2_i1	-2.24785	3.739293	3.79E-09	7.49E-07	NA	UniRef90_A0A0C3PQR8 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PQR8_PHLGI	NA

c6588_g3_i1	-1.86112	4.164711	2.94E-06	0.000205	NA	UniRef90_K5UZ05 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UZ05_PHACS	NA
c6593_g1_i1	-1.17804	3.178772	0.00316	0.045543	NA	NA	NA
c6617_g1_i1	-1.16546	7.252303	0.00205	0.033115	RecName: Full=Ubiquitin-conjugating enzyme E2 2; AltName: Full=Ubiquitin carrier protein UBC2; AltName: Full=Ubiquitin-protein ligase UBC2 [Ustilago maydis 521]	UniRef90_K5WBI6 Uncharacterized protein n=4 Tax=Polyporales RepID=K5WBI6_PHACS	GO:0016881
c6620_g2_i1	-1.79715	8.724993	0.000315	0.008449	RecName: Full=Leukotriene-B4 omega-hydroxylase 3; AltName: Full=Cyp4f-14; AltName: Full=Cytochrome P450 4F14; AltName: Full=Cytochrome P450-LTB-omega; AltName: Full=Leukotriene-B4 20-monooxygenase 3 [Mus musculus]	UniRef90_G5EJM4 Cytochrome P450 n=1 Tax=Phanerochaete chrysosporium RepID=G5EJM4_PHACH	GO:0005506|GO:0016705|GO:0020037|GO:0055114
c6621_g2_i1	-1.44407	7.164038	0.002968	0.043407	NA	UniRef90_K5W534 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W534_PHACS	NA
c6621_g3_i1	-1.45958	6.128367	0.002168	0.03445	NA	UniRef90_K5W534 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W534_PHACS	NA
c6687_g1_i1	-2.64134	1.39835	4.52E-05	0.001831	NA	NA	NA
c671_g1_i1	-5.47946	0.465423	9.08E-05	0.003159	NA	NA	NA
c6755_g2_i1	-1.14295	4.358218	0.002395	0.037218	NA	UniRef90_A0A0C3SD64 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SD64_PHLGI	NA
c678_g1_i1	-3.14272	4.920114	1.94E-10	4.84E-08	RecName: Full=Carbonic anhydrase; AltName: Full=Carbonate dehydratase [Schizosaccharomyces pombe 972h-]	UniRef90_K5WMK7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WMK7_PHACS	GO:0004089|GO:0008270
c6812_g1_i1	-2.68902	1.243933	0.000128	0.00414	NA	NA	NA
c682_g1_i1	-1.46597	1.906662	0.003222	0.04611	NA	NA	NA
c6839_g1_i1	-1.18548	4.547351	0.000843	0.017723	RecName: Full=Putative acyl-coenzyme A synthetase [Aspergillus nidulans FGSC A4]	UniRef90_K5UU00 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UU00_PHACS	GO:0003824|GO:0008152

c6844_g1_i1	-1.83171	9.954504	9.28E-05	0.003218	RecName: Full=[Pyruvate dehydrogenase (acetyl-transferring)] kinase, mitochondrial; Short=Pyruvate dehydrogenase kinase; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_K5X522 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X522_PHACS	NA
c6849_g1_i1	-1.59026	5.590206	0.000483	0.011668	NA	NA	NA
c6849_g1_i2	-1.59026	5.590206	0.000483	0.011668	NA	UniRef90_K5X2X3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X2X3_PHACS	NA
c6855_g1_i1	-1.76497	6.291651	0.000925	0.018942	RecName: Full=Protein arginine N-methyltransferase 1; AltName: Full=Type I protein arginine N-methyltransferase; Short=Type I PRMT [Schizosaccharomyces pombe 972h-]	UniRef90_K5VSF4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSF4_PHACS	GO:0006479|GO:0008168
c6855_g2_i1	-2.11309	4.666202	4.90E-06	0.000308	NA	NA	NA
c6855_g2_i2	-2.11309	4.666202	4.90E-06	0.000308	RecName: Full=Protein arginine N-methyltransferase 1 [Chlamydomonas reinhardtii]	UniRef90_K5VSF4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VSF4_PHACS	NA
c6913_g1_i1	-1.56648	2.300233	0.003378	0.047673	NA	UniRef90_K5VD29 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VD29_PHACS	NA
c6920_g1_i1	-2.34761	7.842311	1.86E-08	2.91E-06	RecName: Full=Lathosterol oxidase; AltName: Full=C-5 sterol desaturase; AltName: Full=Delta(7)-sterol 5-desaturase; AltName: Full=Lathosterol 5-desaturase; AltName: Full=Sterol-C5-desaturase [Homo sapiens]	UniRef90_A0A0C3RZY1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RZY1_PHLGI	GO:0005506|GO:0006633|GO:0016491|GO:0055114
c6920_g2_i1	-1.76783	3.164253	0.00032	0.008538	NA	UniRef90_K5W2H7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2H7_PHACS	NA
c6920_g3_i1	-2.34986	7.224244	7.57E-08	9.61E-06	NA	UniRef90_A0A0C3RZY1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RZY1_PHLGI	NA

c6941_g1_i1	-1.78904	8.847985	1.70E-05	0.000864	RecName: Full=Protoplast secreted protein 2; Flags: Precursor [Saccharomyces cerevisiae S288c]	UniRef90_F1T2K0 1,4-benzoquinone reductase n=1 Tax=Phanerochaete sordida RepID=F1T2K0_9APHY	GO:0010181|GO:0016491
c6948_g1_i1	-1.55866	2.386331	0.001982	0.032327	NA	NA	NA
c7091_g1_i1	-2.10034	1.604441	0.000989	0.019861	NA	UniRef90_K5WAK0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WAK0_PHACS	NA
c70_g1_i1	-1.7252	6.096088	0.000597	0.013672	NA	NA	NA
c7109_g1_i1	-1.56953	5.716129	0.001027	0.020443	NA	UniRef90_K5W8U9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8U9_PHACS	NA
c7131_g1_i1	-1.62443	1.686145	0.002212	0.034976	NA	NA	NA
c7150_g1_i1	-5.04495	0.229179	0.000761	0.016364	NA	NA	NA
c7204_g1_i1	-2.89032	3.526738	3.16E-07	3.23E-05	NA	NA	NA
c7204_g1_i2	-2.89032	3.526738	3.16E-07	3.23E-05	NA	NA	NA
c7204_g1_i3	-2.89032	3.526738	3.16E-07	3.23E-05	NA	UniRef90_K5W8C3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8C3_PHACS	NA
c7204_g1_i4	-2.89032	3.526738	3.16E-07	3.23E-05	NA	NA	NA
c7228_g1_i1	-1.9925	2.713772	5.47E-06	0.00034	NA	NA	NA
c7233_g1_i1	-2.71288	2.484345	3.10E-05	0.001353	NA	UniRef90_K5WEM1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEM1_PHACS	NA
c7242_g2_i1	-1.56034	7.172042	6.79E-05	0.002478	RecName: Full=Succinate dehydrogenase [ubiquinone] cytochrome b subunit, mitochondrial; Flags: Precursor [Saccharomyces cerevisiae S288c]	UniRef90_K5WF33 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WF33_PHACS	NA
c7250_g1_i1	-1.29949	7.208164	0.002495	0.038382	NA	NA	NA
c7250_g1_i2	-1.29949	7.208164	0.002495	0.038382	NA	NA	NA
c7250_g1_i3	-1.29949	7.208164	0.002495	0.038382	NA	UniRef90_K5W774 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W774_PHACS	NA

c7251_g1_i1	-2.78121	1.821783	3.20E-06	0.00022	NA	NA	NA
c7258_g1_i1	-2.08166	2.239506	0.000361	0.009364	RecName: Full=L-serine dehydratase/L-threonine deaminase; Short=SDH; AltName: Full=L-serine deaminase; AltName: Full=L-threonine dehydratase; Short=TDH [Mus musculus]	UniRef90_A0A0C3S660 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S660_PHLGI	NA
c7270_g1_i1	-2.66573	3.061708	0.000118	0.003852	NA	NA	NA
c7277_g1_i1	-2.89364	5.640199	7.58E-10	1.68E-07	NA	NA	NA
c7277_g1_i2	-2.89364	5.640199	7.58E-10	1.68E-07	NA	NA	NA
c7286_g1_i1	-1.20123	4.702832	0.001415	0.025716	NA	UniRef90_K5WQD8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQD8_PHACS	NA
c7316_g1_i1	-1.65651	5.425665	8.09E-06	0.000465	NA	UniRef90_K5WNE7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WNE7_PHACS	NA
c7316_g1_i2	-1.65651	5.425665	8.09E-06	0.000465	NA	NA	NA
c7316_g1_i3	-1.65651	5.425665	8.09E-06	0.000465	NA	NA	NA
c7319_g1_i1	-1.91438	3.062198	0.001098	0.0214	NA	UniRef90_A0A060S4R4 Uncharacterized protein n=1 Tax=Pycnoporus cinnabarinus RepID=A0A060S4R4_PYCCI	NA
c7319_g2_i1	-1.75914	2.333262	0.002604	0.03968	NA	NA	NA
c7319_g2_i2	-1.75914	2.333262	0.002604	0.03968	NA	NA	NA
c7345_g1_i1	-2.20597	7.76193	8.17E-06	0.000467	RecName: Full=Oleate-induced peroxisomal protein POX18; Short=PXP-18; AltName: Full=Lipid-transfer protein [Candida maltosa]	UniRef90_K5WGG4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGG4_PHACS	NA
c7347_g1_i1	-2.51025	1.87998	2.65E-05	0.001199	NA	NA	NA
c7366_g1_i1	-1.51521	2.652505	0.001447	0.026035	NA	NA	NA
c7369_g1_i1	-1.53749	9.048942	0.001315	0.024471	NA	NA	GO:0005509
c7369_g1_i2	-1.53749	9.048942	0.001315	0.024471	RecName: Full=Programmed cell death protein 6; AltName: Full=ALG-257; AltName: Full=PMP41; AltName: Full=Probable calcium-binding protein ALG-2 [Mus musculus]	UniRef90_A0A0C3NUN2 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NUN2_PHLGI	GO:0005509

c7369_g1_i3	-1.53749	9.048942	0.001315	0.024471	NA	NA	GO:0005509
c7401_g1_i1	-2.35492	3.615922	3.37E-08	4.86E-06	NA	UniRef90_A0A0C3NM31 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NM31_PHLGI	NA
c7446_g1_i1	-1.43742	9.161238	0.000334	0.008827	RecName: Full=Synaptobrevin homolog 1 [Schizosaccharomyces pombe 972h-]	UniRef90_K5VPF3 Uncharacterized protein n=6 Tax=Agaricomycetes RepID=K5VPF3_PHACS	GO:0016021|GO:0016192
c7449_g2_i1	-2.09474	2.304126	7.12E-05	0.002575	NA	NA	NA
c7449_g2_i2	-2.09474	2.304126	7.12E-05	0.002575	NA	UniRef90_K5VCG0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VCG0_PHACS	NA
c7474_g1_i1	-1.54822	11.07872	0.00265	0.039981	RecName: Full=AN1-type zinc finger protein TMC1; AltName: Full=Trivalent metalloid-sensitive Cuz1-related protein 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5W8H6 Uncharacterized protein n=2 Tax=Phanerochaetaceae RepID=K5W8H6_PHACS	GO:0008270
c7481_g1_i1	-1.87008	5.663854	0.000236	0.006768	RecName: Full=Hydroxyquinol 1,2-dioxygenase [Rhodococcus opacus]	UniRef90_K5WG12 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WG12_PHACS	GO:0005506|GO:0009712|GO:0018576|GO:0055114
c74_g1_i1	-1.63245	4.901956	1.22E-05	0.000655	NA	UniRef90_K5URX1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5URX1_PHACS	NA
c74_g2_i1	-1.33476	5.988671	0.000486	0.011701	RecName: Full=Uncharacterized protein C9E9.04 [Schizosaccharomyces pombe 972h-]	UniRef90_K5URX1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5URX1_PHACS	NA
c7522_g1_i1	-1.23544	6.862042	0.002033	0.032912	RecName: Full=Homeobox protein Dlx1a; Short=DLX-1; AltName: Full=Distal-less homeobox gene 1a [Danio rerio]	UniRef90_K5WPQ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WPQ5_PHACS	GO:0003677
c7532_g1_i1	-1.58794	4.817877	2.17E-05	0.001032	NA	NA	GO:0046872
c7532_g1_i2	-1.58794	4.817877	2.17E-05	0.001032	RecName: Full=Zinc finger protein MSN4; AltName: Full=Multicopy suppressor of SNF1 protein 4 [Saccharomyces cerevisiae S288c]	UniRef90_K5UXA8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UXA8_PHACS	GO:0046872
c7545_g1_i1	-2.52021	3.867176	4.08E-09	7.78E-07	NA	NA	NA

c7589_g1_i1	-2.18274	4.895976	2.31E-05	0.001093	NA	UniRef90_K5WID0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WID0_PHACS	NA
c7590_g1_i1	-1.32825	4.410896	0.000566	0.01315	NA	UniRef90_K5WB02 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WB02_PHACS	NA
c7592_g1_i1	-2.55996	4.876107	8.17E-06	0.000467	NA	NA	NA
c7592_g1_i2	-2.55996	4.876107	8.17E-06	0.000467	NA	NA	NA
c7604_g1_i1	-1.52894	6.953062	0.000629	0.014289	RecName: Full=Putative agmatinase 1; AltName: Full=Agmatine ureohydrolase 1; Short=AUH 1; Flags: Precursor [Schizosaccharomyces pombe 972h-]	UniRef90_K5V0H8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V0H8_PHACS	GO:0046872
c7607_g1_i1	-3.96429	5.172055	1.88E-14	1.21E-11	RecName: Full=Uncharacterized oxidoreductase C663.09c [Schizosaccharomyces pombe 972h-]	UniRef90_K5WSW5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WSW5_PHACS	GO:0008152|GO:0016491
c7613_g1_i1	-2.44465	1.848519	2.21E-05	0.001049	NA	NA	NA
c7613_g1_i2	-2.44465	1.848519	2.21E-05	0.001049	NA	NA	NA
c7614_g1_i1	-2.13363	1.942335	0.000167	0.005095	NA	UniRef90_K5ULP8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5ULP8_PHACS	NA
c7653_g1_i1	-2.44184	2.727469	3.82E-06	0.000252	NA	UniRef90_K5ULM5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5ULM5_PHACS	NA
c7661_g1_i1	-2.75	2.980358	1.86E-06	0.000137	NA	NA	NA
c7661_g2_i1	-1.95315	6.828225	0.000125	0.004078	RecName: Full=Zinc finger protein C25B8.19c [Schizosaccharomyces pombe 972h-]	UniRef90_A0A0C3NM09 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NM09_PHLGI	GO:0046872
c7683_g1_i1	-2.07938	3.656517	3.87E-05	0.001609	NA	UniRef90_K5VUK3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VUK3_PHACS	NA
c7683_g2_i1	-1.81438	1.918627	0.000741	0.016045	NA	UniRef90_S8FFL9 Uncharacterized protein n=1 Tax=Fomitopsis pinicola (strain FP-58527) RepID=S8FFL9_FOMPI	NA

c7690_g1_i1	-2.0468	10.0072	3.63E-06	0.000241	RecName: Full=Plasma membrane proteolipid 3 [Fusarium graminearum PH-1]	UniRef90_U5H8B0 Uncharacterized protein n=1 Tax=Microbotryum violaceum (strain p1A1 Lamole) RepID=U5H8B0_USTV1	GO:0016021
c7708_g1_i1	-1.61472	9.412764	0.001442	0.025985	NA	NA	NA
c7708_g1_i2	-1.61472	9.412764	0.001442	0.025985	NA	NA	NA
c7722_g1_i1	-1.96097	1.845598	0.003146	0.045386	NA	UniRef90_A0A0C3PTX0 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PTX0_PHLGI	NA
c7722_g1_i2	-1.96097	1.845598	0.003146	0.045386	NA	NA	NA
c7769_g1_i1	-1.87693	4.553003	1.86E-05	0.000915	RecName: Full=UPF0659 protein C216.03 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WKC9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKC9_PHACS	GO:0016620|GO:0051287|GO:0055114
c7769_g2_i1	-1.96668	3.95689	2.40E-05	0.001124	RecName: Full=UPF0659 protein C216.03 [Schizosaccharomyces pombe 972h-]	UniRef90_K5WKC9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKC9_PHACS	NA
c7788_g1_i1	-1.20832	3.810421	0.001107	0.021516	RecName: Full=EKC/KEOPS complex subunit CGI121 [Cryptococcus neoformans var. neoformans B-3501A]	UniRef90_K5WI32 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WI32_PHACS	NA
c7788_g1_i2	-1.20832	3.810421	0.001107	0.021516	NA	NA	NA
c7791_g1_i1	-2.12159	6.045637	1.87E-06	0.000138	NA	UniRef90_K5WUL9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WUL9_PHACS	NA
c7791_g2_i1	-1.53645	5.786771	0.000753	0.016243	NA	UniRef90_K5WUL9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WUL9_PHACS	NA
c7791_g3_i1	-1.44773	3.934005	0.003307	0.046933	NA	NA	NA
c7793_g1_i1	-2.34266	3.858951	2.60E-07	2.72E-05	NA	NA	NA
c7803_g1_i1	-1.43079	7.115475	0.002199	0.034834	NA	UniRef90_A0A0C3SEW5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SEW5_PHLGI	NA
c7825_g1_i1	-1.34251	7.44669	0.001177	0.022573	NA	UniRef90_A0A0C3P0U7 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P0U7_PHLGI	NA

c7828_g1_i1	-2.39582	9.401856	1.58E-07	1.80E-05	RecName: Full=Probable 2-methylcitrate dehydratase [Saccharomyces cerevisiae S288c]	UniRef90_K5W6B4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6B4_PHACS	GO:0019543|GO:0047547
c7828_g1_i2	-2.39582	9.401856	1.58E-07	1.80E-05	NA	NA	GO:0019543|GO:0047547
c7835_g1_i1	-1.04792	4.732312	0.002726	0.040933	NA	NA	NA
c7856_g1_i1	-2.2161	0.958494	0.001701	0.029235	NA	NA	NA
c7865_g1_i1	-1.58935	5.959172	0.000511	0.012217	NA	UniRef90_K5VS78 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VS78_PHACS	NA
c7898_g1_i1	-2.11507	6.675459	1.24E-05	0.000663	NA	UniRef90_K5W049 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W049_PHACS	NA
c7908_g1_i1	-1.40745	2.711372	0.001624	0.028316	NA	NA	NA
c7908_g1_i2	-1.40745	2.711372	0.001624	0.028316	NA	NA	NA
c7910_g1_i1	-2.90067	3.069349	8.19E-07	7.02E-05	NA	NA	NA
c7910_g1_i2	-2.90067	3.069349	8.19E-07	7.02E-05	NA	UniRef90_K5WGQ0 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGQ0_PHACS	NA
c7915_g1_i1	-2.50554	1.474131	0.000335	0.008835	NA	NA	NA
c7919_g1_i1	-2.25285	8.28272	4.54E-06	0.000289	NA	UniRef90_A0A0C3PU53 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PU53_PHLGI	GO:0016021|GO:0055085
c7919_g2_i1	-1.82296	7.396747	7.04E-05	0.002549	RecName: Full=Probable peptide/nitrate transporter At3g43790; AltName: Full=Protein ZINC INDUCED FACILITATOR-LIKE 2 [Arabidopsis thaliana]	UniRef90_A0A0C3PU53 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PU53_PHLGI	GO:0016021|GO:0022857|GO:0055085
c7936_g2_i1	-2.06848	3.972951	2.42E-07	2.58E-05	NA	UniRef90_A0A0C3NEL8 Uncharacterized protein (Fragment) n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NEL8_PHLGI	NA
c7936_g3_i1	-1.81188	6.184057	4.16E-06	0.000269	RecName: Full=Lipase 2; AltName: Full=Triacylglycerol lipase 2 [Saccharomyces cerevisiae S288c]	UniRef90_K5VF57 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VF57_PHACS	NA
c7942_g1_i1	-2.81924	1.090972	0.000589	0.013529	NA	NA	NA

c7942_g2_i1	-2.7109	2.621616	2.74E-06	0.000194	NA	NA	NA
c7942_g2_i2	-2.7109	2.621616	2.74E-06	0.000194	NA	NA	NA
c7942_g2_i3	-2.7109	2.621616	2.74E-06	0.000194	NA	NA	NA
c7975_g1_i1	-4.35902	4.193734	1.04E-16	9.78E-14	RecName: Full=Phosphoenolpyruvate carboxykinase [Candida glabrata CBS 138]	UniRef90_K5VRA1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRA1_PHACS	GO:0004612|GO:0005524|GO:0006094
c7975_g2_i1	-3.68798	0.522574	0.000975	0.019648	NA	NA	GO:0004612|GO:0005524|GO:0006094
c7975_g2_i2	-3.68798	0.522574	0.000975	0.019648	RecName: Full=Phosphoenolpyruvate carboxykinase [Dictyostelium discoideum]	UniRef90_D8QB51 Putative uncharacterized protein n=2 Tax=Schizophyllum commune (strain H4-8 / FGSC 9210) RepID=D8QB51_SCHCM	NA
c7975_g2_i3	-3.68798	0.522574	0.000975	0.019648	NA	NA	GO:0004612|GO:0005524|GO:0006094
c7975_g3_i1	-4.76175	1.851541	1.56E-11	4.82E-09	RecName: Full=Phosphoenolpyruvate carboxykinase [Candida glabrata CBS 138]	UniRef90_M2QL63 Phosphoenolpyruvate carboxykinase n=3 Tax=Agaricomycetes incertae sedis RepID=M2QL63_CERS8	GO:0004612|GO:0005524|GO:0006094
c7975_g3_i2	-4.76175	1.851541	1.56E-11	4.82E-09	NA	NA	GO:0004612|GO:0005524|GO:0006094
c7975_g3_i3	-4.76175	1.851541	1.56E-11	4.82E-09	NA	NA	GO:0004612|GO:0005524|GO:0006094
c79_g1_i1	-5.02513	0.221324	0.00284	0.042066	NA	NA	NA
c8000_g1_i1	-1.25231	4.932222	0.000347	0.009101	RecName: Full=NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9; AltName: Full=B22 subunit of eukaryotic mitochondrial complex I; AltName: Full=Complex I-B22; Short=AtCIB22; Short=CI-B22; AltName: Full=NADH-ubiquinone oxidoreductase B22 subunit [Arabidopsis thaliana]	UniRef90_K5X8R4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X8R4_PHACS	NA
c8004_g1_i1	-2.14817	5.078669	4.59E-07	4.37E-05	NA	UniRef90_K5W1E2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W1E2_PHACS	NA

c8025_g1_i1	-1.09429	5.23021	0.003348	0.047387	RecName: Full=L-rhamnose-1-dehydrogenase [Scheffersomyces stipitis CBS 6054]	UniRef90_K5WPC3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WPC3_PHACS	GO:0008152|GO:0016491
c8071_g1_i1	-2.43674	1.592818	0.001424	0.025724	NA	NA	NA
c8086_g1_i1	-2.33283	4.367679	7.21E-06	0.000421	NA	NA	NA
c8111_g1_i1	-2.64761	9.369199	0.00014	0.004437	NA	UniRef90_K5X0A1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X0A1_PHACS	GO:0005515
c8111_g1_i2	-2.64761	9.369199	0.00014	0.004437	NA	NA	GO:0005515
c8126_g1_i1	-1.53779	6.603595	0.000259	0.007271	NA	UniRef90_A0A0C3SA00 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SA00_PHLGI	NA
c8126_g2_i1	-1.47928	5.774235	0.000303	0.008211	NA	NA	NA
c8131_g1_i1	-1.21168	8.155155	0.003545	0.049389	RecName: Full=Methylsterol monooxygenase; AltName: Full=C-4 methylsterol oxidase [Schizosaccharomyces pombe 972h-]	UniRef90_K5VIW2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VIW2_PHACS	GO:0005506|GO:0006633|GO:0016491|GO:0055114
c8166_g1_i1	-1.34255	8.686018	0.000646	0.014596	NA	NA	NA
c8188_g3_i1	-2.99342	0.963636	0.000926	0.018954	NA	NA	NA
c8188_g3_i2	-2.99342	0.963636	0.000926	0.018954	NA	NA	NA
c8223_g1_i1	-1.40118	4.710315	0.000313	0.008435	NA	UniRef90_K5VM00 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VM00_PHACS	NA
c8229_g1_i1	-1.56233	6.850675	0.000218	0.006365	NA	NA	GO:0006672|GO:0016021|GO:0016811
c8229_g1_i2	-1.56233	6.850675	0.000218	0.006365	NA	UniRef90_K5WQ61 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQ61_PHACS	NA
c8229_g2_i1	-1.65407	7.745231	0.000111	0.003665	RecName: Full=Alkaline ceramidase 3; Short=AlkCDase 3; Short=Alkaline CDase 3; AltName: Full=Alkaline dihydroceramidase SB89; AltName: Full=Alkaline phytoceramidase; Short=aPHC [Homo sapiens]	UniRef90_K5WQ61 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQ61_PHACS	GO:0006672|GO:0016021|GO:0016811

c8235_g1_i1	-1.51552	8.497475	0.000543	0.012772	NA	UniRef90_A0A0C3S327 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S327_PHLGI	NA
c8345_g1_i1	-1.31924	7.264567	0.000689	0.015335	RecName: Full=NEDD8; AltName: Full=Neddylin; AltName: Full=Protein NED-8; AltName: Full=Ubiquitin-like protein Nedd8; Flags: Precursor [Caenorhabditis elegans]	UniRef90_K5X9R9 Uncharacterized protein n=17 Tax=Agaricomycetes RepID=K5X9R9_AGABU	GO:0005515
c8387_g1_i1	-2.20877	2.453684	4.98E-05	0.00196	NA	NA	NA
c8397_g1_i1	-3.4608	1.795355	2.38E-07	2.56E-05	NA	NA	NA
c8406_g1_i1	-3.43781	1.771594	4.61E-06	0.000292	NA	NA	NA
c8410_g1_i1	-1.48969	8.052018	0.001363	0.025053	RecName: Full=Glycerol 2-dehydrogenase (NADP(+)); AltName: Full=Galactose-inducible crystallin-like protein 1 [Saccharomyces cerevisiae S288c]	UniRef90_K5UTR9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UTR9_PHACS	NA
c8410_g1_i2	-1.48969	8.052018	0.001363	0.025053	NA	NA	NA
c8412_g2_i1	-2.73463	1.46914	6.15E-05	0.002298	NA	NA	NA
c8422_g1_i1	-1.81525	1.644606	0.002824	0.041915	NA	NA	NA
c8422_g1_i2	-1.81525	1.644606	0.002824	0.041915	NA	UniRef90_K5WZM7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WZM7_PHACS	NA
c8443_g2_i1	-1.70838	3.234261	0.003215	0.04606	RecName: Full=Carboxypeptidase Y inhibitor; Short=CPY inhibitor; AltName: Full=CDC25 suppressor 1; AltName: Full=I(C); AltName: Full=Ic; AltName: Full=Protein DKA1; AltName: Full=Protein NSP1 [Saccharomyces cerevisiae S288c]	UniRef90_A0A0C3NAY5 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NAY5_PHLGI	NA
c8443_g2_i2	-1.70838	3.234261	0.003215	0.04606	NA	NA	NA
c8482_g1_i1	-2.02617	6.598195	6.05E-06	0.000369	NA	UniRef90_A0A0C3S8Y3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S8Y3_PHLGI	NA
c8482_g2_i1	-1.72717	6.744594	8.87E-06	0.000504	NA	UniRef90_A0A0C3S8Y3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S8Y3_PHLGI	NA

c8487_g3_i1	-1.61606	3.560437	0.002959	0.043333	RecName: Full=Histone H3.2 [Cichorium intybus]	UniRef90_D2I083 Histone H3 (Fragment) n=2 Tax=Ursidae RepID=D2I083_AILME	NA
c8518_g4_i1	-1.49705	3.25175	0.000553	0.012933	NA	UniRef90_K5VZX1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZX1_PHACS	NA
c8519_g1_i1	-1.88578	7.384662	1.45E-06	0.000111	RecName: Full=Superoxide dismutase [Mn], mitochondrial; AltName: Full=Mn-SOD; Flags: Precursor [Ganoderma microsporum]	UniRef90_K5VZE5 Superoxide dismutase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VZE5_PHACS	GO:0004784|GO:0006801|GO:0046872|GO:0055114
c8521_g1_i1	-1.92885	3.881609	0.001325	0.024568	RecName: Full=Uncharacterized oxidoreductase CzcO-like [Geobacillus kaustophilus HTA426]	UniRef90_K5W8F1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8F1_PHACS	NA
c8551_g2_i1	-1.09447	5.733431	0.003378	0.047673	NA	NA	NA
c8551_g2_i2	-1.09447	5.733431	0.003378	0.047673	NA	UniRef90_A0A0C3S973 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S973_PHLGI	NA
c8553_g4_i1	-1.82669	1.652335	0.001958	0.032052	NA	UniRef90_K5XFL2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5XFL2_PHACS	NA
c8564_g1_i1	-1.93172	8.6189	3.11E-05	0.001354	RecName: Full=Upstream activation factor subunit spp27; AltName: Full=Upstream activation factor 27 KDa subunit; Short=p27; AltName: Full=Upstream activation factor 30 KDa subunit; Short=p30; AltName: Full=Upstream activation factor subunit uaf30 [Schizosaccharomyces pombe 972h-]	UniRef90_K5W2T1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2T1_PHACS	GO:0005515
c8577_g1_i1	-1.8554	10.98394	0.000252	0.007108	RecName: Full=Fumarate reductase; Short=FRDS; AltName: Full=FAD-dependent oxidoreductase; AltName: Full=NADH-dependent fumarate reductase [Schizosaccharomyces pombe 972h-]	UniRef90_K5VRN4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VRN4_PHACS	GO:0008033|GO:0016491|GO:0050660|GO:0055114
c8577_g2_i1	-1.85056	8.917713	0.000241	0.006855	RecName: Full=Fumarate reductase; Short=FRDS; AltName: Full=FAD-dependent oxidoreductase; AltName: Full=NADH-	UniRef90_A0A0C3SC36 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SC36_PHLGI	GO:0020037

					dependent fumarate reductase [Schizosaccharomyces pombe 972h-]		
c8582_g1_i1	-2.17484	2.225265	1.37E-05	0.000718	NA	NA	NA
c8582_g1_i2	-2.17484	2.225265	1.37E-05	0.000718	NA	NA	NA
c8582_g1_i3	-2.17484	2.225265	1.37E-05	0.000718	NA	NA	NA
c8582_g1_i4	-2.17484	2.225265	1.37E-05	0.000718	NA	NA	NA
c8594_g1_i1	-2.35271	1.031652	0.002746	0.041146	NA	NA	NA
c8594_g1_i2	-2.35271	1.031652	0.002746	0.041146	NA	NA	NA
c8595_g1_i1	-1.38928	4.986423	0.000364	0.009418	NA	UniRef90_K5VVS9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VVS9_PHACS	NA
c8595_g1_i2	-1.38928	4.986423	0.000364	0.009418	NA	NA	NA
c8603_g1_i1	-1.16591	3.8863	0.00324	0.046249	RecName: Full=Mitochondrial acidic protein MAM33; Flags: Precursor [Saccharomyces cerevisiae S288c]	UniRef90_K5WEZ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEZ5_PHACS	NA
c8603_g1_i2	-1.16591	3.8863	0.00324	0.046249	NA	NA	GO:0005759
c8617_g1_i1	-1.56308	2.372633	0.002003	0.032558	NA	NA	NA
c8624_g1_i1	-2.07785	3.198218	1.13E-06	9.14E-05	NA	NA	NA
c8624_g1_i2	-2.07785	3.198218	1.13E-06	9.14E-05	NA	NA	NA
c8624_g1_i3	-2.07785	3.198218	1.13E-06	9.14E-05	NA	NA	NA
c8652_g1_i1	-1.36205	4.915905	0.003601	0.049941	NA	UniRef90_K5VI00 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VI00_PHACS	NA
c8652_g1_i2	-1.36205	4.915905	0.003601	0.049941	NA	NA	NA
c8656_g2_i1	-1.1133	4.466145	0.001682	0.029012	NA	UniRef90_A0A0C3PGC9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PGC9_PHLGI	NA
c8664_g1_i1	-1.5453	8.431192	0.000211	0.006215	NA	NA	GO:0008152|GO:0016491
c8664_g1_i2	-1.5453	8.431192	0.000211	0.006215	RecName: Full=3-oxoacyl-[acyl-carrier-protein] reductase FabG; AltName: Full=3-ketoacyl-acyl carrier protein reductase; AltName: Full=Beta-Ketoacyl-acyl carrier	UniRef90_K5W9M4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W9M4_PHACS	GO:0008152|GO:0016491

					protein reductase; AltName: Full=Beta-ketoacyl-ACP reductase [Thermotoga maritima MSB8]		
c8696_g1_i1	-1.71804	7.397991	0.001016	0.020254	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	UniRef90_K5WQZ2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQZ2_PHACS	GO:0004190|GO:0006508
c8696_g2_i1	-1.68045	4.124646	0.001657	0.028724	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	UniRef90_K5WQZ2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WQZ2_PHACS	NA
c8711_g1_i1	-2.25491	9.187025	0.000826	0.017512	NA	UniRef90_K5WN81 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WN81_PHACS	NA
c8726_g1_i1	-1.68177	3.727076	1.78E-05	0.000899	RecName: Full=NADPH-dependent 1-acyldihydroxyacetone phosphate reductase; Short=ADR; AltName: Full=1-acyl DHAP reductase; AltName: Full=Acyl/alkyl DHAP reductase; AltName: Full=Acylglycerone-phosphate reductase [Saccharomyces cerevisiae S288c]	UniRef90_K5W654 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W654_PHACS	NA
c8726_g2_i1	-1.80153	5.995995	1.01E-05	0.000561	RecName: Full=NADPH-dependent 1-acyldihydroxyacetone phosphate reductase; Short=ADR; AltName: Full=1-acyl DHAP reductase; AltName: Full=Acyl/alkyl DHAP reductase; AltName: Full=Acylglycerone-phosphate reductase [Schizosaccharomyces pombe 972h-]	UniRef90_K5W654 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W654_PHACS	GO:0003824|GO:0008152|GO:0016491|GO:0050662
c8726_g2_i2	-1.80153	5.995995	1.01E-05	0.000561	NA	NA	GO:0003824|GO:0008152|GO:0016491|GO:0050662
c8734_g1_i1	-1.31592	7.075927	0.002152	0.034269	NA	UniRef90_K5UJ86 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UJ86_PHACS	NA
c8734_g1_i2	-1.31592	7.075927	0.002152	0.034269	NA	NA	NA
c8734_g1_i3	-1.31592	7.075927	0.002152	0.034269	NA	NA	NA

c8751_g1_i1	-2.72857	1.252964	0.000268	0.007474	NA	NA	NA
c8775_g1_i1	-2.86274	4.654668	6.10E-06	0.00037	NA	UniRef90_K5WGQ0 Uncharacterized protein n=2 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WGQ0_PHACS	GO:0003824|GO:0016620|GO:0050662|GO:0051287|GO:0055114
c8775_g2_i1	-2.48443	1.746068	0.000556	0.012983	NA	UniRef90_A0A0C3S475 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S475_PHLGI	NA
c8831_g2_i1	-1.48741	2.84531	0.000531	0.012594	NA	UniRef90_M9PA63 Oligopeptide transporter 11 n=1 Tax=Phanerochaete chrysosporium RepID=M9PA63_PHACH	GO:0055085
c8834_g1_i1	-1.20335	4.317523	0.000843	0.017723	NA	UniRef90_K5UZN4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UZN4_PHACS	NA
c8835_g1_i1	-1.4684	3.132048	0.002198	0.034834	RecName: Full=Citrate synthase 3 [Saccharomyces cerevisiae S288c]	UniRef90_K5WYH4 Citrate synthase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYH4_PHACS	GO:0044262|GO:0046912
c8835_g2_i1	-1.40132	7.665826	0.001949	0.032024	RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor [Neurospora crassa OR74A]	UniRef90_K5WYH4 Citrate synthase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WYH4_PHACS	GO:0044262|GO:0046912
c885_g1_i1	-5.66937	0.579935	4.24E-05	0.001726	NA	NA	NA
c885_g2_i1	-4.95278	1.356719	3.92E-08	5.49E-06	RecName: Full=DnaJ homolog subfamily B member 4 [Mus musculus]	UniRef90_K5X4S7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X4S7_PHACS	NA
c8887_g1_i1	-1.86008	2.735059	5.72E-05	0.002177	NA	NA	NA
c8888_g1_i1	-2.49695	3.348693	7.06E-06	0.000415	NA	NA	NA
c888_g1_i1	-1.93217	7.467923	9.39E-05	0.003251	RecName: Full=Ras-like GTP-binding protein RYL2 [Yarrowia lipolytica CLIB122]	UniRef90_K5W628 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W628_PHACS	GO:0005525|GO:0005622|GO:0005634|GO:0005737|GO:0007264
c8901_g1_i1	-1.55025	2.073615	0.002353	0.036748	NA	NA	NA
c8901_g1_i2	-1.55025	2.073615	0.002353	0.036748	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	UniRef90_A0A0C3S543 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S543_PHLGI	GO:0004190|GO:0006508
c8926_g1_i1	-2.16894	3.726767	1.69E-05	0.000864	NA	NA	NA

c8926_g1_i2	-2.16894	3.726767	1.69E-05	0.000864	NA	UniRef90_K5W5K3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5K3_PHACS	NA
c8962_g1_i1	-1.21541	5.025566	0.000712	0.015696	RecName: Full=N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase; AltName: Full=Phosphatidylinositol-glycan biosynthesis class L protein; Short=PIG-L [Bos taurus]	UniRef90_K5X3V7 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X3V7_PHACS	NA
c8962_g1_i2	-1.21541	5.025566	0.000712	0.015696	NA	NA	NA
c8972_g1_i1	-3.89969	2.786763	1.24E-06	9.76E-05	NA	NA	NA
c8972_g1_i2	-3.89969	2.786763	1.24E-06	9.76E-05	NA	UniRef90_K5WIJ2 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WIJ2_PHACS	NA
c8979_g1_i1	-2.22912	3.670762	4.90E-05	0.001941	NA	NA	NA
c8996_g1_i1	-1.92528	4.230195	0.003173	0.045582	NA	UniRef90_A0A0C3FU39 Uncharacterized protein n=1 Tax=Piloderma croceum F 1598 RepID=A0A0C3FU39_9HOMO	NA
c9011_g1_i1	-1.87666	2.38806	0.000222	0.006476	NA	NA	NA
c9014_g1_i1	-2.27589	9.083764	0.001418	0.025716	RecName: Full=2-deoxyglucose-6-phosphate phosphatase 1; Short=2-DOG-6-P 1; Short=2-deoxyglucose-6-phosphatase 1 [Saccharomyces cerevisiae S288c]	UniRef90_A0A0C3SCM9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SCM9_PHLGI	NA
c9016_g1_i1	-1.70798	7.024832	0.001171	0.02249	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	UniRef90_A0A0C3NXP9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NXP9_PHLGI	GO:0004190|GO:0006508
c9016_g2_i1	-1.56632	5.092409	0.001145	0.02211	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	UniRef90_A0A0C3NXP9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NXP9_PHLGI	GO:0004190|GO:0006508
c9016_g3_i1	-1.33138	4.644636	0.002944	0.043222	RecName: Full=Polyporopepsin; AltName: Full=Aspartic proteinase [Irpex lacteus]	UniRef90_A0A0C3NXP9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NXP9_PHLGI	NA
c9029_g1_i1	-1.3548	3.797479	0.002699	0.040553	NA	UniRef90_K5W7W5 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa	NA

						(strain HHB-10118-sp) RepID=K5W7W5_PHACS	
c9032_g2_i1	-1.98566	7.134207	0.00027	0.007496	NA	NA	NA
c9032_g3_i1	-2.15855	3.241815	0.000176	0.005323	NA	NA	NA
c9061_g1_i1	-1.34634	8.07736	0.00119	0.022682	RecName: Full=RNA polymerase II holoenzyme cyclin-like subunit [Ustilago maydis 521]	UniRef90_K5X805 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X805_PHACS	GO:0016491|GO:0055114
c9139_g1_i1	-1.41997	6.998297	0.001502	0.026795	NA	UniRef90_K5WKI5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WKI5_PHACS	NA
c9148_g1_i1	-1.61467	7.701103	0.000296	0.008079	RecName: Full=GTP-binding protein ypt1 [Neurospora crassa OR74A]	UniRef90_A0A0C3NQM7 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3NQM7_PHLGI	GO:0003924|GO:0005525|GO:0005622|GO:0005634|GO:0005737|GO:0007264
c9182_g2_i1	-1.47311	4.963615	0.000726	0.015863	RecName: Full=Acyl-CoA dehydrogenase family member 11; Short=ACAD-11 [Rattus norvegicus]	UniRef90_K5W3A4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W3A4_PHACS	NA
c9199_g1_i1	-3.1917	3.073737	3.35E-06	0.000227	NA	NA	NA
c9217_g1_i1	-1.17386	7.827276	0.00313	0.04521	NA	UniRef90_K5VPN9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VPN9_PHACS	NA
c9235_g2_i1	-2.14526	1.384487	0.000882	0.018454	NA	NA	NA
c9236_g1_i1	-1.65982	10.08063	0.000225	0.006525	NA	NA	NA
c9236_g1_i2	-1.65982	10.08063	0.000225	0.006525	NA	UniRef90_K5W5J3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5J3_PHACS	NA
c9238_g1_i1	-1.39498	3.012355	0.001009	0.020175	RecName: Full=Pumilio homolog 1; Short=HsPUM; Short=Pumilio-1 [Homo sapiens]	UniRef90_K5W8P1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W8P1_PHACS	GO:0003723
c923_g1_i1	-8.25039	8.21719	2.06E-30	2.52E-26	NA	UniRef90_R7SS05 Ricin B-like lectin n=1 Tax=Dichomitus squalens (strain LYAD-421) RepID=R7SS05_DICSQ	NA
c9250_g1_i1	-2.81201	3.114517	6.23E-10	1.39E-07	NA	NA	NA
c9261_g1_i1	-2.29371	4.262386	2.23E-08	3.40E-06	NA	NA	NA

c9261_g1_i2	-2.29371	4.262386	2.23E-08	3.40E-06	NA	NA	NA
c9264_g1_i1	-1.71304	8.276093	0.00104	0.020613	NA	UniRef90_K5WG47 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WG47_PHACS	NA
c9264_g2_i1	-1.90527	7.057091	0.000241	0.006866	NA	UniRef90_K5WG47 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WG47_PHACS	GO:0003700|GO:0006355|GO:0043565
c9274_g2_i1	-2.10131	5.182277	1.92E-05	0.00094	NA	UniRef90_K5W7G3 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W7G3_PHACS	NA
c9282_g2_i1	-1.68077	3.185574	0.000157	0.004854	NA	UniRef90_K5VY87 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VY87_PHACS	NA
c9282_g2_i2	-1.68077	3.185574	0.000157	0.004854	NA	NA	NA
c9286_g1_i1	-2.12263	11.12551	2.14E-06	0.000154	NA	NA	NA
c9324_g1_i1	-1.3867	4.515125	0.000699	0.01551	RecName: Full=Cytosolic Fe-S cluster assembly factor NBP35; AltName: Full=Nucleotide-binding protein 35 [Yarrowia lipolytica CLIB122]	UniRef90_K5VTT7 Cytosolic Fe-S cluster assembly factor NBP35 n=2 Tax=Phanerochaetaceae RepID=K5VTT7_PHACS	NA
c9324_g2_i1	-1.36911	4.453265	0.000643	0.01455	RecName: Full=Cytosolic Fe-S cluster assembly factor NBP35; AltName: Full=Nucleotide-binding protein 35 [Cryptococcus neoformans var. neoformans B-3501A]	UniRef90_K5VTT7 Cytosolic Fe-S cluster assembly factor NBP35 n=2 Tax=Phanerochaetaceae RepID=K5VTT7_PHACS	NA
c9333_g1_i1	-1.3048	9.189379	0.003314	0.047009	NA	UniRef90_K5UTB6 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UTB6_PHACS	NA
c9333_g1_i2	-1.3048	9.189379	0.003314	0.047009	NA	NA	NA
c9333_g2_i1	-1.45176	10.001	0.001817	0.030719	NA	NA	NA
c9345_g1_i1	-2.8306	3.757759	1.09E-10	2.93E-08	NA	NA	NA
c9346_g1_i1	-1.2431	7.66441	0.00294	0.043184	RecName: Full=Homeobox-leucine zipper protein HDG6; AltName: Full=HD-ZIP protein HDG6; AltName: Full=Homeobox protein	UniRef90_K5WPQ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WPQ5_PHACS	GO:0003677|GO:0006355

					FWA; AltName: Full=Homeodomain GLABRA 2-like protein 6; AltName: Full=Homeodomain transcription factor HDG6; AltName: Full=Protein HOMEODOMAIN GLABROUS 6 [Arabidopsis thaliana]		
c9346_g2_i1	-1.6217	7.056225	0.00035	0.009126	NA	UniRef90_K5WPQ5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WPQ5_PHACS	NA
c9346_g2_i2	-1.6217	7.056225	0.00035	0.009126	NA	NA	NA
c9346_g3_i1	-1.31878	5.061591	0.001245	0.023474	NA	NA	NA
c9360_g1_i1	-1.78913	2.565405	9.91E-05	0.003363	NA	UniRef90_J4HWJ4 Uncharacterized protein n=1 Tax=Fibroporia radiculosa (strain TFFH 294) RepID=J4HWJ4_FIBRA	NA
c9360_g1_i2	-1.78913	2.565405	9.91E-05	0.003363	NA	NA	NA
c9361_g1_i1	-2.48686	3.562349	2.40E-07	2.57E-05	NA	NA	NA
c9409_g1_i1	-2.09194	3.716136	6.82E-07	5.99E-05	RecName: Full=P-type cation-transporting ATPase; AltName: Full=Cadmium resistance protein 2; AltName: Full=Cadmium-translocating P-type ATPase; AltName: Full=Cd(2+)-exporting ATPase [Saccharomyces cerevisiae S288c]	UniRef90_K5VU34 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VU34_PHACS	GO:0000166|GO:0046872
c9448_g2_i1	-1.71108	8.227476	0.003438	0.04826	NA	NA	NA
c9457_g1_i1	-4.23303	6.635356	1.48E-12	5.65E-10	RecName: Full=Protoplast secreted protein 2; Flags: Precursor [Saccharomyces cerevisiae S288c]	UniRef90_A0A0C3RWB3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RWB3_PHLGI	GO:0010181|GO:0016491
c9459_g2_i1	-1.37025	4.570849	0.001522	0.027055	RecName: Full=Sterol O-acyltransferase 2; AltName: Full=ASAT; AltName: Full=Sterol-ester synthase [Candida albicans]	UniRef90_K5VGZ1 O-acyltransferase n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5VGZ1_PHACS	NA
c9460_g1_i1	-1.49564	6.372516	0.000115	0.003768	RecName: Full=Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial; AltName: Full=Isocitric dehydrogenase; AltName: Full=NAD(+)-specific ICDH; Flags: Precursor [Histoplasma capsulatum]	UniRef90_K5V8R8 Uncharacterized protein n=4 Tax=Polyporales RepID=K5V8R8_PHACS	GO:0016616|GO:0055114

c9460_g2_i1	-1.59939	5.928435	0.000195	0.005809	RecName: Full=Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial; AltName: Full=Isocitric dehydrogenase; AltName: Full=NAD(+)-specific ICDH; Flags: Precursor [Histoplasma capsulatum]	UniRef90_K5V8R8 Uncharacterized protein n=4 Tax=Polyporales RepID=K5V8R8_PHACS	GO:0016616|GO:0055114
c9460_g3_i1	-1.62595	5.627501	3.77E-05	0.001586	RecName: Full=Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial; AltName: Full=Isocitric dehydrogenase; AltName: Full=NAD(+)-specific ICDH; Flags: Precursor [Histoplasma capsulatum]	UniRef90_K5V8R8 Uncharacterized protein n=4 Tax=Polyporales RepID=K5V8R8_PHACS	GO:0016616|GO:0055114
c9489_g3_i1	-2.81696	2.62406	4.58E-08	6.25E-06	NA	NA	NA
c9504_g1_i1	-2.3944	2.018598	0.000153	0.00475	NA	UniRef90_K5UKN0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UKN0_PHACS	NA
c9504_g3_i1	-1.48267	3.150602	0.000913	0.018761	NA	NA	NA
c9504_g3_i2	-1.48267	3.150602	0.000913	0.018761	NA	UniRef90_K5UKN0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UKN0_PHACS	GO:0005515
c9504_g3_i3	-1.48267	3.150602	0.000913	0.018761	NA	NA	NA
c9506_g1_i1	-2.11111	6.853938	2.43E-05	0.001132	RecName: Full=Uncharacterized protein AN0679 [Aspergillus nidulans FGSC A4]	UniRef90_K5WIA8 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WIA8_PHACS	NA
c9513_g1_i1	-1.65908	8.118922	0.001189	0.022682	NA	NA	NA
c9513_g1_i2	-1.65908	8.118922	0.001189	0.022682	NA	NA	NA
c9517_g1_i1	-1.82443	4.89956	0.000539	0.012695	RecName: Full=Boletus edulis lectin; Short=BEL [Boletus edulis]	UniRef90_K5WUR4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WUR4_PHACS	NA
c9529_g2_i1	-1.55034	8.168391	0.000523	0.012417	NA	NA	NA
c9529_g2_i2	-1.55034	8.168391	0.000523	0.012417	RecName: Full=Peroxisomal hydratase-dehydrogenase-epimerase; Short=HDE; AltName: Full=Multifunctional beta-oxidation protein; Short=MFP; Includes: RecName: Full=2-enoyl-CoA hydratase; Includes:	UniRef90_K5WDW9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WDW9_PHACS	NA

					RecName: Full=(3R)-3-hydroxyacyl-CoA dehydrogenase [Neurospora crassa OR74A]		
c9537_g1_i1	-1.16391	4.761623	0.000677	0.015155	NA	NA	NA
c9537_g1_i2	-1.16391	4.761623	0.000677	0.015155	RecName: Full=Acyl-CoA dehydrogenase family member 10; Short=ACAD-10 [Mus musculus]	UniRef90_K5W975 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W975_PHACS	NA
c9537_g2_i1	-1.72222	2.019742	0.001403	0.025621	NA	UniRef90_K5W975 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W975_PHACS	NA
c9548_g1_i1	-1.31327	6.466989	0.00196	0.032073	RecName: Full=Delta(24(24(1)))-sterol reductase; AltName: Full=C-24(28) sterol reductase; AltName: Full=Sterol Delta(24(28))-reductase [Schizosaccharomyces pombe 972h-]	UniRef90_K5ULD9 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5ULD9_PHACS	GO:0016020
c9550_g1_i1	-2.26203	3.9973	9.29E-08	1.12E-05	NA	NA	NA
c9550_g2_i1	-1.80927	5.264808	5.89E-07	5.39E-05	NA	UniRef90_K5X8R9 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X8R9_PHACS	NA
c9550_g3_i1	-2.05136	5.024432	3.52E-07	3.52E-05	NA	UniRef90_K5X8R9 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X8R9_PHACS	NA
c9563_g2_i1	-1.66025	3.143147	0.000227	0.006584	NA	UniRef90_A0A0C3RQC3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RQC3_PHLGI	NA
c9563_g2_i2	-1.66025	3.143147	0.000227	0.006584	NA	NA	NA
c9577_g1_i1	-2.20626	7.346916	6.13E-07	5.51E-05	NA	UniRef90_A0A0C3RU22 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RU22_PHLGI	NA
c9577_g2_i1	-1.9202	6.085659	1.41E-05	0.000738	NA	UniRef90_A0A0C3RU22 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3RU22_PHLGI	NA

c9585_g1_i1	-2.70496	2.90696	3.49E-08	4.99E-06	RecName: Full=Uncharacterized oxidoreductase C736.13 [Schizosaccharomyces pombe 972h-]	UniRef90_K5W0R7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W0R7_PHACS	GO:0008152|GO:0016491
c9598_g2_i1	-1.70706	4.730802	2.89E-06	0.000203	RecName: Full=Pantothenate kinase 2; AltName: Full=Pantothenic acid kinase 2 [Oryza sativa Japonica Group]	UniRef90_A0A0C3P1N9 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3P1N9_PHLGI	GO:0004594|GO:0005524|GO:0015937
c9625_g1_i1	-1.14932	6.282969	0.002117	0.033918	NA	NA	NA
c9684_g1_i1	-1.44364	7.07058	0.000365	0.009418	RecName: Full=Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial; Short=MMSDH; Short=Malonate-semialdehyde dehydrogenase [acylating]; AltName: Full=Aldehyde dehydrogenase family 6 member A1; Flags: Precursor [Bos taurus]	UniRef90_K5WB08 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WB08_PHACS	GO:0008152|GO:0016491|GO:0055114
c9690_g1_i1	-2.89346	3.705363	3.78E-06	0.000251	NA	NA	GO:0005199|GO:0009277
c9690_g1_i2	-2.89346	3.705363	3.78E-06	0.000251	NA	UniRef90_K5UV97 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5UV97_PHACS	GO:0005199|GO:0009277
c96_g1_i1	-2.20615	6.828869	1.67E-07	1.87E-05	RecName: Full=DnaJ homolog subfamily B member 5 [Bos taurus]	UniRef90_A0A0C3SEX1 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SEX1_PHLGI	NA
c9717_g1_i1	-1.6573	10.17241	0.001468	0.026298	NA	UniRef90_K5WK96 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WK96_PHACS	NA
c9719_g1_i1	-2.17992	4.580083	6.42E-09	1.13E-06	NA	NA	NA
c9719_g1_i2	-2.17992	4.580083	6.42E-09	1.13E-06	NA	NA	NA
c9722_g1_i1	-2.23132	2.720703	0.000131	0.00421	NA	UniRef90_K5WZS4 Uncharacterized protein n=2 Tax=Agaricus bisporus RepID=K5WZS4_AGABU	NA
c9722_g1_i2	-2.23132	2.720703	0.000131	0.00421	NA	NA	NA
c9723_g1_i1	-1.71894	3.125886	0.00018	0.005406	NA	UniRef90_A0A0C3S2N3 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3S2N3_PHLGI	NA

c9772_g2_i1	-2.23958	8.318353	0.000836	0.017641	NA	UniRef90_A0A0C3SBC4 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3SBC4_PHLGI	NA
c9785_g1_i1	-1.70181	2.660733	0.00057	0.013198	NA	UniRef90_A0A0C3PJD7 Uncharacterized protein n=1 Tax=Phlebiopsis gigantea 11061_1 CR5-6 RepID=A0A0C3PJD7_PHLGI	NA
c97_g2_i1	-1.27556	10.47259	0.00101	0.020175	NA	UniRef90_A6P025 Uncharacterized protein n=1 Tax=Pseudoflavonifractor capillosus ATCC 29799 RepID=A6P025_9FIRM	NA
c9816_g1_i1	-2.77908	5.282362	1.86E-10	4.74E-08	NA	UniRef90_K5WN75 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WN75_PHACS	NA
c9822_g1_i1	-1.32867	4.786154	0.000744	0.016104	NA	UniRef90_K5WLB0 Uncharacterized protein (Fragment) n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WLB0_PHACS	NA
c9838_g1_i1	-1.64643	7.860515	2.71E-05	0.001218	NA	UniRef90_R7T024 Uncharacterized protein n=1 Tax=Dichomitus squalens (strain LYAD-421) RepID=R7T024_DICSQ	NA
c9842_g1_i1	-1.76008	2.392001	0.000313	0.008435	NA	NA	NA
c9858_g1_i1	-2.13139	6.950607	4.39E-07	4.26E-05	RecName: Full=Protein psi1; AltName: Full=Protein psi [Schizosaccharomyces pombe 972h-]	UniRef90_K5X4S7 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X4S7_PHACS	NA
c9861_g1_i1	-1.73872	2.88569	0.002992	0.043626	RecName: Full=Endochitinase 46; AltName: Full=46 kDa endochitinase; AltName: Full=Chitinase 46; Flags: Precursor [Trichoderma harzianum]	UniRef90_K5W5Q5 Glycoside hydrolase family 18 protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W5Q5_PHACS	NA
c9876_g1_i1	-1.86848	7.628655	3.58E-06	0.000239	NA	NA	NA
c9876_g1_i2	-1.86848	7.628655	3.58E-06	0.000239	RecName: Full=Uncharacterized transcriptional regulatory protein C27B12.11c [Schizosaccharomyces pombe 972h-]	UniRef90_K5V030 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V030_PHACS	NA

c9876_g2_i1	-1.18799	3.934326	0.001701	0.029235	NA	UniRef90_K5V030 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5V030_PHACS	NA
c9878_g1_i1	-1.44489	6.186992	0.000361	0.009364	RecName: Full=Uncharacterized endoplasmic reticulum membrane protein YGL010W [Saccharomyces cerevisiae S288c]	UniRef90_K5W6C5 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W6C5_PHACS	NA
c9893_g1_i1	-2.1094	10.10835	6.98E-05	0.002532	NA	UniRef90_K5WEC4 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEC4_PHACS	NA
c9908_g1_i1	-1.60374	2.311782	0.001088	0.021298	NA	NA	NA
c9920_g2_i1	-2.80066	4.566782	4.44E-09	8.22E-07	NA	UniRef90_K5W2A0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5W2A0_PHACS	NA
c993_g1_i1	-3.41242	0.854328	0.000349	0.009118	NA	NA	NA
c9955_g1_i1	-1.1017	4.168567	0.002114	0.033881	NA	NA	NA
c9955_g1_i2	-1.1017	4.168567	0.002114	0.033881	NA	NA	NA
c9955_g1_i3	-1.1017	4.168567	0.002114	0.033881	NA	NA	NA
c9955_g1_i4	-1.1017	4.168567	0.002114	0.033881	NA	UniRef90_K5WY22 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WY22_PHACS	NA
c9970_g1_i1	-1.33765	5.186351	0.000731	0.015938	RecName: Full=DSC E3 ubiquitin ligase complex subunit 2; AltName: Full=Defective for SREBP cleavage protein 2; AltName: Full=UBA domain-containing protein 14 [Schizosaccharomyces pombe 972h-]	UniRef90_K5X9D0 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5X9D0_PHACS	NA
c9986_g1_i1	-2.36451	3.301453	2.81E-05	0.001253	NA	UniRef90_K5WEM1 Uncharacterized protein n=1 Tax=Phanerochaete carnosa (strain HHB-10118-sp) RepID=K5WEM1_PHACS	NA
c9994_g2_i1	-2.19211	2.409657	5.23E-05	0.002034	NA	NA	NA

Table S3 Details of lignin peroxidases and manganese peroxidases of *P. sordida* YK-624 under ligninolytic condition.

Gene description	**Gene id**	**$\log_2$ Fold change**	***P*-value**	**FDR**
Manganese peroxidase	c13441_g4_i1	7.020386	1.90E-24	3.32E-20
	c13441_g2_i1	6.467584	2.28E-23	1.75E-19
	c13441_g3_i1	5.750339	1.14E-20	5.70E-17
	c15662_g1_i1	5.255081	1.10E-12	1.02E-09
	c15662_g2_i1	5.178091	6.36E-14	7.42E-11
Lignin peroxidase	c17468_g3_i2	6.208726	3.74E-21	2.18E-17
	c17468_g1_i1	5.571735	1.31E-20	5.74E-17
	c17468_g2_i1	5.038693	6.08E-07	9.32E-05

FDR: False discovery rate; $\log_2$ Fold change value of transcript upregulated in ligninolytic condition is represented by positive number.

Table S4 Details of lignin peroxidases and manganese peroxidases of *P. chrysosporium* under ligninolytic condition.

Gene description	**Gene id**	**Log$_2$ Fold change**	***P*-value**	**FDR**
Manganese peroxidase	c15948_g1_i2	4.832681	7.53E-13	2.92E-10
Lignin peroxidase	c13618_g2_i1	2.496506	1.02E-05	0.000566
	c6763_g1_i1	2.379883	0.000265	0.007416

FDR: False discovery rate; Log$_2$ Fold change value of transcript upregulated in ligninolytic condition is represented by positive number.

Table S5. Details of DEGs of *P. sordida* YK-624 summarized in figure 2.

Gene description	Gene id	Log_2 Fold change	*P*-value	FDR
aldehyde dehydrogenase	c22536_g1_i1	1.9040497	0.0001088	0.0056442
	c16100_g1_i2	1.4627378	0.0001055	0.0055471
	c16100_g4_i1	1.2826982	0.0003889	0.0144218
	c16100_g3_i1	1.0197686	0.0149889	0.1842835
	c24243_g1_i1	0.8310505	0.4107815	0.885208
	c14166_g1_i3	0.7929187	0.0204382	0.2222832
	c14166_g1_i3	0.7929187	0.0204382	0.2222832
	c16100_g2_i2	0.6185439	0.0854035	0.4699744
	c10926_g2_i1	0.6172908	0.2796543	0.7732398
	c10926_g2_i1	0.6172908	0.2796543	0.7732398
	c18318_g1_i1	0.4516846	0.3852421	0.8670428
	c18396_g1_i1	0.4458002	0.3098128	0.803642
	c3080_g1_i1	0.3835209	0.2777498	0.7714701
	c9139_g1_i1	0.2997931	0.5521634	0.9574438

salicylate hydroxylase	c7235_g1_i1	1.5845855	0.0964772	0.4992484
	c14217_g2_i1	1.0339246	0.0078675	0.1224072
	c16040_g1_i1	0.909708	0.6179296	0.9952689
	c17093_g1_i1	0.7550273	0.1424623	0.593192
	c19987_g1_i1	0.4647824	0.5225729	0.9454734
	c16570_g2_i2	0.2682813	0.5293536	0.9493026
carboxymethylenebutenolidase	c13613_g1_i1	1.055612064	0.098150181	0.504174999
amidase	c9043_g1_i1	3.0009075	4.58E-12	3.34E-09
	c16877_g3_i1	1.6374978	6.26E-05	0.0037066
nitrilase	c5973_g1_i2	1.923446386	0.001199362	0.033984518
phenol 2-monooxygenase	c12326_g2_i1	1.898586	4.79E-06	0.0004826
	c12326_g1_i1	1.7687083	0.0001632	0.0074844
	c11376_g1_i1	1.5149923	0.0013003	0.0360758
	c11376_g2_i1	1.295478	0.0068759	0.1123685
malonate-semialdehyde dehydrogenase (acetylating)/methylmalonate-semialdehyde dehydrogenase	c18180_g1_i1	1.813550819	8.11E-07	0.000117652
pyruvate dehydrogenase E1 component	c18339_g1_i1	0.948805	0.016634	0.196167

beta subunit				
	c14763_g1_i4	0.897952	0.017145	0.200226
glycine hydroxymethyltransferase	c10791_g1_i1	1.762800941	0.000132963	0.006471407
	c10791_g2_i1	1.316995666	0.000205584	0.008941173
isocitrate lyase	c19877_g1_i1	2.147588115	1.41E-05	0.00114523
citrate synthase	c9786_g2_i1	1.6923322	0.0056835	0.0989203
	c9786_g1_i1	1.4080715	0.0001292	0.0063498
	c18209_g1_i1	0.5504108	0.1595933	0.6225639
aconitate hydratase	c2247_g2_i1	1.686370087	2.87E-05	0.002010276
	c2247_g1_i1	1.632785161	7.51E-05	0.004200686
acetyl-CoA synthetase	c11906_g1_i1	1.5405733	0.0001203	0.0060541
	c932_g1_i1	1.0944527	0.312937	0.8066462
	c15471_g1_i1	0.200337	0.5832367	0.9749124
catalase	c798_g2_i1	1.612510964	8.16E-06	0.000744956
fructose-1,6-bisphosphatase I	c11615_g2_i1	1.422242	0.000168	0.00761
	c11615_g1_i2	1.272122	0.002624	0.058619
aryl-alcohol dehydrogenase	c17439_g4_i2	2.471207761	4.73E-07	7.81E-05
	c21326_g1_i1	2.124700152	0.000252491	0.010386568

glucose oxidase	c21424_g1_i1	1.658530445	0.00067	0.021925

.FDR: False discovery rate; Log$_2$ Fold change value of transcript upregulated in ligninolytic condition is represented by positive number.

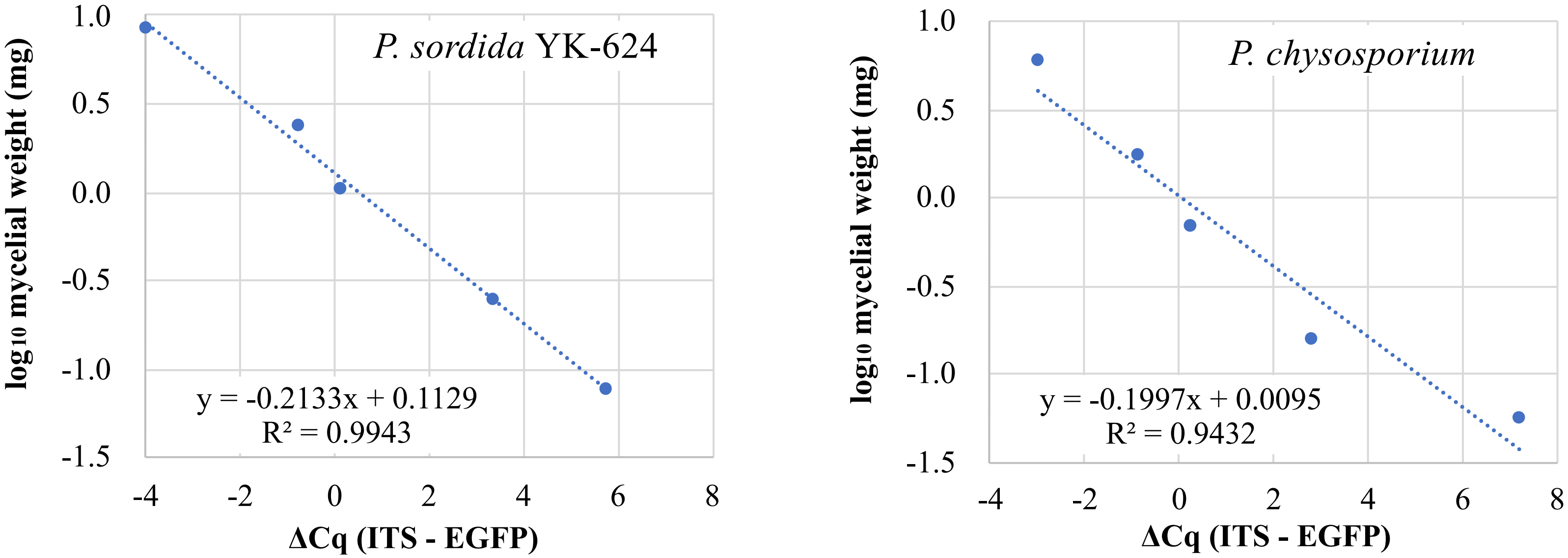

Fig. S1 The calibration curves of biomass and ΔCq for *P. sordida YK-624* and *P. chrysosporium* by qPCR.

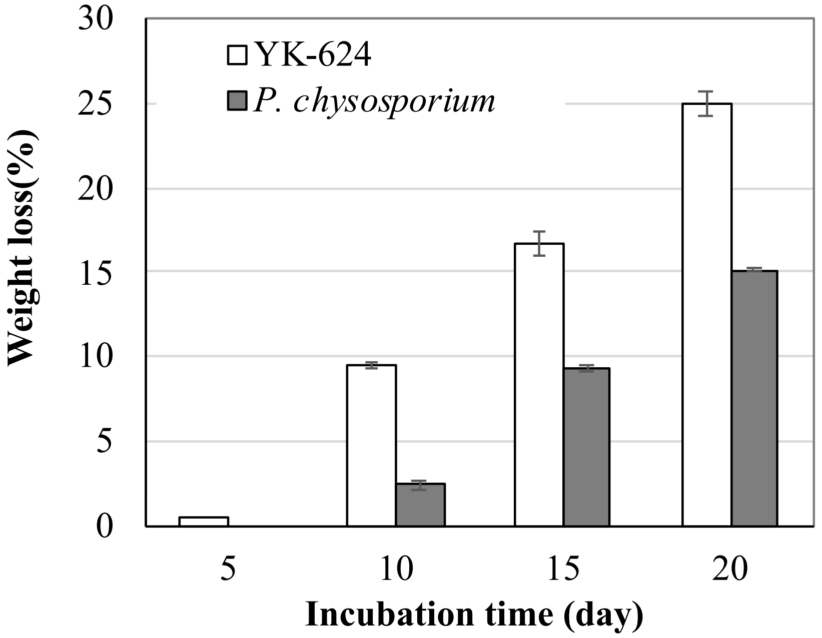

Fig. S2 Time course for the weight loss of *P. sordida* YK-624 and *P. chrysosporium*.