Genome sequencing and analysis of the filamentous fungus Penicillium chrysogenum

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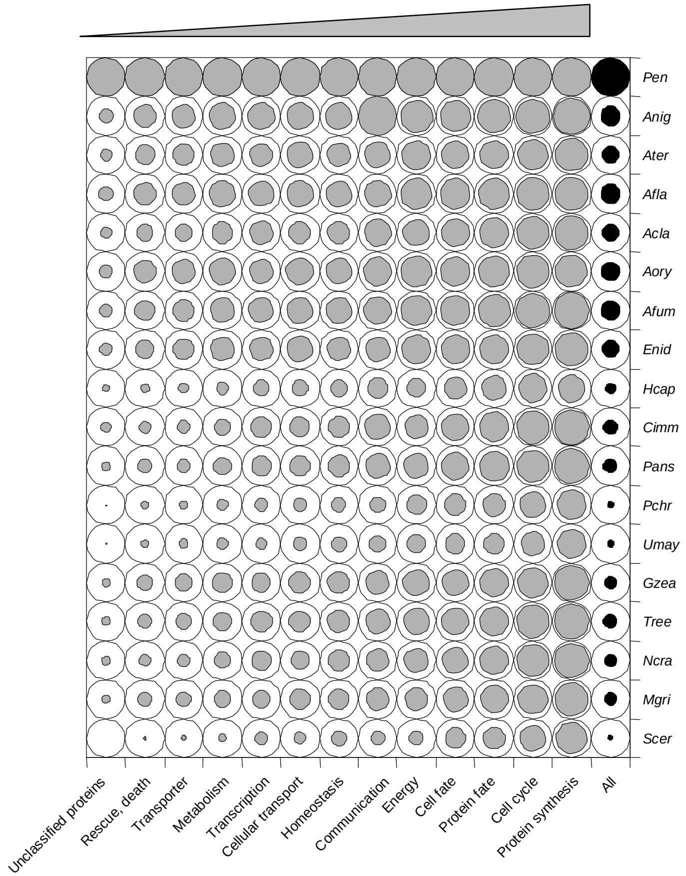
Supplementary Figure 1. Ortholog comparison of main functional classes in different fungal genomes. Pen: *Penicillium chrysogenum*, Anig: *Aspergillus niger*, Ater*: Aspergillus terreus*, Afla: *Aspergillus flavus*, Acla: *Aspergillus clavatus*, Aory: *Aspergillus oryzae*, Afum: *Aspergillus fumigatus*, Enid: *Emericella nidulans*, Hcap: *Histoplasma capsulatum*, Cimm: *Coccidioides immitis*, Pans: *Podospora anserina*, Pchr: *Phanerochaete chrysosporium*, Umay: *Ustilago maydis*, Gzea: *Gibberella zeae*, Tree: *Trichoderma reesei*, Ncra: *Neurospora crassa*, Mgri: *Magnaporthe grisea*, Scer *Saccharomyces cerevisiae*.

The size of the filled circles is proportional to the number of ortholog genes in each category. Categories have been sorted in respect to the number of ortholog genes over all indicated genomes increasing from left to right. Category "All" represents the total number of ortholog genes in respect to *P. chrysogenum* for the listed fungal genomes.



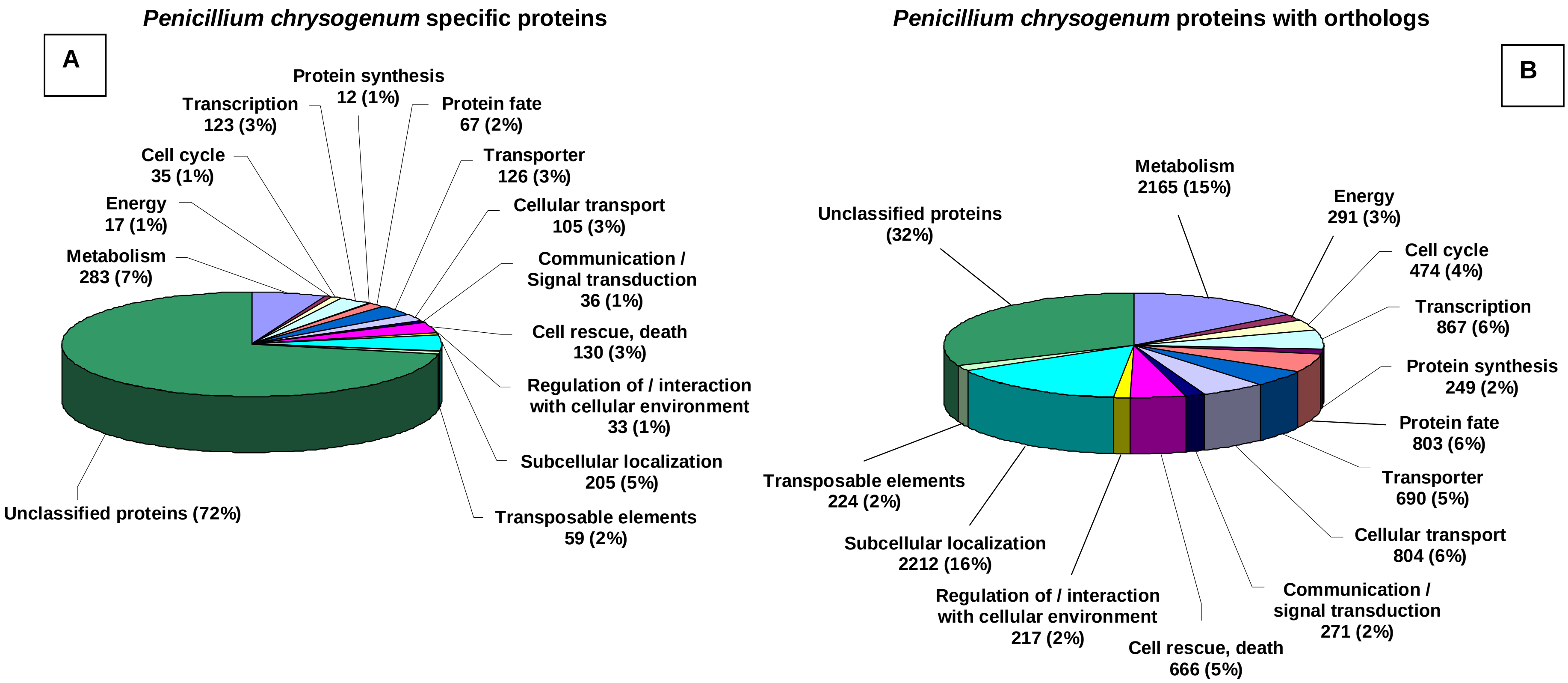
Supplementary Figure 2. Ortholog comparison of functional classes related to metabolism and energy in different fungal genomes. Pen: *Penicillium chrysogenum*, Anig: *Aspergillus niger*, Ater*: Aspergillus terreus*, Afla: *Aspergillus flavus*, Acla: *Aspergillus clavatus*, Aory: *Aspergillus oryzae*, Afum: *Aspergillus fumigatus*, Enid: *Emericella nidulans*, Hcap: *Histoplasma capsulatum*, Cimm: *Coccidioides immitis*, Pans: *Podospora anserina*, Pchr: *Phanerochaete chrysosporium*, Umay: *Ustilago maydis*, Gzea: *Gibberella zeae*, Tree: *Trichoderma reesei*, Ncra: *Neurospora crassa*, Mgri: *Magnaporthe grisea*, Scer *Saccharomyces cerevisiae*.

The size of the filled circles is proportional to the number of ortholog genes in each category. Categories have been sorted in respect to the number of ortholog genes over all indicated genomes increasing from left to right.

The numbers on the x-Axis represent the following functional categories:

1 biosynthesis of nonprotein amino acids, **2** biosynthesis of polyketides, **3** biosynthesis of alkanes, alkenes, alkanals, alkanols, **4** anaerobic aromate catabolism, **5** biosynthesis of aminoglycoside antibiotics, **6** biosynthesis of ß-lactams, **7** biosynthesis of peptide antibiotics, **8** aliphatic hydrocarbon catabolism, **9** biosynthesis of secondary products derived from L-phenylalanine and L-tyrosine, **10** isoprenoid biosynthesis, **11** aerobic aromate catabolism, **12** catabolism of secondary metabolites, **13** biosynthesis of amines, **14** fermentation, **15** aminosaccharide biosynthesis, **16** biosynthesis of alkaloids, **17** nitrogen and sulfur metabolism, **18** degradation of amino acids of the cysteine-aromatic group, **19** biosynthesis of acetoacetate, acetone, hydroxybutyric acid, **20** degradation of amino acids of the glutamate group, **21** assimilation of ammonia, biosynthesis of the glutamate group, **22** breakdown of lipids, fatty acids and isoprenoids, **23** degradation of amino acids of the aspartate group, **24** pentose-phosphate pathway oxidative branch, **25** metabolism of energy reserves (e.g. glycogen, trehalose), **26** fatty acid biosynthesis **27** biosynthesis of derivatives of dehydroquinic acid, shikimic acid and chorismic acid, **28** purine nucleotide metabolism, **29** degradation of amino acids of the pyruvate family, **30** glycolipid biosynthesis, **31** phosphate metabolism, **32** oxidation of fatty acids, **33** polysaccharide biosynthesis, **34** biosynthesis of secondary monosaccharides, **35** biosynthesis of secondary products derived from L-lysine, L-arginine and L-histidine, **36** extracellular metabolism, **37** biosynthesis of the cysteine-aromatic group, **38** glyoxylate cycle, **39** biosynthesis of the aspartate family, **40** glycolysis and gluconeogenesis, **41** metabolism of vitamins, cofactors, and prosthetic groups, **42** polynucleotide degradation, **43** deoxyribonucleotide metabolism, **44** pyrimidine nucleotide metabolism, **45** biosynthesis of the pyruvate family (alanine, isoleucine,

leucine, valine) and D-alanine, **46** biosynthesis of secondary products derived from L-glutamic acid, L-proline and L-ornithine, **47** urea cycle, biosynthesis of polyamines and creatine, **48** biosynthesis of secondary products derived from L-tryptophan, **49** electron transport and membrane-associated energy conservation, **50** tricarboxylic-acid pathway (citrate cycle, Krebs cycle, TCA cycle), **51** respiration, **52** phospholipid biosynthesis, **53** C-1 compound catabolism, **54** biosynthesis of porphyrins, **55** biosynthesis of glycosides, **56** biosynthesis of sulfuric acid and L-cysteine derivatives, **57** metabolism of cyclic and unusual nucleotides, **58** pentose-phosphate pathway non oxidative branch, **59** degradation of amino acids of the hydroxyamino-acid group, **60** biosynthesis of derivatives of homoisopentenyl pyrophosphate, **61** biosynthesis of cobalamins.



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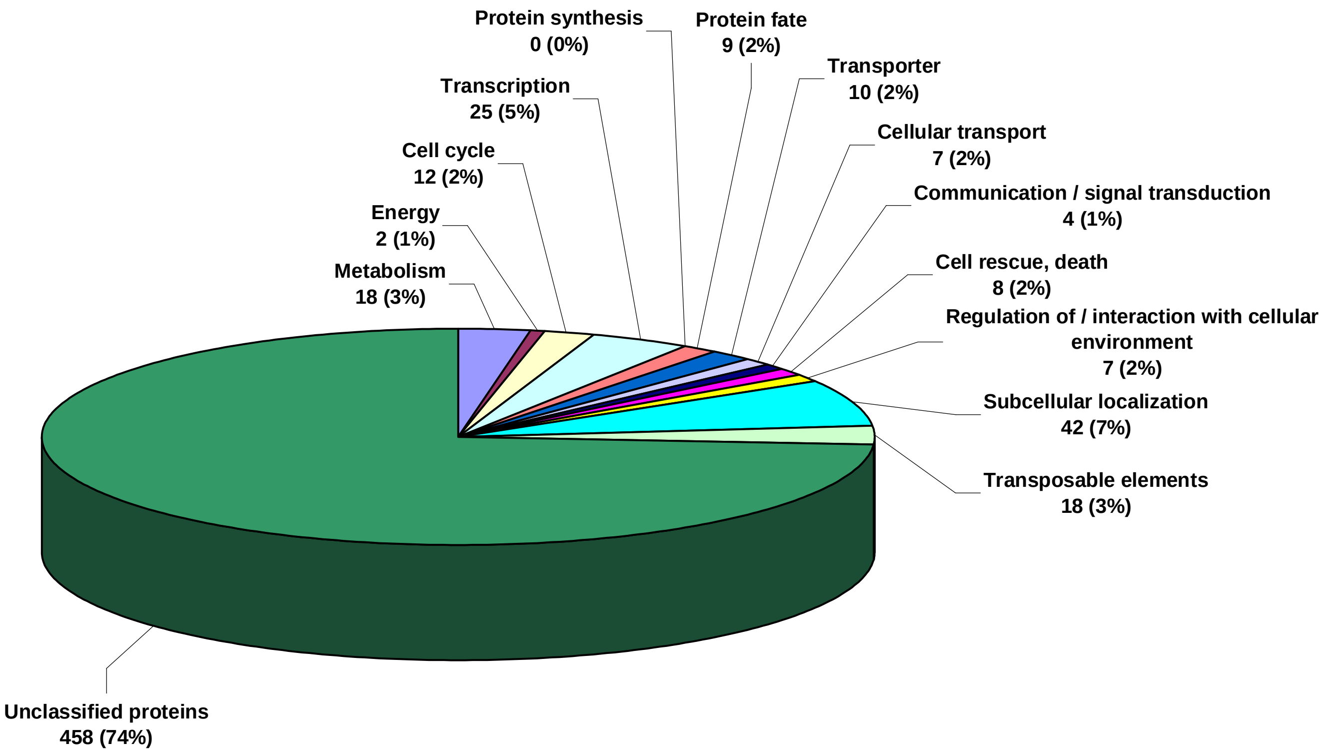
all 4 non-syntenic assemblies



Supplementary Table 1. Genome statistics comparison between different filamentous fungi.

	P. chrysogenum	***A.niger***	***A. nidulans***	***A. fumigatus* Af293**
Chromosomes/Scaffolds				
Total Length (Kb)	32,224	33,931	30,069	28,810
GC content (%)	48.9	50.4	50.0	49.8
Number of Protein Coding Genes	12,941	14,165	10,662	9,632
Mean Gene Length (bp)	1,515	1,573	1,868	1,478.1
Gene Density	2,490	2,395	3,151	2,990
Percent Coding (%)	56.6	55.2	50.0	49.4
Genes with Introns (%)	83.5	87.0	86.9	78.6
Exons				
Average size (bp)	434	370	436	504
Number	41,996	50,629	35,797	28,254
Mean # per Gene	3	3.5	3.4	2.8
GC Content (%)	52.9	53.7	53.3	54
Total Length (bp)	18,238,634	18,733,984	15,477,748	14,241,720
Introns				
Average size (bp)	87.4	97.2	91	82
Number	28,326	36,464	24,792	18,619
Mean # per Gene	2.2	2.6	2.4	1.8
GC Content (%)	45.3	45.3	45.8	46.7
Total Length (bp)	2,475,921	3,544,638	2,243,391	1,521,138
Intergenic Region				
GC Content (%)	44.4	46.4	47.4	45.9
Mean Length (bp)	842	822	1,137	1,322
Longest intergenic region (bp)	44,111	19,212	13,654	55,846
RNA				
tRNA number	145	269	n/a	179
5S rRNA number	28	56	n/a	33

Supplementary table 2. Features of the four non-syntenic supercontigs

Non-syntenic Contigs	67	69	73	74	All four	Genome
Length (Kb)	292	168	229	709	1398	32183
Coding (%)	33.8	37.5	36.3	35.0	35.3	56.6
C+G content (%)	48.6	48.1	48.0	48.1	48.2	48.9
Genes	128	78	103	327	636	13653
Genes (< 100 aa)	6	3	4	8	21	283
Genes with introns (%)	71.1	70.5	82.5	76.1	75.5	83.5
Mean No. exons	2.78	2.50	3.07	2.67	2.75	3.07
Mean protein length (bp)	302	309	307	288	302	446
Mean gene length (aa)	905	927	922	865	905	1338
Repeat element density	0.0177	0.0163	0.0196	0.0158	0.01735	0.0104
TE elements	30	25	11	65	131	559
Pseudogenes	19	11	13	40	83	592

Supplementary Table 3. Detailed analysis of putative key-enzymes in secondairy metabolite synthesis

Analysis was performed using SMURF software (http://www.tigr.org/software/)

Acyl_transf, acyl transferase domain; AMP, adenosyl-monophosphate domain; C, condensation domain; BKS-C, domain with ubiquitin ligase activity, C-terminal; BKS-N, domain with ubiquitin ligase activity, N-terminal; PP, pyrophosphate domain; NAD_4, NAD-binding domain; adh_short, short chain alcohol dehydrogenase domain; DMAT, dimethylallyltransferase domain; arom_pren_DMAT, dimethylallyltransferase domain involved in prenylation of aromatic ring systems; TDMAT, tryptophan-DMAT domain; Lys2, alpha aminoadipate reductase domain; alpha_am_amid - alpha aminoadipate domain

orf code	orf description	Proposed enzyme type	Domains												
			Acyl_transf	AMP	C	BKS-C	BKS-N	PP	NAD_4	adh_short	DMAT	arom_pren_DMAT	TDMAT	Lys2	alpha_am_amid
Pc21g15430	dimethylallyltryptophan synthase dmaW	DMAT	0	0	0	0	0	0	0	0	1	1	1	0	0
Pc14g00080	hybrid NRPS/PKS enzyme, putative	HYBRID	1	1	1	1	1	2	1	1	0	0	0	1	1
Pc16g13930	hybrid NRPS/PKS enzyme, putative	HYBRID	1	1	1	1	1	1	1	1	0	0	0	1	1
Pc13g05250	cyclic peptide AM-toxin synthase like protein An06g01300	NRPS	0	3	6	0	0	6	0	0	0	0	0	0	1
Pc13g14330	HC-toxin peptide synthase HTS	NRPS	0	4	6	0	0	4	0	0	0	0	0	0	1
Pc16g03850	peptide synthase pesA	NRPS	0	1	2	0	0	2	0	0	0	0	0	0	1
Pc16g04690	peptide synthase pesA	NRPS	0	4	6	0	0	5	0	0	0	0	0	0	1
Pc21g01710	peptide synthase like protein An04g06260	NRPS	0	2	1	0	0	2	0	0	0	0	0	0	1
Pc21g10790	HC-toxin peptide synthase HTS	NRPS	0	6	7	0	0	6	0	0	0	0	0	0	1
Pc21g12630	peptide synthase pesA	NRPS	0	2	2	0	0	2	0	0	0	0	0	0	1
Pc21g15480	cyclic peptide AM-toxin synthase like protein An03g00650	NRPS	0	2	2	0	0	2	0	0	0	0	0	0	1
Pc21g21390	nonribosomal alpha-aminoadipyl-cysteinyl-valine synthase PcbAB/AcvA	NRPS	0	3	3	0	0	3	0	0	0	0	0	0	1
Pc22g20400	cyclic peptide AM-toxin synthase AMT	NRPS	0	1	2	0	0	2	0	0	0	0	0	0	1
Pc06g01540	saframycin Mx1 synthase safA	NRPS-Like	0	1	0	0	0	1	1	0	0	0	0	1	1
Pc12g09980	AMP-binding enzyme, putative	NRPS-Like	0	1	0	0	0	1	0	0	0	0	0	0	0
Pc12g13170	polyketide synthase PKS17	NRPS-Like	0	1	0	0	0	1	1	0	0	0	0	1	1
Pc13g12570	saframycin Mx1 synthase safA	NRPS-Like	0	1	0	0	0	1	1	0	0	0	0	1	1
Pc14g01790	polyketide synthase PKS17	NRPS-Like	0	1	0	0	0	0	1	0	0	0	0	1	1
Pc16g09930	FK520 biosynthetic gene cluster polyketide synthase like protein An12g02750	NRPS-Like	0	1	0	0	0	1	0	0	0	0	0	0	0
Pc18g00380	saframycin Mx1 synthase safA	NRPS-Like	0	1	0	0	0	1	1	1	0	0	0	1	1
Pc20g02260	aminoadipate reductase enzyme lys2	NRPS-Like	0	1	0	0	0	0	1	0	0	0	0	1	1
Pc20g02590	saframycin Mx1 synthase safA	NRPS-Like	0	1	0	0	0	1	1	0	0	0	0	1	1
Pc20g09690	polyketide synthase PKS17	NRPS-Like	0	1	0	0	0	1	1	0	0	0	0	1	1
Pc20g12670	hypothetical protein 1457_scaffold_8.tfa_130cg	NRPS-Like	0	1	0	0	0	0	1	0	0	0	0	1	1
Pc21g22530	hypothetical protein contig_1_135_scaffold_11.tfa_110wg	NRPS-Like	0	1	0	0	0	1	0	0	0	0	0	0	1
Pc21g22650	polyketide synthase PKS17	NRPS-Like	0	1	0	0	0	0	1	0	0	0	0	1	1
Pc22g06310	L-aminoadipate-semialdehyde dehydrogenase large subunit Lys2 - Penicillium chrysog	NRPS-Like	0	1	0	0	0	1	1	0	0	0	0	1	1
Pc22g09430	NRPS-like enzyme, putative	NRPS-Like	0	1	0	0	0	0	1	0	0	0	0	1	1
Pc12g05590	nonaketide synthase lovB	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc13g04470	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc13g08690	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc16g00370	6-methylsalicylic acid synthase like protein An10g00140	PKS	1	0	0	1	1	1	0	1	0	0	0	0	0
Pc16g03800	polyketide synthase PKS1	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc16g04890	polyketide synthase like protein An01g01130	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc16g11480	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc21g00960	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	1	1	0	0	0	1	1
Pc21g03930	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc21g03990	polyketide synthase like protein An15g05090	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc21g04840	polyketide synthase PKS1	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc21g05070	polyketide synthase like protein An09g01860	PKS	1	0	0	1	1	1	1	0	0	0	0	1	0
Pc21g05080	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc21g12440	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc21g12450	polyketide synthase wA	PKS	1	0	0	1	1	1	0	0	0	0	0	0	0
Pc21g15160	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc21g16000	polyketide synthase PKS1	PKS	1	0	0	1	1	2	0	0	0	0	0	0	0
Pc22g08170	6-methylsalicylic acid synthase like protein An10g00140	PKS	1	0	0	1	1	1	0	1	0	0	0	0	0
Pc22g22850	polyketide synthase like protein An09g01860	PKS	1	0	0	1	1	1	0	0	0	0	0	0	0
Pc22g23750	lovastatin diketide synthase lovF	PKS	1	0	0	1	1	0	0	1	0	0	0	0	0
Pc12g02940	lovastatin diketide synthase lovF	PKS-Like	1	0	0	1	1	0	0	0	0	0	0	0	0
Pc16g03760	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus [putative	PKS-Like	0	0	0	0	0	0	0	1	0	0	0	0	0
Pc22g09030	3-oxoacyl-[acyl-carrier-protein]-synthase, putative	PKS-Like	0	0	0	1	1	0	0	0	0	0	0	0	0

Supplementary Table 4. PKS and NRPS clusters in *P. chrysogenum* genome

DMAT	
NRPS	
NRPS-Like	
PKS	
PKS-Like	Identified by SMURF (Supplementary Table 7)
PKS-like	Not identified via SMURF
Hybrid	

Secondary metabolite gene or cluster	**ORF code**	**Description of putative *P. chrysogenum* ORF**	**Detailed analyses**	**Average transcript levels @**			
				WIS -PAA	**WIS +PAA**	**DS -PAA**	**DS +PAA**
	Pc06g01490	strong similarity to hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	arabinose efflux permease, weakly similar protein in Ajellomyces capsulatus (35% identity, EDN06642)	57.4	41.2	14.2	0.4
	Pc06g01500	strong similarity to hypothetical protein An12g02740 - Aspergillus niger	Predicted protein with SAM methyltransferase domain, weakly similar proteins in A. terreus (35%identity, EAU36191) and A. niger (32% identity, An12g02740)	84.6	57.8	63.5	35.1
	Pc06g01510	similarity to hypothetical protein AAM35689.1 - Xanthomonas axonopodis	Hypothetical protein, similar proteins in Ajellomyces capsulatus (44% identity, EDN11135)and A. oryzae (43% identity, BAE63447)	55.3	36.4	25.7	9.3
	Pc06g01520	strong similarity to hypothetical protein 1323_scaffold_5.tfa_400cg - Fusarium graminearum	Putative benzoate 4-monooxygenase cytochrome P450, related enzymes in G Zeae (41% identity, XP38819), A. clavatus (39% identity, EAW14333), N. fischeri (39% identity, EAW18955), A. oryzae (39% identity, BAE65144)	52.6	31.0	19.0	5.6
	Pc06g01530	similarity to hypothetical protein 4 - Streptomyces coelicolor	NmrA-family, negative transcriptional regulator, related proteins in Ajellomyces capsulatus	33.9	24.4	56.0	3.0
1	Pc06g01540	strong similarity to saframycin Mx1 synthase safA - Myxococcus xanthus	Monomodular NRPS-like enzyme, 1025 AA, Highly similar NRPS in A. oryzae (64% identity, gi|83773330|dbj|BAE63457.1|), N. fischerii (55% identity, gi|119415803|gb|EAW25740.1|), and Ajellomyces capsulatus (52% identity, gi|150415793|gb|EDN11137.1|)	11.2	5.4	15.6	1.7
	Pc12g02900	strong similarity to transposase Tan1 - Aspergillus niger [putative pseudogene]		135.0	86.7	72.1	26.9
	Pc12g02910	hypothetical protein		983.7	1044.6	575.7	240.9
	Pc12g02920	weak similarity to 2-hydroxyisoflavone reductase IRL - Zea mays		126.3	58.5	152.4	152.5
	Pc12g02930	strong similarity to oxidoreductase like protein An09g01260 - Aspergillus niger		2.4	1.3	24.5	4.7
2	Pc12g02940	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus [putative sequencing error]	PKS-like enzyme, 2523 AA, 13 introns, Related PKS in *A. oryzae* (45% identiy, gi|83764443|dbj|BAE54587.1| and gi|83765672|dbj|BAE55815.1|), *N. fischerii* (45% identity, gi|119406436|gb|EAW16387.1|), *A. niger* (44% identity, gi|119406436|gb|EAW16387.1|), *A. oryzae* (43% identity, gi|83773906|dbj|BAE64031.1|)	4.7	2.2	105.9	20.0
	Pc12g02950	hypothetical protein		424.5	119.3	179.4	22.6
	Pc12g02960	strong similarity to hypothetical protein 1384_scaffold_6.tfa_150cg - Fusarium graminearum	Putative acetyltransferase, similar enzyme in A. terreus (56% identity, gb|EAU33508.1|)	18.9	24.6	82.8	77.8
3	Pc12g05590	strong similarity to nonaketide synthase lovB - Aspergillus terreus	polyketide synthase, related to equisetin synthase, 2715 AA, 10 introns,related enzymes e.g. in A.	3.9	2.9	4.8	6.2
	Pc12g05600	strong similarity to H+-biotin symporter Vht1 - Saccharomyces cerevisiae [putative sequencing error]		1.4	1.9	2.4	1.9
	Pc12g05610	strong similarity to hypothetical protein An01g10470 - Aspergillus niger [putative sequencing error]		69.2	61.8	45.3	47.0
4	Pc12g09980	Monomodular NRPS-like enzyme with additional transferase hexapeptide repeats, 1619 AA, 2	strong similarity to acid-CoA ligase Fat2 - Saccharomyces cerevisiae	5.9	4.1	8.4	6.8
	Pc12g13140	strong similarity to hypothetical molasses resistency protein Rtm1 - Saccharomyces cerevisiae		1.2	1.5	1.4	0.7
	Pc12g13150	strong similarity to cdc25C associated protein kinase like protein An18g01800 - Aspergillus niger		61.4	47.6	33.1	45.3
	Pc12g13160	strong similarity to hypothetical mixed-linked glucanase precursor related protein MLG1 - Neurospora crassa		84.0	32.7	67.1	14.2
5	Pc12g13170	similarity to polyketide synthase PKS17 - Botryotinia fuckeliana	Monomodular NRPS-like enzyme, 1092 AA, 3 introns, Similar enzymes in Aspergilli: A. niger (61% identity, emb|CAK96299.1|), oryzae (60% identity, gi|83768531|dbj|BAE58668.1|), A. terreus (60% identity, gi|114196109|gb|EAU37809.1|), A. nidulans (55% identity, gi|40745358|gb|EAA64514.1|) within orthologous clusters	10.1	3.6	18.8	11.4
	Pc12g13180	strong similarity to 3-dehydroshikimate dehydratase qa-4 - Neurospora crassa		15.5	19.1	18.0	21.5
	Pc12g13190	strong similarity to cDNA O-methyltransferase mt-I - Aspergillus parasiticus		8.0	4.6	12.6	3.3
	Pc12g13200	strong similarity to hypothetical protein contig46_part_ii.tfa_3260wg - Aspergillus fumigatus		466.4	540.0	863.9	1413.8
	Pc13g04460	strong similarity to hypothetical protein contig_1_89_scaffold_6.tfa_690wg - Aspergillus nidulans		153.2	138.1	83.2	54.4
6	Pc13g04470	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, 2591 AA, 6 introns, related enzymes in Solorina crocea (46% identity,	1.9	1.4	0.6	1.8
	Pc13g05170	similarity to multidrug resistance protein mdr1 - Aspergillus flavus		4.8	6.0	5.8	3.0
	Pc13g05180	strong similarity to dicarboxylic amino acid permease Dip5 - Saccharomyces cerevisiae		4.6	3.0	2.3	2.2
	Pc13g05190	weak similarity to 2-haloacid halidohydrolase IVa - Burkholderia cepacia		44.4	34.0	44.8	54.4
	Pc13g05200	strong similarity to hypothetical nuclear migration protein - Neurospora crassa		45.4	36.3	44.9	31.0
	Pc13g05210	similarity to hypothetical protein An08g09910 - Aspergillus niger		3.5	3.8	4.4	2.5
	Pc13g05220	strong similarity to microsomal cytochrome like protein An05g00300 - Aspergillus niger		729.8	864.4	786.0	1126.7
	Pc13g05230	strong similarity to ATP-dependent RNA helicase cdc28p - Schizosaccharomyces pombe		87.2	80.5	60.1	44.9
	Pc13g05240	strong similarity to protein kinase Swe1 - Saccharomyces cerevisiae		69.6	64.2	40.4	39.3
7	Pc13g05250	ferrichrome synthetase, 5081 AA, 5 introns, Similar synthetase in *A. clavatus*	ferrichrome synthetase, 5081 AA, 5 introns, Similar synthetase in A. clavatus (52 % identity, gb|EAW06285.1|), which however has an intact second A-domain, thus producing presumably ferricrocin	52.7	61.2	69.2	80.5

	Pc13g05260	strong similarity to L-ornithine N5-hydroxylase psbA - Pseudomonas sp.		64.9	66.5	57.1	57.0
	Pc13g05270	strong similarity to ankyrin repeat-containing protein Akr1 - Saccharomyces cerevisiae		243.1	231.2	206.0	137.1
	Pc13g08640	strong similarity to FAD dependent L-sorbose dehydrogenase SDH - Gluconobacter oxydans		44.8	55.2	100.0	149.2
	Pc13g08650	similarity to integral membrane protein PTH11 from patent WO9913094-A2 - Magnaporthe grisea		0.2	0.6	0.6	2.2
	Pc13g08660	hypothetical protein		2.8	2.1	5.2	4.9
	Pc13g08670	weak similarity to hypothetical protein YER080w - Saccharomyces cerevisiae		4.0	2.3	4.9	2.4
	Pc13g08680	similarity to trichothecene 3-O-acetyltransferase TRI101 - Gibberella zeae		1.6	1.5	8.7	0.9
8	Pc13g08690	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, 2526 AA , 6 introns, Related enzyme in A. oryzae (45% identity,	61.9	33.2	41.6	14.4
	Pc13g08700	weak similarity to hypothetical protein BAB11562.1 - Arabidopsis thaliana		71.0	39.9	79.6	52.0
9	Pc13g12570	strong similarity to saframycin Mx1 synthase safA - Myxococcus xanthus	Monomodular NRPS-like enzyme, 1037 AA, Similar enzymes in Aspergilli, e.g. A. oryzae (57% identity, dbj|BAE64320.1|), A. niger (56% identity, emb|CAK38572.1|)	1.0	0.2	1.6	0.6
	Pc13g12580	strong similarity to 8-amino-7-oxononanoate synthase KAPA synthase BioF - Kurthia sp.		0.4	2.5	2.4	0.9
	Pc13g14310	similarity to methyl chloride transferase AAC72357.1 - Batis maritima	methyl transferase, similar enzymes in A. niger (53% identity, emb|CAK38144.1|), andA. nidulans (47% identity, gb|EAA58069.1|),	39.4	49.1	119.3	86.8
	Pc13g14320	strong similarity to multidrug resistance protein atrD - Aspergillus nidulans [putative sequencing error]		0.7	0.2	2.4	1.5
10	Pc13g14330	weak similarity to HC-toxin peptide synthase HTS - Cochliobolus carbonum	nonribosomal peptide synthase, 5267 AA , 3 introns, Related NRPSA in A. terreus (52% identity,	3.5	2.6	7.0	6.4
	Pc14g00010	strong similarity to methionine aminopeptidase-like protein F6E13.31 - Arabidopsis thaliana		172.1	150.0	138.6	129.8
	Pc14g00020	weak similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe		85.6	132.7	153.2	343.6
	Pc14g00030	weak similarity to hypothetical protein PA1213 - Pseudomonas aeruginosa		41.5	123.1	170.5	711.3
	Pc14g00040	strong similarity to hypothetical protein ncu00758.1 - Neurospora crassa		1.5	1.5	2.3	1.7
	Pc14g00050	hypothetical protein		4.7	2.9	6.0	4.2
	Pc14g00060	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae		12.6	7.1	30.1	70.8
	Pc14g00070	hypothetical protein		1.4	2.6	4.3	3.0
11	Pc14g00080	strong similarity to nonaketide synthase lovB - Aspergillus terreus	hybrid NRPS/PKS enzyme, putative, 4049 AA, 6 introns, related NRPS/PKS in M. grisea (41 and 42%	24.4	17.5	28.6	23.0
	Pc14g00090	strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus		1.4	0.4	0.9	1.4
	Pc14g00100	similarity to hypothetical protein 162_scaffold_1.tfa_20wg - Fusarium graminearum		1.5	1.3	1.4	3.3
	Pc14g00110	weak similarity to hypothetical protein An03g00160 - Aspergillus niger		7.3	0.8	10.2	3.4
	Pc14g00120	strong similarity to cytochrome P450 trichodiene oxygenase TRI4 - Fusarium sporotrichioides		252.4	321.3	877.0	474.9
	Pc14g00130	hypothetical protein		12.9	10.1	7.9	8.8
	Pc14g00140	strong similarity to hypothetical protein contig_1_62_scaffold_4.tfa_510cg - Aspergillus nidulans		69.7	126.0	163.7	95.9
	Pc14g00150	strong similarity to lysine permease Lyp1 - Saccharomyces cerevisiae		38.7	14.5	45.6	54.0
12	Pc14g01790	strong similarity to polyketide synthase PKS17 - Botryotinia fuckeliana	Adenylate domain containing enzyme, 1075 AA, 3 introns, likely acyl substrate, Only in Ascomycetes and Basidiomycetes, related enzymes in Aspergilli, e.g. A. oryzae (50% identity, gi|83776108|dbj|BAE66227.1|), A. terreus (48% identity, gi|114188579|gb|EAU30279.1|), a related enzyme in P. nordicum (45% identity, gi|46452157|gb|AAS98174.1|) is involved in ochratoxin biosynthesis	1.2	3.7	2.2	1.5
	Pc15g00040	strong similarity to hypothetical protein contig17.tfa_80wg - Aspergillus fumigatus	Related to integral membrane protein in Aspergillus fumigatus (31% identity, EAL86542), Clustered with a PKS (Afu3g02570) not related to Pc15g00050	3.9	0.5	2.0	2.2
13	Pc15g00050	Polyketide synthase, 2198 AA, 2 introns, fragment, related PKS in *Gibberella moniliformis*	Polyketide synthase, 748 AA, 2 introns, presumably non-functional fragment, related PKS in Gibberella moniliformis (40% identity, gi|40806905|gb|AAR92212.1|)	1.2	0.3	0.4	3.0
	Pc15g00060	strong similarity to amino-acid N-acetyltransferase - Neurospora crassa		46.0	48.6	51.9	64.0
	Pc15g00070	similarity to arylalkylamine N-acetyltransferase AANAT1 - Esox lucius		256.8	251.5	192.8	147.1
	Pc16g00350	strong similarity to hypothetical protein An10g00160 - Aspergillus niger		1.8	2.5	5.5	1.8
	Pc16g00360	strong similarity to cytochrome P450 trichodiene oxygenase TRI4 - Fusarium sporotrichioides		0.4	1.0	1.1	3.8
14	Pc16g00370	strong similarity to 6-methylsalicylic acid synthase like protein An10g00140 - Aspergillus niger	polyketide synthase, 6-methylsalicylic acid synthase like protein, 1783 AA,also found in P. griseofulvum (85% identity, gi|1888549|gb|AAB49684.1|), while known6-MSA synthases have less similarity, e.g. in Byssochlamys nivea (48% identity,gi|13899024|gb|AAK48943.1|AF360398_1), A. terreus (47% identity, gi|114213489|dbj|BAA20102.2|), P. griseofulvum (48% identity, gi|3212|emb|CAA39295.1|)related clusters in A. niger (around An10g00140), A. fumigauts (Afu8g02350), and N. fischeri (NFIA_096030).	27.5	32.1	29.4	30.2
	Pc16g00380	similarity to para-hydroxybenzoate--polyprenyltransferase ppt1p - Schizosaccharomyces pombe	Polyprenyltransferase, related enzymes in A. niger (An10g00130), N. fischeri (NFIA_096080), A. nidulans (AN8142.3), and A. fumigatus (Afu8g02350)	3.5	3.6	5.9	4.1
	Pc16g00390	similarity to hypothetical meta-cleavage compound hydrolase gene ren71 - Streptomyces aureofaciens		1.9	0.5	1.3	0.5
	Pc16g00400	strong similarity to cytochrome P450 eln2 - Coprinus cinereus		0.2	0.6	0.5	0.8
	Pc16g03740	weak similarity to siderophore biosynthesis repressor sREA - Aspergillus nidulans	High regional similarity to siderophore biosynthesis repressors sREA in Aspergilli (70 % identity)	2.2	1.8	0.6	2.2
	Pc16g03750	strong similarity to hypothetical protein contig_1_61_scaffold_4.tfa_2170cg - Aspergillus nidulans	Myosin cross reactive antigen family – various related proteins in Aspergilli (35-52% identity)	4.5	5.1	10.4	11.7

15	Pc16g03760	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus [putative pseudogene]	Polyketide synthase, 711 AA fragment, 50% identity to internal segments of G. zeae gi|82779926|gb|ABB90283.1| and gi|42544370|gb|EAA67213.1|	0.8	0.5	2.2	1.5
	Pc16g03770	strong similarity to conserved hypothetical protein - Brucella suis	Contains cupin domain, highly similar proteins in A. oryzae (88% identity, dbj|BAE59540.1|) and various Brucella suis sp. (88% identityx, e.g. gb|ABQ61818.1|)	116.2	75.2	103.2	149.1
	Pc16g03780	strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	Zn-binding dehydrogenase, related protein in A. niger (62% identity, emb|CAK40659.1|), ToxD-like, e.g. inA. fumigatus (53% identity, gb|EAL88863.1|)	32.6	25.8	71.1	87.4
	Pc16g03790	hypothetical protein		1.0	1.3	2.8	0.3
15	Pc16g03800	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	polyketide synthase, Siderophore associated, producing acyl component of triacetyl-fusarinine like siderophore, 2357 AA , 7 introns, related enzymes in A. niger (54% identity, emb|CAK40660.1|, and 52% identity, emb|CAK41112.1|))	56.8	31.4	84.8	93.7
	Pc16g03810	strong similarity to hypothetical protein F28J12.200 - Arabidopsis thaliana		1.6	2.3	5.4	6.3
	Pc16g03820	similarity to hypothetical protein 1145_scaffold_2.tfa_290cg - Fusarium graminearum		109.0	80.2	120.4	101.7
	Pc16g03830	similarity to hypothetical protein An12g06250 - Aspergillus niger		4.4	2.5	14.3	57.9
	Pc16g03840	hypothetical protein		2.0	0.6	2.4	1.9
15	Pc16g03850	similarity to peptide synthase pesA - Metarhizium anisopliae	nonribosomal siderophore peptide synthase, 1900 AA, 1 intron, highly similar synthetase in A. terreus (67% identity, gb|EAU31750.1|), and related NRPS in Coccidioides immitis (52% identity, gb|EAS36075.1|) and N. crassa (50% identity, gb|EAA34175.2|)	17.6	11.8	11.7	25.0
	Pc16g03860	acetylase		43.5	32.4	37.5	24.8
	Pc16g03870	strong similarity to multidrug resistance protein atrD - Aspergillus nidulans		36.7	23.1	31.4	36.0
	Pc16g03880	strong similarity to hypothetical protein contig_1_7_scaffold_1.tfa_250wg - Aspergillus nidulans		61.3	78.9	45.8	75.4
	Pc16g03890	weak similarity to hypothetical protein SPAC56E4.07 - Schizosaccharomyces pombe		71.6	72.7	69.7	112.5
	Pc16g03900	strong similarity to hypothetical protein An18g01950 - Aspergillus niger [putative sequencing error]		4.1	4.6	6.1	5.5
	Pc16g03910	strong similarity to ferrioxamine B permease Sit1 - Saccharomyces cerevisiae		80.9	95.8	179.6	162.5
	Pc16g03920	weak similarity to trichodiene synthase - Gibberella pulicaris		2.0	2.8	3.3	3.7
	Pc16g04670	strong similarity to cadmium resistance protein Ycf1 - Saccharomyces cerevisiae		852.6	755.9	669.9	577.4
	Pc16g04680	hypothetical protein		6.4	5.0	7.9	7.6
16	Pc16g04690	similarity to peptide synthase pesA - Metarhizium anisopliae	nonribosomal peptide synthase, presumably cyclopentapeptide synthetase, Related NRPS systems in all Aspergilli with best regional identities between 52 and 56% (A. clavatus gb|EAW07799.1|, N. fischerii gb|EAW22836.1|, A. fumigatus gb|EAL90366.1|, A. oryzae dbj|BAE64185.1| , A. terreus gb|EAU38874.1|,A. niger emb|CAK48225.1|, A. nidulans gb|EAA65335.1| and gb|EAA65835.1|)	597.1	563.0	394.5	408.5
	Pc16g04700	strong similarity to polyamine transport protein Tpo1 - Saccharomyces cerevisiae	Major facilitator superfamily, highly similar in Aspergilli (75-80% identity)	25.8	41.7	23.1	30.8
	Pc16g04710	strong similarity to hypothetical protein YKR018c - Saccharomyces cerevisiae	Hypothetical protein, highly similar in Aspergilli (64-69% identity)	147.0	218.2	266.9	307.8
	Pc16g04720	weak similarity to hypothetical protein YDR363w-a - Saccharomyces cerevisiae	Putative proteasome complex subunit, similar proteins in Aspergilli (65-72% identity)	201.0	240.6	238.8	265.8
	Pc16g04860	similarity to hypothetical protein An07g02510 - Aspergillus niger [putative pseudogene]	178 AA fragment, related to a hypothetical protein in A. oryzae (695 AA, regional 42% identity, dbj|BAE54609.1|)	1.9	1.0	0.6	2.6
	Pc16g04870	strong similarity to cytochrome P450 protein like protein An15g05070 - Aspergillus niger		0.2	0.4	4.6	5.6
	Pc16g04880	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	Fungal transcription factor, similar protein in Ajellomyces capsulatus (56% identity, gb|EDN11107.1|),A. terreus (56% identity, gb|EAU37616.1|) and A. niger (54% identity, emb|CAK42482.1|)	375.1	389.1	381.9	377.1
17	Pc16g04890	strong similarity to polyketide synthase like protein An01g01130 - Aspergillus niger	polyketide synthase, 2546 AA, 3 introns, highly similar PKS in an orthologous cluster A. niger (66% identity, emb|CAK42483.1|), and PKS with related N-terminally regions (52% identity) in A. terreus (gi|114192117|gb|EAU33817.1|) and N. crassa (gi|28919501|gb|EAA28933.1|)	39.9	27.7	56.6	43.5
	Pc16g04900	strong similarity to hypothetical protein contig1477_1.tfa_1070cg - Aspergillus fumigatus	Related proteins with weak similarity in Aspergilli (31%), e.g. N. fischeri (35%, gb|EAW21131.1|), and30%, gb|EAW20557.1|), A. fumigatus (31%, gb|EAL84504.1|, and gb|EAL85603.1|)	6.8	8.8	7.6	11.4
	Pc16g04910	strong similarity to protein involved in cercosporin production CFP - Cercospora kikuchii	Major Facilitator Superfamily, highly similar proteins in A. niger (81% identity, emb|CAK42480.1|) and A. terreus (80% identity, gb|EAU37617.1|)	5.6	18.3	12.4	7.5
18	Pc16g09930	strong similarity to FK520 biosynthetic gene cluster polyketide synthase like protein An12g02750 - Aspergillus niger	Monomodular NRPS-like enzyme, 967 AA, 1 intron, only weakly related enzymes in *A. terreus* (34% identity, gb|EAU37830.1|) and *A. niger* (33% identity, emb|CAK41114.1|)	11.3	9.6	4.7	3.8
	Pc16g09940	strong similarity to hypothetical protein 1324_scaffold_5.tfa_120cg - Fusarium graminearum	2-oxoglutarate Fe(II) oxygenase superfamily, related proteins in *Sclerotinia sclerotiorum* (40% identity, EDN92102) and *A. clavatus* (39% identity, EAW14281)	21.3	9.9	11.8	8.0
	Pc16g09950	similarity to conserved hypothetical protein - Pseudomonas syringae	Similarity to conserved hypothetical proteins in *Sclerotinia sclerotiorum* (41% identity, EDN92101), *A. clavatus* (40%, EAW14280) and *Phaeosphaeria nodorum* (38%, EAT86602)	5.7	5.7	3.3	3.1
	Pc16g11440	hypothetical protein	hypothetical protein, partially related proteins in Aspergilli (e.g. in *A. oryzae* , BAE66300.1) and *A. fumigatus* (EAE90389), related to superoxide dismutase	27.2	28.1	75.4	36.9
	Pc16g11450	strong similarity to hypothetical protease Mch5 - Saccharomyces cerevisiae	Moncarboxylate permease homolog, similar *A. niger* (CAK43292, 62% identity), *A. terreus* (EAU36164, 55% identity) and *A. nidulans* (EAA64469, 512% identity)	3.0	2.6	18.7	23.6
	Pc16g11460	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae		128.3	89.8	142.2	351.1
	Pc16g11470	strong similarity to ATP-binding cassette multidrug transport protein atrB - Aspergillus nidulans		73.8	65.5	249.8	116.6
19	Pc16g11480	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, 2624 AA, 7 introns, Related enzymes in *N. fischerii* (46% identity, gi|119406936|gb|EAW16886.1|), *A. clavatus* (46% identity, gi|119401914|gb|EAW12336.1|), *A. oryzae* (46% identity, gi|83764427|dbj|BAE54571.1|), *A. fumigatus* (46% identity, gi|66846091|gb|EAL86424.1|), *A. terreus* (41% identity, gi|66846091|gb|EAL86424.1|)in related clusters, presumably ochratoxin-type biosynthesis	7.3	2.7	688.5	208.1
	Pc16g11490	weak similarity to hypothetical dihydrofolate reductase CAB16576.1 - Schizosaccharomyces pombe	DUF341 domain protein, hypothetical dihydrofolate reductase, homologs in all Aspergilli, 66-71% identity	0.7	1.6	252.2	94.9
	Pc16g11500	strong similarity to hypothetical integral membrane protein - Schizosaccharomyces pombe	DUF1212 domain membrane protein, homologs in Aspergilli (60-68% identity)	82.1	79.1	644.7	345.2

	Pc16g13880	strong similarity to hypothetical oxidoreductase PC14 - Phytophthora capsici [truncated ORF][putative pseudogene]	strong similarity (83% identity) to hypothetical oxidoreductase PC14 - *Phytophthora capsiciindu* ced by interaction with host plant	2.1	1.5	1.4	3.1
	Pc16g13890	strong similarity to hypothetical membrane transport protein SPAC3H1.06c - Schizosaccharomyces pombe	Major facilitator superfamily, efflux pump, similar genes (53% identity) in *A. niger* (An07g00060 and An02g08330) and *B. fuckeliana* (BC1G_00699)	10.2	8.1	17.4	30.4
	Pc16g13900	strong similarity to hypothetical protein Z - Streptomyces hygroscopicus	Putative hydrolase, related genes in Aspergilli (51-52% identity): *A. fumigatus* (EAL85114), *A. terreus* (EAU78973), *A. niger* (An07g00020), *A. clavatus* (EAW15063)	19.4	10.0	7.1	6.1
	Pc16g13910	similarity to hypothetical protein contig14.tfa_150wg - Aspergillus fumigatus	Putative integral membrane protein, weak similarity (34% identity) to *N. fischeri* EAW19777and EAW 15333, *A. clavatus* (31% identity)	0.4	1.3	5.0	4.5
	Pc16g13920	strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	Putative Zn-binding oxidoreductase, related enzymes in *N. fischeri* (43% identity, EAW16807; 37% identity, EAW16241), *A. nidulans* (41% identity, AN8409), *A. clavatus* (38% identity,EAW06525), *A. fumigatus* (37% identity, EAL88863)	2.1	1.0	5.6	2.4
20	Pc16g13930	strong similarity to lovastatin nonaketide synthase lovB - Aspergillus terreus	hybrid NRPS/PKS enzyme, 4096 AA, 4 introns, related multienzymes in Aspergilli (38% identity): *A. clavatus* gi|119404686|gb|EAW15062.1|, *A. fumigatus* gi|66844776|gb|EAL85113.1|, *A. terreus* gi|114197271|gb|EAU38971.1|in related clusters	103.2	88.5	68.0	52.2
	Pc16g13940	strong similarity to hypothetical protein mg09154.1 - Magnaporthe grisea	similarity to hypothetical proteins in *Magnaporthe grise*) (43% identity, EAQ71548), *Phaeosphaeria nodorum* (41% identity, EAT49431*), A. niger* (38% identity, CAK46265)	69.0	68.4	42.8	43.8
	Pc18g00330	strong similarity to hypothetical phd finger transcription regulator - Schizosaccharomyces pombe	hypothetical phd finger transcription regulator, related proteins in A. clavatus (57% identity, EAW09774), *N. fischeri* (56% identity, EAW21364), *A. fumigatus* (55% identity, EAL92380)	36.0	29.3	27.4	27.3
	Pc18g00340	similarity to hypothetical protein BAB75479.1 - Nostoc sp.	hypothetical protein containing tetratricopeptid-domain, related proteins in *C. globosum* (46-49% identity, e.g. EAQ83821, 84130, 88760, 93491)	29.6	18.9	28.3	28.8
	Pc18g00350	hypothetical protein	hypothetical protein, weakly related proteins in in *G. zeae* (28% identity, FG08961), *C. globosum* (27% identity, EAQ93177), *A. fumigtus* (28% identity, EAL85340)	108.1	80.4	140.1	91.9
	Pc18g00360	strong similarity to hypothetical protein contig336.tfa_290wg - Aspergillus fumigatus [putative sequencing error]	sigma-70 region 2 family protein, related proteins in all Aspergilli, e.g. A. clavatus (44% identity, EAW09773), *N. fischeri* (45% identity, EAW21364), *A. fumigatus* (55% identity, EAL92380)	2.8	4.0	27.5	26.4
	Pc18g00370	hypothetical protein	hypothetical protein, no significant similarity found	2.7	2.0	6.4	2.4
21	Pc18g00380	strong similarity to saframycin Mx1 synthase safA - Myxococcus xanthus	Monomodular NRPS-like enzyme, 1318 AA, Highly similar enzymes in Aspergilli, presumably primary metabolism, *A. terreus* (75% identity, gi|114195665|gb|EAU37365.1|), *N. fischerii* (73% identity, gi|119407835|gb|EAW17784.1|), *A. fumigatus* (72% identity, gi|66851266|gb|EAL91592.1|), *A . nidulans* (72% identity, gi|66851266|gb|EAL91592.1|)	393.4	398.1	386.6	366.8
	Pc18g00390	strong similarity to high-affinity glucose transporter HGT1 - Kluyveromyces lactis	high-affinity glucose transporter , related proteins in all Aspergilli, e.g. A. clavatus (57% identity, EAW09772), *N. fischeri* (65% identity, EAW21366), *A. fumigatus* (66% identity, EAL92382)	45.5	36.5	54.4	46.3
	Pc18g00400	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	Transcription factor, GAL4-like Zn2Cys6 binuclear cluster DNA-binding domain, related proteinsin all Aspergilli, e.g. A. clavatus (64% identity, EAW09771), *N. fischeri* (65% identity, EAW21367), *A. fumigatus* (65% identity, EAL92384)	197.6	174.3	178.0	122.0
	Pc18g00410	strong similarity to prolyl-4-hydroxylase-alpha like protein An02g07870 - Aspergillus niger	prolyl-4-hydroxylase-alpha like protein, related proteins in all Aspergilli, e.g. A. clavatus (63% identity, EAW09770), *N. fischeri* (58% identity, EAW21368), *A. fumigatus* (62% identity, EAL92385)	8.7	8.0	10.3	11.4
	Pc18g00420	transcription factor pacC - Penicillium chrysogenum	transcription factor pacC, related proteins in all Aspergilli, e.g. A. clavatus (64% identity, EAW09769), *A. niger* (69% identity, CAK37752), *A. parasiticus* (70% identity, AF408430)	211.5	171.5	219.2	151.2
22	Pc20g02260	similarity to aminoadipate reductase enzyme lys2 - Acremonium chrysogenum	Monomodular NRPS-like enzyme, 1080 AA, 1 intron, Weakly related enzymes in G. zeae (46% identity, ref|XP_382427.1|) , Botryotinia fuckeliana (45% identity, gb|EDN18359.1|) and A. nidulans (43% identity, gb|EAA60062.1|)	3.0	1.8	2.9	2.8
23	Pc20g02590	strong similarity to saframycin Mx1 synthase safA - Myxococcus xanthus	Monomodular NRPS-like enzyme, 1045 AA, related enzymes in N. fischerii (46% identity, gi|119407216|gb|EAW17166.1|), A. terreus (43% identity, gi|114192344|gb|EAU34044.1|), A. oryzae (41% identity, gi|83774195|dbj|BAE64320.1|)	0.5	0.9	2.1	0.8
	Pc20g04890	similarity to salicylate hydroxylase nahG - Pseudomonas putida	Monooygenase, highly similar enzymes in A. oryzae (80% identity, BAE64963), A. terreus(79% identity, EAU33487), N. fischeri (78% identity, EAW23864)	7.6	7.5	20.7	15.9
24	Pc20g04900	strong similarity to hypothetical protein An08g08230 - Aspergillus niger	3123 AA, 6 introns, similar protein in A. niger (42% identity, emb|CAK45810.1|), related proteins in Aspergilli with 28-29% identity	2.7	2.2	4.2	2.2
	Pc20g04910	hypothetical protein		1.1	3.1	7.0	3.0
	Pc20g04920	similarity to fluconazole resistance protein like protein An16g02330 - Aspergillus niger		3.9	1.3	5.4	5.7
	Pc20g04930	similarity to polyketide synthase like protein An12g07070 - Aspergillus niger		0.6	0.6	3.0	1.1
	Pc20g09620	strong similarity to multidrug resistance protein Hol1 - Saccharomyces cerevisiae	Major facilitator superfamily protein, related transporters in *Pichia guilliermondii* (44%identity, EDK41085), *Phaeosphaeria nodorum* (39% identity, EEEAT81452), *A. terreus* (38% identity, EAU38738)	0.8	1.5	2.7	1.1
	Pc20g09630	similarity to lipase LipP - Pseudomonas sp.	Putative hydrolase, lipase, similar proteins in *A. terreus* (59% identity, EAU29496), *A. clavatus* (56% identity, EAW09316), *N. fischeri* (55% identity, EAW21829)	17.6	27.9	34.8	45.4
	Pc20g09640	strong similarity to hypothetical sugar transporter encoded by DRA0271 - Deinococcus radiodurans	5S rRNA	139.4	129.9	134.6	113.1
	Pc20g09650	hypothetical protein	Sugar transporter, similar proteins in A. terreus (81% identity, EAU32826 and 66% identity, EAW29729), *A. oryzae* (71% identity, BAE60291), *A. clavatus* (65% identity, EAW21829)	0.4	0.7	1.5	1.0
	Pc20g09660	similarity to hypothetical protein required for biosynthesis of the host-specific AK-toxin Akt2 - Alternaria alternata		0.6	1.9	1.5	3.6
	Pc20g09670	strong similarity to hypothetical conserved protein CC0299 - Caulobacter crescentus [putative sequencing error]	Small noncoding RNA	0.4	0.3	2.5	0.4
	Pc20g09680	strong similarity to astaxanthin synthetase like protein An07g00250 - Aspergillus niger	Putative AK-toxin biosynthesis protein, related proteins in *N. fischeri* (57% identity, EAW24908), *A.*	2.3	2.0	3.1	0.6

25	Pc20g09690	strong similarity to polyketide synthase PKS17 - Botryotinia fuckeliana	Predicted phosphotransferase**,** related proteins in *A. oryzae* (55% identity, BAE55799), *N. fischeri* (55% identity, EAW23466), *A. fumigatus* (55% identity, EAL88000), *A. nidulans* (53% identity, AN2272),*A. terreus* (51% identity, EAU37482), *A. clavatus* (54% identity, EAW08403), *A. niger* (55% identity, An01g05030)	2.3	2.0	6.3	4.3
	Pc20g09700	hypothetical protein	P450 oxygenase, similarity to *A niger* (44% identity, An07g00250), *A. terreus* (42% identity, EAU30769),	0.5	0.4	0.4	1.8
	Pc20g09710	strong similarity to hypothetical protein An15g06870 - Aspergillus niger	Monomodular NRPS-like enzyme, 1072 AA, 3 introns, Related enzymes in Aspergilli, e.g. *A. terreus*	166.6	111.5	48.2	51.1
	Pc20g09720	similarity to hypothetical protein An01g07110 - Aspergillus niger [putative pseudogene]	Small noncoding RNA	58.9	46.5	24.5	17.4
	Pc20g09730	similarity to glutamyl endoprotease polypeptide like protein An11g07120 - Aspergillus niger		56.2	47.0	10.8	26.6
	Pc20g09740	similarity to hypothetical zinc-finger protein SPBC15D4.02 - Schizosaccharomyces pombe	Putative phosphotransferase, related proteins in *Sclerotinia sclerotiorum* (43% identity, EDO00056	104.3	159.8	88.6	141.2
26	Pc20g12670	strong similarity to hypothetical protein 1457_scaffold_8.tfa_130cg - Fusarium graminearum	Monomodular NRPS-like enzyme, 1283 AA, 1 intron, related enzyme in A. terreus (40% identity, gi|114190456|gb|EAU32156.1|)	3.6	0.7	5.7	5.8
	Pc21g00890	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	Major facilitator superfamily, related genes in A. niger (65% identity, An11g08880), C. immitis (61% identity, EAS28823), A. terreus (44% identity, EAU30298),	11.5	9.0	11.8	11.3
	Pc21g00900	strong similarity to methicillin resistance gene HmrA - Staphylococcus aureus	Predicted peptidase, related enzymes in A. oryzae (67% identity, BAE55394),C. immitis (61% identity, EAS28824), A. niger (56% identity, An11g08890),	4.9	5.1	4.8	13.2
	Pc21g00910	strong similarity to acetamidase amds - Aspergillus oryzae	Predicted amidase, related enzymes in A. oryzae (70% identity, BAE55395),A. terreus (66% identity, EAU32722), A. clavatus (65% identity, EAW09194),	86.0	144.3	129.7	237.0
	Pc21g00920	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	predicted transcription activator, weakly similar proteins in A. niger (34% identity, An11g08910 and An03g01500), A. oryzae (39% identity, BAE55396)	104.9	102.1	114.0	126.9
	Pc21g00930	similarity to SR protein kinase Sky1 - Saccharomyces cerevisiae	S/T-kinase, related proteins in A. clavatus (77% identity, EAW11545), N. fischerii (76%identity, EAW16825), A. terreus (73% identity, EAU34098),	17.6	11.1	14.4	28.4
	Pc21g00940	strong similarity to hypothetical protein An08g05350 - Aspergillus niger	Predicted transferase, LysR family regulatory protein, related proteins in N. fischeri (39% identity,EAW20697 and EAW20091), A. clavatus (39% identity, EAW13628)	15.8	3.1	9.8	11.2
	Pc21g00950	similarity to hypothetical protein contig_1_168_scaffold_14.tfa_260wg - Aspergillus nidulans	hypothetical protein, weak similarity to A. oryzae (30% identity, BAE64032) and A. nidulans (31% identity, AN9006),	700.0	148.6	436.1	328.0
27	Pc21g00960	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, 2988 AA, 5 introns, Similar enzymes in some Aspergilli: N. fischerii (53% identity; gi|119406436|gb|EAW16387.1|); A. oryzae (52% identity, gi|83764443|dbj|BAE54587.1|, and 41% identity, gi|83773906|dbj|BAE64031.1|), A. terreus (47% idfetnity, gi|114188537|gb|EAU30237.1|)	81.0	16.6	138.1	116.3
	Pc21g00970	strong similarity to hex1 - Aspergillus nidulans	Woronin body protein HexA, related proteins in N. fischerii (60%identity, EAW17907),A. terreus (62% identity, EAU62125), A. fumigatus (53% identity, EAL91716),	2685.5	2952.6	2926.5	2448.5
	Pc21g00980	hypothetical protein		0.5	0.5	1.0	0.9
	Pc21g00990	hypothetical protein	Predicted membrane protein, similar protein in Phaeosphaeria nodorum (53% identity, EAT82522)	19.3	17.0	32.4	58.8
	Pc21g01000	weak similarity to hypothetical protein SPBC1685.08 - Schizosaccharomyces pombe	Predicted protein containing PHD Zn finger, related proteins in A. terreus 66% identity, EAU33124), A.	25.9	24.2	18.8	14.9
	Pc21g01690	strong similarity to hypothetical membrane protein YOL119c - Saccharomyces cerevisiae	Putative MFS monocarboxylate transporter, related proteins in A. clavatus (74% identity, EAW12156),A. fumigatus (73% identity, EAL86614), N. fischerii (72%identity, EAW17188)	2.8	2.7	10.9	2.1
	Pc21g01700	similarity to mitochondrial respiratory function protein Mrf1 - Saccharomyces cerevisiae	mitochondrial Zn-dependent oxidoreductase, related proteins in A. clavatus (65% identity, EAW12157),A. fumigatus (65% identity, EAL86615), N. fischerii (65%identity, EAW17189)	2.8	2.7	10.9	2.1
28	Pc21g01710	strong similarity to peptide synthase like protein An04g06260 - Aspergillus niger	nonribosomal peptide synthase, cyclodipeptide synthetase, 2174 AA, 1 intron, Related NRPS in A.	47.9	27.7	46.0	11.9
	Pc21g01720	similarity to hypothetical neutral amino acid permease - Neurospora crassa		9.0	12.6	27.1	140.3
	Pc21g01730	strong similarity to quinate transport protein qutD - Aspergillus nidulans	transmembrane neutral amino acid permease, related proteins in Sclerotinia sclerotiorum (44% identity, EDN93972, EDN92524 and EDN03493) and Botryotinia fuckeliana (42% identity, EDN48995)	49.8	36.5	73.7	75.1
	Pc21g03820	similarity to lactone-specific esterase estf1 - Pseudomonas fluorescens [putative pseudogene]		0.9	0.6	0.5	1.8
	Pc21g03830	similarity to lactone-specific esterase estf1 - Pseudomonas fluorescens [putative pseudogene]		0.3	1.7	3.2	0.7
	Pc21g03840	similarity to hypothetical sterigmatocystin biosynthesis monooxygenase stcW - Aspergillus nidulans [putative pseudogene]		2.1	2.1	2.4	1.4
	Pc21g03850	hypothetical protein		0.6	0.1	0.5	0.4
	Pc21g03860	strong similarity to hypothetical protein An05g02110 - Aspergillus niger [putative pseudogene]		1.9	2.6	2.0	1.8
	Pc21g03870	similarity to ankyrin 3 (splice form 3) - Mus musculus		34.0	24.9	95.6	46.2
	Pc21g03880	strong similarity to hypothetical protein An05g02110 - Aspergillus niger [putative pseudogene]		0.9	0.9	2.3	2.5
	Pc21g03890	hypothetical protein		2.6	1.7	4.3	6.1
	Pc21g03900	similarity to hypothetical mixed-linked glucanase precursor related protein MLG1 - Neurospora crassa [putative pseudogene]		2.7	2.1	7.0	4.3
	Pc21g03910	similarity to hypothetical protein SMb20606 - Sinorhizobium meliloti		2.9	1.9	7.5	3.3
	Pc21g03920	strong similarity to hypothetical short chain dehydrogenase SPCC736.13 - Schizosaccharomyces pombe		0.9	1.2	6.1	12.3
29	Pc21g03930	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, related to compactin synthase, 2642 AA, 5 introns, Related enzymes in A. clavatus	7.4	2.9	14.5	10.4
	Pc21g03940	strong similarity to transposase Tan1 - Aspergillus niger [putative pseudogene]		2.9	1.5	4.4	5.0
	Pc21g03950	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe		21.6	14.9	23.5	16.0
	Pc21g03960	strong similarity to hypothetical oxidoreductase DR2595 - Deinococcus radiodurans	Oxidoreductase, orthologs in *N. fischeri* (58% identity, EAW19764), *A. terreus* (57% identity, EAU38660), *A. clavatus* (58% identity, EAW07338), *A. fumigatus* (55% identity, EAL85138)	1.5	2.6	4.0	5.4

	Pc21g03970	strong similarity to alcohol dehydrogenase alkJ - Pseudomonas oleovorans	Predicted oxidoreductase, orthologs in *N. fischeri* (61% identity, EAW19762), *A. terreus* (56% identity, EAU36858),	4.7	1.8	5.7	6.8
	Pc21g03980	strong similarity to hypothetical protein contig_1_155_scaffold_12.tfa_40wg - Aspergillus nidulans	hypothetical protein, weakly related to *A. terreus* (33% identity, EAU36859), *A. nidulans* (33% identity, AN8523),*N. fischeri* (32% identity, EAW17812),	1.2	1.8	1.0	0.7
30	Pc21g03990	strong similarity to polyketide synthase like protein An15g05090 - Aspergillus niger	polyketide synthase, 2445 AA, 5 introns, PKS in orthologous clusters in *Coccidioides immitis* (51% identity, gi|90307413|gb|EAS37044.1|), *N. fischerii* (39% identity, gi|119409812|gb|EAW19759.1|), *A. terreus* (40% identity, gi|114195156|gb|EAU36856.1|); weak similarity to compactin synthase in *P*. *citrinum* (35% identity, gi|23574645|dbj|BAC20566.1|)	1.7	1.2	1.0	1.9
	Pc21g04000	hypothetical protein		0.3	0.5	1.5	0.7
	Pc21g04010	similarity to 4-Hydroxyacetophenone monooxygenase hapE - Pseudomonas fluorescens	Predicted flavoprotein, related to *C. immitis* (48% identity, EAS37043), *C. globosum* (47% identity, EAQ92010),*N. fischeri* (43% identity, EAW19766), *A. terreus* (39% identity, EAU36862),	2.4	2.3	2.9	2.1
	Pc21g04020	weak similarity to trichothecene 3-O-acetyltransferase TRI101 - Gibberella zeae	Transferase family protein, weakly related to *A. clavatus* (34% identity, EAW12165), *M. grisea* (33% identity, EDJ97457),*N. fischeri* (31% identity, EAW19760),	2.0	0.7	2.0	1.9
	Pc21g04030	strong similarity to levodione reductase lvr - Corynebacterium aquaticum	Putative short-chain dehydrogenase, orthologs in in *N. fischeri* (64% identity, EAW19761), *A. terreus* (61% identity, EAU36857), *C. globosum* (47% identity, EAQ92004),	0.5	0.3	0.7	1.2
	Pc21g04040	strong similarity to monooxygenase paxM - Penicillium paxilli	FAD-binding oxidoreductase, UbiH-related, orthologs in in *N. fischeri* (43% identity, EAW19765), *C. globosum* (42% identity, EAQ92008),	3.5	3.0	4.1	4.8
	Pc21g04050	similarity to hypothetical protein An08g03600 - Aspergillus niger	Hypothetical protein, related proteins in in *N. fischeri* (41% identity, EAW19768), *A. terreus* (37% identity, EAU36864), *C. globosum* (39% identity, EAQ92003),	5.2	1.7	3.7	5.1
	Pc21g04750	similarity to aflatoxin biosynthesis regulatory protein aflR - Aspergillus parasiticus	Fungal transcription factor, related proteins in *A. oryzae* (61% identity, BAE63808), *A. terreus* (65% identity, EAU33888), *A. niger* (48% identity, An04g07240)	68.6	49.0	50.7	39.3
	Pc21g04760	strong similarity to cysteine dioxygenase CDO1 - Rattus norvegicus		109.5	23.1	157.7	78.2
	Pc21g04770	strong similarity to cytochrome-b5 reductase Mcr1 - Saccharomyces cerevisiae		4.8	3.4	8.5	11.3
	Pc21g04780	hypothetical protein		84.5	136.5	102.8	177.4
	Pc21g04790	similarity to hypothetical protein YER080w - Saccharomyces cerevisiae		95.7	87.8	96.2	86.7
	Pc21g04800	strong similarity to hypothetical protein An02g13770 - Aspergillus niger		22.8	35.4	44.7	56.6
	Pc21g04810	similarity to hypothetical protein contig42.tfa_2390wg - Aspergillus fumigatus [truncated ORF]		69.1	131.8	26.4	48.6
	Pc21g04820	similarity to precursor of triacylglycerol lipase like protein An13g00480 - Aspergillus niger [truncated ORF]		275.9	327.9	571.1	891.6
	Pc21g04830	strong similarity to hexokinase-like protein xprF - Aspergillus nidulans [putative sequencing error]		2669.1	2759.8	3620.1	3220.0
31	Pc21g04840	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	polyketide synthase, 2292 AA, 4 introns, highly similar to A. niger PKS (59% identity, emb|CAK46336.1|),related enzymes in N. crassa (43% identity, gi|28919463|gb|EAA28899.1|), A. terreus (43% identity, gi|114190751|gb|EAU32451.1|), C. globosum (42% identity, gi|88177264|gb|EAQ84732.1|), B. fuckeliana (42% identity, gi|40787340|gb|AAR90244.1|) and M. grisea (41% identity, gi|39941356|ref|XP_360215.1| and gi|39943482|ref|XP_361278.1|; 40% identity, gi|39945586|ref|XP_362330.1|)	3.4	1.4	8.6	11.1
	Pc21g04850	weak similarity to hypothetical protein C25G4.2 - Caenorhabditis elegans		3.9	1.9	7.3	9.9
	Pc21g04860	hypothetical protein		11.9	12.0	9.7	7.0
	Pc21g05030	hypothetical protein		19.7	20.6	22.3	21.4
	Pc21g05040	hypothetical protein		7.3	6.3	10.5	12.1
	Pc21g05050	weak similarity to positive regulator qa-1F - Neurospora crassa		480.5	770.1	1169.9	973.6
	Pc21g05060	strong similarity to salicylate hydroxylase nahW - Pseudomonas stutzeri		19.9	150.1	182.0	68.3
32	Pc21g05070	strong similarity to polyketide synthase like protein An09g01860 - Aspergillus niger	polyketide synthase, related to citrinin synthase, 2754 AA, 3 introns, similar PKS in C. globosum (57% identity, gi|88175714|gb|EAQ83182.1|), related to citrinin synthase (Monascus purpureus, 41%identity, gi|52000443|dbj|BAD44749.1|)	71.6	69.0	65.5	29.9
32	Pc21g05080	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, 2667 AA, 5 introns, related NRPS in A. terreus (48% identity, gi|114190221|gb|EAU31921.1|), C. immitis (48% identity, gi|90304914|gb|EAS34545.1|), A. nidulans (47% identity, gi|40739419|gb|EAA58609.1|, 46% identity, gi|40746448|gb|EAA65604.1|), and 45% identity, gi|40745711|gb|EAA64867.1|), A. oryzae (47% identity, gi|83772350|dbj|BAE62480.1|)	26.4	123.9	93.8	38.4
	Pc21g05090	weak similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans		117.8	181.5	128.6	128.1
	Pc21g05100	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae		8.9	37.8	23.7	13.2
	Pc21g05110	strong similarity to hypothetical protein contig_1_54_scaffold_3.tfa_480wg - Aspergillus nidulans		27.0	207.9	151.1	66.5
	Pc21g10750	strong similarity to hypothetical protein contig5_part_i.tfa_2940wg - Aspergillus fumigatus		168.5	186.7	169.9	264.9
	Pc21g10760	hypothetical protein		17.5	16.8	18.4	23.4
	Pc21g10770	strong similarity to aristolochene synthase Ari1 - Penicillium roqueforti		47.4	45.6	56.4	83.6
	Pc21g10780	weak similarity to hypothetical protein ncu00302.1 - Neurospora crassa		4.8	3.0	6.0	6.1
33	Pc21g10790	strong similarity to HC-toxin peptide synthase HTS - Cochliobolus carbonum	cyclopeptide synthetase, 7287 AA, 4 introns, highly similar NRPS in A. oryzae (64% identity,	23.9	17.3	21.0	13.2
	Pc21g10800	strong similarity to acetylglutamate kinase N-acetyl-gamma-glutamyl-phosphate reductase precursor arg-6 - Neurospora crassa		2.6	2.6	4.0	2.7
	Pc21g10810	similarity to erythrocyte ankyrin like protein An04g07710 - Aspergillus niger		3.1	1.3	2.6	0.8
	Pc21g10820	strong similarity to branched-chain amino acid aminotransferase bcaT - Lactococcus lactis		0.2	0.5	1.9	0.5
	Pc21g10830	strong similarity to cytochrome P450 monooxygenase TRI11 - Fusarium sporotrichioides		3.2	2.7	3.3	5.2
	Pc21g10840	strong similarity to fatty acid synthase alpha subunit fas2p - Schizosaccharomyces pombe		3.6	1.1	14.9	10.0
	Pc21g10850	strong similarity to cadmium resistance protein Ycf1 - Saccharomyces cerevisiae		4.0	5.1	11.3	8.7
	Pc21g10860	similarity to hypothetical protein YBR096w - Saccharomyces cerevisiae		4.1	3.0	7.3	3.2
	Pc21g10870	strong similarity to fatty-acyl-CoA synthase beta chain fas1p - Schizosaccharomyces pombe		202.5	106.7	281.6	140.2

	Pc21g10880	similarity to 7-aminocholesterol resistance protein Rta1 - Saccharomyces cerevisiae		347.4	175.0	872.2	572.7
	Pc21g12340	similarity to hypothetical transcription regulator SPAC139.03 - Schizosaccharomyces pombe		5.8	4.6	81.2	57.5
	Pc21g12350	strong similarity to hypothetical membrane protein YBR043c - Saccharomyces cerevisiae		0.4	0.4	2.0	2.4
	Pc21g12360	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus		3.3	3.2	13.2	15.3
	Pc21g12370	similarity to multidrug resistance protein like protein An11g07820 - Aspergillus niger		0.9	0.7	0.9	1.8
	Pc21g12380	strong similarity to hypothetical neutral amino acid permease - Neurospora crassa [putative sequencing error]		33.2	74.7	56.8	133.9
	Pc21g12390	strong similarity to hypothetical protein B2J23.120 - Neurospora crassa		74.6	65.4	556.6	487.8
	Pc21g12400	similarity to hypothetical protein An11g02890 - Aspergillus niger		8.1	3.4	6.2	6.1
	Pc21g12410	hypothetical protein		28.4	34.4	9.4	9.0
	Pc21g12420	strong similarity to cercosporin transporter CFP - Cercospora kikuchii		49.7	40.2	27.0	33.7
	Pc21g12430	strong similarity to hypothetical protein contig_1_46_scaffold_3.tfa_100wg - Aspergillus nidulans		115.1	109.8	192.1	188.5
34	Pc21g12440	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, 2397 AA, 1 intron, related PKS in G. zeae (60% identity, gi|42544370|gb|EAA67213.1| and gi|82779926|gb|ABB90283.1|)	4.2	0.8	5.1	4.4
34	Pc21g12450	strong similarity to polyketide synthase wA - Aspergillus nidulans	polyketide synthase, 2098 AA, related PKS in *G. zeae* (56% identity, gb|ABB90282.1| and 61% identity, only N-terminal region ref|XP_382571.1|), *M. grisea* (41% identity, gb|EDK04302.1|)	2.1	3.1	7.9	9.2
	Pc21g12460	strong similarity to histone acetyltransferase Gcn5 - Saccharomyces cerevisiae [putative pseudogene]		1.4	0.3	0.9	0.5
	Pc21g12470	weak similarity to heterokaryon incompatibility protein het-6 - Neurospora crassa		8.8	9.9	38.3	49.4
	Pc21g12480	strong similarity to rhamnogalacturonase B precursor rhgB - Aspergillus aculeatus		6.8	3.3	6.9	10.6
	Pc21g12490	hypothetical protein		142.2	152.5	176.5	200.4
	Pc21g12500	hypothetical protein		1.6	0.5	1.3	2.5
	Pc21g12510	similarity to esterase like protein An11g04020 - Aspergillus niger [putative pseudogene]		3.7	3.4	5.8	2.2
	Pc21g12520	similarity to hypothetical protein An08g01890 - Aspergillus niger [putative pseudogene]		3.0	1.8	2.4	3.2
	Pc21g12530	strong similarity to hypothetical nicotinate phosphoribosyltransferase Npt1 - Saccharomyces cerevisiae [putative sequencing error]		100.2	108.8	108.2	137.6
	Pc21g12540	strong similarity to hypothetical protein An01g11750 - Aspergillus niger		0.3	0.3	1.5	0.3
	Pc21g12550	hypothetical protein		0.6	0.3	1.3	1.0
	Pc21g12560	hypothetical protein		0.3	0.8	3.9	2.5
	Pc21g12570	similarity to hypothetical protein SPAC13C5.04 - Schizosaccharomyces pombe		51.1	52.7	1113.7	872.7
	Pc21g12580	hypothetical protein		0.7	2.4	2.0	1.1
	Pc21g12590	similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans		56.7	100.6	2145.6	1607.9
	Pc21g12600	strong similarity to hypothetical protein 1465_scaffold_9.tfa_470wg - Fusarium graminearum		585.3	599.2	2024.5	2102.3
	Pc21g12610	weak similarity to 7alpha-cephem-methoxylase subunit cmcJ - Streptomyces lactamdurans		15.2	18.5	567.4	386.5
	Pc21g12620	strong similarity to asparagine synthase asnB - Bacillus subtilis		55.4	64.3	1901.5	1359.0
35	Pc21g12630	similarity to peptide synthase pesA - Metarhizium anisopliae	nonribosomal peptide synthase, cyclodipeptide synthetase, 2382 AA, 2 introns, similar NRPS in G.	44.4	15.2	1486.7	792.0
	Pc21g12640	strong similarity to cutinase transcription factor beta CTF1b - Fusarium solani		114.8	123.5	122.5	178.5
	Pc21g12650	similarity to mitochondrial protein TOM6 - Neurospora crassa		730.2	740.5	627.9	537.8
	Pc21g12660	strong similarity to hypothetical conserved protein SPAC1952.06c - Schizosaccharomyces pombe		59.6	67.6	72.7	89.6
	Pc21g12670	hypothetical protein		2.2	0.8	3.5	1.1
	Pc21g12680	strong similarity to 138 kD subunit of DNA-dependent RNA polymerase II rpb2p - Schizosaccharomyces pombe		538.1	517.3	528.4	463.9
	Pc21g12690	strong similarity to hypothetical protein CAD21276.1 - Neurospora crassa		2594.8	2682.4	3200.6	2583.1
	Pc21g12700	strong similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae		8.8	7.8	8.0	7.5
	Pc21g15110	hypothetical protein		0.4	0.4	0.4	1.1
	Pc21g15120	hypothetical protein		4.5	3.0	3.8	1.5
	Pc21g15130	strong similarity to hypothetical protein CAB91439.2 - Neurospora crassa		12.6	23.0	11.7	16.4
	Pc21g15140	strong similarity to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase hpcH - Escherichia coli		8.3	22.0	40.1	98.7
	Pc21g15150	strong similarity to hypothetical protein contig_1_139_scaffold_11.tfa_60cg - Aspergillus nidulans		0.3	1.5	3.5	1.5
36	Pc21g15160	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, related to fumonisin synthase, 2447 AA, 17 introns, related PKS in Aspergilli (*A. oryzae* , 41% identity, dbj|BAE54587.1|; *N. fischerii* , 41% identity, gb|EAW16387.1|; *A. niger* , 42% identity, emb|CAK43811.1|; *A. clavatus* , 40% identity), and *G. moniliformis* (40% identiy, gb|AAD43562.2|AF155773_1)	0.9	0.7	3.3	2.0
	Pc21g15170	strong similarity to GTP-binding associated protein like protein An02g10400 - Aspergillus niger [putative sequencing error]		279.7	246.6	175.0	189.9
	Pc21g15420	strong similarity to cercosporin transporter CFP - Cercospora kikuchii		1629.0	807.3	2564.7	668.8
37	Pc21g15430	strong similarity to dimethylallyltryptophan synthase dmaW - Claviceps purpurea	dimethylallyltryptophan synthase DmaW , 422 AA, 1 intron, Strong similarity *in Neosartorya fischerii* (67% identity, gb|EAW17508.1|), similar enzymes in *N. fischerii* (50% identity, gb|EAW19789.1|) and *A. fumigatus* (50% identity, gb|EAL85105.2|)	883.9	595.2	2123.9	823.6
	Pc21g15440	weak similarity to hypothetical UbiE COQ5 family methyltransferase - Caulobacter crescentus		769.1	614.6	3302.2	1796.0
	Pc21g15450	strong similarity to cytochrome P450 monooxygenase P450I - Gibberella fujikuroi		344.1	281.2	1420.2	617.7
	Pc21g15460	strong similarity to maackiain detoxification protein MAK1 - Nectria haematococca		345.6	167.9	1829.6	653.9
	Pc21g15470	similarity to mitochondrial 25-hydroxyvitamin D3 24-hydroxylase cP450cc24 - Gallus gallus		241.7	115.5	742.6	98.6

37	Pc21g15480	strong similarity to cyclic peptide AM-toxin synthase like protein An03g00650 - Aspergillus niger	nonribosomal peptide synthase, cyclodipeptide synthetase, 2372 AA, 3 introns, related NRPS in N.	562.2	207.4	1488.2	162.2
	Pc21g15490	strong similarity to protein phosphatase PP2A0 B subunit gamma isoform - Oryctolagus cuniculus		109.7	97.1	90.7	83.7
	Pc21g15990	similarity to brown 2 protein abr2 - Aspergillus fumigatus [putative pseudogene]		0.7	1.4	1.0	0.3
38	Pc21g16000	strong similarity to polyketide synthase PKS1 - Colletotrichum lagenarium	polyketide synthase, conidial yellow pigment synthase PksP, 2138 AA, 4 introns, highly similar PKS in Aspergilli (*A. oryzae* , 70% identity, dbj|BAE61567.1| ; *A. niger* , 68% identity, emb|CAL00851.1|; *A . nidulans* , 66% identity, emb|CAA46695.2| ; *A. clavatus* , 66% identity,gb|EAW14609.1|; *N. fischerii* , 66% identity, gb|EAW19338.1|; *A. fumigatus* , 65% identity, gb|AAC39471.1| ; and *A. nidulans* wA, 65% identity, prf||1905375A	8.0	4.7	12.7	4.6
	Pc21g16010	hypothetical protein		2.0	1.8	4.6	4.7
	Pc21g21240	similarity to retrotransposon like protein An11g08670 - Aspergillus niger [putative pseudogene]		0.1	0.1	0.8	0.1
	Pc21g21250	strong similarity to hypothetical protein An02g09120 - Aspergillus niger [putative pseudogene]		0.6	0.5	0.9	0.3
	Pc21g21260	weak similarity to OSJNBa0038P21.10 - Oryza sativa [putative pseudogene]		1.4	1.5	2.2	3.6
	Pc21g21270	strong similarity to hypothetical protein B9I2.20 - Neurospora crassa		3.0	1.9	2.6	1.7
	Pc21g21280	strong similarity to methyl sterol oxidase Erg25 - Saccharomyces cerevisiae		44.0	81.5	542.2	971.5
	Pc21g21290	strong similarity to hypothetical protein mg02069.1 - Magnaporthe grisea		119.4	955.7	3398.5	2598.6
	Pc21g21300	hypothetical protein		6.2	4.1	9.4	9.6
	Pc21g21310	hypothetical protein		0.3	0.4	0.7	0.6
	Pc21g21320	strong similarity to sequence 1 - unknown organism		3.9	15.0	24.8	65.1
	Pc21g21330	similarity to hypothetical protein An13g03520 - Aspergillus niger [putative pseudogene]		1.9	1.7	1.7	5.3
	Pc21g21340	similarity to hypothetical protein alr1138 - Nostoc sp.		12.1	51.8	9.3	23.1
	Pc21g21350	weak similarity to hypothetical conserved protein PA2776 - Pseudomonas aeruginosa		127.1	741.5	585.0	1037.2
	Pc21g21360	hypothetical protein		1.4	10.8	5.3	10.7
	Pc21g21370	acyl-coenzyme A:isopenicillin N acyltransferase (acyltransferase) AAT/PenDE	acyl-coenzyme A:isopenicillin N acyltransferase (acyltransferase) AAT/PenDE	1031.3	1827.0	1993.7	2714.6
	Pc21g21380	isopenicillin N synthase ips/PcbC	isopenicillin N synthase ips/PcbC	1312.0	2381.9	5107.0	5111.8
39	Pc21g21390	alpha-aminoadipyl-cysteinyl-valine synthetase pcbAB/acvA, 3790 AA, Isofunctional NRPS in	alpha-aminoadipyl-cysteinyl-valine synthetase pcbAB/acvA, 3790 AA, Isofunctional NRPS in A. oryzae (79% identity, gi|83774189|dbj|BAE64314.1|), A. nidulans (66% identity, gi|40743782|gb|EAA62968.1|), A. cephalosporium (55% identity, gi|113315|sp|P25464|ACVS_CEPAC), and Kallichroma thetys (53% identity, gi|13398458|gb|AAK21902.1|AF335329_1), bacterial ACV synthetases have more than 40% identity	1056.7	2068.8	4321.8	4376.0
	Pc21g21400	hypothetical protein		0.9	1.7	2.5	2.0
	Pc21g21410	strong similarity to hypothetical protein ncu05765.1 - Neurospora crassa		2.6	1.7	5.4	6.3
	Pc21g21420	strong similarity to hypothetical protein An09g04870 - Aspergillus niger		8.8	5.6	87.6	107.0
40	Pc21g22530	strong similarity to hypothetical protein contig_1_135_scaffold_11.tfa_110wg - Aspergillus	Monomodular NRPS-like enzyme, 878 AA, 2 introns, unique, only distantly related domains in A.	7.8	3.2	1.3	2.5
41	Pc21g22650	strong similarity to polyketide synthase PKS17 - Botryotinia fuckeliana	Monomodular NRPS-like enzyme, 1225 AA, 1 intron, Highly similar enzymes in Aspergilli, A. terreus	23.4	16.9	14.3	18.2
	Pc22g08110	strong similarity to cytochrome P450 eln2 - Coprinus cinereus		31.6	12.9	108.9	81.6
	Pc22g08120	similarity to hypothetical meta-cleavage compound hydrolase gene ren71 - Streptomyces aureofaciens [putative sequencing error]		1.3	1.1	8.8	11.5
	Pc22g08130	weak similarity to protein involved in cercosporin production CFP - Cercospora kikuchii [putative pseudogene]		1.7	0.2	1.6	2.4
	Pc22g08140	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe		121.6	106.9	86.5	90.4
	Pc22g08150	strong similarity to cytochrome p450 related protein eln2 - Coprinus cinereus		0.2	1.7	1.9	1.3
	Pc22g08160	strong similarity to hypothetical protein An10g00180 - Aspergillus niger		3.5	2.2	3.5	5.4
42	Pc22g08170	strong similarity to 6-methylsalicylic acid synthase like protein An10g00140 - Aspergillus niger	6-methylsalicylic acid synthase, 1776 AA, 1 intron, 6-MSA synthases from *P. griseofulvum* (89% identity, emb|CAA39295.1|), *A. clavatus* (77% identity, gb|EAW11667.1|), *Byssochlamys nivea* (73% identiy, gb|AAK48943.1|AF360398_1)	3.2	2.8	3.3	3.0
	Pc22g08180	strong similarity to hypothetical protein mg05770.1 - Magnaporthe grisea		192.5	221.2	159.4	184.7
	Pc22g08190	similarity to retroviral-like transposable element like protein An03g03110 - Aspergillus niger [truncated ORF]		2.1	3.0	17.5	15.1
	Pc22g08200	hypothetical protein		0.3	0.6	1.1	0.4
	Pc22g08210	weak similarity to hypothetical protein - Plasmodium falciparum		2.5	1.3	2.2	1.8
	Pc22g08220	strong similarity to hypothetical protein contig14.tfa_150wg - Aspergillus fumigatus		59.8	61.5	101.3	117.8
	Pc22g08230	hypothetical protein		1.8	1.0	8.6	2.7
	Pc22g08240	strong similarity to hypothetical protein - Danio rerio		12.6	8.8	44.9	50.6
	Pc22g08250	strong similarity to protein involved in cercosporin production CFP - Cercospora kikuchii		2.6	1.7	2.5	1.6
	Pc22g08260	similarity to aminotriazole resistance protein Atr1 - Saccharomyces cerevisiae		1.1	0.6	1.6	1.4
43	Pc22g09430	similarity to nonribosomal peptide synthase MxaA - Stigmatella aurantiaca	Monomodular NRPS-like enzyme, 1030 AA, 3 introns, Related enzymes in *Ajellomyces capsulatus* (54% identity, gb|EDN05769.1|), *A. oryzae* (49% identity, dbj|BAE66286.1|), *A . clavatus* (44% identity, gb|EAW07472.1|)	696.1	129.9	108.3	21.4
	Pc22g20360	strong similarity to siderophore-iron transporter for enterobactin Enb1 - Saccharomyces cerevisiae		1.9	4.3	19.4	67.3
	Pc22g20370	strong similarity to carnitine racemase like protein An03g03550 - Aspergillus niger		0.7	1.6	4.9	43.3
	Pc22g20380	strong similarity to aerobactin biosynthesis protein iucB - Escherichia coli		6.5	15.0	32.7	90.2

	Pc22g20390	strong similarity to multidrug resistance protein atrD - Aspergillus nidulans		15.2	22.1	33.3	100.0
44	Pc22g20400	weak similarity to cyclic peptide AM-toxin synthase AMT - Alternaria alternata	triacetylfusarinin synthetase, 2076 AA, 1 intron, Highly similar NRPS in N. fischerii (68% identity, gb|EAW17196.1|), A. fumigatus (69% identity, gb|EAL86624.1|, and 68% identity, gb|AAX11421.1|), A. oryzae (72% identity, dbj|BAE65630.1|,dbj|BAE65630.1|, and 71% identity, dbj|BAC78651.1|), A. clavatus (68% identity, gb|EAW12140.1|), A. niger (65% identity, emb|CAK47792.1|), A. nidulans (62% identity, gb|EAA58620.1|), Botryotinia fuckeliana (67% identity, gb|EDN31507.1|, and 65% identity, gb|AAX11420.1|), Sclerotinia sclerotiorum (68% identity, gb|EDO01775.1|)	16.1	18.6	34.2	77.4
	Pc22g20410	strong similarity to hypothetical protein contig43.tfa_360wg - Aspergillus fumigatus		29.6	46.1	73.1	151.5
	Pc22g20420	weak similarity to exo-alpha-sialidase - Trypanosoma cruzi		289.3	251.7	157.7	111.6
45	Pc22g22580	strong similarity to hypothetical protein contig_1_153_scaffold_12.tfa_490wg - Aspergillus nidulans	adenylate domain containing protein, 797 AA, 1 intron, related proteins in *A. nidulans* (47% identity, gb|EAA67055.1|), *N. fischerii* (45% identity, gb|EAW24710.1|),*A. terreus* (42% identity, gb|EAU30093.1|), *C. globosum* (42% identity, gb|EAQ91494.1|)	5.9	3.3	33.1	4.3
	Pc22g22590	similarity to alcohol dehydrogenase pan2 - Mus musculus		17.3	71.7	54.2	44.7
	Pc22g22600	weak similarity to hypothetical protein B24P7.350 - Neurospora crassa		4.6	0.8	71.9	14.7
	Pc22g22610	similarity to cytochrome P450 monooxygenase avnA - Aspergillus parasiticus		5.9	2.2	44.6	10.9
	Pc22g22820	strong similarity to cytochrome P450 monooxygenase P450I - Gibberella fujikuroi		0.6	1.0	11.8	0.7
	Pc22g22830	hypothetical protein		1.5	1.3	3.0	2.8
	Pc22g22840	strong similarity to ATP-binding cassette multidrug transport protein atrA - Aspergillus nidulans		2.9	1.7	3.9	4.4
46	Pc22g22850	strong similarity to polyketide synthase like protein An09g01860 - Aspergillus niger [putative sequencing error]	polyketide synthase, 2522 AA, 4 introns, related PKS in *A. nidulans* (53% identity, gb|EAA67005.1|), and *A . terreus* (53% identiy, gb|EAU29529.1|)	6.4	3.3	13.1	9.1
	Pc22g22860	similarity to cinnamyl-alcohol dehydrogenase CAD1 - Eucalyptus gunnii		0.7	0.6	5.1	2.1
	Pc22g22870	strong similarity to levodione reductase lvr - Corynebacterium aquaticum		0.5	1.5	3.4	1.0
	Pc22g22880	similarity to para-hydroxybenzoate--polyprenyltransferase ppt1p - Schizosaccharomyces pombe		2.0	0.6	2.2	2.3
	Pc22g22890	strong similarity to hypothetical monooxygenase paxM - Penicillium paxilli		0.7	0.3	2.5	2.0
	Pc22g23700	weak similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus		12.4	15.1	32.4	52.0
	Pc22g23710	strong similarity to pyrroline-5-carboxylate reductase P5CR - Zalerion arboricola		10.4	14.4	25.3	37.3
	Pc22g23720	strong similarity to hypothetical membrane transport protein SPAC3H1.06c - Schizosaccharomyces pombe		23.2	11.3	19.7	6.9
	Pc22g23730	hypothetical protein		2.6	0.4	1.3	2.5
	Pc22g23740	strong similarity to protein involved in betaine lipid production btaA like protein An02g02840 - Aspergillus niger		6.5	4.4	11.0	7.2
47	Pc22g23750	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	polyketide synthase, 3061 AA, 12 introns, N-terminal part has weak similarity to PKS in *N. crassa* (32% identity, gb|EAA28933.1|), *A. terreus* (31% identitygb|EAU33817.1|), *A. clavatus* (32% identity, gb|EAW08895.1|), *G. moniliformis (* 31% identity, gb|AAD43562.2|AF155773_1)	1.8	1.6	4.3	1.4

@ Values given are the average of three independent experiments

Supplementary Table 5. ORFs on the amplified region of industrial *Penicillium* strains

orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF *			Average transcript levels @				mRNA ratio #		mRNA ratio $	
		Description (Species)	Accession number	e-value	WIS - PAA	WIS + PAA	DS - PAA	DS + PAA	WIS	DS17690	non-producing	producing
Pc21g21240	similarity to retrotransposon like protein An11g08670 - Asperg	strong similarity to retrotransposon Tto1 of Nic	An11c0280	4e-62	0.1	0.1	0.8	0.1	0.8	0.1	6.3	1.0
Pc21g21250	strong similarity to hypothetical protein An02g09120 - Aspergi	strong similarity to hypothetical retrotransposo	An02c0270	1e-28	0.6	0.5	0.9	0.3	0.9	0.3	1.6	0.5
Pc21g21260	weak similarity to OSJNBa0038P21.10 - Oryza sativa [putativ	gene: "OSJNBa0038P21.10"; Oryza sativa ger	OSJN00241_10	2e-06	1.4	1.5	2.2	3.6	1.1	1.6	1.5	2.3
Pc21g21270	strong similarity to hypothetical protein B9I2.20 - Neurospora	similarity to hypothetical protein B9I2.20 - Neu	An08g03170	3e-48	3.0	1.9	2.6	1.7	0.6	0.6	0.9	0.9
Pc21g21280	strong similarity to methyl sterol oxidase Erg25 - Saccharomy	probable c-4 methyl sterol oxidase - fission ye	T38986	1e-89	44.0	81.5	542.2	971.5	1.9	1.8	12.3	11.9
Pc21g21290	strong similarity to hypothetical protein mg02069.1 - Magnapo	probable lactoylglutathione lyase (EC 4.4.1.5)	AG3272	7e-23	119.4	955.7	3398.5	2598.6	8.0	0.8	28.5	2.7
Pc21g21300	hypothetical protein	-	-	-	6.2	4.1	9.4	9.6	0.7	1.0	1.5	2.4
Pc21g21310	hypothetical protein	unnamed protein product [Aspergillus oryzae].	BAE61984.1	4e-10	0.3	0.4	0.7	0.6	1.3	0.8	2.1	1.3
Pc21g21320	similar to AA sequence:TREMBL:AX100446.1	Sequence 1 from Patent WO0121779 (Penicill	AX100446_1	5e-72	3.9	15.0	24.8	65.1	3.8	2.6	6.3	4.3
Pc21g21330	similarity to hypothetical protein An13g03520 - Aspergillus nig	strong similarity to hypothetical protein encode	An13g03520	1e-13	1.9	1.7	1.7	5.3	0.9	3.0	0.9	3.2
Pc21g21340	similarity to hypothetical protein alr1138 - Nostoc sp.	unnamed protein product [Aspergillus oryzae].	BAE61986.1	0.0	12.1	51.8	9.3	23.1	4.3	2.5	0.8	0.4
Pc21g21350	weak similarity to hypothetical conserved protein PA2776 - Ps	similarity to hypothetical oxidoreductase PA53	An03g05870	1e-60	127.1	741.5	585.0	1037.2	5.8	1.8	4.6	1.4
Pc21g21360	hypothetical protein	-	-	-	1.4	10.8	5.3	10.7	7.6	2.0	3.7	1.0
Pc21g21370	acyl-coenzyme A:isopenicillin N acyltransferase (acyltransfera	acyl-CoA-6-aminopenicillanic acid acyltransfer	JQ0118	0.0	1031.3	1827.0	1993.7	2714.6	1.8	1.4	1.9	1.5
Pc21g21380	isopenicillin N synthase ips PcbC - Penicillium chrysogenum	isopenicillin N synthase (EC 1.14.11.-) ips [sin	S04441	0.0	1312.0	2381.9	5107.0	5111.8	1.8	1.0	3.9	2.1
Pc21g21390	alpha-aminoadipyl-cysteinyl-valine synthetase pcbAB acvA - P	alpha-aminoadipyl-cysteinyl-valine synthetase	YGPLV8	0.0	1098.0	2060.0	4345.2	4557.4	1.9	1.0	4.0	2.2
Pc21g21400	hypothetical protein	-	-	-	0.9	1.7	2.5	2.0	1.9	0.8	2.8	1.2
Pc21g21410	strong similarity to hypothetical protein ncu05765.1 - Neurosp	unnamed protein product [Aspergillus oryzae]	BAE66036.1	5e-134	2.6	1.7	5.4	6.3	0.6	1.2	2.1	3.7
Pc21g21420	strong similarity to hypothetical protein An09g04870 - Aspergi	weak similarity to polypeptide SEQ ID NO:618	An09g04870	0.0	8.8	5.6	87.6	107.0	0.6	1.2	9.9	19.2
Pc21g21430	similarity to hypothetical protein An09g03770 - Aspergillus nig	hypothetical protein CHGG_05465 [Chaetomiu	XP_001221560.1	2e-16	4.4	3.2	22.5	41.3	0.7	1.8	5.1	12.8
Pc21g21440	hypothetical protein	-	-	-	20.0	9.1	533.7	170.9	0.5	0.3	26.7	18.8
Pc21g21450	strong similarity to hypothetical protein contig_1_94_scaffold_	hypothetical protein (Aspergillus_nidulans_FG	contig_1_94_scaffold_6.tfa_	0.0	2.2	0.8	1.3	0.7	0.4	0.5	0.6	0.8
Pc21g21460	hypothetical protein	-	-	-	121.7	87.8	711.9	614.2	0.7	0.9	5.8	7.0
Pc21g21470	strong similarity to hypothetical protein contig_1_94_scaffold_	hypothetical protein (Aspergillus_nidulans_FG	contig_1_94_scaffold_6.tfa_	1e-165	112.6	92.1	700.9	694.7	0.8	1.0	6.2	7.5
Pc21g21480	hypothetical protein	-	-	-	27.9	22.1	90.9	55.5	0.8	0.6	3.3	2.5
Pc21g21490	hypothetical protein	-	-	-	4.4	3.2	22.0	25.3	0.7	1.1	5.0	7.9
Pc21g21500	strong similarity to hypothetical isoamyl alcohol oxidase mreA	FAD binding domain protein [Neosartorya fisch	XP_001261742	0.0	4.9	4.3	2.7	6.1	0.9	2.3	0.5	1.4
Pc21g21510	strong similarity to cercosporin transporter CFP - Cercospora	strong similarity to cercosporin transporter CF	An01g11290	6e-93	0.1	0.2	0.5	0.8	1.3	1.5	4.0	5.0
Pc21g21520	similarity to C-8,7 sterol isomerase - Arabidopsis thaliana	strong similarity to emopamil-binding protein	An01g13260	6e-56	24.9	7.9	48.6	133.8	0.3	2.8	2.0	16.9
Pc21g21530	strong similarity to allantoate permease Dal5 - Saccharomyce	strong similarity to allantoate permease Dal5	An12g01960	1e-180	0.7	1.2	3.2	3.6	1.8	1.1	4.8	3.1
Pc21g21540	strong similarity to lipase lip1 - Geotrichum candidum	strong similarity to triacylglycerol lipase lipI of	An09g02270	1e-178	6.8	12.4	27.8	53.8	1.8	1.9	4.1	4.3
Pc21g21550	strong similarity to beta transducin-like protein like protein An0	similarity to beta transducin-like protein het-e	An01g01380	1e-163	1.4	0.8	0.2	0.8	0.6	3.3	0.2	1.0
Pc21g21560	similarity to histidine kinase like protein An07g08100 - Aspergi	strong similarity to histidine kinase nik-1 of Ne	An07g08100	1e-11	1.5	0.9	1.3	0.7	0.6	0.6	0.8	0.8
Pc21g21570	strong similarity to hypothetical impala transposase - Fusariu	strong similarity to hypothetical impala transpo	An03g03020	2e-25	77.0	82.1	84.1	99.1	1.1	1.2	1.1	1.2
Pc21g21580	strong similarity to hypothetical protein An04g09900 - Aspergi	strong similarity to hypothetical protein encode	An04g09900	6e-65	147.8	104.9	123.1	102.7	0.7	0.8	0.8	1.0
Pc21g21590	strong similarity to glucose transporter rco-3 - Neurospora cra	strong similarity to monosaccharide transporte	An15g03940	1e-139	665.7	166.9	88.1	29.8	0.3	0.3	0.1	0.2
Pc21g21600	hypothetical protein	-	-	-	5.3	2.0	1.6	3.6	0.4	2.2	0.3	1.7
Pc21g21610	strong similarity to P-type ATPase ENA1 - Schwanniomyces	strong similarity to P-type ATPase ENA1 of Sch	An09g00690	0.0	-	-	-	-	-	-	-	-
Pc21g21620	weak similarity to retrotransposon Tto1 - Nicotiana tabacum [	strong similarity to retrotransposon Tto1 of Nic	An10g00740	1e-105	0.1	0.3	1.5	0.5	3.0	0.4	15.0	1.8
Pc21g21630	similarity to hypothetical protein B24P11.150 - Neurospora cra	similarity to hypothetical protein B24P11.150 o	An16g05580	7e-16	0.7	2.3	3.9	2.3	3.4	0.6	5.8	1.0
Pc21g21640	similarity to 7-aminocholesterol resistance protein Rta1 - Sac	similarity to 7-aminocholesterol resistance pro	An14g07050	1e-101	1.3	0.7	3.1	3.4	0.6	1.1	2.4	4.6
Pc21g21650	strong similarity to alcohol dehydrogenase ADH like protein Ar	strong similarity to alcohol dehydrogenase AD	An01g14780	1e-147	6.2	6.9	7.6	6.6	1.1	0.9	1.2	1.0
Pc21g21660	weak similarity to zinc-finger transcription factor amdA - Aspe	strong similarity to zinc-finger transcription fac	An01g14770	0.0	16.4	15.8	21.2	20.3	1.0	1.0	1.3	1.3
Pc21g21670	weak similarity to hypothetical RNA polymerase II transcriptio	similarity to gene expression regulator At14 fro	An14g07040	8e-91	2.8	1.0	3.9	2.1	0.4	0.5	1.4	2.0
Pc21g21680	strong similarity to hypothetical C6 hypothetical protein CAD3	strong similarity to hypothetical C6 hypothetica	An08g07710	8e-52	71.9	63.8	42.1	16.3	0.9	0.4	0.6	0.3
Pc21g21690	strong similarity to ATP-dependent RNA helicase like protein	strong similarity to ATP-dependent RNA helica	An08g07610	0.0	108.9	99.0	96.6	61.2	0.9	0.6	0.9	0.6

* Best non-Penicillium chrysogenum blast hits are given

@ Values given are the average of three independent experiments

\# Interesting ratio's are indicated in blue (i.e. ratio >2 and one of the values above the background of 12)

$ Interesting ratio's are indicated in orange (i.e. ratio >2 and one of the values above the background of 12)

Supplementary Table 6. Putative β-lactam related ORFs located outside the amplified region of industrial *Penicillium* strains

orf code	Description of putative *P. chrysogenum* ORF	Identification method	e-value	Average transcript levels @				mRNA ratio #		mRNA ratio $		length [aa]	Mw [Da]	pI	CAI
				WIS - PAA	WIS + PAA	DS - PAA	DS + PAA	WIS	DS17690	non-producing	producing				
Pc12g04030	strong similarity to cephalosporin esterase - Rhodosporidium toruloides	blastP with cephalosporin esterase	6e-33	3.1	2.3	3.9	1.9	0.8	0.5	1.3	0.8	653	70940	6.07	0.383
Pc12g11540	similarity to isopenicillin N epimerase cefD - Streptomyces clavuligerus	blastP with Streptomyces clavuligerus cefD	3.4e-16	272.6	431.8	805.3	1032.8	1.6	1.3	3.0	2.4	476	53175.8	6.14	0.477
Pc12g13400	strong similarity to cephalosporin esterase - Rhodosporidium toruloides	blastP with cephalosporin esterase	1e-49	159.5	214.3	104.2	68.3	1.3	0.7	0.7	0.3	542	59792.3	5.22	0.421
Pc13g04050	strong similarity to hypothetical protein npgA - Aspergillus nidulans	blastP with Aspergillus nidulans npgA	2.6e-51	144.9	117.9	139.7	160.2	0.8	1.1	1.0	1.4	422	47080.4	5.76	0.514
Pc13g04140	strong similarity to precursor of cephalosporin esterase - Rhodosporidium toruloides	blastP with cephalosporin esterase	1e-56	6.1	5.3	9.3	14.0	0.9	1.5	1.5	2.6	542	60032.6	6.15	0.442
Pc13g04180	strong similarity to 7alpha-cephem-methoxylase subunit cmcJ - Streptomyces lactamdurans	blastP with Streptomyces clavuligerus cmcJ	1.5e-23	15.4	6.8	11.0	47.8	0.4	4.3	0.7	7.0	314	35521.7	6.01	0.493
Pc13g04680	strong similarity to 7alpha-cephem-methoxylase subunit cmcJ - Streptomyces lactamdurans	blastP with Streptomyces clavuligerus cmcJ	5.9e-19	93.5	190.3	178.5	249.5	2.0	1.4	1.9	1.3	296	33556.6	5.6	0.443
Pc13g09140	strong similarity to isopenicillin N acyltransferase aAT - Aspergillus nidulans	blastP with Penicillium chrysogenum aAT	1e-43	1.7	2.2	2.1	1.3	1.3	0.6	1.3	0.6	362	39525.3	5.4	0.440
Pc13g12270	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	blastP with Penicillium chrysogenum pclA	2.4e-103	92.2	100.8	57.3	133.4	1.1	2.3	0.6	1.3	556	61635.9	7.61	0.454
Pc13g14300	similarity to hypothetical beta-lactamase XF1621 - Xylella fastidiosa	blastP with beta-lactamase	2e-21	77.1	49.1	120.9	116.3	0.6	1.0	1.6	2.4	570	63924.9	5.8	0.407
Pc15g00420	strong similarity to very long-chain fatty acyl-CoA synthase Fat1	blastP with Acremonium chrysogenum cefD1	2e-77	3.1	1.5	3.6	8.4	0.5	2.3	1.2	5.7	634	69269.2	7.56	0.508
Pc16g14010	strong similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae	blastP with Aspergillus nidulans laeA	2.4e-145	365.6	361.9	373.8	395.3	1.0	1.1	1.0	1.1	427	48548.5	6.98	0.460
Pc16g14410	strong similarity to 7alpha-cephem-methoxylase subunit cmcJ - Streptomyces lactamdurans	blastP with Streptomyces clavuligerus cmcJ	2.5e-16	13.0	13.9	12.2	16.8	1.1	1.4	0.9	1.2	282	32241.8	6.8	0.408
Pc18g05710	strong similarity to very long-chain fatty acyl-CoA synthase Fat1	blastP with Acremonium chrysogenum cefD1	e-100	79.2	84.9	103.7	101.3	1.1	1.0	1.3	1.2	658	73218.7	8.61	0.523
Pc20g04080	strong similarity to gene involved in the regulation of penicillin biosynthesis suAprgA1 - Aspergillus	blastP with Aspergillus nidulans suAprgA1	2e-82	545.4	568.9	444.0	384.5	1.0	0.9	0.8	0.7	285	32198.9	4.46	0.773
Pc20g10590	similarity to hypothetical beta-lactamase XF1621 - Xylella fastidiosa	blastP with beta-lactamase	1e-26	75.8	37.5	48.8	29.0	0.5	0.6	0.6	0.8	560	61921.3	6.58	0.390
Pc20g13500	strong similarity to very long-chain fatty acyl-CoA synthase Fat1	blastP with Acremonium chrysogenum cefD1	e-171	54.7	25.9	45.7	143.7	0.5	3.1	0.8	5.5	632	70529.4	7.01	0.478
Pc21g12610	weak similarity to 7alpha-cephem-methoxylase subunit cmcJ - Streptomyces lactamdurans	blastP with Streptomyces clavuligerus cmcJ	0.019	15.2	18.5	567.4	386.5	1.2	0.7	37.4	20.9	392	43818.3	5.53	0.399
Pc21g18210	strong similarity to homoserine O-acetyltransferase metE - Aspergillus nidulans	blastP with Acremonium chrysogenum cefG	7e-88	179.8	176.4	224.8	209.0	1.0	0.9	1.3	1.2	499	54534.8	5.27	0.565
Pc21g20650	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	blastP with Penicillium chrysogenum pclA	2.8e-86	72.6	62.9	52.6	123.1	0.9	2.3	0.7	2.0	566	62478.9	6.57	0.463
Pc21g22010	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	blastP with Penicillium chrysogenum pclA	2.1e-69	50.8	45.3	22.0	11.7	0.9	0.5	0.4	0.3	560	61901.3	6.32	0.417
Pc22g00550	similarity to hypothetical beta-lactamase XF1621 - Xylella fastidiosa	blastP with beta-lactamase	2e-35	20.1	27.6	23.1	36.2	1.4	1.6	1.1	1.3	511	56664.7	6.5	0.432
Pc22g13680	strong similarity to hypothetical protein contig1495_1.tfa_1650cg - Aspergillus fumigatus	blastP with Acremonium chrysogenum cefD2	e-143	17.3	13.7	12.3	15.4	0.8	1.3	0.7	1.1	377	41017	5.86	0.431
Pc22g14900	phenylacetyl-CoA ligase pclA - Penicillium chrysogenum	blastP with Penicillium chrysogenum pclA	0.0	108.5	140.0	222.5	381.6	1.3	1.7	2.1	2.7	578	62629.2	8.63	0.489
Pc22g16570	strong similarity to serine O-acetyltransferase cysA - Aspergillus nidulans	blastP with Acremonium chrysogenum cefG	2e-39	196.2	242.1	280.8	422.6	1.2	1.5	1.4	1.7	529	57623.2	6.53	0.493
Pc22g20270	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	blastP with Penicillium chrysogenum pclA	2.7e-103	111.8	173.9	186.3	458.8	1.6	2.5	1.7	2.6	562	62639.9	8.46	0.537
Pc22g24630	similarity to protein involved in cephalosporin C biosynthesis like protein An09g06420 - Aspergillus	blastP with Acremonium chrysogenum cefD2	2.4e-22	3.8	5.4	6.0	7.0	1.4	1.2	1.6	1.3	118	12524	5.41	0.407
Pc22g24780	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	blastP with Penicillium chrysogenum pclA	3.9e-80	11.6	44.1	18.2	252.3	3.8	13.9	1.6	5.7	549	60915.1	7.2	0.436

* Acremonium chrysogenum cefD2 gene for isopenicillin N-CoA epimerase

@ Values given are the average of three independent experiments

\# Interesting ratio's are indicated in blue (i.e. ratio >2 and one of the values above the background of 12)

$ Interesting ratio's are indicated in orange (i.e. ratio >2 and one of the values above the background of 12)

Supplementary Table 7. *In silico* identified putative *P. chrysogenum* microbody matrix proteins

		Average transcript levels				Putative	Putative
ORF code	**Description of putative *P. chrysogenum* ORF**	**WIS - PAA**	**WIS + PAA**	**DS - PAA**	**DS + PAA**	**PTS1**	**PTS2**
Pc04g00160	hypothetical protein	4.87	5.23	9.13	4.53		KLRCISCHL
Pc04g00190	hypothetical protein	9.37	6.60	15.73	9.95	CKI	
Pc06g01180	strong similarity to probable acyl-CoA dehydrogenase - Glomus intraradices	0.93	0.53	4.07	0.48	AKI	
Pc06g02280	strong similarity to cadmium resistance protein - Saccharomyces cerevisiae	435.60	379.10	427.67	409.90	SKI	
Pc07g00070	hypothetical protein	na	na	na	na	CKI	
Pc09g00320	hypothetical protein	na	na	na	na	CKI	
Pc12g00910	strong similarity to hypothetical protein AACU01001693_2 - Magnaporthe grisea	19.87	24.37	38.83	56.23		RLSRLSKHL
Pc12g01170	strong similarity to hypothetical protein Afu2g14850 - Aspergillus fumigatus	145.40	92.33	183.83	187.33	AKL	
Pc12g01670	similarity to ankyrin repeat protein E3_19 - Synthetic construct	4.67	2.73	4.33	1.80	AKM	
Pc12g02020	similarity to delta-6 desaturase like protein An07g06770 - Aspergillus niger	0.40	1.70	2.47	1.88		RLGVVAGQL
Pc12g04590	similarity to beta transducin-like protein het-e1 - Podospora anserina	482.53	499.20	514.20	486.03		RLTELLDQL
Pc12g05400	strong similarity to citrate synthase citA - Aspergillus niger	665.60	586.47	417.17	266.80	AKL	
Pc12g05520	strong similarity to long-chain-fatty-acid--CoA ligase Faa2 - Saccharomyces cerevisiae	366.53	169.77	224.33	235.20	AKL	
Pc12g07380	weak similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	22.67	10.50	12.17	8.25	CHI	
Pc12g08530	strong similarity to long-chain acyl-CoA dehydrogenase like protein An13g03940 - Aspergillus niger	135.73	126.77	178.30	352.00	AKI	
Pc12g09130	similarity to hypothetical protein ncu04017.1 - Neurospora crassa	291.80	245.33	212.33	224.95	SHL	
Pc12g09740	strong similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	79.50	53.60	42.57	63.08	AKL	
Pc12g09950	alcohol oxidase aox - Penicillium chrysogenum	6.23	4.13	9.13	2.73	SRL	
Pc12g13480	similarity to protein #3345 from patent US6562958-B1 - Acinetobacter baumannii	4.40	2.93	52.57	104.65	SKL	
Pc12g14790	strong similarity to AK-toxin production protein Akt3-1 - Alternaria alternata	2.43	0.27	2.87	1.18	AKL	
Pc12g15900	hypothetical protein	1.57	1.63	2.87	2.23	ARI	
Pc13g01380	strong similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	7.57	7.00	9.13	11.18	SKL	
Pc13g01530	strong similarity to hypothetical protein Afu2g02950 - Aspergillus fumigatus	34.17	42.67	67.90	123.28	CKI	
Pc13g01660	similarity to herbicidally active polypeptide SEQ ID NO 2512 from patent WO200210210-A2 - Arabidopsis thaliana	10.33	16.87	70.13	374.68	SKL	
Pc13g01890	strong similarity to acyl-CoA synthase like protein An18g03800 - Aspergillus niger	144.97	223.63	132.00	391.13		RLSGLLGHFI
Pc13g02660	strong similarity to hypothetical protein AN7738_2 - Aspergillus nidulans	6.83	3.10	6.47	9.45	AKL	
Pc13g02710	strong similarity to multifunctional beta-oxidation protein - Neurospora crassa	441.87	416.23	460.40	853.38	SKL	
Pc13g02990	strong similarity to pyruvate dehydrogenase phosphatase isoenzyme 1 PDP1 - Rattus norvegicus	231.50	238.93	200.73	179.30	SKL	
Pc13g03100	weak similarity to hypothetical protein An12g03380 - Aspergillus niger [putative sequencing error]	11.70	11.10	15.73	18.35	ARL	
Pc13g03340	strong similarity to succinate-semialdehyde dehydrogenase NAD(P)+ gabD - Escherichia coli	1.37	0.20	2.90	1.53	SKL	
Pc13g03350	strong similarity to copper amine oxidase AO-I - Aspergillus niger	15.10	20.60	22.10	18.93	CRL	
Pc13g03610	strong similarity to hypothetical protein AAF47250.1 - Drosophila melanogaster	85.20	199.30	180.13	524.75	SKI	
Pc13g03720	hypothetical protein	1.80	3.17	4.23	1.23	ARM	
Pc13g04270	strong similarity to dimethylglycine dehydrogenase precursor DMGDH - Homo sapiens	17.03	15.13	36.57	30.08	SRL	
Pc13g04370	similarity to peroxisomal membrane protein PEX17 - Yarrowia lipolytica	262.23	271.40	245.67	273.85	SKL	
Pc13g04510	strong similarity to NADP-dependent malate dehydrogenase mdh - Homo sapiens	97.87	98.20	81.33	33.35	AKL	
Pc13g05130	strong similarity to acetyl coenzyme A synthase - Tetrahymena pyriformis	64.07	60.80	39.87	56.75	SKL	
Pc13g05220	strong similarity to microsomal cytochrome like protein An05g00300 - Aspergillus niger	729.80	864.43	786.00	1126.73	AKL	
Pc13g05940	strong similarity to trifunctional protein of the beta-oxidation fox-2 - Neurospora crassa	491.57	263.90	427.53	322.68	AKL	
Pc13g06220	strong similarity to hypothetical protein brt1 - Schizophyllum commune	276.40	309.57	404.73	383.55	SRL	
Pc13g06300	strong similarity to acetamidase amdS - Aspergillus nidulans	6.63	146.67	32.77	225.40	SKI	
Pc13g06370	strong similarity to hypothetical protein 1148_scaffold_2.tfa_890cg - Fusarium graminearum	4.40	4.30	16.43	15.85	AKL	
Pc13g07280	strong similarity to hypothetical protein 1158_scaffold_2.tfa_100wg - Fusarium graminearum	19.97	6.33	22.23	4.33		KVLHLLQHA
Pc13g07430	strong similarity to hypothetical protein Afu4g07940 - Aspergillus fumigatus	57.53	37.17	106.77	226.33	SKL	
Pc13g09070	strong similarity to hypothetical protein B23L21.110 - Neurospora crassa	64.30	48.83	48.10	54.45	ARL	
Pc13g09740	strong similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	48.27	43.43	117.77	193.65	AKL	
Pc13g11580	strong similarity to hypothetical protein Afu1g12880 - Aspergillus fumigatus	120.37	326.87	112.03	458.30	ARL	
Pc13g11930	strong similarity to acyl CoA dehydrogenase aidB - Escherichia coli	1.37	2.83	51.37	108.40	SKL	
Pc13g12080	similarity to acetyl-hydrolase chnC - Acinetobacter sp.	111.07	147.07	180.30	440.23	ARL	
Pc13g12270	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	92.17	100.77	57.33	133.35	AKL	
Pc13g12580	strong similarity to 8-amino-7-oxononanoate synthase/KAPA synthase BioF - Kurthia sp.	0.43	2.50	2.37	0.90	ARL	KILSQKLQF

Pc13g12620	strong similarity to spindle assembly checkpoint protein like protein An08g06660 - Aspergillus niger	105.27	90.77	66.83	63.78	ARM	
Pc13g12760	strong similarity to pyruvate decarboxylase dcpY - Aspergillus parasiticus	0.57	1.23	5.53	3.98		RLHQVGLHA
Pc13g12930	strong similarity to peroxisomal acetyl-CoA C-acyltransferase POT1 - Yarrowia lipolytica	444.73	317.80	446.53	442.33		RLSSLLSHL
Pc13g14410	strong similarity to hypothetical protein Afu7g06090 - Aspergillus fumigatus	5.47	4.70	7.07	20.60	SKL	
Pc13g14420	strong similarity to malonyl CoA synthase matB - Rhizobium trifolii	4.67	8.50	7.73	86.88	ARL	
Pc13g14580	hypothetical protein	2.30	2.00	2.43	2.58	AKL	
Pc13g15940	strong similarity to copper amine oxidase AO-I - Aspergillus niger	200.00	365.70	98.40	195.53	SHI	
Pc14g00140	strong similarity to hypothetical protein AN3880_2 - Aspergillus nidulans	69.67	126.00	163.67	95.90	ARI	
Pc14g00560	strong similarity to hypothetical protein EAA30321.1 - Neurospora crassa	36.20	39.47	34.57	53.25	AKL	
Pc14g00970	similarity to D-amino-acid oxidase DAO - Fusarium solani	2.23	0.63	2.17	3.03	SKL	
Pc14g01040	strong similarity to aldehyde dehydrogenase aldA - Aspergillus niger	1.33	1.03	0.90	1.33	ARL	
Pc14g01070	strong similarity to actVA-ORF4-like protein from patent WO9911793-A1 - Homo sapiens	15.50	8.43	12.37	10.70	SKI	
Pc14g01090	strong similarity to NADH oxidase nadA - Aspergillus parasiticus	2.13	0.23	2.13	0.78	SKL	
Pc14g01270	strong similarity to hypothetical 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase BH2000 - Bacillus halodurans	269.07	364.33	481.37	806.98	SKL	
Pc15g00240	weak similarity to hypothetical protein Afu6g10160 - Aspergillus fumigatus	1.27	0.43	2.40	0.70	SRI	
Pc15g00410	strong similarity to peroxisomal acetyl-CoA C-acyltransferase POT1 - Yarrowia lipolytica	185.87	149.63	163.77	271.45		RLNSVANQL
Pc15g00420	strong similarity to very long-chain fatty acyl-CoA synthase Fat1 - Saccharomyces cerevisiae	3.07	1.47	3.60	8.35	AKI	
Pc15g00830	strong similarity to hypothetical protein AN0303_2 - Aspergillus nidulans	87.37	91.40	74.53	72.90		RQVDHAAHA
Pc16g00190	strong similarity to NADH oxidase nadA - Aspergillus parasiticus	2.43	3.13	3.77	9.68	SHL	
Pc16g03770	strong similarity to conserved hypothetical protein - Brucella suis	116.23	75.23	103.23	149.05	SRL	
Pc16g03970	strong similarity to hypothetical conserved protein SPCP1E11.11 - Schizosaccharomyces pombe	130.23	124.37	119.77	49.53	SKI	
Pc16g04350	strong similarity to hypothetical protein An02g13300 - Aspergillus niger	3.53	2.33	5.70	12.73	SKL	
Pc16g05060	strong similarity to 3-hydroxy-3-methylglutaryl coenzyme A reductase HmgA - Sulfolobus solfataricus	0.23	0.33	1.90	1.68	SKI	
Pc16g05620	strong similarity to protein kinase CK2 (casein kinase II) beta subunit ckb1p - Schizosaccharomyces pombe [truncated ORF]	331.80	348.57	219.47	192.68	AKM	
Pc16g05900	similarity to salicylate hydroxylase nahG - Pseudomonas putida	0.27	0.23	0.53	0.25	ARM	
Pc16g06490	strong similarity to hypothetical protein An04g06530 - Aspergillus niger	2.33	0.63	3.87	3.43	SRL	
Pc16g07060	strong similarity to catalase C catC - Aspergillus nidulans	4.33	2.07	3.20	2.88	SRL	
Pc16g07070	strong similarity to aryl-alcohol oxidase precursor aao - Pleurotus eryngii	3.53	2.33	3.87	2.75	SKL	
Pc16g07440	strong similarity to cytoplasmic proline--tRNA ligase like protein An08g02860 - Aspergillus niger	44.50	41.83	44.73	51.28	AKL	
Pc16g10060	strong similarity to methylmalonate-semialdehyde dehydrogenase precursor MMSDH - Bos taurus [putative sequencing error]	6.97	4.93	6.13	2.75	SHL	
Pc16g10070	strong similarity to 2-nitropropane dioxygenase ncd-2 - Neurospora crassa	10.67	13.97	12.17	13.00	SKL	
Pc16g10670	strong similarity to cyclohexanone monooxygenase chnB - Acinetobacter sp.	10.80	11.73	14.17	14.35	SKL	
Pc16g11360	similarity to tripeptidylaminopeptidase Tap - Streptomyces lividans	143.60	109.83	125.30	98.03		RQVRQAHQA
Pc16g11450	strong similarity to hypothetical protease Mch5 - Saccharomyces cerevisiae	2.97	2.63	18.70	23.63	AKI	
Pc16g11790	strong similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	5.57	10.43	10.60	14.30	SKI	
Pc16g11910	similarity to hypothetical protein BAB09014.1 - Arabidopsis thaliana	5.17	2.37	5.90	6.00	SKL	
Pc16g14240	strong similarity to acetamidase amdS - Aspergillus oryzae	220.13	169.30	228.40	272.30	AKL	
Pc16g14920	similarity to zinc-finger protein like protein An12g08230 - Aspergillus niger	0.50	0.93	2.23	1.25	AKL	
Pc17g00250	hypothetical protein	25.30	18.23	21.57	17.03	SRM	
Pc17g00720	similarity to hypothetical protein AN0335_2 - Aspergillus nidulans	0.63	2.23	2.80	1.58	ARL	
Pc17g00980	hypothetical protein	na	na	na	na	CKI	
Pc18g01590	strong similarity to glycolate oxidase GOX - Mus musculus	13.97	16.50	19.80	35.85	ARL	
Pc18g01860	strong similarity to D-amino-acid oxidase DAO - Fusarium solani	10.13	8.27	6.93	6.78	SHL	
Pc18g03000	strong similarity to hypothetical protein YMR099c - Saccharomyces cerevisiae	455.80	460.13	554.63	501.10	SRL	
Pc18g03470	strong similarity to lysine aminopeptidase apsA - Aspergillus niger	436.43	450.17	305.93	236.55	SKL	
Pc18g04530	similarity to hypothetical coiled-coil protein SPAC13A11.03 - Schizosaccharomyces pombe	48.00	45.50	46.90	47.25		KQDLILTHL
Pc19g00210	strong similarity to hypothetical protein 1190_scaffold_2.tfa_540wg - Fusarium graminearum [putative pseudogene]	2.63	2.50	3.17	0.38	ARI	
Pc20g01800	strong similarity to hypothetical protein Afu7g06090 - Aspergillus fumigatus	438.57	118.13	125.37	230.88	SKL	
Pc20g01980	strong similarity to phenol 2-monooxygenase - Trichosporon beigelii	9.70	60.60	12.40	79.53	SRL	
Pc20g03400	hypothetical protein	3.17	2.33	3.77	3.25	ARL	
Pc20g03610	strong similarity to precursor of mitochondrial isocitrate dehydrogenase icdA - Aspergillus niger	867.90	1270.00	943.53	1200.78	ARL	
Pc20g03630	strong similarity to acetamidase amdS - Aspergillus nidulans	4.33	2.90	2.37	2.83	ARL	
Pc20g04300	strong similarity to hypothetical protein An16g02770 - Aspergillus niger	50.20	83.93	237.90	507.25	ARL	
Pc20g06660	strong similarity to D-amino-acid oxidase DAO - Fusarium solani	29.83	24.80	63.20	79.48	SRL	

Pc20g08300	strong similarity to hypothetical protein 12F11.200 - Neurospora crassa	51.20	76.80	72.30	150.13	SKI	
Pc20g09430	similarity to hypothetical ureidoglycolate hydrolase SPAC19G12.04 - Schizosaccharomyces pombe	19.73	31.90	40.17	51.18	AKL	
Pc20g10430	strong similarity to D-mandelate dehydrogenase - Rhodotorula graminis	1.77	2.87	4.77	2.58	SKL	
Pc20g10520	similarity to hypothetical protein An12g07270 - Aspergillus niger	11.90	22.20	13.67	29.63	AKM	
Pc20g10700	strong similarity to hypothetical protein 1143_scaffold_2.tfa_210cg - Fusarium graminearum	1.43	3.27	3.23	4.43	SKI	
Pc20g11660	strong similarity to mitochondrial mRNA processing protein Pet127 - Saccharomyces cerevisiae	71.93	61.13	51.40	26.65	CKM	
Pc20g13550	strong similarity to malate synthase acuE - Aspergillus nidulans	164.57	123.83	397.17	188.58	AKL	
Pc20g14920	similarity to hypothetical oxidoreductase PA5309 - Pseudomonas aeruginosa	11.73	39.70	29.90	96.10	ARL	
Pc20g15650	strong similarity to hypothetical protein AN5853_2 - Aspergillus nidulans	6.77	2.00	11.70	41.18	ARL	
Pc20g15660	strong similarity to sterol carrier protein-X/sterol carrier protein-2 SCP2 - Homo sapiens	6.03	6.27	23.63	107.70	ARI	
Pc21g00200	hypothetical protein	na	na	na	na		KLRCISCHL
Pc21g00230	hypothetical protein	na	na	na	na	CKI	
Pc21g00970	strong similarity to hex1 - Aspergillus nidulans	2685.47	2952.60	2926.47	2448.45	SRL	
Pc21g01040	similarity to hypothetical protein AN7405_2 - Aspergillus nidulans	89.63	86.97	83.97	77.23	SRM	
Pc21g01650	strong similarity to hypothetical conserved protein PA5185 - Pseudomonas aeruginosa	97.43	132.47	117.50	237.35	AKL	
Pc21g02970	strong similarity to phenol 2-monooxygenase - Trichosporon beigelii	64.27	80.87	73.63	104.65	SRL	
Pc21g03400	strong similarity to triose-phosphate-isomerase tpiA from patent WO8704464-A - Aspergillus niger	1488.47	1672.60	2271.77	1813.75	ARI	
Pc21g03940	strong similarity to transposase Tan1 - Aspergillus niger [putative pseudogene]	2.90	1.47	4.43	5.00	ARI	
Pc21g04900	strong similarity to hypothetical protein AN4261_2 - Aspergillus nidulans	89.97	83.13	83.87	126.78	SKL	
Pc21g05470	strong similarity to mannase man1 - Aspergillus aculeatus	6.40	4.53	6.27	9.05	SKI	
Pc21g05490	strong similarity to sn-glycerol-3-phosphate acyltransferase like protein An18g01960 - Aspergillus niger	189.90	157.30	188.90	201.75	AKL	
Pc21g05590	strong similarity to D-amino-acid oxidase DAO - Fusarium solani	304.87	383.33	278.93	372.93	AKL	
Pc21g05690	weak similarity to hypothetical protein An09g06720 - Aspergillus niger	1.90	0.93	3.13	2.18	SHM	
Pc21g06590	strong similarity to hypothetical protein Afu8g02420 - Aspergillus fumigatus	2.87	1.90	6.93	9.45	SRL	
Pc21g06860	strong similarity to endopeptidase La 2 lonD - Myxococcus xanthus	316.17	291.53	356.00	378.08	SRL	
Pc21g07100	similarity to transposase Taf1 - Aspergillus fumigatus [putative pseudogene]	2.70	1.20	0.73	0.73	SKI	
Pc21g07210	weak similarity to S-layer protein CipA - Clostridium thermocellum	348.73	315.87	215.77	190.35	SKL	
Pc21g07490	strong similarity to hypothetical protein AN0070_2 - Aspergillus nidulans	65.43	62.93	62.67	71.93	SRI	
Pc21g08790	strong similarity to NADP-dependent leukotriene B4 12-hydroxydehydrogenase like protein An13g01120 - Aspergillus niger	58.93	45.00	86.93	99.93	AKL	
Pc21g09440	strong similarity to hypothetical protein AN5270_2 - Aspergillus nidulans	1.10	2.87	5.53	4.23	SKL	
Pc21g09460	strong similarity to propionyl-CoA carboxylase, beta subunit - Mycobacterium tuberculosis	1.40	0.63	1.63	0.20	ARI	
Pc21g09470	strong similarity to feruloyl-CoA synthase like protein An06g01320 - Aspergillus niger	0.23	0.20	0.80	0.33	AKL	
Pc21g09480	strong similarity to 3-hydroxy-3-methylglutaryl CoA lyase HMG-CoA lyase - Rattus norvegicus	4.87	1.63	5.23	5.33	SKL	
Pc21g09780	strong similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	8.17	4.53	30.70	43.25	SRL	
Pc21g10640	strong similarity to cadmium resistance protein - Saccharomyces cerevisiae	374.47	342.17	413.80	371.18	SKI	
Pc21g11080	strong similarity to hypothetical protein AN1437_2 - Aspergillus nidulans	93.57	64.93	52.63	32.83	SRM	
Pc21g11670	strong similarity to quinone reductase like protein An12g00170 - Aspergillus niger	84.90	77.50	102.33	139.55	SKL	
Pc21g11780	strong similarity to 3-dehydroshikimate dehydratase qa-4 - Neurospora crassa	3.07	4.57	11.43	32.60	SRI	
Pc21g12260	strong similarity to alcohol dehydrogenase C ADHC - Mycobacterium smegmatis	20.73	12.07	22.40	23.20	AKL	
Pc21g13110	strong similarity to polyprotein of retrotransposon REAL pol - Alternaria alternata [putative pseudogene]	0.17	0.40	0.63	1.40	SRI	
Pc21g13270	strong similarity to hypothetical protein AN3770_2 - Aspergillus nidulans	37.13	37.77	40.27	52.38	SRM	
Pc21g14590	strong similarity to protease involved in a-factor processing Ste23 - Saccharomyces cerevisiae	299.93	303.43	362.53	285.30	AKL	
Pc21g14640	strong similarity to hypothetical protein YDR196c - Saccharomyces cerevisiae	53.07	62.70	82.40	175.88	AKL	
Pc21g15970	strong similarity to cytosolic exopolyphosphatase Ppx1 - Saccharomyces cerevisiae	31.23	29.47	54.83	83.50	AKL	
Pc21g16050	strong similarity to hypothetical protein YGL067w - Saccharomyces cerevisiae	76.30	122.50	93.77	154.23	SKI	
Pc21g16080	strong similarity to hypothetical protein encoded by gene B18D24.50 - Neurospora crassa	184.10	242.00	576.63	431.73	AHI	
Pc21g16580	hypothetical protein	6.00	3.23	5.40	4.50	AKI	
Pc21g16710	strong similarity to hypothetical protein AACM01000094_6 - Fusarium graminearum	22.20	72.73	14.67	62.95	ARL	
Pc21g17590	strong similarity to acyl-CoA dehydrogenase like protein An17g01150 - Aspergillus niger	529.80	553.13	838.73	1248.65	SHL	
Pc21g20650	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	72.60	62.87	52.57	123.08	ARL	
Pc21g21120	strong similarity to monoamine oxidase N mao-N - Aspergillus niger	0.83	11.57	0.53	14.25	SHL	
Pc21g21140	similarity to hypothetical protein - Gloeobacter violaceus	2.63	1.00	3.37	5.15	AHL	
Pc21g21370	acyl-coenzyme A:isopenicillin N acyltransferase (acyltransferase) AAT/PenDE - Penicillium chrysogenum	1031.33	1827.00	1993.70	2714.55	ARL	
Pc21g21410	strong similarity to hypothetical protein ncu05765.1 - Neurospora crassa	2.63	1.70	5.40	6.30	SRM	
Pc21g21810	strong similarity to levodione reductase lvr - Corynebacterium aquaticum	79.30	82.27	154.37	241.25		RLQALSKQ
Pc21g22010	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	50.77	45.30	22.03	11.73	SKL	
Pc21g23700	strong similarity to long-chain-fatty-acid alcohol oxidase fao1 - Candida cloacae	54.73	66.50	40.03	55.33	ARL	
Pc22g00060	similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	93.93	177.60	137.93	334.18	AKL	
Pc22g00300	strong similarity to flavocytochrome b2 L-lactate dehydrogenase CYB2 - Pichia anomala	8.87	7.37	9.57	4.35	SKL	

Pc22g00460	strong similarity to hypothetical protein An06g01070 - Aspergillus niger	62.90	67.23	227.67	87.93	ARI	
Pc22g00860	strong similarity to cytochrome-c peroxidase precursor Ccp1 - Saccharomyces cerevisiae	62.63	3.03	5.67	1.98	ARL	
Pc22g01300	similarity to lipid transfer protein POX18 - Candida tropicalis	407.10	286.73	628.57	403.55	AKL	
Pc22g01600	strong similarity to histidine triad protein Hnt1 - Saccharomyces cerevisiae	882.90	1065.03	1135.30	1128.53	SKM	
Pc22g02570	hypothetical protein	6.17	6.83	5.93	7.35	AHI	
Pc22g02620	strong similarity to monoglyceride lipase mgll - Mus musculus	71.67	119.07	89.37	238.30	AKL	
Pc22g03680	strong similarity to NADPH-dependent beta-ketoacyl reductase RhlG - Pseudomonas aeruginosa	161.83	130.50	370.53	460.73	AKL	
Pc22g05640	similarity to hypothetical protein required for biosynthesis of the host-specific AK-toxin Akt2 - Alternaria alternata	13.07	18.37	13.57	29.08	SKL	
Pc22g06120	strong similarity to SR-protein-specific kinase SRPK2 - Mus musculus	460.47	397.50	324.80	220.25	SHM	
Pc22g06820	strong similarity to peroxisomal acetyl-CoA C-acyltransferase POT1 - Yarrowia lipolytica	475.30	194.27	244.33	157.40		RLSQVSSHF
Pc22g07740	strong similarity to acyl-CoA oxydase tylP - Streptomyces fradiae	2.73	0.87	2.30	2.33	AKL	
Pc22g08120	similarity to hypothetical meta-cleavage compound hydrolase gene ren71 - Streptomyces aureofaciens [putative sequencing error]	1.30	1.13	8.80	11.53	ARI	
Pc22g10030	strong similarity to betaine-aldehyde dehydrogenase betB - Escherichia coli	373.37	568.73	212.27	232.75	AKL	
Pc22g11470	strong similarity to L-lactate dehydrogenase precursor Cyb2 - Saccharomyces cerevisiae	142.77	177.83	147.63	271.18	ARL	
Pc22g13390	strong similarity to alcohol dehydrogenase like protein An02g02060 - Aspergillus niger	258.07	301.53	529.07	917.10	SKL	
Pc22g13680	strong similarity to hypothetical protein Afu5g03740 - Aspergillus fumigatus	17.27	13.67	12.30	15.40	SKI	
Pc22g14270	strong similarity to hypothetical protein Afu5g09600 - Aspergillus fumigatus	231.20	118.90	318.57	333.53	SKL	
Pc22g14900	phenylacetyl-CoA ligase pclA - Penicillium chrysogenum	108.53	139.97	222.50	381.63	SKI	
Pc22g15030	strong similarity to peroxisomal 2,4-dienoyl-CoA reductase involved in sporulation Sps19 - Saccharomyces cerevisiae	428.20	555.93	388.37	813.73	SKL	
Pc22g15400	similarity to hypothetical protein required for biosynthesis of the host-specific AK-toxin Akt2 - Alternaria alternata	8.67	0.97	0.73	0.58	SKI	
Pc22g17230	strong similarity to aldehyde dehydrogenase aldA - Aspergillus niger	9.00	6.43	14.70	11.60	SKL	
Pc22g18190	strong similarity to L-lactate dehydrogenase precursor Cyb2 - Saccharomyces cerevisiae	39.83	59.00	70.93	113.65	SKL	
Pc22g18380	strong similarity to salicylate hydroxylase nahG - Pseudomonas putida	14.47	40.33	38.87	69.70	SRL	
Pc22g18490	strong similarity to hypothetical protein T22K18.2 - Arabidopsis thaliana	107.20	136.47	111.80	189.13	CRM	
Pc22g18850	similarity to secretory polypeptide SPTM SEQ ID NO 850 from patent WO200283876-A2 - Homo sapiens	113.83	109.43	122.23	117.63	ARL	
Pc22g19270	strong similarity to glycolate oxidase GOX - Mus musculus	0.13	1.60	0.60	0.23	SKL	
Pc22g19440	strong similarity to cytosolic aspartate transaminase Aat2 - Saccharomyces cerevisiae	626.00	780.57	930.77	1212.05	AKL	
Pc22g19490	strong similarity to trans-2-enoyl-ACP reductase like protein An16g05340 - Aspergillus niger	923.17	504.00	1072.27	956.15	SKL	
Pc22g20270	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	111.83	173.90	186.27	458.80	AKL	
Pc22g20320	strong similarity to myo-inositol 2-dehydrogenase yisS - Bacillus subtilis	75.60	63.33	53.03	66.13	ARL	
Pc22g20370	strong similarity to carnitine racemase like protein An03g03550 - Aspergillus niger	0.67	1.60	4.93	43.33	SKL	
Pc22g20380	strong similarity to aerobactin biosynthesis protein iucB - Escherichia coli	6.47	15.03	32.73	90.15	AKL	
Pc22g20960	strong similarity to urate oxidase uaz - Aspergillus flavus	107.13	97.33	318.03	96.15	AKL	
Pc22g21240	strong similarity to catalase cta1p - Schizosaccharomyces pombe	54.93	61.93	34.00	35.80	ARL	
Pc22g21670	strong similarity to endocytosis protein Ede1 - Saccharomyces cerevisiae	417.50	370.63	304.93	205.28		RVFFQLFQA
Pc22g22110	strong similarity to glycerol-3-phosphate dehydrogenase (NAD+) precursor Gpd1 - Saccharomyces cerevisiae	316.37	311.97	248.20	201.75	ARL	
Pc22g22390	strong similarity to AK-toxin production protein Akt3-1 - Alternaria alternata	28.37	30.93	51.27	141.38	SKL	
Pc22g23350	strong similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	0.50	1.80	1.50	3.53	AKL	
Pc22g23700	weak similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	12.37	15.13	32.37	52.00	SRL	
Pc22g24630	similarity to protein involved in cephalosporin C biosynthesis like protein An09g06420 - Aspergillus niger	3.77	5.43	6.03	7.00	AKI	
Pc22g24780	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	11.60	44.10	18.17	252.33	AKL	
Pc22g25120	strong similarity to hypothetical protein 1141_scaffold_2.tfa_360cg - Fusarium graminearum	12.03	20.07	14.80	38.23	SKL	
Pc22g25150	strong similarity to acyl CoA dehydrogenase aidB - Escherichia coli	46.17	17.53	96.90	189.28	SKL	
Pc22g26560	hypothetical protein	na	na	na	na		KLRCISCHL
Pc22g26600	hypothetical protein	na	na	na	na	CKI	
Pc23g00390	similarity to hypothetical protein ncu04490.1 - Neurospora crassa	36.70	42.07	51.67	34.03	AKL	
Pc24g00180	hypothetical protein [truncated ORF]	na	na	na	na	CKI	
Pc24g01320	similarity to hypothetical S-layer protein - Clostridium thermocellum	231.23	353.20	314.27	357.38	SRM	
Pc24g02680	strong similarity to copia-like retrotransposable element - Arabidopsis thaliana	4.30	2.20	2.30	3.90	CRL	
Pc32g00010	strong similarity to protein encoded by ORF1 of transposon Ant1 - Aspergillus niger	23.17	30.97	13.63	2.55	CHL	

Supplementary Table 8: Summary of the global transcriptional response to phenylacetic acid in chemostat cultures of *P. chrysogenum.* Transcript levels of strains Wisconsin54-1255 and DS17690 were analysed in triplicate glucose-limited chemostat cultures in the absence and presence of phenylacetic acid (PAA); **A.** Numbers of genes whose transcript levels were below the detection limit in each situation. Transcript levels of 3970 genes were below detection limit in all four situation; **B.** Pairwise comparisons, showing the numbers of genes that showed a significantly different transcript level between the two strains or in response to PAA addition. Transcript levels of 2470 genes were significantly different in at least one of the four situations.

A.

	Below detection limit
DS17690 - PAA	4552
DS17690+ PAA	5054
Wis 54-1255 - PAA	4755
Wis 54-1255 + PAA	5213

B.

	Higher transcript level	**Lower transcript level**
DS17690 + PAA vs. DS1760 - PAA	443	411
Wis54-1255 + PAA vs. Wis54-1255 - PAA	252	338
DS17690 + PAA vs. Wis54-1255 + PAA	861	744
DS17690 - PAA vs. Wis54-1255 - PAA	492	549

Supplementary Table 9. K-mean cluster 1
@=Values given are the average of three independent experiments

orf code	**Description of putative *P. chrysogenum* ORF**	**Best blast homolog to putative *P. chrysogenum* ORF**			**Average transcript levels @**				**FunCat (auto)**	
		p-value	**Gene code**	**description**	**WIS - PAA**	**WIS + PAA**	**DS - PAA**	**DS + PAA**	**pval**	**category**
Pc06g01600	strong similarity to FAD dependent L-sorbose dehydrogenase SDH - Gluconc	2e-69	GOD622_2	product: "L-sorbose dehydrogenase,	41.2	2373.4	20.6	2223.1	0.0	02.11 electron transport and membrane-associated energ
Pc12g02570	strong similarity to cytochrome P450 monooxygenase TRI11 - Fusarium spor	4e-84	AF155773_13	gene: "FUM12"; product: "Fum12p";	12.0	295.5	12.0	922.2	1e-100	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc12g07980	similarity to benzoylformate decarboxylase - Pseudomonas putida	1e-129	NCB2G14_13	gene: "B2G14.130"; product: "relatec	29.2	424.1	63.5	1227.0	1e-136	01.01.01 amino acid biosynthesis
Pc12g09020	strong similarity to maleylacetoacetate isomerase maiA - Aspergillus nidulans	2e-76	EN1836_1	gene: "maiA"; product: "maleylaceto	47.0	3267.8	106.3	3479.8	5e-57	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc12g09030	strong similarity to fumarylacetoacetase - Homo sapiens	0.0	ENFUHY_1	gene: "fahA"; product: "fumarylaceto	138.0	3786.2	279.5	3905.8	0.0	01 METABOLISM
Pc12g09040	strong similarity to 3,4-dihydroxyphenylacetate 2,3-dioxygenase hmgA - Aspe	0.0	A57435	3,4-dihydroxyphenylacetate 2,3-diox	135.0	3551.7	202.7	3736.3	0.0	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc12g13630	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	0.0	BX842634_3	gene: "B16B8.030"; product: "relatec	12.0	85.7	12.0	140.9	5e-64	01.05.07 C-compound, carbohydrate transport
Pc12g13800	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	5e-80	T41604	probable membrane transport protei	12.0	482.7	12.0	470.8	2e-53	01.04.07 phosphate transport
Pc13g06300	strong similarity to acetamidase amdS - Aspergillus nidulans	1e-126	T41382	acetamidase - fission yeast (Schizos	12.0	146.7	32.8	225.4	7e-95	01.01.10 amino acid degradation (catabolism)
Pc13g10030	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyce	1e-103	NC64C2_19	gene: "64C2.200"; product: "related t	22.9	487.1	125.0	1344.0	2e-53	01.04.07 phosphate transport
Pc13g10900	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyce	1e-180	BX649605_57	product: "transporter, putative"; Aspe	22.9	487.1	125.0	1344.0	1e-56	01.04.07 phosphate transport
Pc16g01770	strong similarity to phenylacetate hydroxylase pahA - Penicillium chrysogenum	1e-112	AF057559_1	gene: "pahA"; product: "phenylacetat	12.0	2661.0	32.8	2533.9	1e-117	01.01.01 amino acid biosynthesis
Pc16g07590	strong similarity to acetamidase amdS - Aspergillus oryzae	0.0	AF349510_1	gene: "gmdB"; product: "general ami	66.0	2790.0	76.8	3542.9	1e-63	01.01.10 amino acid degradation (catabolism)
Pc18g01290	strong similarity to dityrosine transporter Dtr1 - Saccharomyces cerevisiae	3e-71	AF141925_12	product: "unknown"; Aspergillus terre	20.4	175.2	42.8	224.3	6e-55	01.05.07 C-compound, carbohydrate transport
Pc20g02710	weak similarity to DOPA-dioxygenase dodA - Amanita muscaria	3e-51	BX897679_2	gene: "B2C22.020"; product: "conse	13.9	89.1	31.3	373.8	0	0
Pc20g14540	strong similarity to alcohol dehydrogenase like protein An15g07870 - Aspergil	1e-27	AP005953_4	gene: "blr4874"; Bradyrhizobium jap	98.2	868.9	127.6	798.8	9e-77	01.05 C-compound and carbohydrate metabolism
Pc21g04400	strong similarity to mandelate like protein An13g00920 - Aspergillus niger	3.00E-90	AB0793	probable MR-MLE-family protein ST	12.0	239.3	12.0	309.3	6e-75	01 METABOLISM
Pc21g12990	strong similarity to polyamine transport protein Tpo1 - Saccharomyces cerevi	1e-149	BX908812_25	gene: "G17A4.250"; product: "relatec	12.0	76.6	12.0	109.1	8e-54	01.05.07 C-compound, carbohydrate transport
Pc21g14280	phenylacetate hydroxylase pahA - Penicillium chrysogenum	0.0	AF056978_1	gene: "pahA"; product: "phenylacetat	12.0	93.0	40.2	202.2	1e-111	01.01.10 amino acid degradation (catabolism)
Pc21g19470	strong similarity to mitochondrial succinate-fumarate transporter Sfc1 - Sacch	1e-125	BX897673_8	gene: "B13M15.080"; product: "prob	25.0	344.1	48.3	361.2	3e-77	01.05.04 regulation of C-compound and carbohydrate util
Pc21g21750	strong similarity to flavin-containing monooxygenase like protein An13g02690	1e-45	SPBP16F5_8	gene: "SPBP16F5.08c"; S.pombe c	25.0	344.1	48.3	361.2	1e-112	01.02.01.09.99 other catabolism of nitrogenous compour
Pc22g07320	strong similarity to mycocerosate synthase like protein An02g14970 - Aspergi	2e-91	NCB8P8_9	gene: "B8P8.090"; product: "probabl	16.8	94.7	47.6	647.5	1e-80	01 METABOLISM
Pc22g07360	strong similarity to 1,2-dichlorophenol hydroxylase tfdB - Pseudomonas putida	1e-124	AY078159_14	gene: "tfdB"; product: "dichlorophenc	33.2	476.9	57.7	501.2	1e-78	01.05.01.01.09 aerobic aromate catabolism
Pc22g07410	strong similarity to trihydroxytoluene oxygenase dntD - Burkholderia cepacia	2e-45	AF076848_1	gene: "dntD"; product: "trihydroxytolu	12.0	97.8	12.0	199.8	0	0
Pc22g24780	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	1e-98	AY254381_1	Emericella nidulans adenylate-formin	110.2	558.2	94.8	818.2	1e-128	01 METABOLISM
Pc22g24860	strong similarity to aldehyde dehydrogenase aldA - Aspergillus niger	1e-131	NCB11B23_10	gene: "B11B23.110"; product: "proba	12.0	44.1	18.2	252.3	0.0	01.05 C-compound and carbohydrate metabolism
Pc20g02930	strong similarity to D-lactate dehydrogenase dld - Kluyveromyces lactis	1e-141	BX842682_10	gene: "B13C5.100"; product: "probal	12.0	968.8	48.3	1655.9	1e-157	01.05.01 C-compound and carbohydrate utilization
Pc16g02700	weak similarity to cutinase transcription factor beta CTF1b - Fusarium solani	7e-11	T38690	probable regulatory protein - fission y	44.3	308.8	71.3	526.7	4e-77	01.01.04 regulation of amino acid metabolism
Pc16g02690	strong similarity to benomyl methotrexate resistance protein MDR1 - Candida	1e-78	BX649607_11	gene: "mdR"; product: "mfs-family m	12.0	97.0	20.8	129.6	2e-48	01.04.07 phosphate transport
Pc21g01300	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae	0.0	ACH487683_1	gene: "cefT"; product: "multidrug resi	12.0	280.7	12.0	910.0	9e-67	01.05.07 C-compound, carbohydrate transport
Pc21g09220	strong similarity to fluconazole resistance transporter Flr1 - Saccharomyces c	4e-90	BX649607_11	gene: "mdR"; product: "mfs-family m	12.0	81.1	12.0	591.1	4e-51	01.05.04 regulation of C-compound and carbohydrate util
Pc21g14210	similarity to polyamine transport protein Tpo3 - Saccharomyces cerevisiae	2e-23	T41018	probable membrane transporter - fiss	15.2	402.4	158.4	1118.5	7e-55	01.04.07 phosphate transport
Pc22g14600	strong similarity to ATP-binding cassette multidrug transport protein atrB - Asp	0.0	AB028872_1	gene: "BMR1"; product: "BMR1"; Bc	12.0	272.6	12.0	111.2	0.0	01.06.13 lipid and fatty-acid transport
Pc22g20580	strong similarity to multidrug resistance protein Qdr1 - Saccharomyces cerevi	9e-67	S49888	probable membrane protein YIL121w	35.0	399.5	176.0	567.2	7e-58	01.05.07 C-compound, carbohydrate transport
Pc12g13810	strong similarity to methicillin resistance gene HmrA - Staphylococcus aureus	3e-96	NCB14A21_24	gene: "B14A21.240"; product: "relate	12.2	140.9	52.5	163.4	9e-87	01.01 amino acid metabolism
Pc22g06840	similarity to arylamine N-acetyltransferase - Gallus gallus	2e-07	AY228175_2	product: "putative arylamine N-acety	31.1	2001.2	98.9	2710.2	9e-82	01 METABOLISM
Pc22g08750	strong similarity to mitomycin C translocase mct - Streptomyces lavendulae	1e-44	BX908808_43	gene: "G21B4.430"; product: "relatec	19.6	150.7	33.6	345.9	2e-48	01.05.04 regulation of C-compound and carbohydrate util
Pc22g08950	strong similarity to cytochrome P450 pisatin demethylase PDAT9 - Nectria ha	4e-62	S45583	pisatin demethylase (EC 1.14.-.-) cyt	12.0	78.5	12.0	120.5	1e-105	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc12g02210	similarity to hypothetical protein contig_1_67_scaffold_4.tfa_580cg - Aspergil	3e-09	H95268	hypothetical protein SMa0112 [impo	30.7	554.9	52.7	547.9	0	0
Pc12g02220	strong similarity to hypothetical protein mg00678.1 - Magnaporthe grisea	1e-34	T41554	hypothetical protein SPCC70.08c - fi	12.0	1051.1	21.5	864.5	1e-35	01.07.01 biosynthesis of vitamins, cofactors, and prosthe
Pc13g06330	similarity to hypothetical membrane protein YOL119c - Saccharomyces cerev	3e-51	NCB23B10_3	gene: "B23B10.030"; product: "relate	12.0	266.8	130.3	724.7	1e-44	01.04.07 phosphate transport
Pc16g09960	strong similarity to hypothetical protein contig_1_43_scaffold_2.tfa_610cg - A	6e-48	BX842647_291	product: "Major facilitator family tran	12.0	159.7	26.4	355.4	9e-45	01.04.07 phosphate transport
Pc16g13530	strong similarity to hypothetical protein contig_1_130_scaffold_10.tfa_180cg	0	0	0	12.0	63.0	12.0	90.8	0	0
Pc19g00540	similarity to membrane steroid hormone-binding protein MSBP - Bos taurus	4e-25	S65181	hypothetical protein YPL170w - yeas	12.0	223.0	12.0	175.2	8e-47	04.05.01.04 transcriptional control
Pc22g07140	strong similarity to hypothetical protein An04g06070 - Aspergillus niger	0	0	0	12.0	162.0	12.0	217.4	0	0
Pc22g07310	strong similarity to hypothetical protein binA - Aspergillus nidulans	5e-21	ANI011295_1	gene: "binA"; product: "hypothetical p	237.4	3840.0	338.7	3996.3	0	0
Pc22g07350	strong similarity to hypothetical protein SPCC757.02c - Schizosaccharomyce	4e-49	T41593	hypothetical protein SPCC757.02c -	12.0	206.7	22.8	184.6	1e-137	11.01 stress response
Pc22g07370	strong similarity to hypothetical protein contig_1_168_scaffold_14.tfa_410wg	7e-30	NCB14A6_3	gene: "B14A6.030"; product: "probal	12.0	70.6	12.0	234.1	1e-108	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc22g07400	strong similarity to hypothetical 2-hydroxyhepta-2,4-diene-1,7-dioate isomeras	2.00E-51	BX897674_13	gene: "B2N18.140"; product: "conse	12.0	180.5	12.0	197.8	2e-85	01 METABOLISM
Pc22g09710	weak similarity to hypothetical protein PA1213 - Pseudomonas aeruginosa	1e-160	NCG15G9_2	gene: "G15G9.020"; product: "conse	47.5	1043.5	36.7	1180.6	0	0
Pc22g15280	hypothetical protein	0	0	0	162.8	1715.7	508.0	2631.8	0	0
Pc22g16820	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosa	8.00E-14	T40524	hypothetical protein SPBC530.08 - fi	12.0	222.6	12.0	131.7	2e-61	01.01.04 regulation of amino acid metabolism
Pc22g22960	strong similarity to hypothetical protein B2J23.80 - Neurospora crassa	6e-91	NCB2J23_8	gene: "B2J23.080"; product: "conser	155.8	898.3	177.8	1502.1	4e-61	01.01.10 amino acid degradation (catabolism)

Supplementary Table 10. K-mean cluster 2

@=Values given are the average of three independent experiments

orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels @				FunCat (auto)	
		p-value	Gene code	description	WIS - PAA	WIS + PAA	DS - PAA	DS + PAA	pval	category
Pc06g00650	strong similarity to hypothetical protein 1147_scaf	7e-43	AP005025_101	product: "putative hydrolase"; Streptomyces avermitilis genomic DNA,	222.1	488.9	431.0	1108.5	0	0
Pc06g01070	strong similarity to membrane protein Tpo2 - Sacc	1e-122	NCB19C19_12	gene: "B19C19.140"; product: "related to fluconazole resistance protei	12.0	57.7	25.5	62.0	5e-62	01.05.07 C-compound, carbohydrate transport
Pc06g01350	strong similarity to bifunctiona xylosidase-arabinos	3e-26	AE016937_194	product: "periplasmic beta-glucosidase precursor"; Bacteroides thetaic	14.1	48.3	14.9	22.1	1e-117	01.05.01.01 C-compound, carbohydrate catabolism
Pc06g01360	similarity to bifunctiona xylosidase-arabinosidase	1e-17	BFAF6658_1	product: "beta-glucosidase"; Bacteroides fragilis beta-glucosidase gen	15.1	64.7	12.9	25.6	7e-41	01.05.01.01 C-compound, carbohydrate catabolism
Pc06g01370	strong similarity to hypothetical membrane protein	1e-139	AY236409_1	gene: "mct"; product: "monocarboxylate transporter-like protein"; Emer	17.4	57.7	12.0	23.0	1e-42	01.04.07 phosphate transport
Pc08g00080	weak similarity to scytalone dehydratase - Pyricula	0	0	0	62.9	517.1	384.5	530.1	0	0
Pc12g03690	strong similarity to hypothetical protein contig_1_1	1e-94	A78767_1	unnamed ORF; Sequence 1 from Patent EP0565172.	70.7	455.4	151.6	108.6	6e-64	02.11 electron transport and membrane-associated energy conservation
Pc12g06820	strong similarity to hypothetical protein BAA10688.	8e-25	S76996	hypothetical protein - Synechocystis sp. (strain PCC 6803)	49.5	73.2	24.1	56.5	3e-38	04.05.01.04 transcriptional control
Pc12g09010	weak similarity to transcription factor Aro80 - Sacc	3e-27	S69704	hypothetical protein YDR421w - yeast (Saccharomyces cerevisiae)	24.0	83.2	49.3	128.8	1e-118	04.05.01.04 transcriptional control
Pc12g10830	strong similarity to cytochrome b5 - Mortierella alp	4e-38	NCB23L21_12	gene: "B23L21.190"; product: "probable cytochrome b5"; Neurospora	819.9	2287.4	816.9	2887.2	1e-30	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc12g10870	strong similarity to lanosterol 14 alpha-demethylas	0.0	AB030178_1	gene: "PDCYP51"; product: "cytochrome P-450 14DM"; Penicillium dig	136.6	252.5	86.2	188.2	1e-106	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc12g11110	strong similarity to beta-glucosidase 1 bgl1 - Aspe	0.0	AF029913_4	gene: "BGL1"; product: "beta glucosidase homolog"; Cochliobolus het	130.1	96.8	60.4	140.2	0.0	01.05.01.01 C-compound, carbohydrate catabolism
Pc12g11140	strong similarity to hypothetical protein SC8D11.1	3e-32	SCO939132_1	gene: "SCO7720"; "SC8D11.11"; product: "hypothetical protein SC8D1	12.0	69.0	13.3	81.7	0	0
Pc12g11950	strong similarity to hypothetical protein SPAC11D	2e-88	AE016865_237	product: "conserved hypothetical protein"; Pseudomonas syringae pv.	28.8	90.8	67.5	127.7	2e-76	99 UNCLASSIFIED PROTEINS
Pc12g11990	strong similarity to fluconazole resistance transpor	3e-79	UMPLOC_5	gene: "pig6"; product: "related to multidrug resistant protein"; Ustilago	54.3	172.2	63.1	214.5	1e-52	01.04.07 phosphate transport
Pc12g12000	similarity to zinc-finger transcription factor amdA -	6e-11	S61908	DNA-binding protein amdA - Emericella nidulans	35.5	74.4	40.1	53.7	3e-87	04 TRANSCRIPTION
Pc12g12010	weak similarity to hypothetical mll5689 - Mesorhiz	2e-23	AP006569_36	Gloeobacter violaceus PCC 7421 DNA, complete genome, section 2/1	274.3	751.7	737.6	1366.3	0	0
Pc12g12960	weak similarity to transcription factor Arg81 - Sacc	0	0	0	31.2	59.0	46.5	114.3	0	0
Pc12g13110	strong similarity to hypothetical protein SPAC227.	2e-35	NCB7H23_12	gene: "B7H23.120"; product: "conserved hypothetical protein"; Neuros	26.8	53.0	21.7	54.0	7e-44	01 METABOLISM
Pc12g13590	similarity to acid phosphatase PHO2 - Yarrowia lip	2e-22	S19993	acid phosphatase (EC 3.1.3.2) - yeast (Yarrowia lipolytica)	12.0	20.8	12.0	43.2	0	0
Pc12g13640	strong similarity to hypothetical conserved protein	1e-142	BX842634_4	gene: "B16B8.040"; product: "conserved hypothetical protein"; Neuros	36.5	96.6	54.4	154.8	1e-130	99 UNCLASSIFIED PROTEINS
Pc12g14890	strong similarity to fluconazole resistance protein F	1e-123	T41018	probable membrane transporter - fission yeast (Schizosaccharomyces	12.0	66.9	17.8	95.2	1e-58	01.05.07 C-compound, carbohydrate transport
Pc12g16010	hypothetical protein	0	0	0	18.6	68.5	36.2	56.3	0	0
Pc13g01890	strong similarity to acyl-CoA synthase like protein	1e-103	B83121	probable AMP-binding enzyme PA4198 [imported] - Pseudomonas aer	145.0	223.6	132.0	391.1	1e-115	01 METABOLISM
Pc13g04680	strong similarity to 7alpha-cephem-methoxylase s	1e-45	AP005958_178	gene: "bll6449"; Bradyrhizobium japonicum USDA 110 DNA, complete	93.5	190.3	178.5	249.5	0	0
Pc13g04990	strong similarity to hypothetical protein contig31_p	3e-12	AK051230_1	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-lengt	43.5	87.6	77.4	102.6	2e-47	13.05 cell motility
Pc13g07240	similarity to p-nitrobenzyl esterase pnbA - Bacillus	5e-77	T41347	probable carboxylesterase-lipase family member - fission yeast (Schiz	16.0	64.0	12.0	70.5	1e-113	13 REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT
Pc13g07540	similarity to subunit 13 of glutathione S-transferas	1e-52	NCB7K22_4	gene: "B7K22.040"; product: "related to glutahione s-transferase subu	105.4	281.5	148.5	726.9	1e-87	01 METABOLISM
Pc13g08560	strong similarity to hypothetical protein An14g028	0	0	0	12.1	38.5	31.8	20.4	0	0
Pc13g10520	strong similarity to hypothetical protein yraM - Bac	2e-82	BX842653_296	product: "conserved hypothetical protein"; Bdellovibrio bacteriovorus c	42.7	74.9	43.2	87.1	1e-159	99 UNCLASSIFIED PROTEINS
Pc13g10810	strong similarity to acetoacetyl-CoA synthase acs	0.0	BX649605_63	product: "acetoacetyl-coa synthetase, putative"; Aspergillus fumigatus	108.2	224.2	213.9	409.9	1e-157	01 METABOLISM
Pc13g10880	hypothetical protein	0	0	0	12.0	133.9	14.2	37.0	0	0
Pc13g10910	strong similarity to hypothetical protein An08g0401	0	0	0	56.3	170.2	82.4	126.8	0	0
Pc13g11150	similarity to protein PRIB - Lentinus edodes	2e-11	PRIB_LENED	PRIB PROTEIN.	12.7	81.1	29.5	67.7	0	0
Pc13g11540	strong similarity to hypothetical oxidoreductase of	1e-39	AY458641_40	product: "oxidoreductase, short-chain dehydrogenase/reductase family	12.0	80.7	13.2	12.8	6e-58	01 METABOLISM
Pc13g11580	strong similarity to hypothetical protein contig46_p	6e-87	BX649606_31	product: "epoxide hydrolase, putative"; Aspergillus fumigatus BAC pilot	120.4	326.9	112.0	458.3	4e-66	01 METABOLISM
Pc13g11590	similarity to hypothetical protein SPCC1393.04 - S	1e-10	T40952	hypothetical protein SPCC1393.04 - fission yeast (Schizosaccharomyc	48.5	133.4	39.5	98.1	0	0
Pc13g11860	strong similarity to androgen-inducible aldehyde r	1e-166	BX649606_86	product: "aflatoxin b1 aldehyde reductase-like protein, putative"; Asper	131.9	282.7	255.7	271.0	4e-82	01 METABOLISM
Pc13g12110	strong similarity to hypothetical protein AAO49461	0.0	BX649606_68	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot project	75.1	153.5	134.6	175.8	0	0
Pc13g13030	strong similarity to nonsense mRNA-reducing prot	9e-24	AE014829_55	product: "regulator of nonsense transcripts, putative"; Plasmodium falc	12.0	17.1	12.0	25.3	1e-108	03.03.01 mitotic cell cycle and cell cycle control
Pc13g15930	similarity to hypothetical transcription regulator SP	6e-09	ENU56097_1	gene: "facB"; product: "acetate regulatory DNA binding protein FacB";	34.4	149.9	22.8	165.3	1e-114	01.01.04 regulation of amino acid metabolism
Pc13g15940	strong similarity to copper amine oxidase AO-I - As	0.0	AF362473_1	product: "copper amine oxidase"; Aspergillus niger strain AKU 3302 c	200.0	365.7	98.4	195.5	0.0	01 METABOLISM
Pc13g15950	strong similarity to choline permease Hnm1 - Sacc	1e-59	S11175	choline transport protein - yeast (Saccharomyces cerevisiae)	12.0	62.2	12.0	34.1	4e-78	01.01.07 amino acid transport
Pc16g00500	strong similarity to hypothetical membrane protein	1e-43	NC64C2_19	gene: "64C2.200"; product: "related to PUTATIVE TARTRATE TRANS	33.5	70.5	178.1	716.8	0.0	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS
Pc16g00610	strong similarity to hypothetical membrane protein	4e-91	CNS07TIX_2	DNA centromeric region sequence from BAC DP15B03, DP38F06 of c	55.3	122.1	220.2	656.8	2e-71	01.01.07 amino acid transport
Pc16g00790	similarity to hypothetical transcription activator SP	2e-45	BX842620_25	gene: "B11E5.250"; product: "conserved hypothetical protein"; Neuros	35.2	89.0	53.8	98.2	1e-86	01.01.04 regulation of amino acid metabolism
Pc16g00830	similarity to hypothetical protein contig_1_108_sc	0	0	0	12.0	62.1	27.3	13.7	0	0
Pc16g00840	similarity to O-methyltransferase A omtA - Aspergil	2e-13	BX908810_7	gene: "G3C5.070"; product: "related to O-methyltransferase"; Neurosp	35.3	121.2	83.0	86.1	3e-46	01.20 secondary metabolism
Pc16g00860	similarity to hypothetical protein contig17.tfa_50cg	0	0	0	58.4	186.0	118.5	164.4	0	0
Pc16g02950	strong similarity to aryl-alcohol oxidase precursor	4e-76	CNS07TIX_17	DNA centromeric region sequence from BAC DP15B03, DP38F06 of c	19.2	22.1	18.7	45.5	0.0	02.11 electron transport and membrane-associated energy conservation
Pc16g04300	hypothetical protein	0	0	0	285.2	754.2	547.6	809.9	0	0
Pc16g04830	strong similarity to pyridoxine 4-dehydrogenase P	6e-70	T39218	pyridoxal reductase - fission yeast (Schizosaccharomyces pombe)	12.0	24.4	24.6	34.6	4e-82	01.05.01.01.01 sugar, glucoside, polyol and carboxylate catabolism
Pc16g05120	weak similarity to hypothetical protein attM - Agro	4e-08	AY052389_4	gene: "attM/aiiB"; product: "AttM/AiiB"; Agrobacterium tumefaciens AttJ	165.6	187.7	136.6	276.5	0	0
Pc16g05680	strong similarity to alpha-L-arabinofuranosidase a	2e-95	G72395	alpha-L-arabinofuranosidase - Thermotoga maritima (strain MSB8)	112.9	128.1	38.3	198.5	0.0	01.05.01.01 C-compound, carbohydrate catabolism
Pc16g06760	strong similarity to hypothetical protein SC5H1.34	1e-45	T35350	hypothetical protein SC5H1.34 - Streptomyces coelicolor	27.4	115.5	57.9	124.7	5e-33	01.02 nitrogen and sulfur metabolism
Pc16g06970	strong similarity to short-chain alcohol dehydroger	1e-28	APU76621_1	gene: "adhA"; product: "short-chain alcohol dehydrogenase"; Aspergill	21.8	27.5	23.7	60.2	3e-58	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc16g08590	similarity to NAD+-dependent 15-hydroxyprostagl	4e-22	CNS09S4S_94	DNA centromeric region sequence from BAC DP26B06, DP34F04, DP	51.3	81.4	33.7	75.8	1e-65	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc16g09230	strong similarity to urease URE1 - Cryptococcus n	0.0	U81509_1	gene: "URE"; product: "urease"; Coccidioides immitis urease (URE) ge	39.0	188.6	47.9	193.4	0.0	01.01.01.03.01 urea cycle
Pc16g10090	strong similarity to cytosine deaminase FCA1 - Ca	1e-46	AJ616007_1	gene: "fca1"; product: "putative cytosine deaminase"; Candida albican	75.2	152.8	154.6	294.6	1e-31	01.02 nitrogen and sulfur metabolism
Pc16g10640	weak similarity to transcription factor Arg81 - Sacc	8e-08	S49627	regulatory protein ARGR2 - yeast (Saccharomyces cerevisiae)	25.2	64.0	54.8	131.0	0.0	01.01.04 regulation of amino acid metabolism
Pc16g11760	weak similarity to hypothetical transcription regula	2e-04	T37601	probable trancription factor - fission yeast (Schizosaccharomyces pom	92.4	197.9	187.7	217.1	2e-60	01.01.04 regulation of amino acid metabolism
Pc16g11770	strong similarity to choline monooxygenase like pr	3e-27	BX248345_40	gene: "Mb3186c"; product: "POSSIBLE DIOXYGENASE"; Mycobacteri	45.0	125.6	56.9	89.8	1e-148	01.20.17.03 biosynthesis of amines
Pc16g12280	strong similarity to membrane protein Tpo2 - Sacc	0.0	BX649607_11	gene: "mdR"; product: "mfs-family multidrug resistance protein, putative	37.5	291.2	163.4	364.0	2e-63	01.05.07 C-compound, carbohydrate transport
Pc16g12810	strong similarity to hypothetical protein CAC28784	6e-76	BX649607_60	product: "hypothetical protein, conserved"; Aspergillus fumigatus BAC	561.7	691.9	537.3	1168.0	0	0
Pc16g13180	strong similarity to L-galactonolactone oxidase Alo	2e-90	AF031228_1	gene: "ALO"; product: "D-arabinono-1,4-lactone oxidase"; Candida alb	35.1	99.5	58.8	94.0	1e-171	01.05.01 C-compound and carbohydrate utilization
Pc16g13370	similarity to hypothetical protein contig_1_13_scaf	2e-04	AC115684_23	product: "hypothetical protein"; Dictyostelium discoideum chromosome	23.7	70.3	42.4	71.4	0	0
Pc16g13490	strong similarity to short branched chain specific a	1e-121	HSM803134_1	gene: "DKFZp451K202"; product: "hypothetical protein"; Homo sapien	301.5	432.9	290.4	744.8	1e-138	01.01.10.04 degradation of amino acids of the pyruvate family
Pc16g13540	similarity to positive regulator of purine utilisation	4e-30	S54779	purine utilization positive regulator - Emericella nidulans	12.0	39.3	12.0	46.8	1e-100	01.01.04 regulation of amino acid metabolism
Pc17g00430	weak similarity to hypothetical membrane protein	0	0	0	184.8	562.3	238.2	264.8	0	0
Pc17g00440	weak similarity to retrotransposon Tto1 - Nicotian	1e-145	T02206	hypothetical protein - common tobacco retrotransposon Tto1	38.7	309.2	32.6	113.1	0.0	10.01.01 unspecified signal transduction
Pc17g00590	strong similarity to retrotransposon Tto1 - Nicotian	1e-140	T02206	hypothetical protein - common tobacco retrotransposon Tto1	65.5	470.5	45.4	153.2	0.0	10.01.01 unspecified signal transduction
Pc17g00590	strong similarity to retrotransposon Tto1 - Nicotian	1e-140	T02206	hypothetical protein - common tobacco retrotransposon Tto1	65.5	470.5	45.4	153.2	0.0	10.01.01 unspecified signal transduction
Pc18g00150	strong similarity to high affinity glucose transporte	3e-38	AF136235_1	gene: "asd-3"; product: "ascus development protein 3"; Neurospora cr	39.1	113.2	117.6	68.9	9e-76	01.05.07 C-compound, carbohydrate transport
Pc18g00160	strong similarity to hypothetical protein 1357_scaf	0	0	0	37.9	92.3	62.7	62.3	0	0
Pc18g00500	strong similarity to hypothetical protein contig336.	4e-99	BX842620_43	gene: "B11E5.430"; product: "related to dihydrodipicolinate synthase";	70.5	114.4	68.1	149.5	9e-92	01.01.01.07.06 biosynthesis of lysine
Pc18g02660	strong similarity to hypothetical protein An18g040	0	0	0	17.6	39.5	21.4	17.2	0	0
Pc18g02670	strong similarity to salicylaldehyde dehydrogenas	5e-96	ACPCAOP_34	gene: "hcaB"; product: "vanillin dehydrogenase"; Acinetobacter sp. AD	143.3	374.7	102.8	332.4	0.0	01.05 C-compound and carbohydrate metabolism
Pc18g03010	strong similarity to choline permease Hnm1 - Sacc	1e-75	S11175	choline transport protein - yeast (Saccharomyces cerevisiae)	60.3	125.0	36.8	75.2	2e-75	01.01 amino acid metabolism
Pc18g05670	strong similarity to hypothetical protein SPCC16A1	2e-23	T41080	hypothetical protein SPCC16A11.07 - fission yeast (Schizosaccharomy	58.1	92.4	51.6	113.1	7e-44	04.05.01.04 transcriptional control

Pc18g05780	strong similarity to multidrug resistance protein fnx	9e-79	T40380	major facilitator family transporter - fission yeast (Schizosaccharomyce	101.4	283.6	218.6	530.3	1e-49	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc18g06290	strong similarity to hypothetical NADPH dehydroge	1e-104	BX908808_9	gene: "G21B4.090"; product: "probable NADPH2 dehydrogenase chair	12.1	45.6	26.0	65.1	3e-81	01.20 secondary metabolism	
Pc19g00090	weak similarity to retrotransposon Tto1 - Nicotiana	1e-125	T02206	hypothetical protein - common tobacco retrotransposon Tto1	13.6	29.3	13.1	16.2	0.0	10.01.01 unspecified signal transduction	
Pc19g00550	strong similarity to cutinase transcription factor bet	1e-56	CT1B_FUSSO	CUTINASE TRANSCRIPTION FACTOR 1 BETA.	226.3	450.3	165.4	332.6	9e-68	01.01.04 regulation of amino acid metabolism	
Pc20g00130	strong similarity to myo-inositol transport protein Itı	1e-141	NCB17B1_7	gene: "B17B1.070"; product: "related to myo-inositol transporter"; Neu	168.2	567.6	149.7	679.4	2e-72	01.05.07 C-compound, carbohydrate transport	
Pc20g01500	strong similarity to 2,3-dihydroxybenzoic acid deca	1e-69	AF2887	conserved hypothetical protein Atu2529 [imported] - Agrobacterium tum	76.3	292.0	224.7	280.1	1e-133	99 UNCLASSIFIED PROTEINS	
Pc20g01980	strong similarity to phenol 2-monooxygenase - Tric	1e-132	AY450844_1	product: "m-hydroxybenzoate hydroxylase"; Comamonas testosteroni m	12.0	60.6	12.4	79.5	2e-92	01.01.10.05.07 degradation of tryptophan	
Pc20g02630	strong similarity to Gly-X carboxypeptidase precurs	5e-85	SCCPS1_1	gene: "CPS1"; product: "carboxypeptidase s"; S.cerevisiae CPS1 gene	17.8	38.4	21.0	104.5	1e-48	01.01 amino acid metabolism	
Pc20g04510	similarity to multidrug resistance protein Hol1 - Sac	2e-39	T39346	probable major facilitator family multi-drug resistance protein - fission y	12.0	43.5	12.0	41.7	3e-47	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc20g06080	strong similarity to hypothetical protein An02g114(	0.0	NCB19A17_11	gene: "B19A17.110"; product: "hypothetical protein"; Neurospora crass	219.6	230.2	150.0	374.1	0		0
Pc20g06140	strong similarity to hypothetical protein An02g1132	1e-108	NCB19A17_12	gene: "B19A17.120"; product: "hypothetical protein"; Neurospora crass	203.1	271.4	111.2	630.0	5e-86	01.03 nucleotide metabolism	
Pc20g06200	strong similarity to hypothetical membrane protein	1e-118	S50361	probable membrane protein YIL166c - yeast (Saccharomyces cerevisia	12.0	25.6	95.6	525.6	2e-99	01.01.04 regulation of amino acid metabolism	
Pc20g06650	hypothetical protein	0	0	0	136.4	162.0	113.6	281.5	0		0
Pc20g07520	similarity to hypothetical protein An01g15120 - Asp	2e-04	BX649605_78	product: "hypothetical protein, conserved"; Aspergillus fumigatus BAC	127.2	105.9	88.0	242.1	0		0
Pc20g08300	strong similarity to hypothetical protein 12F11.200	5e-59	NC12F11_20	gene: "12F11.200"; product: "hypothetical protein"; Neurospora crassa	51.2	76.8	72.3	150.1	0		0
Pc20g08400	similarity to hypothetical transcriptional regulator F	2e-12	AF057038_1	gene: "FCR1"; product: "zinc cluster transcription factor Fcr1p"; Candic	26.4	63.4	58.0	95.1	6e-19	01.01.04 regulation of amino acid metabolism	
Pc20g08470	strong similarity to protease Mch5 - Saccharomyce	8e-65	NCB23B10_3	gene: "B23B10.030"; product: "related to monocarboxylate transporter"	21.2	64.9	77.5	239.3	1e-112	01 METABOLISM	
Pc20g10520	similarity to hypothetical protein An12g07270 - Asp	0	0	0	12.0	22.2	13.7	29.6	0		0
Pc20g12910	strong similarity to hypothetical protein An08g1215	0	0	0	25.2	63.0	45.6	34.4	0		0
Pc20g14130	strong similarity to hypothetical protein 1160_scaff	1e-156	AP004600_12	gene: "OB2083"; product: "hypothetical conserved protein"; Oceanoba	111.0	124.2	84.3	186.4	1e-68	01.05 C-compound and carbohydrate metabolism	
Pc20g14390	strong similarity to mitochondrial phosphate transp	1e-97	S50556	hypothetical protein YER053c - yeast (Saccharomyces cerevisiae)	12.0	65.9	35.6	233.5	1e-87	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g01650	strong similarity to hypothetical conserved protein	1e-22	E82998	conserved hypothetical protein PA5185 [imported] - Pseudomonas aeru	97.4	132.5	117.5	237.4	0		0
Pc21g02160	weak similarity to TRAF5 - Mus musculus	4e-31	NCB23E9_9	gene: "B23E9.090"; product: "related to traf5 protein"; Neurospora cra	83.7	159.1	81.4	177.5	6e-81	04.05.01.04 transcriptional control	
Pc21g03190	strong similarity to hydroxypyruvate dehydrogenas	6e-72	BX649606_114	product: "glycerate dehydrogenase, putative"; Aspergillus fumigatus B	93.1	111.2	72.9	189.5	1e-100	01 METABOLISM	
Pc21g04410	strong similarity to glucose 1-dehydrogenase gdhI	9e-47	TACID3_96	gene: "Ta0747"; product: "glucose 1-dehydrogenase related protein";	12.0	13.7	12.0	27.8	6e-63	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g05110	strong similarity to hypothetical protein contig_1_5	4e-79	T49756	related to berberine bridge enzyme [imported] - Neurospora crassa	27.0	207.9	151.1	66.5	1e-100	01.05.01 C-compound and carbohydrate utilization	
Pc21g05550	strong similarity to multidrug resistance protein fnx	5e-70	NCB13O8_14	gene: "B13O8.150"; product: "conserved hypothetical protein"; Neuros	42.6	156.1	45.0	104.4	5e-50	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc21g05750	strong similarity to fatty acid regulation protein like	8e-49	NCB9B15_9	gene: "B9B15.090"; product: "conserved hypothetical protein"; Neuros	901.2	2504.4	1322.7	3172.5	2e-76	01.06.10 regulation of lipid, fatty-acid and isoprenoid metabolism	
Pc21g05850	strong similarity to allantoate permease Dal5 - Sac	1e-84	T41604	probable membrane transport protein - fission yeast (Schizosaccharom	21.9	100.6	127.3	554.3	1e-104	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS	
Pc21g06300	strong similarity to hypothetical protein contig5_pa	3e-84	BX908808_19	gene: "G21B4.190"; product: "related to NADPH2 quinone reductase";	111.9	515.6	233.5	1088.0	9e-74	01 METABOLISM	
Pc21g06670	strong similarity to carboxypeptidase S1 - Penicilliu	4e-85	AF394242_1	gene: "cpl"; product: "carboxypeptidase S1"; Aspergillus oryzae strain T	53.3	52.0	30.5	170.3	1e-105	06.07 protein modification	
Pc21g07740	similarity to beta-ketoacyl reductase rhlG - Pseudo	1e-48	NCB23B10_7	gene: "B23B10.070"; product: "related to gluconate 5-dehydrogenase";	143.5	317.3	240.3	541.0	8e-67	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g07900	strong similarity to hypothetical protein contig_1_1	0	0	0	295.9	504.4	292.6	594.1	0		0
Pc21g08400	strong similarity to 3-hydroxyisobutyryl-coenzyme	1e-137	NCB18D24_21	gene: "B18D24.230"; product: "related to enoyl-CoA-hydratase"; Neur	92.2	206.2	88.2	379.8	1e-111	01 METABOLISM	
Pc21g08920	strong similarity to norsolorinic acid reductase nor	1e-119	AP24698_1	gene: "nor"; product: "norsolorinic acid reductase"; Aspergillus parasiti	78.1	294.0	333.2	414.6	8e-88	01.01.10 amino acid degradation (catabolism)	
Pc21g10100	weak similarity to glutathione S-transferase omega	3e-11	TCTCAC2X_1	product: "TcAc2"; Trypanosoma cruzi stress and GST superfamily rela	131.1	637.8	260.2	1015.8	4e-41	03.01.05.01 DNA repair	
Pc21g12380	strong similarity to hypothetical neutral amino acid	2e-66	S47892	neutral amino acid permease - Neurospora crassa	33.2	74.7	56.8	133.9	2e-67	01.01.07 amino acid transport	
Pc21g13520	weak similarity to hypothetical protein YKL051w -	4e-43	NCB2F7_3	gene: "B2F7.030"; product: "conserved hypothetical protein"; Neurosp	123.3	272.4	136.5	167.6	0		0
Pc21g14050	strong similarity to mannase man1 - Aspergillus ac	1e-140	AAMANNA_1	gene: "man1"; product: "mannanase"; Aspergillus aculeatus mannanas	56.7	48.2	35.7	77.0	1e-123	01.05 C-compound and carbohydrate metabolism	
Pc21g14230	strong similarity to hypothetical nadh-dependent fl	5e-89	T39956	probable nadh-dependent flavin oxidoreductase - fission yeast (Schizo	74.5	266.9	249.7	775.7	0		0
Pc21g14260	strong similarity to high-affinity nicotinic acid perm	1e-120	SPBC1683_12	gene: "SPBC1683.12"; Schizosaccharomyces pombe cosmids c1683.	43.6	88.4	407.3	1042.9	1e-84	01.01.10 amino acid degradation (catabolism)	
Pc21g14270	similarity to hypothetical transcription regulator SP	2e-16	T40521	hypothetical protein SPBC530.05 - fission yeast (Schizosaccharomyce	67.2	256.1	91.8	245.5	8e-91	01.01.04 regulation of amino acid metabolism	
Pc21g14290	strong similarity to hypothetical protein An12g073(	0	0	0	12.0	23.2	12.0	36.6	0		0
Pc21g14380	similarity to hypothetical protein SPBC31F10.02 -	3e-22	NC18F11_2	gene: "18F11.015"; product: "conserved hypothetical protein"; Neuros	168.2	370.3	196.8	370.7	8e-40	47.03.01.01.01.99 other brain areas	
Pc21g14740	similarity to hypothetical intracellular protease ami	3e-17	G87469	ThiJ/PfpI family protein [imported] - Caulobacter crescentus	30.6	82.0	35.4	96.9	0		0
Pc21g16710	weak similarity to hypothetical protein DR0703 - D	7e-10	H69851	hypothetical protein yjlB - Bacillus subtilis	22.2	72.7	14.7	63.0	3e-53	99 UNCLASSIFIED PROTEINS	
Pc21g17040	weak similarity to beta transducin-like protein het-	5e-05	AF323585_1	gene: "het-d"; product: "beta transducin-like protein HET-D2Y"; Podos	89.4	176.1	68.5	409.3	0		0
Pc21g19280	strong similarity to 25D9-5p - Aspergillus fumigatu	1e-89	AY080962_7	gene: "25d9-5"; product: "25D9-5p"; Aspergillus fumigatus Mvp1p (25d	43.9	139.3	27.8	160.0	0		0
Pc21g20580	strong similarity to Fe(II)-dependent sulfonate alph	7e-55	S50963	hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae)	164.1	192.9	142.1	717.9	1e-152	11.07.01 detoxification involving cytochrome P450	
Pc21g20650	strong similarity to 4-coumarate-CoA ligase 4CL -	5e-81	AP005036_223	product: "putative 4-coumarate:CoA ligase"; Streptomyces avermitilis g	72.6	62.9	52.6	123.1	1e-125	01 METABOLISM	
Pc21g20890	strong similarity to NADPH cytochrome P450 oxid	0.0	AX684154_1	Sequence 5 from Patent WO0246386.	912.0	2551.3	626.1	2715.6	0.0	01.02.01.07 nitric oxide biosynthesis	
Pc21g21340	similarity to hypothetical protein alr1138 - Nostoc s	2e-17	AG1948	hypothetical protein alr1138 [imported] - Nostoc sp. (strain PCC 7120)	12.1	51.8	12.0	23.1	0		0
Pc21g21350	weak similarity to hypothetical conserved protein F	2e-28	NC5F3_10	gene: "5F3.100"; product: "conserved hypothetical protein"; Neurospo	127.1	741.5	585.0	1037.2	0		0
Pc21g23440	strong similarity to hypothetical aminotransferase	1e-144	BX897674_17	gene: "B2N18.180"; product: "conserved hypothetical protein"; Neuros	201.0	388.1	66.6	213.0	1e-133	01.01 amino acid metabolism	
Pc21g23730	strong similarity to feruloyl-CoA synthase like prot	0.0	CNS07TIX_8	DNA centromeric region sequence from BAC DP15B03, DP38F06 of cl	36.7	81.0	52.3	129.8	1e-143	01 METABOLISM	
Pc22g00060	similarity to fructosyl amine oxygen oxidoreductase	1e-174	AB035128_1	gene: "soxC"; product: "sarcosine oxidase"; Cylindrocarpon didymum s	93.9	177.6	137.9	334.2	1e-100	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g00110	strong similarity to hypothetical oxidoreductase SF	1e-105	AB119281_1	Alternaria alternata AMT2 gene for aldo-keto reductase, complete	100.5	99.2	28.9	532.6	5e-87	01.01.10 amino acid degradation (catabolism)	
Pc22g00130	strong similarity to hypothetical protein 1110_scaff	1e-50	BX842620_43	gene: "B11E5.430"; product: "related to dihydrodipicolinate synthase";	25.4	96.0	34.0	125.4	4e-83	01.01.01.07.06 biosynthesis of lysine	
Pc22g00140	strong similarity to exo-alpha-sialidase - Micromon	1e-97	A45244	exo-alpha-sialidase (EC 3.2.1.18) - Micromonospora viridifaciens	12.9	72.6	16.6	74.4	1e-137	01.05 C-compound and carbohydrate metabolism	
Pc22g00270	strong similarity to transcription activator Put3 - Sa	3e-27	A39792	transcription activator PUT3 - yeast (Saccharomyces cerevisiae)	99.3	208.8	140.7	337.3	1e-92	01.01.04 regulation of amino acid metabolism	
Pc22g01120	strong similarity to hypothetical protein PA2326 - F	1e-132	A83356	hypothetical protein PA2326 [imported] - Pseudomonas aeruginosa (st	71.3	131.8	135.5	830.8	3e-51	01.05.07 C-compound, carbohydrate transport	
Pc22g01340	strong similarity to D-arabinitol 2-dehydrogenase	1e-37	D70635	hypothetical protein Rv1928c - Mycobacterium tuberculosis (strain H37	12.0	31.5	13.3	28.6	3e-64	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g01530	strong similarity to hypothetical protein YAL049c -	4e-53	AY465528_1	product: "dienelactone hydrolase"; Chaetomium globosum dienelacton	234.0	787.2	740.1	845.0	2e-68	98 CLASSIFICATION NOT YET CLEAR-CUT	
Pc22g01540	strong similarity to hypothetical protein SPBC3B8.	1e-125	CNS09S4S_72	DNA centromeric region sequence from BAC DP26B06, DP34F04, DP	447.3	654.3	176.2	454.6	8e-90	02.13 respiration	
Pc22g01660	similarity to uroporphyrinogen-III synthase Hem4 -	1e-52	CNS09S4S_38	DNA centromeric region sequence from BAC DP26B06, DP34F04, DP	30.9	32.3	17.0	49.6	4e-92	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	
Pc22g02620	strong similarity to monoglyceride lipase mgll - Mu	6e-52	NC7F4_20	gene: "7F4.210"; product: "conserved hypothetical protein"; Neurospo	71.7	119.1	89.4	238.3	9e-41	01.05.01.01.09 aerobic aromate catabolism	
Pc22g02720	weak similarity to hypothetical conserved protein \	6e-61	NC104H10_16	gene: "104H10.140"; product: "hypothetical protein"; Neurospora crass	29.9	26.7	21.9	45.9	0		0
Pc22g03710	strong similarity to hypothetical membrane protein	1e-168	NCB8P8_18	gene: "B8P8.200"; product: "related to dityrosine transporter"; Neurosp	14.3	49.7	26.5	82.4	3e-59	01.05.07 C-compound, carbohydrate transport	
Pc22g03940	strong similarity to Succinyl CoA: 3-oxoacid CoA tr	1e-155	BT008292_1	product: "Homo sapiens 3-oxoacid CoA transferase"; Synthetic constr	204.4	897.9	170.5	775.0	0.0	01 METABOLISM	
Pc22g04190	similarity to protein Mog1 - Saccharomyces cerevi	6e-05	S57093	hypothetical protein YJR074w - yeast (Saccharomyces cerevisiae)	35.4	48.6	35.0	75.5	5e-13	06.04 protein targeting, sorting and translocation	
Pc22g05400	strong similarity to hypothetical monocarboxylate p	4e-76	S38065	hypothetical protein YKL221w - yeast (Saccharomyces cerevisiae)	22.7	89.1	67.2	266.8	0		0
Pc22g06010	similarity to hypothetical protein YBR151w - Sacch	7e-21	S46022	hypothetical protein YBR151w - yeast (Saccharomyces cerevisiae)	39.9	74.6	42.9	96.4	7e-15	01.05 C-compound and carbohydrate metabolism	
Pc22g06830	similarity to inhibitor of endosome-lysosome fusion	4e-16	AP005027_159	product: "putative dimethylmenaquinone methyltransferase family prote	33.2	56.6	22.2	90.6	6e-81	99 UNCLASSIFIED PROTEINS	
Pc22g07330	strong similarity to hypothetical protein An16g066	2e-09	AF230811_1	gene: "PIG1"; product: "putative transcription factor Pig1p"; Pyricularia	131.8	309.5	103.9	296.7	6e-96	04.05.01.04 transcriptional control	
Pc22g07440	strong similarity to benzoate 4-monooxygenase cy	1e-154	NCB14A6_3	gene: "B14A6.030"; product: "probable benzoate 4-monooxygenase cy	25.9	76.4	57.9	88.0	1e-101	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc22g09840	strong similarity to cytochrome P450 monooxygen	4e-92	T49413	probable cytochrome P450 monooxygenase (lovA) [imported] - Neuros	20.6	63.6	46.8	57.5	5e-84	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc22g12250	strong similarity to NADPH-ferrihemoprotein reduc	1e-179	NCB9B15_10	gene: "B9B15.100"; product: "conserved hypothetical protein"; Neuros	86.3	107.8	46.5	128.6	1e-178	01.02.01.07 nitric oxide biosynthesis	
Pc22g14620	hypothetical protein	0	0	0	123.7	332.3	296.4	261.7	0		0
Pc22g15030	strong similarity to peroxisomal 2,4-dienoyl-CoA re	2e-67	S50729	sporulation protein SPS19 - yeast (Saccharomyces cerevisiae)	428.2	555.9	388.4	813.7	1e-67	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g15050	hypothetical protein	0	0	0	45.5	93.8	81.3	58.9	0		0
Pc22g15140	weak similarity to hypothetical protein SPAC57A7.	7e-39	T38949	hypothetical protein SPAC57A7.05 - fission yeast (Schizosaccharomyc	68.4	188.1	88.7	281.0	0		0
Pc22g15300	similarity to hypothetical scaffold protein CG6385	5e-40	AF329477_2	gene: "dmg"; product: "N,N-dimethylglycine oxidase"; Arthrobacter glob	18.8	30.6	39.4	153.0	1e-66	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc22g15370	similarity to regulator protein Ppr1 - Saccharomyce	1e-12	RGBYP1	regulatory protein PPR1 - yeast (Saccharomyces cerevisiae)	12.5	40.8	16.1	49.2	7e-86	01.01.04 regulation of amino acid metabolism	
Pc22g15690	strong similarity to O-methylsterigmatocystin oxido	1e-130	AF017151_1	gene: "ordA"; product: "oxidoreductase"; Aspergillus parasiticus oxidore	110.8	280.6	221.7	389.3	1e-113	01.20 secondary metabolism	

Pc22g15710	similarity to hypothetical protein An08g08410 - Asp	0	0	0	24.4	66.0	62.6	91.6	0		0
Pc22g16060	strong similarity to UDP-glucose:dolichyl-phospha	1e-142	T44819	dolichyl-phosphate beta-glucosyltransferase (EC 2.4.1.117) [imported]	92.4	169.3	84.2	287.0	2e-85	01 METABOLISM	
Pc22g17060	strong similarity to hypothetical protein An12g104	0	0	0	46.3	50.9	27.5	59.7	0		0
Pc22g17250	strong similarity to hypothetical protein mg02084.1	2e-32	D86873	dehydrogenase [imported] - Lactococcus lactis subsp. lactis (strain IL1	85.3	163.0	131.0	277.1	1e-104	01 METABOLISM	
Pc22g17810	weak similarity to hypothetical protein yciI - Esche	4e-19	NC20H10_30	gene: "20H10.300"; product: "conserved hypothetical protein"; Neuros	280.3	840.9	455.9	1365.2	0		0
Pc22g18380	strong similarity to salicylate hydroxylase nahG - F	2e-35	AP005214_117	product: "putative salicylate hydroxylase"; Corynebacterium efficiens Y	14.5	40.3	38.9	69.7	2e-85	01.01.10 amino acid degradation (catabolism)	
Pc22g19410	weak similarity to hypothetical protein YJR154w -	4e-89	SCO939129_2	gene: "SCO6985"; "SC8F11.11c"; product: "hypothetical protein SC8F	15.1	20.6	12.0	29.0	0		0
Pc22g20490	strong similarity to cinnamyl-alcohol dehydrogenas	5e-77	NCB23E9_11	gene: "B23E9.110"; product: "conserved hypothetical protein"; Neuros	158.3	368.5	291.4	357.4	5e-52	01.03 nucleotide metabolism	
Pc22g21310	weak similarity to hypothetical protein 192_scaffol	0	0	0	15.5	149.1	113.6	269.2	0		0
Pc22g22590	similarity to alcohol dehydrogenase pan2 - Mus m	8e-18	BC063926_1	gene: "MGC76232"; product: "MGC76232 protein"; Xenopus tropicalis	17.3	71.7	54.2	44.7	3e-56	01 METABOLISM	
Pc22g24570	similarity to putative integral membrane protein CA	5e-71	BX908810_10	gene: "G3C5.100"; product: "related to integral membrane protein PTH	16.6	16.3	12.6	48.0	0		0
Pc22g24790	similarity to cutinase transcription factor alpha CT	3e-30	T50198	probable transcription activator protein [imported] - fission yeast (Schiz	51.1	120.9	73.1	91.0	1e-126	01.01.04 regulation of amino acid metabolism	
Pc22g25120	strong similarity to hypothetical protein 1141_scaf	7e-67	BX572594_63	product: "probable enoyl CoA-hydratase/isomerase"; Rhodopseudomo	12.0	20.1	14.8	38.2	1e-71	01 METABOLISM	
Pc22g26000	weak similarity to retrotransposon Tto1 - Nicotian	7e-61	S04273	retrovirus-related reverse transcriptase homolog - common tobacco ret	19.3	59.6	33.8	38.2	0.0	10.01.01 unspecified signal transduction	
Pc22g26000	weak similarity to retrotransposon Tto1 - Nicotian	7e-61	S04273	retrovirus-related reverse transcriptase homolog - common tobacco ret	19.3	59.6	33.8	38.2	0.0	10.01.01 unspecified signal transduction	
Pc24g03100	weak similarity to retrotransposon Tto1 - Nicotian	1e-137	T02206	hypothetical protein - common tobacco retrotransposon Tto1	89.6	230.0	83.8	95.1	0.0	10.01.01 unspecified signal transduction	

Supplementary Table 11. K-mean cluster 3

@=Values given are the average of three independent experiments

orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels @				FunCat (auto)	
		p-value	Gene code	description	WIS - PAA	WIS + PAA	DS - PAA	DS + PAA	pval	category
Pc06g00690	hypothetical protein	7e-04	AB069670_	product: "envelope glycoprotein precursor"; Crimean-Congo her	12.0	20.8	72.9	120.5	0	0
Pc06g01340	strong similarity to high affinity glucose transporter HGT1 - Kluyveromyces lactis	6e-59	AY081846_	gene: "mstB"; product: "putative sugar transporter"; Aspergillus	12.0	73.6	12.0	12.0	2e-69	01.05.04 regulation of C-compound and carbohydrate utilization
Pc06g01480	strong similarity to maltose transport protein Mal31 - Saccharomyces cerevisiae	1e-82	NC5E6_16	gene: "5E6.180"; product: "probable alpha-glucoside transport p	579.9	991.6	458.9	1161.1	3e-82	01.05.07 C-compound, carbohydrate transport
Pc06g01670	strong similarity to hypothetical protein AAL60010.1 - Arabidopsis thaliana	1e-123	AY072188_	gene: "At1g18270"; product: "unknown protein"; Arabidopsis tha	24.7	63.6	61.4	155.2	4e-40	01 METABOLISM
Pc06g01800	strong similarity to quinone oxidoreductase P1 - Arabidopsis thaliana	2e-96	AF525909_	gene: "RED1"; product: "reductase RED1"; Cochliobolus heteros	81.9	93.2	140.2	586.4	7e-89	01.01 amino acid metabolism
Pc12g00180	strong similarity to oxidoreductase of short-chain ORF11 - Streptomyces coelicolor	1e-47	T41028	short chain dehydrogenase - fission yeast (Schizosaccharomyce	12.0	12.0	18.8	90.1	1e-80	01.05 C-compound and carbohydrate metabolism
Pc12g00450	weak similarity to hypothetical protein PA2336 - Pseudomonas aeruginosa	6e-77	BX649607_	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot p	16.9	32.8	34.9	129.4	0	0
Pc12g00460	strong similarity to multidrug resistance protein fnx1p - Schizosaccharomyces pombe	1e-178	NCB13O8_	gene: "B13O8.150"; product: "conserved hypothetical protein";	12.7	21.9	17.9	40.9	1e-52	01.05.07 C-compound, carbohydrate transport
Pc12g01130	strong similarity to aldehyde reductase II ARII - Sporidiobolus salmonicolor	2e-52	AF160799_	gene: "ARII"; product: "aldehyde reductase II"; Sporidiobolus sal	153.2	668.0	1706.7	1867.3	1e-138	01 METABOLISM
Pc12g01840	strong similarity to methicillin resistance gene HmrA - Staphylococcus aureus	1e-100	NCB14A21_	gene: "B14A21.240"; product: "related to amidohydrolase AmhX	12.0	13.3	28.3	71.9	4e-84	01.05 C-compound and carbohydrate metabolism
Pc12g02470	strong similarity to xylitol dehydrogenase xdh - Galactocandida mastotermitis	3e-94	AF428150_	gene: "xdh1"; product: "xylitol dehydrogenase"; Hypocrea jecorin	12.0	12.0	18.1	90.8	5e-53	01.05.07 C-compound, carbohydrate transport
Pc12g03550	strong similarity to p-nitrobenzyl esterase pnbA - Bacillus subtilis	1e-30	BSP27806	gene: "estA1"; product: "type B carboxylesterase"; Bacillus sp. e	12.0	12.0	29.2	129.5	0.0	01.04 phosphate metabolism
Pc12g03640	weak similarity to hypothetical isochorismatase Ta0729 - Thermoplasma acidophilum	4e-24	F83435	conserved hypothetical protein PA1677 [imported] - Pseudomon	40.8	113.6	195.8	674.6	2e-47	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc12g05530	similarity to hypothetical glutathione S-transferase BAB68404.1 - Gibberella fujikuroi	4e-22	AB071861_	product: "putative glutathione S-transferase"; Gibberella fujikuro	12.0	12.0	20.3	67.3	9e-70	01.01.99 other amino acid metabolism activities
Pc12g06200	strong similarity to hypothetical glutathione S-transferase CAA19067.1 - Schizosaccharomyces pombe	3e-44	T41660	Glutathione S-transferase - fission yeast (Schizosaccharomyces	23.3	123.2	67.6	245.6	2e-41	01.04.07 phosphate transport
Pc12g07050	strong similarity to polyamine transport protein Tpo1 - Saccharomyces cerevisiae	5e-52	BX908812_	gene: "G17A4.250"; product: "related to multidrug resistant prot	19.4	21.0	38.5	102.3	7e-45	01.03 nucleotide metabolism
Pc12g07750	strong similarity to hypothetical protein contig_1_46_scaffold_3.tfa_190cg - Aspergillus nidulans	3e-19	T41002	hypothetical protein SPCC1494.01 - fission yeast (Schizosaccha	12.0	12.0	13.0	184.8	0	0
Pc12g07810	strong similarity to extracellular alpha-glucosidase aglU - Aspergillus niger	0.0	JC4217	alpha-glucosidase (EC 3.2.1.20) - Aspergillus oryzae	24.7	32.9	105.0	196.3	1e-130	01.01.01 amino acid biosynthesis
Pc12g08340	strong similarity to hypothetical membrane protein YOL119c - Saccharomyces cerevisiae	2e-57	NCB23B10_	gene: "B23B10.030"; product: "related to monocarboxylate trans	31.0	59.5	85.4	209.0	0	0
Pc12g08560	similarity to hemagglutinating surface lectin - Arthrobotrys oligospora	3e-18	A47688	hemagglutinating surface lectin - nematode-trapping fungus (Art	12.0	12.0	12.0	77.3	4e-55	01.05.04 regulation of C-compound and carbohydrate utilization
Pc12g09570	strong similarity to integral membrane protein PTH11 - Magnaporthe grisea	3e-30	AF119671_	gene: "PTH11"; product: "integral membrane protein"; Magnapo	12.0	19.7	48.8	110.9	0	0
Pc12g10000	similarity to hypothetical protein CC3654 - Caulobacter crescentus	2e-23	BX569693_	product: "conserved hypothetical protein"; Synechococcus sp. W	90.1	757.9	1558.6	2036.1	2e-83	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups
Pc12g11220	weak similarity to 2-hydroxyisoflavone reductase IRL - Zea mays	4e-92	BX649605_	product: "isoflavone reductase, putative"; Aspergillus fumigatus	12.0	26.8	44.7	137.1	2e-68	01 METABOLISM
Pc12g11870	strong similarity to benzoylformate decarboxylase - Pseudomonas putida	0.0	NCB2G14_	gene: "B2G14.130"; product: "related to BENZOYLFORMATE D	22.8	90.3	73.6	390.5	2e-82	01.05 C-compound and carbohydrate metabolism
Pc12g12020	similarity to lactoylglutathione lyase glyoxalase-I - Lycopersicon esculentum	3e-16	F83006	lactoylglutathione lyase PA5111 [imported] - Pseudomonas aeru	12.0	12.3	23.2	55.7	1e-89	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM
Pc12g13130	strong similarity to hypothetical protein SPAC869.06c - Schizosaccharomyces pombe	1e-39	T39117	hypothetical protein SPAC869.06c - fission yeast (Schizosaccha	17.8	64.3	144.4	215.5	2e-61	99 UNCLASSIFIED PROTEINS
Pc12g13280	strong similarity to hypothetical protein encoded by all1319 - Nostoc sp.	2e-34	D83426	hypothetical protein PA1752 [imported] - Pseudomonas aerugin	12.0	12.0	52.9	159.1	0	0
Pc12g13310	strong similarity to starvation-sensing protein like protein An04g02760 - Aspergillus niger	1e-112	AP004600_	gene: "OB2215"; product: "unknown conserved protein (partial)"	12.0	12.0	36.2	128.1	0	0
Pc12g13440	strong similarity to alcohol dehydrogenase adh1p - Schizosaccharomyces pombe	1e-106	AY170473_	gene: "ADH"; product: "alcohol dehydrogenase"; Cercospora ze	13.0	14.9	23.5	151.3	1e-111	01.01.07 amino acid transport
Pc12g13480	weak similarity to hypothetical oxidoreductase PA5309 - Pseudomonas aeruginosa	2e-24	NC5F3_10	gene: "5F3.100"; product: "conserved hypothetical protein"; Ne	12.0	12.0	52.6	104.7	2e-50	01.05.01.01.01 sugar, glucoside, polyol and carboxylate catabolism
Pc12g13540	strong similarity to quinate transport protein qutD - Aspergillus nidulans	1e-61	S08498	quinate transport protein - Emericella nidulans	180.7	231.0	147.9	360.1	3e-77	01.05.04 regulation of C-compound and carbohydrate utilization
Pc12g14180	strong similarity to urea transport protein Dur3 - Saccharomyces cerevisiae	1e-114	S46830	urea transport protein - yeast (Saccharomyces cerevisiae)	12.0	12.0	12.0	60.7	2e-53	01.04.07 phosphate transport
Pc12g14370	strong similarity to lysine permease Lyp1 - Saccharomyces cerevisiae	1e-130	BX908808_	gene: "G21B4.270"; product: "probable amino acid transporter";	84.7	99.3	260.2	528.6	6e-34	01.03 nucleotide metabolism
Pc12g14630	strong similarity to hypothetical protein contig1477_1.tfa_1140cg - Aspergillus fumigatus	1e-22	AP005024_	product: "hypothetical protein"; Streptomyces avermitilis genom	122.5	288.4	350.6	862.7	0	0
Pc12g14970	similarity to hypothetical conserved protein 99H12.80 - Neurospora crassa	1e-154	BX649605_	product: "hypothetical protein, conserved"; Aspergillus fumigatus	18.1	27.3	81.8	180.3	9e-21	01.01.01.01.02 biosynthesis of the glutamate group (proline, hydroxyprolin, arginine, glutamine, glutamate)
Pc12g15400	similarity to hypothetical protein An03g00840 - Aspergillus niger	3e-09	AY164486_	gene: "Pkd1l3"; product: "polycystic kidney disease 1-like 3"; Mu	137.6	380.4	729.2	1172.0	9e-67	01 METABOLISM
Pc12g15450	similarity to hypothetical protein contig1492_0.tfa_1310cg - Aspergillus fumigatus	0	0	0	16.8	24.2	75.1	90.5	0.0	99 UNCLASSIFIED PROTEINS
Pc12g15730	strong similarity to novobiocin biosynthetic gene novR - Streptomyces spheroides	3e-63	AE2021	hypothetical protein all1723 [imported] - Nostoc sp. (strain PCC	18.7	47.8	111.3	370.8	8e-85	01.05 C-compound and carbohydrate metabolism
Pc13g01660	weak similarity to phenylcoumaran benzylic ether reductase PT1 - Pinus taeda	2e-78	BX649605_	product: "isoflavone reductase, putative"; Aspergillus fumigatus	12.0	16.9	70.1	374.7	3e-71	01.01.04 regulation of amino acid metabolism
Pc13g02040	strong similarity to myo-inositol 2-dehydrogenase yisS - Bacillus subtilis	2e-54	AP003185_	gene: "CPE0093"; product: "probable dehydrogenase"; Clostrid	13.3	12.0	36.3	93.9	1e-113	01.01.10.04 degradation of amino acids of the pyruvate family
Pc13g02570	strong similarity to polyamine transport protein Tpo1 - Saccharomyces cerevisiae	3e-89	BX649607_	gene: "mdR"; product: "mfs-family multidrug resistance protein, p	12.0	41.4	12.0	17.3	4e-55	01.05.04 regulation of C-compound and carbohydrate utilization
Pc13g03330	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	4e-09	SCARGRII_	S. cerevisiae ARGR II regulatory gene	15.9	43.2	132.4	148.8	4e-89	01.05.01 C-compound and carbohydrate utilization
Pc13g03610	strong similarity to hypothetical protein AAF47250.1 - Drosophila melanogaster	2e-24	AE003464_	product: "CG3663-PA"; Drosophila melanogaster chromosome	85.2	199.3	180.1	524.8	0	0
Pc13g05900	strong similarity to sulfur dioxygenase like protein An04g09670 - Aspergillus niger	3e-57	AY396519_	Gordonia sp. CYKS2 putative transposases, dibenzothiophene	55.9	49.7	59.6	348.5	0.0	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS
Pc13g07960	strong similarity to alcohol dehydrogenase ADH like protein An04g02690 - Aspergillus niger	5e-82	T39671	alcohol dehydrogenase - fission yeast (Schizosaccharomyces p	17.9	45.4	178.3	514.4	0.0	01.05 C-compound and carbohydrate metabolism
Pc13g08080	strong similarity to bile acid transporter Ybt1 - Saccharomyces cerevisiae	0.0	S64800	probable membrane protein YLL048c - yeast (Saccharomyces c	16.9	30.8	72.4	96.9	1e-109	01.01.10.04 degradation of amino acids of the pyruvate family
Pc13g08250	strong similarity to hypothetical protein 1144_scaffold_2.tfa_20cg - Fusarium graminearum	1e-136	SCO93910	gene: "SCO0371"; "SCF41.30c"; product: "putative secreted pro	12.0	17.6	23.7	62.6	1e-169	01.02.01 nitrogen and sulfur utilization
Pc13g09130	strong similarity to beta-glucosidase bgl4 - Humicola grisea	1e-143	AF439322_	gene: "bg1"; product: "beta-glucosidase 1"; Talaromyces emers	40.4	82.9	89.6	186.5	1e-127	01 METABOLISM
Pc13g11140	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae	4e-89	NCB19C19_	gene: "B19C19.140"; product: "related to fluconazole resistance	12.0	109.1	133.1	176.7	0.0	01 METABOLISM
Pc13g11930	strong similarity to acyl CoA dehydrogenase aidB - Escherichia coli	1e-74	NC2E4_2	gene: "2E4.020"; product: "conserved hypothetical protein"; Ne	12.0	12.0	51.4	108.4	1e-48	01.05 C-compound and carbohydrate metabolism
Pc13g13290	strong similarity to succinat-CoA ligase alpha chain Lsc1 - Saccharomyces cerevisiae	2e-72	AE003726_	product: "CG6255-PA"; Drosophila melanogaster chromosome	38.4	69.1	88.8	266.2	1e-109	01 METABOLISM
Pc13g14030	similarity to ferulic acid esterase A faeA - Aspergillus niger	1e-130	AF274320_	product: "alkaline lipase"; Penicillium cyclopium alkaline lipase r	55.7	144.7	137.2	591.2	8e-61	01.04.07 phosphate transport
Pc13g14180	strong similarity to hypothetical protein An02g09040 - Aspergillus niger	0	0	0	74.5	90.5	286.6	439.0	1e-136	01 METABOLISM
Pc13g14420	strong similarity to malonyl CoA synthase matB - Rhizobium trifolii	7e-56	AY084636_	product: "putative long-chain acyl-CoA synthetase"; Arabidopsis	12.0	12.0	12.0	86.9	1e-109	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc13g14920	strong similarity to hypothetical protein An09g01070 - Aspergillus niger	1e-121	AE016866_	product: "xenobiotic compound monooxygenase, DszA family"; F	40.9	78.7	275.6	841.8	7e-59	01 METABOLISM
Pc13g14930	strong similarity to hypothetical sterigmatocystin biosynthesis monooxygenase stcW - Aspergillus nidulans	1e-101	BX842595_	Neurospora crassa DNA linkage group II BAC clone B24N4;	12.0	42.6	79.9	530.8	0	0
Pc13g14940	strong similarity to hypothetical short chain dehydrogenase SPCC736.13 - Schizosaccharomyces pombe	1e-121	NCB13O8_	gene: "B13O8.020"; product: "related to light induced alcohol de	12.0	12.0	12.0	61.7	1e-83	01.01.99 other amino acid metabolism activities
Pc13g15280	similarity to integral membrane protein PTH11 - Magnaporthe grisea	3e-25	AF329397_	gene: "pth"; product: "integral membrane protein"; Blumeria gra	29.3	102.7	100.2	283.8	0	0
Pc13g15880	strong similarity to hypothetical oxidoreductase PA0147 - Pseudomonas aeruginosa	2e-48	AP003010_	gene: "mlr6892"; Mesorhizobium loti DNA, complete genome, se	17.1	52.7	101.5	251.7	0	0
Pc14g00030	weak similarity to hypothetical protein PA1213 - Pseudomonas aeruginosa	1e-133	NCG15G9_	gene: "G15G9.020"; product: "conserved hypothetical protein";	41.5	123.1	170.5	711.3	0	0
Pc14g00060	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	4e-62	T41604	probable membrane transport protein - fission yeast (Schizosac	12.6	12.0	30.1	70.8	0.0	02.11 electron transport and membrane-associated energy conservation
Pc14g00320	strong similarity to alkane-inducible cytochrome P450 gene ALK1 - Yarrowia lipolytica	1e-133	AB010388_	gene: "ALK1"; product: "ALK1"; Yarrowia lipolytica gene for ALK	96.2	133.5	219.7	561.0	0	0
Pc14g00350	strong similarity to carboxypeptidase y CPY - Candida albicans	4e-68	CBPY_CAN	CARBOXYPEPTIDASE Y PRECURSOR (EC 3.4.16.5) (CARBOX	12.0	35.8	35.3	70.1	1e-103	01.20.05.99 other biosynthesis of acetic acid derivatives
Pc14g00990	strong similarity to alcohol dehydrogenase alkJ - Pseudomonas oleovorans	1e-134	SCO93912	gene: "SCO4829"; "SC2A6.14"; product: "putative oxidoreductas	12.0	12.0	49.7	63.5	3e-76	01.05 C-compound and carbohydrate metabolism
Pc14g01680	strong similarity to L-fucose permease fucP - Escherichia coli	7e-53	A81394	probable sugar transporter Cj0486 [imported] - Campylobacter j	44.9	72.8	105.6	210.0	2e-40	01.04.01 phosphate utilization
Pc15g00520	weak similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	2e-07	AF141925_	gene: "lovC"; product: "enoyl reductase"; Aspergillus terreus lov	12.0	15.4	30.0	202.8	1e-143	01 METABOLISM
Pc15g00530	strong similarity to hypothetical protein SPAC922.05c - Schizosaccharomyces pombe	5e-28	T39038	hypothetical protein SPAC6F6.04c - fission yeast (Schizosaccha	12.0	16.0	33.2	225.4	1e-129	01.02.01.09.99 other catabolism of nitrogenous compounds
Pc16g00270	strong similarity to glycosylphosphatidylinositol-anchored beta(1-3)glucanosyltransferase gel3 - Aspergillu	1e-136	AX710542_	unnamed ORF; Sequence 34 from Patent WO03018626.	75.4	114.1	231.1	548.1	1e-27	01.05 C-compound and carbohydrate metabolism
Pc16g00510	strong similarity to arylsulfatase ars-1 - Neurospora crassa	0.0	CNS07TIX_	DNA centromeric region sequence from BAC DP15B03, DP38F0	155.5	443.0	639.2	1926.6	1e-115	01.02.01.09.99 other catabolism of nitrogenous compounds
Pc16g00620	strong similarity to glucan 1,4-alpha-glucosidase glaA - Aspergillus niger	0.0	JQ1346	glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Aspergillus oryzae	445.6	823.3	3082.2	3034.4	2e-80	01.05.04 regulation of C-compound and carbohydrate utilization
Pc16g00850	similarity to polyamine transport protein Tpo4 - Saccharomyces cerevisiae	6e-12	BX649607_	gene: "mdR"; product: "mfs-family multidrug resistance protein, p	58.5	229.8	111.1	157.4	1e-28	01.05.04 regulation of C-compound and carbohydrate utilization
Pc16g03830	similarity to hypothetical protein An12g06250 - Aspergillus niger	0	0	0	12.0	12.0	14.3	57.9	5e-58	01.03 nucleotide metabolism
Pc16g04560	strong similarity to lactone-specific esterase estf1 - Pseudomonas fluorescens	1e-102	SCO93911	gene: "SCO3172"; "SCE87.23c"; product: "putative monooxyger	35.2	17.6	28.8	160.3	2e-72	01 METABOLISM
Pc16g05670	strong similarity to glucose transporter rco-3 - Neurospora crassa	2e-63	NCB8B8_9	gene: "B8B8.110"; product: "related to sugar transport protein S	116.3	124.4	62.1	505.3	5e-70	01.05.04 regulation of C-compound and carbohydrate utilization
Pc16g05700	strong similarity to sugar transporter Sut2 - Pichia stipitis	4e-42	BX842681_	gene: "B13N4.080"; product: "probable maltose permease"; Neu	12.0	12.3	35.6	64.3	4e-86	01.05.01 C-compound and carbohydrate utilization
Pc16g05930	similarity to cold-adapted lipase lipP - Pseudomonas sp.	2e-32	G70671	probable lipase/esterase - Mycobacterium tuberculosis (strain H	12.0	17.1	48.2	123.8	4e-55	01 METABOLISM
Pc16g06150	strong similarity to alpha-amylase precursor amy - Bacillus amyloliquefaciens	1e-177	AB078784_	product: "hypothetical protein"; Aspergillus oryzae gene for hyp	101.5	128.0	265.7	523.1	1e-158	01.05 C-compound and carbohydrate metabolism
Pc16g06910	strong similarity to hypothetical sterigmatocystin biosynthesis monooxygenase stcW - Aspergillus nidulans	1e-116	BX842629_	gene: "B20J13.060"; product: "related to steroid monooxygenas	12.0	12.9	12.0	57.7	3e-71	01.01.10 amino acid degradation (catabolism)
Pc16g10040	strong similarity to flavohemoglobin Fhp - Alcaligenes eutrophus	3e-92	AB016807_	product: "flavohemoglobin"; Fusarium oxysporum mRNA for flav	12.0	16.0	45.5	158.5	1e-118	06.01 protein folding and stabilization
Pc16g10320	strong similarity to hypothetical protease Mch5 - Saccharomyces cerevisiae	4e-80	NCB23B10_	gene: "B23B10.030"; product: "related to monocarboxylate trans	12.0	18.3	31.9	76.8	0.0	14.04.03.03 pheromone response, mating-type determination, sex-specific proteins
Pc16g10390	strong similarity to oxidoreductase protein like protein An11g08950 - Aspergillus niger	1e-118	NCB8P8_9	gene: "B8P8.090"; product: "probable NADPH quinone oxidored	57.8	130.3	141.7	296.9	0	0
Pc16g10620	similarity to beta transducin-like protein het-e1 - Podospora anserina	5e-14	AF323585_	gene: "het-d"; product: "beta transducin-like protein HET-D2Y";	26.6	37.6	78.2	157.7	1e-44	01.04.07 phosphate transport
Pc16g12050	strong similarity to lactonohydrolase - Fusarium oxysporum	1e-135	AB010465_	product: "lactonohydrolase"; Fusarium oxysporum mRNA for lac	20.1	48.5	52.4	140.0	2e-54	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc16g12750	strong similarity to beta-galactosidase lacA - Aspergillus niger [putative frameshift]	0.0	AJ629057_	gene: "lac"; product: "beta-galactosidase"; Penicillium sp. partial	16.0	41.3	106.2	338.3	1e-96	01.01.10 amino acid degradation (catabolism)
Pc16g12790	strong similarity to hypothetical UDP-glucose 4-epimerase - Alcaligenes eutrophus	1e-130	BX649607_	product: "possible epimerase"; Aspergillus fumigatus BAC pilot	18.5	44.9	77.2	291.3	0	0
Pc16g13310	strong similarity to short-chain dehydrogenase sou1 - Candida albicans	1e-54	SOU1_CAN	SORBITOL UTILIZATION PROTEIN SOU1.	21.4	49.7	51.6	151.2	5e-55	01 METABOLISM
Pc16g13520	strong similarity to 1,2-dichlorophenol hydroxylase tfdB - Pseudomonas putida	9e-48	AJ628861_	gene: "tfdB"; product: "dichlorophenol hydroxylase"; Sphingomo	12.0	18.1	54.3	80.6	0.0	01.05 C-compound and carbohydrate metabolism
Pc16g13960	strong similarity to probable amidase - Mesorhizobium loti	1e-153	AP002999_	gene: "mlr2310"; product: "probable amidase"; Mesorhizobium lo	12.0	12.0	19.2	65.0	0	0
Pc16g14380	strong similarity to P-type ATPase ENA1 - Schwanniomyces occidentalis	0.0	NCR24352	gene: "ena-1"; product: "putative sodium P-type ATPase"; Neur	49.8	144.6	210.2	311.5	6e-55	01.05.04 regulation of C-compound and carbohydrate utilization
Pc16g15340	hypothetical protein	0	0	0	12.0	65.3	60.3	126.2	0	0
Pc18g03610	weak similarity to canalicular multidrug resistance protein cMrp - Rattus norvegicus	0.0	NCB7A16_	gene: "B7A16.190"; product: "related to ATP-binding cassette tr	12.0	34.7	52.6	68.6	9e-53	01.04.07 phosphate transport
Pc18g04250	strong similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae	2e-37	AF359361_	gene: "OrfF"; product: "methyltransferase"; Gibberella zeae stra	26.5	40.0	94.8	254.4	0	0
Pc18g05800	strong similarity to hypothetical protein SPAC922.05c - Schizosaccharomyces pombe	2e-43	T50270	hypothetical protein SPAC922.05c [imported] - fission yeast (Scl	12.0	12.0	12.0	51.0	0	0
Pc20g00050	similarity to hypothetical protein An08g01250 - Aspergillus niger	0	0	0	12.0	12.0	22.9	57.2	0	0
Pc20g01870	strong similarity to hypothetical protein contig1490_3.tfa_160wg - Aspergillus fumigatus	2e-11	A75567	conserved hypothetical protein - Deinococcus radiodurans (stra	26.5	88.3	213.1	337.8	0	0
Pc20g02040	strong similarity to methicillin resistance gene HmrA - Staphylococcus aureus	1e-84	NCB14A21_	gene: "B14A21.240"; product: "related to amidohydrolase AmhX	12.0	12.0	12.0	269.6	0	0
Pc20g02160	similarity to lipase LipP - Pseudomonas sp.	1e-27	F84000	carboxylesterase BH2806 [imported] - Bacillus halodurans (strai	13.5	12.0	17.7	83.0	1e-111	01.02.01.09.99 other catabolism of nitrogenous compounds
Pc20g02410	strong similarity to succinate-semialdehyde dehydrogenase NAD(P)+ gabD - Escherichia coli	1e-123	SPAC1002_	gene: "SPAC1002.12c"; product: "succinate-semialdehyde dehy	29.0	56.0	75.7	160.9	1e-71	01.05 C-compound and carbohydrate metabolism
Pc20g03770	strong similarity to hypothetical protein An14g06100 - Aspergillus niger	2e-32	AP005037_	product: "hypothetical protein"; Streptomyces avermitilis genom	57.4	70.8	93.3	356.7	5e-63	01.05.07 C-compound, carbohydrate transport
Pc20g04300	strong similarity to hypothetical protein An16g02770 - Aspergillus niger	4e-41	SPBP16F5_	gene: "SPBP16F5.08c"; S.pombe chromosome II p1 p16F5.	50.2	83.9	237.9	507.3	0.0	11.07.01 detoxification involving cytochrome P450
Pc20g05270	strong similarity to aflatoxin B1 aldehyde reductase AFAR - Rattus norvegicus	3e-50	BX649606_	product: "aflatoxin b1 aldehyde reductase-like protein, putative";	12.2	135.2	138.7	321.7	1e-104	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc20g05830	strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	1e-110	TOXD_CO	TOXD PROTEIN.	26.9	87.5	175.0	370.7	1e-101	01.05.01.01.01 sugar, glucoside, polyol and carboxylate catabolism
Pc20g06160	similarity to hypothetical glutathione S-transferase BAB68404.1 - Gibberella fujikuroi	2e-15	AB071861_	product: "putative glutathione S-transferase"; Gibberella fujikuro	50.3	92.7	205.7	465.1	0	0
Pc20g06210	strong similarity to Fe(II)-dependent sulfonate alpha-ketoglutarate dioxygenase YLL057c - Saccharomyces	5e-83	S50963	hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae	17.4	155.0	445.0	1790.6	2e-35	01.03 nucleotide metabolism
Pc20g07320	strong similarity to hypothetical protein SPAC922.05c - Schizosaccharomyces pombe	8e-44	T50270	hypothetical protein SPAC922.05c [imported] - fission yeast (Scl	12.0	16.5	44.6	63.7	1e-36	01.05.01 C-compound and carbohydrate utilization
Pc20g09370	strong similarity to multidrug resistance protein Hol1 - Saccharomyces cerevisiae	9e-54	T39346	probable major facilitator family multi-drug resistance protein - fi	31.7	32.3	83.2	152.6	2e-70	01.05.07 C-compound, carbohydrate transport
Pc20g09380	similarity to endo-1,4-beta-xylanase XynD - Bacillus polymyxa	1e-148	AB093564_	product: "xylosidase"; Penicillium herquei mRNA for xylosidase,	12.0	12.0	12.0	98.0	2e-78	01.05.07 C-compound, carbohydrate transport
Pc20g10710	similarity to hypothetical regulator protein CAB16735.1 - Schizosaccharomyces pombe	5e-19	T38690	probable regulatory protein - fission yeast (Schizosaccharomyce	14.7	17.8	40.8	89.7	2e-57	01.03 nucleotide metabolism

Pc20g10850	similarity to hypothetical protein An11g00150 - Aspergillus niger	8e-12	T01145	probable acetone-cyanohydrin lyase [imported] - Arabidopsis th	12.6	12.0	25.0	77.3	0		0
Pc20g13380	weak similarity to cytidine deaminase - Homo sapiens	6e-36	S41571	blasticidin-S deaminase (EC 3.5.4.23) - Aspergillus terreus	15.9	33.9	52.6	96.2	0		0
Pc20g13920	weak similarity to hypothetical protein SPBC2A9.02 - Schizosaccharomyces pombe	1e-09	T40093	hypothetical protein SPBC2A9.02 - fission yeast (Schizosacchar	24.0	27.2	92.1	140.4	0		0
Pc20g14890	weak similarity to 2-haloacid halidohydrolase IVa - Pseudomonas cepacia	1e-05	AP005962_	gene: "dhlB"; product: "2-haloalkanoic acid dehalogenase"; Bra	12.0	13.9	47.4	243.4	7e-99	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc20g14920	similarity to hypothetical oxidoreductase PA5309 - Pseudomonas aeruginosa	1e-36	NC5F3_10	gene: "5F3.100"; product: "conserved hypothetical protein"; Ne	12.0	39.7	29.9	96.1	0		0
Pc20g14970	weak similarity to hypothetical membrane protein YDL237w - Saccharomyces cerevisiae	0	0	0	60.8	214.3	143.8	639.9	0		0
Pc20g15400	strong similarity to hypothetical protein jhp0295 - Helicobacter pylori	6e-59	AE016871_	product: "polysaccharide deacetylase family protein"; Pseudom	17.1	17.9	47.9	103.9	1e-134	01.01.10.04 degradation of amino acids of the pyruvate family	
Pc20g15440	weak similarity to peroxisomal membrane protein Pmp27 - Saccharomyces cerevisiae	2e-07	AX052571_	unnamed ORF; Sequence 1 from Patent WO0071579.	17.8	38.8	48.2	112.5	4e-39	01.04.07 phosphate transport	
Pc20g15480	strong similarity to hypothetical protein An04g04470 - Aspergillus niger	0	0	0	23.6	55.1	106.1	243.4	0		0
Pc20g15640	strong similarity to hypothetical protein - Bradyrhizobium japonicum	1e-138	AP005959_	gene: "bll6791"; Bradyrhizobium japonicum USDA 110 DNA, cor	12.0	12.0	37.1	105.0	0		0
Pc20g15660	strong similarity to sterol carrier protein-X sterol carrier protein-2 SCP2 - Homo sapiens	1e-171	NCB9B11_	gene: "B9B11.130"; product: "probable sterol carrier protein"; N	12.0	12.0	23.6	107.7	1e-108	01.07 metabolism of vitamins, cofactors, and prosthetic groups	
Pc20g15670	strong similarity to NAD-GSH-dependent formaldehyde dehydrogenase flhA - Paracoccus denitrificans	2e-62	B95865	conserved hypothetical protein [imported] - Sinorhizobium melilo	12.0	12.0	49.0	119.1	5e-91	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g00870	strong similarity to vacuolar aminopeptidase Y Ape3 - Saccharomyces cerevisiae	1e-125	BX908808_	gene: "G21B4.310"; product: "related to aminopeptidase Y prec	277.6	268.5	537.8	1981.5	1e-107	06.01 protein folding and stabilization	
Pc21g01720	similarity to hypothetical neutral amino acid permease - Neurospora crassa	4e-13	S47892	neutral amino acid permease - Neurospora crassa	12.0	12.6	27.1	140.3	0		0
Pc21g02640	strong similarity to hypothetical protein contig31_part_i.tfa_460cg - Aspergillus fumigatus	0	0	0	47.5	45.5	76.8	213.4	2e-57	99 UNCLASSIFIED PROTEINS	
Pc21g04130	similarity to hypothetical protein SC1C3.21 - Streptomyces coelicolor	5e-11	T34713	hypothetical protein SC1C3.21 SC1C3.21 - Streptomyces coelic	215.5	369.3	744.2	1317.5	6e-63	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g04310	strong similarity to hypothetical protein SPAC1039.06 - Schizosaccharomyces pombe	1e-74	T50056	hypothetical protein SPAC1039.06 [imported] - fission yeast (Sc	12.0	12.0	38.1	90.1	5e-92	01.01.01.15 biosynthesis of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine	
Pc21g05760	similarity to integral membrane protein PTH11 - Magnaporthe grisea	1e-120	BX649605_	product: "integral membrane protein, putative"; Aspergillus fumi	12.0	14.9	12.0	82.7	3e-77	01 METABOLISM	
Pc21g05770	strong similarity to cytochrome P450 eln2 - Coprinus cinereus	0.0	BX649605_	product: "cytochrome p450, putative"; Aspergillus fumigatus BAC	12.0	25.7	27.9	89.1	1e-128	11.07.01 detoxification involving cytochrome P450	
Pc21g05900	strong similarity to hypothetical short chain dehydrogenase SPAC521.03 - Schizosaccharomyces pombe	1e-110	BX897675_	gene: "B2E7.120"; product: "conserved hypothetical protein"; N	144.9	291.9	404.8	779.3	6e-83	01.01.01.07.06 biosynthesis of lysine	
Pc21g06580	strong similarity to benzoate 4-monooxygenase cytochrome P450 53 bphA - Aspergillus niger	3e-40	AF169016_	gene: "cypX"; product: "cytochrome P450 monooxigenase"; Asp	12.0	12.0	32.1	91.5	2e-97	01.05.01 C-compound and carbohydrate utilization	
Pc21g06600	strong similarity to taurine dioxygenase, 2-oxoglutarate-dependent tauD - Escherichia coli	3e-33	AE016756_	gene: "tauD"; product: "Alpha-ketoglutarate-dependent taurine	12.0	12.0	12.0	53.1	0.0	01.01 amino acid metabolism	
Pc21g09020	strong similarity to alcohol dehydrogenase alcB - Aspergillus nidulans	1e-159	S62746	alcohol dehydrogenase (EC 1.1.1.1) B - Emericella nidulans	77.1	41.9	154.6	391.5	4e-91	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	
Pc21g09300	strong similarity to gamma-glutamyl transpeptidase GGT1 - Homo sapiens	1e-150	T49441	gamma-glutamyltransferase related protein [imported] - Neurosp	12.0	12.0	43.5	68.0	1e-160	01.05.01 C-compound and carbohydrate utilization	
Pc21g09410	strong similarity to monoamine oxidase maoN - Aspergillus niger	0.0	S55273	amine oxidase (flavin-containing) (EC 1.4.3.4) N - Aspergillus nig	12.0	28.9	12.0	167.8	1e-107	98 CLASSIFICATION NOT YET CLEAR-CUT	
Pc21g09430	weak similarity to peroxisomal transporter Ant1 - Saccharomyces cerevisiae	1e-42	S69019	hypothetical protein YPR128c - yeast (Saccharomyces cerevisia	20.4	30.2	48.3	125.3	4e-48	01.05.07 C-compound, carbohydrate transport	
Pc21g09940	strong similarity to hypothetical protein contig5_part_i.tfa_3420cg - Aspergillus fumigatus	4e-97	BX908809_	gene: "29E8.120"; product: "related to 3-hydroxyisobutyrate deh	19.7	28.9	54.6	292.0	0		0
Pc21g10950	strong similarity to prolidase - Aureobacterium esteraromaticum	1e-128	NC64C2_2	gene: "64C2.270"; product: "conserved hypothetical protein"; N	13.7	28.1	75.7	168.1	1e-117	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS	
Pc21g12160	strong similarity to flavocytochrome b2 L-lactate dehydrogenase CYB2 - Pichia anomala	3e-98	KLA24332	gene: "cyb2"; product: "cytochrome b2"; Kluyveromyces lactis cy	12.0	12.0	12.0	52.0	2e-62	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g12190	strong similarity to hypothetical protein contig_1_135_scaffold_11.tfa_530wg - Aspergillus nidulans	5e-47	BX842620_	gene: "B11E5.430"; product: "related to dihydrodipicolinate synt	19.1	41.0	47.1	129.4	0		0
Pc21g12200	similarity to hypothetical protein MRI1 - Arabidopsis thaliana	1e-110	AE016757_	gene: "c0759"; product: "Hypthetical protein"; Escherichia coli C	12.0	12.0	14.7	54.3	1e-114	01.20 secondary metabolism	
Pc21g13940	strong similarity to hypothetical protein An03g01270 - Aspergillus niger	0	0	0	64.1	74.2	151.9	306.9	1e-118	99 UNCLASSIFIED PROTEINS	
Pc21g14250	strong similarity to hypothetical protein SPAC5H10.01 - Schizosaccharomyces pombe	7e-67	S55479	hypothetical protein SPAC5H10.01 - fission yeast (Schizosaccha	22.0	85.4	240.3	1064.1	2e-93	01.04 phosphate metabolism	
Pc21g14780	strong similarity to hypothetical protein An16g01890 - Aspergillus niger	0	0	0	21.0	12.0	49.7	103.5	0		0
Pc21g15140	strong similarity to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase hpcH - Escherichia coli	4e-44	BX649605_	product: "2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase"; Asp	12.0	22.0	40.1	98.7	7e-65	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g15410	strong similarity to hypothetical protein An07g04880 - Aspergillus niger [putative sequencing error]	4e-06	A53731	translation initiation factor eIF-2 alpha chain kinase (EC 2.7.1.-)	14.5	15.6	66.2	86.5	0		0
Pc21g16840	similarity to NAD+-dependent 15-hydroxyprostaglandin dehydrogenase PDGH - Homo sapiens	8e-18	BC052123_	gene: "zgc:56585"; product: "similar to hydroxyprostaglandin del	36.7	158.0	171.5	507.2	3e-73	11.05.01 resistance proteins	
Pc21g17020	strong similarity to hypothetical protein An04g08050 - Aspergillus niger	0	0	0	12.0	12.0	18.1	64.0	0		0
Pc21g17030	similarity to hypothetical protein An04g08060 - Aspergillus niger	0	0	0	12.0	16.6	26.0	72.9	4e-63	01.03 nucleotide metabolism	
Pc21g17620	weak similarity to hypothetical conserved protein TM1177 - Thermotoga maritima	3e-08	AE017006_	product: "hydrolase (HAD superfamily)"; Bacillus cereus ATCC 1	34.0	28.6	105.0	239.5	0		0
Pc21g18260	weak similarity to hypothetical protein YLL056c - Saccharomyces cerevisiae	1e-06	S50964	hypothetical protein YLL056c - yeast (Saccharomyces cerevisia	37.5	52.5	128.2	190.6	1e-166	99 UNCLASSIFIED PROTEINS	
Pc21g18570	similarity to isochorismate pyruvate-lyase - Pseudomonas syringae	3e-09	AE016865_	gene: "pchB"; product: "isochorismate pyruvate-lyase"; Pseudo	25.5	60.8	104.3	169.5	2e-68	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g18580	strong similarity to p-sulfobenzyl alcohol dehydrogenase TsaC - Comamonas testosteroni	7e-70	AL646069_	gene: "tsaC"; "RSc2351"; "RS01195"; product: "PROBABLE TOI	86.4	436.2	587.1	949.1	1e-105	01.01.07 amino acid transport	
Pc21g18680	strong similarity to 1,4-butanediol diacrylate esterase BDA1 - Brevibacterium linens	7e-51	BX572594_	product: "putative esterase"; Rhodopseudomonas palustris CGA	116.6	254.3	310.0	608.8	4e-88	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g19460	strong similarity to hypothetical sterol transporter YMR034c - Saccharomyces cerevisiae	1e-57	S53951	probable membrane protein YMR034c - yeast (Saccharomyces	12.0	21.9	24.6	94.8	2e-76	01 METABOLISM	
Pc21g19590	strong similarity to hypothetical protein mg00056.1 - Magnaporthe grisea	3e-35	AE3150	dehydrogenase Atu4825 [imported] - Agrobacterium tumefacien	16.7	26.0	35.4	96.1	0		0
Pc21g19600	strong similarity to hypothetical protein 1329_scaffold_5.tfa_150cg - Fusarium graminearum	3e-26	E70900	probable lipase - Mycobacterium tuberculosis (strain H37RV)	39.5	102.4	175.7	323.9	1e-99	01.01.01.15 biosynthesis of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine	
Pc21g20520	strong similarity to hypothetical protein contig1469.tfa_1450cg - Aspergillus fumigatus	1e-11	AX196125_	Sequence 197 from Patent WO0151639.	12.0	21.6	83.7	129.0	0		0
Pc21g20910	strong similarity to hypothetical 3-hydroxyisobutyrate dehydrogenase - Aspergillus fumigatus	1e-145	AFA12H2_	gene: "AfA12H2.02"; product: "putative 3-hydroxyisobutyrate de	122.7	194.0	265.2	576.8	0		0
Pc21g20960	strong similarity to lysine-specific permease lysP - Escherichia coli	0.0	AFA12H2_	gene: "AfA12H2.07"; product: "putative lysine-specific permease	68.8	115.0	171.7	481.3	0		0
Pc21g21320	strong similarity to sequence 1 - unknown organism	5e-72	AX100446_	Sequence 1 from Patent WO0121779.	12.0	15.0	24.8	65.1	7e-81	01.01.01.07.06 biosynthesis of lysine	
Pc21g21520	similarity to C-8,7 sterol isomerase - Arabidopsis thaliana	8e-31	A56122	emopamil-binding protein - guinea pig	24.9	12.0	48.6	133.8	4e-52	01.04.07 phosphate transport	
Pc21g21740	similarity to taurine dioxygenase, 2-oxoglutarate-dependent like protein An13g02700 - Aspergillus niger [p	0	0	0	12.0	12.0	12.0	55.7	9e-99	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g21950	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	1e-169	NC64C2_1	gene: "64C2.200"; product: "related to PUTATIVE TARTRATE T	12.0	14.1	17.8	80.5	1e-97	01.20.35.01 biosynthesis of phenylpropanoids	
Pc21g22240	similarity to cholesterol 7alpha-monooxygenase CYP7 - Oryctolagus cuniculus	2e-17	AF127090_	gene: "CYP7B1"; product: "oxysterol 7alpha-hydroxylase"; Hom	12.0	12.0	49.2	87.8	0.0	01.01.01 amino acid biosynthesis	
Pc21g22270	strong similarity to cytochrome P450 monooxygenase P450I - Gibberella fujikuroi	1e-119	GFP450I_1	gene: "P450I"; product: "cytochrome P450 monooxygenase"; G	31.5	12.0	51.7	177.3	1e-153	13 REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT	
Pc22g00100	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	4e-62	BX842634_	gene: "B16B8.030"; product: "related to allantoate permease";	12.0	12.0	12.0	37.2	1e-52	01.04.07 phosphate transport	
Pc22g00120	strong similarity to hypothetical protein mg10417.1 - Magnaporthe grisea	0	0	0	57.2	121.6	99.1	849.3	1e-171	01.02.01 nitrogen and sulfur utilization	
Pc22g00220	strong similarity to hypothetical protein contig589.tfa_1770cg - Aspergillus fumigatus	4e-46	BX842620_	gene: "B11E5.430"; product: "related to dihydrodipicolinate synt	12.2	27.7	30.6	113.1	0.0	01.02.01 nitrogen and sulfur utilization	
Pc22g00290	strong similarity to ATP-hydrolyzing 5-oxoprolinase - Rattus norvegicus	0.0	T37524	probable oxoprolinase - fission yeast (Schizosaccharomyces po	223.3	254.0	1089.9	1649.8	1e-120	01 METABOLISM	
Pc22g00570	strong similarity to triacylglycerol lipase lipI - Geotrichum candidum	2e-42	S41091	triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (Geotrichu	85.2	245.2	257.5	740.6	0		0
Pc22g00840	strong similarity to 3-isopropylmalate dehydrogenase leu2B - Aspergillus niger	1e-153	S72210	3-isopropylmalate dehydrogenase (EC 1.1.1.85) B - Aspergillus	15.6	86.7	46.0	327.0	0.0	01.05 C-compound and carbohydrate metabolism	
Pc22g01110	strong similarity to urea transport protein Dur3 - Saccharomyces cerevisiae	1e-138	T39959	probable urea active transporter - fission yeast (Schizosaccharo	12.0	12.0	12.0	60.0	0.0	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc22g01150	strong similarity to nitrilotriacetate monooxygenase component A - Mesorhizobium loti	0.0	AP003011_	gene: "mlr7299"; product: "nitrilotriacetate monooxygenase com	37.8	117.3	157.8	502.9	5e-96	01.05.01 C-compound and carbohydrate utilization	
Pc22g03060	strong similarity to tartrate transport protein ttuB - Agrobacterium vitis	1e-174	NC5F3_25	gene: "5F3.250"; product: "conserved hypothetical protein"; Ne	24.1	35.2	23.4	72.5	4e-53	01.05.07 C-compound, carbohydrate transport	
Pc22g06170	strong similarity to hypothetical oxidoreductase SPAC977.14c - Schizosaccharomyces pombe	1e-103	T50285	probable oxidoreductase [imported] - fission yeast (Schizosacch	31.3	80.7	173.8	359.3	0		0
Pc22g07690	weak similarity to AK-toxin regulating protein AktR-1 - Alternaria alternata	0	0	0	31.3	43.5	70.9	168.8	0.0	01.01.01 amino acid biosynthesis	
Pc22g08520	weak similarity to heparanase - Homo sapiens	0	0	0	228.0	980.7	1417.9	1718.0	1e-95	01.01.01.11.09 biosynthesis of phenylalanine	
Pc22g08560	strong similarity to fluconazole resistance transporter Flr1 - Saccharomyces cerevisiae	1e-124	BX908812_	gene: "G17A4.250"; product: "related to multidrug resistant prot	12.0	23.6	19.9	54.2	2e-53	01.05.07 C-compound, carbohydrate transport	
Pc22g09210	strong similarity to alpha-glucosidase - Bacillus thermoamyloliquefaciens	0.0	SCO93910	gene: "SCO1055"; "SCG22.01c"; "SCG20A.35c"; product: "puta	12.0	13.8	51.3	98.0	4e-59	01.05.07 C-compound, carbohydrate transport	
Pc22g09220	strong similarity to hypothetical protein ncu08183.1 - Neurospora crassa [putative sequencing error]	1e-12	AE011062_	gene: "MA3534"; product: "methylase"; Methanosarcina acetivor	12.0	19.0	61.5	72.7	3e-70	01.20.99 other secondary metabolism activities	
Pc22g09680	similarity to hypothetical protein PA4204 - Pseudomonas aeruginosa	7e-17	AE016869_	product: "conserved hypothetical protein"; Pseudomonas syring	226.1	224.8	575.4	1100.4	0		0
Pc22g11250	strong similarity to oligopeptide transporter like protein An15g07460 - Aspergillus niger	5e-77	AY054590_	gene: "Z97341.3"; product: "Unknown protein"; Arabidopsis thali	12.0	12.0	25.2	127.9	0		0
Pc22g11360	strong similarity to dihydroxy-acid dehydratase like protein An07g09870 - Aspergillus niger	0.0	BX640427_	gene: "ilvD"; product: "putative dihydroxy-acid dehydratase"; Bo	12.0	29.4	27.2	154.2	0.0	01.05.01.01 C-compound, carbohydrate catabolism	
Pc22g11440	strong similarity to hypothetical protein contig1483_1.tfa_360wg - Aspergillus fumigatus	5e-26	AH2794	polyketide biosynthesis associated protein Atu1775 [imported] -	27.1	79.0	72.1	169.8	0		0
Pc22g13600	strong similarity to hypothetical protein SPAC922.05c - Schizosaccharomyces pombe	9e-41	T50270	hypothetical protein SPAC922.05c [imported] - fission yeast (Sc	12.0	12.0	49.0	375.3	1e-121	99 UNCLASSIFIED PROTEINS	
Pc22g14520	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	4e-89	T41604	probable membrane transport protein - fission yeast (Schizosac	12.0	12.0	18.8	62.8	1e-157	01.01.01.15 biosynthesis of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine	
Pc22g14710	strong similarity to bifunctiona xylosidase-arabinosidase xarB - Thermoanaerobacter ethanolicus	1e-148	AF135015_	gene: "xarB"; product: "xylosidase/arabinosidase"; Thermoanae	12.0	12.0	12.3	58.0	0.0	01.01.01.15 biosynthesis of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine	
Pc22g15100	strong similarity to dicarboxylic amino acid permease Dip5 - Saccharomyces cerevisiae	1e-109	UFA30825	gene: "AAT1"; product: "amino acid transporter"; Uromyces faba	186.2	281.1	233.6	491.2	1e-105	01.01.07 amino acid transport	
Pc22g15170	strong similarity to propionyl-CoA carboxylase beta chain precursor like protein An15g02830 - Aspergillus	5e-87	BX572604_	product: "possible methylmalonyl-CoA decarboxylase alpha chai	12.0	12.0	14.8	100.7	1e-148	01 METABOLISM	
Pc22g15180	strong similarity to pyruvate carboxylase like protein An15g02820 - Aspergillus niger	4e-93	A83978	pyruvate carboxylase pycA [imported] - Bacillus halodurans (stra	12.0	44.1	31.8	297.3	6e-84	01 METABOLISM	
Pc22g16410	strong similarity to long-chain-fatty-acid acyl-CoA ligase like protein An07g05210 - Aspergillus niger	1e-163	BX842641_	gene: "B22I21.020"; product: "related to long-chain fatty-acid-Co	22.3	84.2	54.8	291.5	1e-126	01 METABOLISM	
Pc22g17460	strong similarity to cytochrome P450 pisatin demethylase PDAT9 - Nectria haematococca	3e-50	S45583	pisatin demethylase (EC 1.14.-.-) cytochrome P450 CYP57 - fun	30.7	50.9	168.4	177.0	1e-107	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g18500	weak similarity to monophenol monooxygenase melC2 - Streptomyces antibioticus	2e-61	NCB1D14_	gene: "B1D14.090"; product: "hypothetical protein"; Neurospora	12.0	12.0	17.0	241.8	0.0	01.20.37.03 biosynthesis of peptide antibiotics	
Pc22g18510	weak similarity to integral membrane protein PTH11 - Magnaporthe grisea	1e-11	AF329397_	gene: "pth"; product: "integral membrane protein"; Blumeria gra	12.0	12.0	54.8	334.0	0		0
Pc22g18600	similarity to serine-type carboxypeptidase precursor cpdS - Aspergillus phoenicis	5e-34	NCB11H7_	gene: "B11H7.050"; product: "probable SERINE-TYPE CARBOX	12.0	12.0	12.1	59.2	8e-54	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc22g19710	strong similarity to hypothetical protein RTS-beta - Homo sapiens	1e-151	AE013861_	gene: "y2598"; product: "hypothetical"; Yersinia pestis KIM secti	22.5	30.9	47.9	156.5	1e-175	01.02.01 nitrogen and sulfur utilization	
Pc22g20360	strong similarity to siderophore-iron transporter for enterobactin Enb1 - Saccharomyces cerevisiae	1e-172	AY131330_	gene: "mirB"; product: "major facilitator MIRB"; Emericella nidula	12.0	12.0	19.4	67.3	1e-90	01 METABOLISM	
Pc22g20380	strong similarity to aerobactin biosynthesis protein iucB - Escherichia coli	1e-143	AB087619_	gene: "aceI"; product: "acetylase"; Aspergillus oryzae aceI gene	12.0	15.0	32.7	90.2	0		0
Pc22g20390	strong similarity to multidrug resistance protein atrD - Aspergillus nidulans	0.0	AB087618_	gene: "sidT"; product: "ABC transporter"; Aspergillus oryzae sidT	15.2	22.1	33.3	100.0	3e-88	01.01 amino acid metabolism	
Pc22g20400	weak similarity to cyclic peptide AM-toxin synthase AMT - Alternaria alternata	0.0	AB087617_	gene: "sid2"; product: "peptide synthetase"; Aspergillus oryzae s	16.1	18.6	34.2	77.4	1e-93	01.05.01 C-compound and carbohydrate utilization	
Pc22g20410	strong similarity to hypothetical protein contig43.tfa_360wg - Aspergillus fumigatus	5e-38	SPAPB24D	gene: "SPAPB24D3.06c"; S.pombe chromosome I BAC pB24D3	29.6	46.1	73.1	151.5	1e-42	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g21090	strong similarity to hypothetical protein An12g09150 - Aspergillus niger	1e-117	AE017238_	product: "hypothetical protein"; Mycobacterium avium subsp. pa	12.0	49.4	50.3	634.6	1e-85	01.05.01 C-compound and carbohydrate utilization	
Pc22g21400	strong similarity to thermostable alcohol dehydrogenase adhT - Bacillus stearothermophilus	3e-59	S47643	alcohol dehydrogenase (EC 1.1.1.1) - Bacillus stearothermophil	12.0	12.0	47.6	104.3	7e-78	01 METABOLISM	
Pc22g21550	similarity to alpha-1,6-mannosyltransferase Hoc1 - Saccharomyces cerevisiae	8e-70	AF374353_	product: "putative mannosyltransferase"; Paracoccidioides brasi	81.4	70.3	186.8	397.0	1e-129	01.04 phosphate metabolism	
Pc22g22390	strong similarity to AK-toxin production protein Akt3-1 - Alternaria alternata	1e-58	AB070713_	gene: "AFT3-1"; product: "Aft3-1"; Alternaria alternata AFT3-1	28.4	30.9	51.3	141.4	0.0	01.01.01 amino acid biosynthesis	
Pc22g23120	strong similarity to hypothetical glutathione S-transferase like protein - Bradyrhizobium japonicum	7e-42	AP005955_	gene: "bll5700"; product: "hypothetical glutathione S-transferase	42.9	98.7	237.2	260.4	1e-176	01 METABOLISM	
Pc22g23320	strong similarity to acid phosphatase aph, 3-phytase phyB - Aspergillus niger	3e-72	JN0890	acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori	24.5	25.4	85.8	131.4	4e-51	01.04.07 phosphate transport	
Pc22g23330	strong similarity to ATP-hydrolyzing 5-oxoprolinase - Rattus norvegicus	0.0	T37524	probable oxoprolinase - fission yeast (Schizosaccharomyces po	12.0	22.5	19.5	88.8	2e-49	01.04.07 phosphate transport	
Pc22g23580	similarity to trichothecene efflux pump TRI12 - Fusarium sporotrichioides	1e-126	NCB2J23_	gene: "B2J23.030"; product: "conserved hypothetical protein";	18.4	12.0	54.7	162.9	3e-55	01.04.07 phosphate transport	
Pc22g24910	strong similarity to hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	1e-36	T41145	probable amine transporter - fission yeast (Schizosaccharomyce	38.8	90.1	154.2	236.8	2e-47	01.01.10 amino acid degradation (catabolism)	
Pc22g24950	strong similarity to hypothetical protein SCE6.29 - Streptomyces coelicolor	4e-50	G87515	secreted protein, probable [imported] - Caulobacter crescentus	15.1	17.5	38.6	127.1	0		0
Pc22g24960	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	1e-140	T50054	probable transporter [imported] - fission yeast (Schizosacharon	122.7	141.6	560.6	995.7	1e-61	01.03 nucleotide metabolism	
Pc22g25250	strong similarity to hypothetical protein ncu00715.1 - Neurospora crassa	2e-96	AP005949_	gene: "bll3876"; product: "aldehyde dehydrogenase"; Bradyrhiz	14.0	18.5	53.6	92.8	0		0
Pc22g25970	strong similarity to hypothetical protein contig1492_0.tfa_3120wg - Aspergillus fumigatus [putative pseudo	0	0	0	12.0	13.1	39.9	93.5	0		0

Supplementary Table 12. K-mean cluster 4

@=Values given are the average of three independent experiments

orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels @				FunCat (auto)	
		p-value	Gene code	description	WIS - PAA	WIS + PAA	DS - PAA	DS + PAA	pval	category
Pc12g00830	strong similarity to sorbitol utilization protein sou2 - Candida albicans	1e-125	AF387300_	gene: "MtDH"; product: "NADP-dependent mannitol dehydr	65.6	91.0	1200.5	787.5	0	0
Pc12g01900	strong similarity to nuclear migration factor nudF - Aspergillus nidulans	1e-118	NCB7H23_	gene: "B7H23.150"; product: "related to NUCLEAR MIGRAT	16.6	12.0	126.7	66.9	2e-40	01.01.04 regulation of amino acid metabolism
Pc12g01930	similarity to ribonuclease III like protein An03g00790 - Aspergillus niger	0	0	0	75.9	73.6	423.7	396.1	2e-25	06.04 protein targeting, sorting and translocation
Pc12g05550	weak similarity to fructosamine-3-kinase FN3K - Homo sapiens	2e-14	NCB3E4_	gene: "B3E4.080"; product: "conserved hypothetical protein	18.9	22.3	116.1	165.4	0	0
Pc12g07500	strong similarity to alpha-1,3-glucanase mutA - Penicillium purpurogenum	1e-173	PFU50838	gene: "mutA"; product: "alpha-1,3-glucanase"; Penicillium f	137.0	16.3	982.1	130.4	1e-80	01.05.07 C-compound, carbohydrate transport
Pc12g07820	similarity to chitosanase csnA - Aspergillus oryzae	1e-87	AB159785_	gene: "csnC"; product: "chitosanase"; Aspergillus oryzae c	31.4	26.4	1190.9	1569.5	0	0
Pc12g07910	similarity to potassium transport protein Trk2 - Saccharomyces cerevisiae	1e-112	SOC29045	gene: "trk1"; product: "high-affinity potassium uptake transp	12.0	12.0	66.7	87.0	2e-99	01.20 secondary metabolism
Pc12g08710	strong similarity to sugar transport protein Stl1 - Saccharomyces cerevisiae	1e-44	S69591	sugar transport protein STP1 - yeast (Saccharomyces cer	34.3	12.0	134.0	180.4	3e-86	01.01.01.15 biosynthesis of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine
Pc12g14380	strong similarity to ribonuclease T1 precursor rntA - Aspergillus oryzae	1e-45	A23620	ribonuclease T1 (EC 3.1.27.3) - Penicillium chrysogenum	12.0	12.0	234.4	72.5	1e-28	01.05 C-compound and carbohydrate metabolism
Pc12g14640	strong similarity to hypothetical protein An06g00160 - Aspergillus niger	0	0	0	98.1	45.7	1520.7	3156.7	0	0
Pc13g06200	similarity to pyoverdine biosynthesis protein PvcA - Pseudomonas aeruginosa	2e-23	BX571868_	Photorhabdus luminescens subsp. laumondii TTO1 compl	22.7	12.2	345.8	35.1	0	0
Pc13g07080	similarity to hypothetical protein An15g00820 - Aspergillus niger	0	0	0	68.9	15.1	678.1	429.5	1e-86	01.05.01 C-compound and carbohydrate utilization
Pc13g07890	similarity to 3-hydroxyisobutyrate dehydrogenase mmsB - Pseudomonas aeruginosa	2e-17	AE010190_	gene: "PF0716"; product: "3-hydroxyisobutyrate dehydroge	12.3	17.3	77.2	134.7	1e-44	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc13g10890	similarity to hypothetical protein PA1213 - Pseudomonas aeruginosa	1e-37	NCG15G9_	gene: "G15G9.020"; product: "conserved hypothetical prote	67.5	58.0	305.2	367.1	0	0
Pc13g11940	strong similarity to glucan 1,4-alpha-glucosidase glaA - Aspergillus niger	1e-134	BX842595_	Neurospora crassa DNA linkage group II BAC clone B24N4	91.2	156.0	3281.4	3681.9	1e-111	01.20.17.03 biosynthesis of amines
Pc13g14720	strong similarity to pisatin demethylase PDA6-1 - Nectria haematococca	7e-35	S34286	pisatin demethylase PDA6-1 - fungus (Nectria haematococ	12.0	18.4	112.8	164.1	0	0
Pc13g14980	weak similarity to developmental protein C-factor csgA - Myxococcus xanthus	4e-20	BX572098_	product: "Short-chain dehydrogenase/reductase (SDR) su	93.0	107.4	568.5	336.0	2e-97	01.05.01 C-compound and carbohydrate utilization
Pc16g00100	strong similarity to choline monooxygenase like protein An04g09810 - Aspergillus niger	1e-29	AP006580_	Gloeobacter violaceus PCC 7421 DNA, complete genome,	12.0	12.0	80.4	61.1	0.0	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis
Pc16g00630	strong similarity to alpha-amylase precursor amy - Aspergillus niger	0.0	AB008370_	product: "acid-stable alpha-amylase"; Aspergillus kawachii	48.3	68.4	503.4	910.0	4e-58	01.01.01 amino acid biosynthesis
Pc16g03010	strong similarity to hypothetical 6-hydroxy-D-nicotine oxidase related protein 13E11.250 - Neurospora crassa	2e-61	T48777	6-HYDROXY-D-NICOTINE OXIDASE related protein [impo	12.0	12.0	112.4	109.1	0	0
Pc16g03020	weak similarity to integral membrane protein PTH11 - Magnaporthe grisea	0	0	0	12.0	12.0	176.4	105.8	0.0	99 UNCLASSIFIED PROTEINS
Pc16g07460	strong similarity to hypothetical neutral amino acid permease - Neurospora crassa	1e-143	BX842615_	gene: "B4B2.030"; product: "related to neutral amino acid p	32.3	68.2	359.3	411.1	0	0
Pc16g10920	strong similarity to hypothetical protein mg07765.1 - Magnaporthe grisea	0	0	0	21.9	12.0	92.8	90.2	1e-116	01.01.01 amino acid biosynthesis
Pc16g11480	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	0.0	CHU68040	gene: "PKS1"; product: "polyketide synthase"; Cochliobolus	12.0	12.0	688.5	208.1	2e-53	01.05.07 C-compound, carbohydrate transport
Pc16g11490	weak similarity to hypothetical dihydrofolate reductase CAB16576.1 - Schizosaccharomyces pombe	1e-11	OSJN0004	gene: "OSJNBa0086B14.2"; Oryza sativa genomic DNA, c	12.0	12.0	252.2	94.9	1e-113	01.20 secondary metabolism
Pc16g11500	strong similarity to hypothetical integral membrane protein - Schizosaccharomyces pombe	1e-134	T39090	probable integral membrane protein - fission yeast (Schizo	82.1	79.1	644.7	345.2	0	0
Pc16g12080	strong similarity to allergen rAsp f 4 - Aspergillus fumigatus	5e-55	AFRASPF	gene: "rasp f 4"; product: "rAsp f 4"; Aspergillus fumigatus r	88.0	54.8	2292.5	902.5	5e-76	01.01.07 amino acid transport
Pc16g13290	strong similarity to hypothetical protein CP0630 - Chlamydophila pneumoniae	1e-176	NCB13B3_	gene: "B13B3.110"; product: "conserved hypothetical prote	12.0	12.0	60.5	77.3	0	0
Pc16g15360	weak similarity to hypothetical protein An14g05070 - Aspergillus niger	0	0	0	32.3	52.6	518.3	196.9	0	0
Pc18g03640	similarity to hypothetical protein dag11 - Agaricus bisporus	5e-16	ABI271703	gene: "dag11"; product: "hypothetical protein"; Agaricus bis	40.3	25.3	130.1	204.2	1e-112	99 UNCLASSIFIED PROTEINS
Pc20g03900	strong similarity to hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	1e-39	T41145	probable amine transporter - fission yeast (Schizosacchar	28.1	62.3	482.7	274.0	2e-94	01.05 C-compound and carbohydrate metabolism
Pc20g06790	strong similarity to trichothecene 3-O-acetyltransferase TRI101 - Fusarium sporotrichioides	1e-144	S50957	probable membrane protein YLL063c - yeast (Saccharomy	12.0	12.0	201.9	61.9	1e-104	02.11 electron transport and membrane-associated energy conservation
Pc20g09750	strong similarity to fructose-1,6-bisphosphate aldolase - Thermus aquaticus	1e-72	BX908809_	gene: "29E8.130"; product: "related to fructose-bisphospha	12.0	12.0	57.4	65.8	0	0
Pc20g10040	strong similarity to choline permease Hnm1 - Saccharomyces cerevisiae [putative sequencing error]	1e-78	S11175	choline transport protein - yeast (Saccharomyces cerevisia	12.0	12.0	114.9	83.5	0	0
Pc20g10750	strong similarity to hypothetical protein An06g01170 - Aspergillus niger [truncated ORF]	0	0	0	34.2	17.3	315.1	347.9	0	0
Pc20g10870	strong similarity to cytochrome P450 trichodiene oxygenase TRI4 - Fusarium sporotrichioides	1e-100	MRAF9417	gene: "TRI4"; product: "cytochrome P450"; Myrothecium ro	47.3	12.0	125.6	156.7	1e-95	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc20g15260	strong similarity to glutaminase A gtaA - Aspergillus oryzae	1e-107	AB029553_	gene: "gtaA"; product: "glutaminase A"; Emericella nidulans	14.8	16.7	89.0	114.6	2e-93	01.04 phosphate metabolism
Pc20g15490	strong similarity to cytochrome P450 monooxygenase P450I - Gibberella fujikuroi	7e-79	GFP450I_1	gene: "P450I"; product: "cytochrome P450 monooxygenase	12.0	12.0	287.0	44.8	2e-71	01.05.04 regulation of C-compound and carbohydrate utilization
Pc21g02690	strong similarity to phosphate-repressible phosphate permease pho-4 - Neurospora crassa	1e-105	JQ0116	phosphate-repressible phosphate permease - Neurospora	12.0	12.0	72.0	55.0	0	0
Pc21g07690	similarity to hypothetical conserved protein SCIF3.07c - Streptomyces coelicolor	5e-21	AB071418_	gene: "ACMSD"; product: "2-amino-3-carboxylmuconate-6-	16.9	23.2	134.1	221.1	0	0
Pc21g08480	hypothetical protein	0	0	0	14.7	12.0	115.4	141.2	0	0
Pc21g08490	weak similarity to hypothetical short chain dehydrogenase SPCC736.13 - Schizosaccharomyces pombe	5e-44	AE011685_	gene: "XAC0583"; product: "oxidoreductase"; Xanthomonas	12.0	12.0	61.4	59.0	0	0
Pc21g09230	similarity to hypothetical protein 1185_scaffold_2.tfa_130cg - Fusarium graminearum	0	0	0	61.7	63.0	288.4	317.1	4e-61	01.01.04 regulation of amino acid metabolism
Pc21g09240	strong similarity to signal peptidase subunit like protein An01g00560 - Aspergillus niger	1e-20	BC061447_	gene: "MGC76332"; product: "MGC76332 protein"; Xenopu	12.0	12.0	113.4	124.0	5e-82	01.01.07 amino acid transport
Pc21g09270	strong similarity to hypothetical protein B11B22.80 - Neurospora crassa	5e-29	T49806	hypothetical protein B11B22.80 [imported] - Neurospora cr	12.0	12.0	190.6	345.7	5e-69	01.05.01.01.02 polysaccharide degradation
Pc21g09830	strong similarity to high affinity glucose transporter HGT1 - Kluyveromyces lactis	4e-80	NCB8G12_	gene: "B8G12.230"; product: "related to hexose transporter	43.4	21.0	184.6	141.9	0	0
Pc21g12340	similarity to hypothetical transcription regulator SPAC139.03 - Schizosaccharomyces pombe	1e-19	BX908809_	gene: "29E8.250"; product: "conserved hypothetical protein	12.0	12.0	81.2	57.5	6e-41	01.01 amino acid metabolism
Pc21g12390	strong similarity to hypothetical protein B2J23.120 - Neurospora crassa	2e-62	NCG65A3_	gene: "G65A3.130"; product: "probable DFG5 protein"; Neu	74.6	65.4	556.6	487.8	0.0	01.20.37.03 biosynthesis of peptide antibiotics
Pc21g12570	similarity to hypothetical protein SPAC13C5.04 - Schizosaccharomyces pombe	5e-13	AX513228_	unnamed ORF; Sequence 1 from Patent WO02063018.	51.1	52.7	1113.7	872.7	0	0
Pc21g12590	similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans	1e-15	HDNO_AR	6-HYDROXY-D-NICOTINE OXIDASE (EC 1.5.3.6) (6-HDN	56.7	100.6	2145.6	1607.9	1e-130	01.01.01 amino acid biosynthesis
Pc21g12610	weak similarity to 7alpha-cephem-methoxylase subunit cmcJ - Streptomyces lactamdurans	1e-23	GFU41749	gene: "des"; product: "GA4 desaturase"; Gibberella fujikuroi	15.2	18.5	567.4	386.5	4e-51	01.05.07 C-compound, carbohydrate transport
Pc21g12620	strong similarity to asparagine synthase asnB - Bacillus subtilis	2e-83	BX294156_	gene: "asnB"; product: "asparagine synthetase"; Pirellula s	55.4	64.3	1901.5	1359.0	3e-78	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc21g12630	similarity to peptide synthase pesA - Metarhizium anisopliae	0.0	AF469045_	gene: "tex1"; product: "nonribosomal peptide synthetase";	44.4	15.2	1486.7	792.0	1e-112	99 UNCLASSIFIED PROTEINS
Pc21g05190	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	3e-53	NC64C2_1	gene: "64C2.200"; product: "related to PUTATIVE TARTRA	94.7	161.9	74.3	176.8	6e-57	01.05.04 regulation of C-compound and carbohydrate utilization
Pc21g14620	strong similarity to lysophospholipase like protein An16g01880 - Aspergillus niger	1e-77	AX952977_	unnamed ORF; Sequence 5 from Patent WO03097825.	66.1	45.0	250.2	697.6	0	0
Pc21g15310	weak similarity to hypothetical intracellular protease amidase related enzyme of the ThiJ family CAC2826 - Clc	2e-15	AE016866_	product: "ThiJ/PfpI family protein"; Pseudomonas syringae	33.0	12.0	392.0	71.1	0	0
Pc21g15460	strong similarity to maackiain detoxification protein MAK1 - Nectria haematococca	9e-46	S70702	maackiain detoxification protein 1 - fungus (Nectria haemat	345.6	167.9	1829.6	653.9	1e-65	01 METABOLISM
Pc21g17820	strong similarity to hypothetical protein sll1024 - Synechocystis sp.	1e-119	NC64C2_2	gene: "64C2.210"; product: "conserved hypothetical protein	92.7	103.8	738.5	1038.6	2e-76	01 METABOLISM
Pc21g17980	strong similarity to hypothetical protein contig5_part_ii.tfa_2530cg - Aspergillus fumigatus	0	0	0	77.9	35.7	896.2	144.5	0	0
Pc21g18040	similarity to conserved domain protein - Pseudomonas syringae	2e-24	AE016873_	product: "conserved domain protein"; Pseudomonas syring	132.4	77.5	606.4	461.7	0	0
Pc21g18920	similarity to cyanate lyase cynS - Escherichia coli	6e-56	NCB10N12	gene: "B10N12.060"; product: "probable cyanate lyase"; Ne	31.8	18.1	159.5	171.4	0	0
Pc21g21280	strong similarity to methyl sterol oxidase Erg25 - Saccharomyces cerevisiae	1e-89	T38986	probable c-4 methyl sterol oxidase - fission yeast (Schizos	44.0	81.5	542.2	971.5	3e-91	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc21g21290	strong similarity to hypothetical protein mg02069.1 - Magnaporthe grisea	7e-23	AG3272	probable lactoylglutathione lyase (EC 4.4.1.5) [imported] - E	119.4	955.7	3398.5	2598.6	0	0
Pc21g21420	strong similarity to hypothetical protein An09g04870 - Aspergillus niger	1e-122	BX842620_	gene: "B11E5.350"; product: "conserved hypothetical prote	12.0	12.0	87.6	107.0	0	0
Pc21g21440	hypothetical protein	0	0	0	20.0	12.0	533.7	170.9	0	0
Pc21g21460	hypothetical protein	0	0	0	121.7	87.8	711.9	614.2	1e-127	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis
Pc21g21470	strong similarity to hypothetical protein contig_1_94_scaffold_6.tfa_290wg - Aspergillus nidulans	0	0	0	112.6	92.1	700.9	694.7	0	0
Pc21g22230	strong similarity to hypothetical protein 1158_scaffold_2.tfa_20wg - Fusarium graminearum	7e-90	BC055631_	gene: "dhcr7"; product: "7-dehydrocholesterol reductase";	39.3	12.0	103.1	198.3	0	0
Pc21g22250	similarity to T-2 toxin biosynthesis protein TRI7 - Fusarium sporotrichioides	9e-22	AF336365_	gene: "Tri7"; product: "TRI7"; Gibberella zeae 88-1 trichoth	27.9	13.3	168.2	494.8	1e-59	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc21g22260	similarity to cholesterol 7alpha-monooxygenase CYP7 - Oryctolagus cuniculus	6e-14	RRCHOL	gene: "CYP7A1"; product: "cholesterol 7a-hydroxylase"; R.	34.9	13.7	106.3	399.9	2e-90	01.01.01 amino acid biosynthesis
Pc21g22710	strong similarity to hypothetical neutral amino acid permease - Neurospora crassa	7e-49	S47892	neutral amino acid permease - Neurospora crassa	12.0	12.0	74.4	148.6	1e-101	14.04.03.05 sporulation and germination
Pc21g23810	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus	8e-31	BX649607_	product: "transcriptional regulator, putative"; Aspergillus fu	12.7	13.3	467.3	648.1	0.0	08.19 cellular import
Pc21g23820	strong similarity to hypothetical protein contig1495_1.tfa_1060wg - Aspergillus fumigatus	0	0	0	32.2	24.4	2288.7	2557.1	0	0
Pc22g00190	strong similarity to hypothetical cell wall protein binB - Aspergillus nidulans	2e-47	ANI011296	gene: "binB"; product: "putative cell wall protein"; Aspergill	409.0	265.9	1384.8	2908.5	3e-50	99 UNCLASSIFIED PROTEINS
Pc22g00670	strong similarity to sorbitol utilization protein sou2 - Candida albicans	1e-55	SOU2_CAI	SORBITOL UTILIZATION PROTEIN SOU2.	12.0	12.0	109.6	273.6	0.0	01.05.01 C-compound and carbohydrate utilization
Pc22g01090	strong similarity to hypothetical protein An11g02070 - Aspergillus niger	0	0	0	25.1	48.3	631.9	85.5	1e-164	01.05.01 C-compound and carbohydrate utilization
Pc22g04940	strong similarity to 2-ketoaldonate reductase like protein An01g07030 - Aspergillus niger	1e-96	BX649607_	product: "NAD-dependant D-isomer specific 2-hydroxyacid	17.4	30.6	141.2	301.5	1e-110	01.07 metabolism of vitamins, cofactors, and prosthetic groups
Pc22g07880	strong similarity to alpha-1-6-glucosidase glcA - Aspergillus parasiticus	0.0	AB044389_	gene: "malT"; product: "maltase"; Aspergillus oryzae malP	132.9	118.5	719.4	1007.1	1e-151	01.05 C-compound and carbohydrate metabolism
Pc22g08110	strong similarity to cytochrome P450 eln2 - Coprinus cinereus	8e-82	BX842624_	gene: "B10D6.150"; product: "related to O-methylsterigmat	31.6	12.9	108.9	81.6	2e-71	01 METABOLISM
Pc22g12680	weak similarity to hypothetical protein PA5433 - Pseudomonas aeruginosa	2e-05	S50347	hypothetical protein YIR042c - yeast (Saccharomyces cere	62.1	67.8	309.2	333.5	7e-61	01.02 nitrogen and sulfur metabolism
Pc22g13580	strong similarity to diglycosidase related protein like protein An03g00500 - Aspergillus niger	0.0	THA24382	gene: "P2"; product: "P2 protein"; Trichoderma harzianum	21.0	12.8	128.0	1308.7	0	0
Pc22g13590	strong similarity to hypothetical protein - Gloeobacter violaceus	0.0	AP006580_	Gloeobacter violaceus PCC 7421 DNA, complete genome,	54.2	40.9	877.7	456.0	0	0
Pc22g18620	strong similarity to proline iminopeptidase - Arabidopsis thaliana	2e-86	AY059916_	gene: "At2g14260; T1O16.15"; product: "proline iminopeptic	172.0	134.9	664.4	841.7	0	0
Pc22g19330	strong similarity to nitrilase - Rhodococcus rhodochrous	8e-69	AY487547_	product: "nitrilase"; Uncultured organism clone 2A11 nitrila	12.0	12.0	272.0	389.4	4e-59	01.04.07 phosphate transport
Pc22g19520	strong similarity to hypothetical protein contig10.tfa_410cg - Aspergillus fumigatus	0	0	0	60.2	39.7	247.7	189.6	0	0
Pc22g19620	strong similarity to arabinofuranosidase B abfB - Aspergillus niger	0.0	AB073860_	gene: "abfB"; product: "alpha-L-arabinofuranosidase B"; As	26.9	22.6	118.0	300.3	0.0	01.01.01 amino acid biosynthesis
Pc22g20210	strong similarity to yeast phase specific gene yps-3 - Histoplasma capsulatum	2e-26	HTOYSPC	gene: "yps-3"; product: "yeast phase specific protein"; Ajell	50.8	18.0	539.9	461.8	4e-77	01.05 C-compound and carbohydrate metabolism
Pc22g22290	strong similarity to IgE-binding protein - Aspergillus fumigatus	6e-37	AFU6688_	product: "IgE-binding protein"; Aspergillus fumigatus mRN	273.7	311.2	1417.9	1970.8	0	0
Pc22g22420	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	1e-178	BX842680_	gene: "90C4.090"; product: "related to allantoate permease	64.4	14.2	379.7	306.4	5e-70	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc22g23110	strong similarity to acetolactate synthase precursor ALS - Schizosaccharomyces pombe	0.0	AF013601_	product: "acetolactate synthase"; Magnaporthe grisea acet	36.3	105.3	911.5	884.5	0	0
Pc22g24990	strong similarity to hypothetical protein contig589.tfa_1960wg - Aspergillus fumigatus	9e-64	AE011478_	product: "alcohol dehydrogenase"; Leptospira interrogans	17.9	17.2	86.5	148.3	0	0

Supplementary Table 13. K-mean cluster 5

@=Values given are the average of three independent experiments

orf code	**Description of putative *P. chrysogenum* ORF**	**Best blast homolog to putative *P. chrysogenum* ORF**			**Average transcript levels @**				**FunCat (auto)**	
		p-value	**Gene code**	**description**	**WIS - PAA**	**WIS + PAA**	**DS - PAA**	**DS + PAA**	**pval**	**category**
Pc12g0021	strong similarity to quinate transport protein qutD - Aspergillus nidulans	2e-50	S08498	quinate transport protein - Emericella nidulans	400.3	375.9	571.3	1262.1	2e-47	01.04.07 phosphate transport
Pc12g0022	strong similarity to galactoside acetyltransferase lacA - Escherichia coli	1e-33	AL935260_	gene: "thgA3"; product: "galactoside O-acetyltransferase"; Lactobaci	471.6	364.9	544.7	960.3	1e-169	01.01.01 amino acid biosynthesis
Pc12g0025	strong similarity to transmembrane transporter liz1p - Schizosaccharomyces pombe	1e-71	T40485	transmembrane transporter Liz1p - fission yeast (Schizosaccharomy	17.0	12.0	24.1	32.0	2e-79	01.05 C-compound and carbohydrate metabolism
Pc12g0102	strong similarity to threonine aldolase Gly1 - Saccharomyces cerevisiae	9e-87	AGAJ5442	gene: "GLY1"; product: "threonine aldolase"; Eremothecium gossypii	279.2	401.4	777.8	546.7	0	0
Pc12g0114	strong similarity to alcohol dehydrogenase alcB - Aspergillus nidulans	5e-49	AB046446_	gene: "alcB"; product: "alcohol dehydrogenase II"; Monascus anka a	12.0	12.0	12.0	32.0	1e-102	01 METABOLISM
Pc12g0232	weak similarity to phosphinothricin acetyltransferase pat - Streptomyces coelicolor	9e-07	AP005935_	gene: "bll0009"; Bradyrhizobium japonicum USDA 110 DNA, comple	21.8	17.1	32.6	58.4	0	0
Pc12g0268	strong similarity to 3-phosphoglycerate dehydrogenase like protein An12g01580 - Aspergillus	5e-46	AB3200	phosphoglycerate dehydrogenase serA [imported] - Agrobacterium tu	12.0	12.0	12.0	26.4	8e-75	01.05.07 C-compound, carbohydrate transport
Pc12g0292	weak similarity to 2-hydroxyisoflavone reductase IRL - Zea mays	2e-11	NC5F3_3	gene: "5F3.030"; product: "hypothetical protein"; Neurospora crassa	126.3	58.5	152.4	152.5	2e-57	01 METABOLISM
Pc12g0322	strong similarity to high-affinity glucose transporter HGT1 - Kluyveromyces lactis	1e-84	AF168613_	gene: "hxtA"; product: "hexose transporter protein"; Aspergillus para	65.9	21.8	30.3	51.4	0.0	01.05.01.01 C-compound, carbohydrate catabolism
Pc12g0351	similarity to lipase LipP - Pseudomonas sp.	1e-23	F84000	carboxylesterase BH2806 [imported] - Bacillus halodurans (strain C-	90.2	28.9	159.5	108.4	1e-135	01.01 amino acid metabolism
Pc12g0363	strong similarity to beta-glucosidase bgln - Candida molischiana	0.0	A46838_1	unnamed ORF; Sequence 5 from Patent WO9530009.	36.1	31.9	51.8	117.4	1e-107	01.01 amino acid metabolism
Pc12g0437	strong similarity to phosphoserine transaminase Ser1 - Saccharomyces cerevisiae	1e-121	NCB20D17	gene: "B20D17.010"; product: "related to 3-phosphoserine aminotran	343.4	363.1	808.0	757.1	8e-78	01.05.07 C-compound, carbohydrate transport
Pc12g0542	strong similarity to O-acetylhomoserine (thiol)-lyase cysD - Aspergillus nidulans	0.0	CYSD_EM	O-ACETYLHOMOSERINE (THIOL)-LYASE (EC 4.2.99.10) (O-ACE	697.3	788.1	1322.9	1708.2	0	0
Pc12g0544	strong similarity to maltose transport protein Mal31 - Saccharomyces cerevisiae	6e-93	NC5E6_16	gene: "5E6.180"; product: "probable alpha-glucoside transport protei	235.5	296.4	595.9	933.0	1e-120	01.01.10.04 degradation of amino acids of the pyruvate family
Pc12g0830	strong similarity to precursor of tannase - Aspergillus oryzae	0.0	TST50593	gene: "faeC"; product: "ferulic acid esterase"; Talaromyces stipitatus	29.7	37.6	35.6	79.9	2e-80	01.01.01.01 assimilation of ammonia, biosynthesis of the glutamate group
Pc12g0853	strong similarity to long-chain acyl-CoA dehydrogenase like protein An13g03940 - Aspergillu	1e-101	AY033936_	product: "probable acyl-CoA dehydrogenase"; Glomus intraradices pr	135.7	126.8	178.3	352.0	6e-93	01.01.10 amino acid degradation (catabolism)
Pc12g0886	weak similarity to thyroid hormone-binding protein mu-crystallin Crym - Homo sapiens	2e-98	ANAJ3459	gene: "prnX"; product: "PrnX protein"; Aspergillus nidulans prnD, prn	44.7	74.4	79.0	187.2	1e-147	01.01 amino acid metabolism
Pc12g0988	strong similarity to acetamidase amdS - Aspergillus oryzae	0.0	AY048582_	gene: "gmdA"; product: "general amidase"; Emericella nidulans gene	45.7	61.8	166.9	198.6	0	0
Pc12g1035	similarity to L-2,4-diaminobutyrate decarboxylase dat - Acinetobacter baumannii	1e-104	NC123A4_	gene: "123A4.310"; product: "related to L-2, 4-diaminobutyrate decar	31.1	30.1	92.4	84.3	5e-49	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc12g1092	strong similarity to secretory lipase LIP2 - Candida albicans	1e-117	AX015710_	unnamed ORF; Sequence 1 from Patent WO9950420.	93.1	32.4	29.5	107.2	7e-54	01.05 C-compound and carbohydrate metabolism
Pc12g1154	similarity to isopenicillin N epimerase cefD - Streptomyces clavuligerus	2e-45	T40624	probable class v pyridoxal phosphate dependent aminotransferase - f	272.6	431.8	805.3	1032.8	1e-108	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc12g1175	similarity to beta-glucuronidase GUSB - Canis lupus	2e-82	SCO93913	gene: "SCO7506"; "SCBAC17A6.39"; product: "putative hydrolase";	31.2	39.2	112.3	101.4	3e-74	01 METABOLISM
Pc12g1233	strong similarity to cytochrome P450 monooxygenase TRI11 - Fusarium sporotrichioides	1e-104	AY102594_	gene: "TRI11"; product: "trichothecene C-15 hydroxylase"; Gibberell	44.3	34.7	57.2	69.6	1e-174	01 METABOLISM
Pc12g1336	strong similarity to aliphatic nitrilase - Rhodococcus rhodochrous	3e-93	NCB23G1_	gene: "B23G1.100"; product: "related to aliphatic nitrilase"; Neurosp	18.0	13.8	25.4	40.9	9e-66	01.05 C-compound and carbohydrate metabolism
Pc12g1366	strong similarity to indole-3-acetaldehyde dehydrogenase iad1 - Ustilago maydis	1e-101	T51919	related to aldehyde dehydrogenase (NAD+) [imported] - Neurospora	213.9	147.6	360.4	484.5	4e-63	01.01 amino acid metabolism
Pc12g1420	similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	2e-42	AF500213_	product: "putative dehydrogenase"; Podospora anserina idi-2 locus,	129.9	179.2	196.2	407.2	0	0
Pc12g1467	strong similarity to choline permease Hnm1 - Saccharomyces cerevisiae	3e-57	ENI131668	gene: "gabA"; product: "GABA permease"; Emericella nidulans gabA	46.9	36.6	71.1	114.5	1e-101	01 METABOLISM
Pc13g0251	similarity to L-2-haloalkanoic acid dehalogenase hadL - Pseudomonas putida	1e-19	HAD_PSE	2-HALOALKANOIC ACID DEHALOGENASE (EC 3.8.1.2) (L-2-HAL	15.4	15.9	47.6	60.8	3e-39	01.01.01 amino acid biosynthesis
Pc13g0271	strong similarity to multifunctional beta-oxidation protein - Neurospora crassa	4e-32	BX572603_	product: "MaoC-like dehydratase:Asparaginase/glutaminase"; Rhodo	441.9	416.2	460.4	853.4	0	0
Pc13g0406	strong similarity to hypothetical pyridoxine synthesis protein PDX2 - Cercospora nicotianae	1e-100	AF363613_	gene: "pyroB"; product: "pyridoxine"; Aspergillus nidulans pyridoxine	82.7	101.3	164.3	241.5	1e-145	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc13g0418	similarity to 7alpha-cephem-methoxylase subunit cmcJ - Streptomyces lactamdurans	1e-49	AP005958_	gene: "bll6449"; Bradyrhizobium japonicum USDA 110 DNA, comple	15.4	12.0	12.0	47.8	7e-59	01.01.10 amino acid degradation (catabolism)
Pc13g0440	strong similarity to diacylglycerol acyltransferase DAGAT - Arabidopsis thaliana	9e-63	AF251794_	product: "putative diacylglycerol acyltransferase"; Brassica napus pu	59.7	46.2	65.9	110.0	1e-141	01.01.99 other amino acid metabolism activities
Pc13g0512	strong similarity to phenol 2-monooxygenase - Trichosporon beigelii	0.0	BX908810_	gene: "G3C5.110"; product: "probable phenol 2-monooxygenase"; N	116.8	95.9	195.8	238.7	0.0	01.01.01 amino acid biosynthesis
Pc13g0540	strong similarity to leukotriene-A4 hydrolase - Mus musculus	1e-161	S61099	leukotriene-A4 hydrolase homolog YNL045w - yeast (Saccharomyces	168.0	167.0	253.6	386.9	0	0
Pc13g0551	strong similarity to ATP-hydrolyzing 5-oxoprolinase - Rattus norvegicus	0.0	T37524	probable oxoprolinase - fission yeast (Schizosaccharomyces pombe)	43.7	38.0	101.5	95.8	6e-89	01 METABOLISM
Pc13g0663	strong similarity to C4-dicarboxylate transport protein mae1p - Schizosaccharomyces pombe	1e-70	NCB21D9_	gene: "B21D9.140"; product: "related to C4-dicarboxylate transport pr	12.0	12.0	13.8	34.1	0.0	01.05 C-compound and carbohydrate metabolism
Pc13g0686	similarity to phenazine biosynthesis oxidoreductase phzF - Pseudomonas fluorescens	4e-22	S75237	hypothetical protein - Synechocystis sp. (strain PCC 6803)	213.7	268.4	417.6	610.9	7e-79	01.05.07 C-compound, carbohydrate transport
Pc13g0779	strong similarity to succinate-semialdehyde dehydrogenase NAD(P)+ gabD - Escherichia col	1e-158	AE016857_	gene: "gabD-2"; product: "succinate-semialdehyde dehydrogenase";	30.4	52.8	76.6	120.3	0.0	02.11 electron transport and membrane-associated energy conservation
Pc13g0863	strong similarity to high-affinity glucose transporter HGT1 - Kluyveromyces lactis	1e-73	A31776	lactose permease - yeast (Kluyveromyces marxianus var. lactis)	85.8	31.3	56.9	116.5	1e-124	01.01.01 amino acid biosynthesis
Pc13g0864	strong similarity to FAD dependent L-sorbose dehydrogenase SDH - Gluconobacter oxydans	7e-53	AP003001_	gene: "mll3225"; product: "dehydrogenase; polyethylene glycol dehyd	44.8	55.2	100.0	149.2	1e-150	01.01 amino acid metabolism
Pc13g0899	strong similarity to homoserine dehydrogenase YJR139c - Saccharomyces cerevisiae	1e-109	T49733	probable homoserine dehydrogenase [imported] - Neurospora crassa	325.2	392.6	652.7	671.2	3e-89	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc13g0935	strong similarity to glutamate decarboxylase 1 - Felis silvestris catus	2e-81	AF149833_	gene: "GAD67"; product: "glutamic acid decarboxylase isoform 67";	22.8	18.9	39.7	46.3	1e-85	01.03.01 purine nucleotide metabolism
Pc13g0974	strong similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	0.0	PJFAOP_1	gene: "faoP"; product: "fructosyl amino acid oxidase"; P.janthinellum	48.3	43.4	117.8	193.7	2e-83	01.01.01.15 biosynthesis of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine
Pc13g1108	similarity to inosine-uridine nucleosid hydrolase IUNH - Crithidia fasciculata	1e-154	BX649605_	product: "possible nucleoside hydrolase"; Aspergillus fumigatus BAC	101.0	101.8	201.4	205.8	3e-55	01 METABOLISM
Pc13g1198	similarity to 3-hydroxyisobutyrate dehydrogenase mmsB - Pseudomonas aeruginosa	6e-35	BX649606_	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot proje	23.7	30.1	43.8	74.1	6e-62	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc13g1208	similarity to acetyl-hydrolase chnC - Acinetobacter sp.	2e-87	BX649606_	product: "esterase/lipase/thioesterase family protein, putative"; Asper	111.1	147.1	180.3	440.2	1e-143	01.06.99 other lipid, fatty-acid and isoprenoid metabolism activities
Pc13g1341	strong similarity to hypothetical short-chain dehydrogenase PA1379 - Pseudomonas aerugin	2e-36	BX649607_	product: "short-chain oxidoreductase, putative"; Aspergillus fumigatu	90.1	176.9	198.7	223.2	1e-172	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc13g1417	strong similarity to glycosylphosphatidylinositol-anchored beta(1-3)glucanosyltransferase gel	1e-123	NCB17B1_	gene: "B17B1.110"; product: "related to beta (1-3) glucanosyltransfer	64.6	73.7	128.5	184.9	9e-74	01.01 amino acid metabolism
Pc13g1568	strong similarity to indoleamine 2,3-dioxygenase IDO - Mus musculus	9e-83	S57097	indoleamine-pyrrole 2,3-dioxygenase homolog YJR078w - yeast (Sac	53.3	67.0	127.8	108.5	2e-84	01.05.01.01.01 sugar, glucoside, polyol and carboxylate catabolism
Pc13g1580	strong similarity to serine racemase - Mus musculus	1e-107	NCB11H24	gene: "B11H24.140"; product: "related to threonine dehydratase"; Ne	56.2	60.5	114.2	136.1	1e-110	01.01.07 amino acid transport
Pc13g1592	strong similarity to endo 1,5-alpha-arabinanase abnA - Aspergillus niger	1e-122	ABNA_ASI	ARABINAN ENDO-1,5-ALPHA-L-ARABINOSIDASE A PRECURSO	131.4	255.9	402.0	547.5	1e-175	01.01 amino acid metabolism
Pc14g0015	strong similarity to lysine permease Lyp1 - Saccharomyces cerevisiae	1e-129	S60914	lysine transport protein - yeast (Saccharomyces cerevisiae)	38.7	14.5	45.6	54.0	4e-58	01.05.07 C-compound, carbohydrate transport
Pc14g0024	strong similarity to aromatic-L-amino-acid decarboxylase DDC - Rattus norvegicus	1e-103	RN31884_	product: "aromatic L-amino acid decarboxylase"; Rattus norvegicus a	76.5	95.8	125.7	224.4	0.0	01 METABOLISM
Pc14g0040	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	9e-62	BX842680_	gene: "90C4.090"; product: "related to allantoate permease"; Neuros	290.2	412.3	479.6	962.1	1e-76	01.04 phosphate metabolism
Pc14g0059	strong similarity to succinyl-CoA:3-ketoacid-CoA transferase SCOT - Homo sapiens	1e-131	BT008292_	product: "Homo sapiens 3-oxoacid CoA transferase"; Synthetic cons	24.1	20.3	26.5	46.2	5e-37	01.04.01 phosphate utilization
Pc14g0081	weak similarity to sphingoid long chain base kinases Lcb4 - Saccharomyces cerevisiae	1e-07	AB018110_	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K19M	131.3	185.6	278.0	406.6	1e-121	01.05 C-compound and carbohydrate metabolism
Pc15g0021	similarity to glucan 1,3-beta-glucosidase Bgl2 - Saccharomyces cerevisiae	2e-25	AF359360_	gene: "OrfC"; product: "glucosidase"; Fusarium sporotrichioides trich	1180.7	1237.5	2819.4	2262.1	1e-132	01 METABOLISM
Pc15g0151	strong similarity to brown 2 protein abr2 - Aspergillus fumigatus	1e-77	AF104823_	gene: "abr2"; product: "brown 2"; Aspergillus fumigatus brown 2 (abr	181.4	175.6	444.7	397.5	8e-75	01.05.04 regulation of C-compound and carbohydrate utilization
Pc16g0012	strong similarity to hypothetical protein RTS-beta - Homo sapiens	1e-118	AE013861_	gene: "y2598"; product: "hypothetical"; Yersinia pestis KIM section 26	12.0	12.0	15.2	25.9	7e-64	01 METABOLISM
Pc16g0014	strong similarity to high affinity hexose transporter Hxt1 - Saccharomyces cerevisiae	3e-77	S69591	sugar transport protein STP1 - yeast (Saccharomyces cerevisiae)	12.0	12.0	15.6	30.6	6e-82	01.01.04 regulation of amino acid metabolism
Pc16g0034	similarity to alcohol dehydrogenase pan2 - Mus musculus	1e-19	BC009830_	product: "retinol dehydrogenase 14 (all-trans and 9-cis)"; Homo sapi	29.9	44.3	65.9	65.3	8e-76	01.05.07 C-compound, carbohydrate transport
Pc16g0356	similarity to thiamine repressible gene thi1p - Schizosaccharomyces pombe	8e-17	T40521	hypothetical protein SPBC530.05 - fission yeast (Schizosaccharomy	19.2	12.0	21.7	43.9	6e-69	01.05 C-compound and carbohydrate metabolism
Pc16g0365	strong similarity to myo-inositol transporter 2 itr2p - Schizosaccharomyces pombe	5e-94	T43400	myo-inositol transporter - fission yeast (Schizosaccharomyces pombe	80.1	61.2	168.0	199.2	0.0	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis
Pc16g0378	strong similarity to enoyl reductase of the lovastatin biosynthesis lovC - Aspergillus terreus	2e-78	TOXD_CO	TOXD PROTEIN.	32.6	25.8	71.1	87.4	1e-157	01.05 C-compound and carbohydrate metabolism
Pc16g0380	strong similarity to polyketide synthase PKS1 - Cochliobolus heterostrophus	0.0	AY495597_	gene: "PKS7"; product: "polyketide synthase"; Gibberella moniliformis	56.8	31.4	84.8	93.7	6e-93	01.05 C-compound and carbohydrate metabolism
Pc16g0522	strong similarity to alpha-xylosidase XylS - Sulfolobus solfataricus	0.0	G83906	hypothetical protein BH2055 [imported] - Bacillus halodurans (strain	48.0	29.8	86.4	68.4	9e-80	01.05.07 C-compound, carbohydrate transport
Pc16g0637	strong similarity to cellulose synthase protein like protein An03g05740 - Aspergillus niger	2e-21	AG3170	conserved hypothetical protein Atu5090 [imported] - Agrobacterium tu	114.8	133.0	125.6	327.0	5e-51	01.04.07 phosphate transport
Pc16g0685	strong similarity to high affinity glucose transporter HGT1 - Kluyveromyces lactis [putative se	1e-68	A31776	lactose permease - yeast (Kluyveromyces marxianus var. lactis)	26.4	12.0	18.9	29.5	2e-79	01.05.07 C-compound, carbohydrate transport
Pc16g0694	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	3e-68	T41604	probable membrane transport protein - fission yeast (Schizosaccharo	12.0	12.0	13.5	35.8	1e-102	01 METABOLISM
Pc16g0849	strong similarity to maltose transport protein Mal31 - Saccharomyces cerevisiae	4e-99	BX842681_	gene: "B13N4.080"; product: "probable maltose permease"; Neurosp	52.8	67.5	75.5	152.7	0.0	01.01.01 amino acid biosynthesis
Pc16g0960	strong similarity to NAD(P)H-dependent xylose reductase XYL1 - Pachysolen tannophilus	1e-155	AF219625_	gene: "xyrA"; product: "D-xylose reductase"; Aspergillus niger D-xylos	14.7	16.6	33.1	64.5	5e-99	01.03 nucleotide metabolism
Pc16g1002	sulfate permease SutB - Penicillium chrysogenum	0.0	AF163974_	gene: "sutB"; product: "sulfate permease SutB"; Penicillium chrysoge	472.9	577.1	926.6	1470.3	0.0	01 METABOLISM
Pc16g1053	strong similarity to adenosine deaminase Aah1 - Saccharomyces cerevisiae	1e-133	AF123460_	gene: "nadA"; product: "adenine deaminase"; Emericella nidulans ade	14.3	27.5	33.3	41.2	9e-75	01.05.04 regulation of C-compound and carbohydrate utilization
Pc16g1120	strong similarity to copper amine oxidase AO-I - Aspergillus niger	1e-163	BX649606_	gene: "ao-I"; product: "copper amine oxidase 1, putative"; Aspergillus	12.0	12.0	17.1	27.4	3e-76	25.05.25 gametogenesis
Pc16g1122	strong similarity to hexose transporter ght2p - Schizosaccharomyces pombe	2e-93	NC13E11_	gene: "13E11.140"; product: "probable sugar transporter"; Neurospo	12.7	12.0	41.3	42.2	1e-101	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc16g1135	strong similarity to novobiocin biosynthetic gene novR - Streptomyces spheroides	1e-69	AL646066_	gene: "RSc1767"; "RS02954"; product: "CONSERVED HYPOTHET	221.1	414.4	430.5	967.3	0	0
Pc16g1162	strong similarity to hypothetical sterigmatocystin biosynthesis p450 monooxygenase stcB - A	8e-71	AF169016_	gene: "cypX"; product: "cytochrome P450 monooxigenase"; Aspergil	12.0	12.0	41.1	19.4	0	0
Pc16g1163	strong similarity to arylsulfate sulfotransferase like protein An13g03160 - Aspergillus niger	2e-57	BX649607_	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot proje	38.0	33.7	54.0	71.8	5e-81	01.05 C-compound and carbohydrate metabolism
Pc16g1184	strong similarity to phosphinothricin acetyltransferase like protein An04g09830 - Aspergillus	5e-07	NCB13B3_	gene: "B13B3.050"; product: "conserved hypothetical protein"; Neuro	227.8	204.1	287.7	449.3	1e-87	01 METABOLISM
Pc16g1236	strong similarity to glutathione-dependent formaldehyde dehydrogenase FDH - Methylobacte	8e-51	AF1918	alcohol dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)	35.3	15.9	25.1	44.8	3e-50	01.04.07 phosphate transport
Pc16g1298	strong similarity to D-mandelate dehydrogenase - Rhodotorula graminis	1e-150	BX649607_	product: "NAD-dependant D-isomer specific 2-hydroxyacid dehydrog	12.0	12.0	12.0	36.6	6e-63	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc16g1395	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	3e-70	T41604	probable membrane transport protein - fission yeast (Schizosaccharo	12.0	12.0	12.0	26.6	1e-79	01.05.07 C-compound, carbohydrate transport
Pc16g1423	strong similarity to beta-ketoacyl reductase rhlG - Pseudomonas aeruginosa	1e-86	NCB9B15_	gene: "B9B15.060"; product: "probable NADPH-dependent beta-keto	100.9	52.0	139.4	241.1	1e-35	01.03 nucleotide metabolism
Pc16g1444	strong similarity to glucose transporter rco-3 - Neurospora crassa	0.0	ANI251561	gene: "mstA"; product: "MSTA protein"; Aspergillus nidulans mstA ge	1238.9	1228.0	2726.4	2906.0	1e-101	01 METABOLISM
Pc16g1451	similarity to orotidine-5-phosphate decarboxylase pyrA - Aspergillus niger	2e-08	DCASOE	orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Emericella nidu	153.9	193.3	310.1	337.3	1e-89	01.01.10 amino acid degradation (catabolism)
Pc16g1464	strong similarity to cytochrome P450 monooxygenase stcS - Aspergillus nidulans	9e-41	STCS_EM	PROBABLE STERIGMATOCYSTIN BIOSYNTHESIS P450 MONO	12.0	12.0	12.2	25.3	2e-62	01.05 C-compound and carbohydrate metabolism

Pc16g1477	strong similarity to phenol 2-monooxygenase - Trichosporon beigelii	6e-88	BX908810_	gene: "G3C5.110"; product: "probable phenol 2-monooxygenase"; N	12.0	12.0	23.1	30.8	1e-179	01.01.01 amino acid biosynthesis	
Pc18g0049	weak similarity to myo-inositol 2-dehydrogenase yisS - Bacillus subtilis	1e-177	BX842620_	gene: "B11E5.420"; product: "conserved hypothetical protein"; Neuro	20.6	25.5	28.3	53.2	1e-118	01.05.01 C-compound and carbohydrate utilization	
Pc18g0133	strong similarity to saccharopine reductase LYS3 - Magnaporthe grisea [putative sequencing	1e-133	T40337	probable saccharopine dehydrogenase (NADP, L-glutamate-forming)	80.4	121.8	168.8	267.4	1e-32	01.02 nitrogen and sulfur metabolism	
Pc18g0159	strong similarity to glycolate oxidase GOX - Mus musculus	4e-78	AF104312_	product: "glycolate oxidase"; Mus musculus glycolate oxidase mRNA	14.0	16.5	19.8	35.9	2e-82	01.01 amino acid metabolism	
Pc18g0213	similarity to epoxide hydrolase - Rattus norvegicus	8e-14	AF2333	hypothetical protein all4221 [imported] - Nostoc sp. (strain PCC 7120	29.1	34.5	61.3	104.8	3e-90	01.05 C-compound and carbohydrate metabolism	
Pc18g0348	strong similarity to high affinity methionine permease Mup1 - Saccharomyces cerevisiae	1e-150	S61943	methionine transport protein, high affinity - yeast (Saccharomyces ce	127.2	67.3	98.0	278.4	1e-100	01 METABOLISM	
Pc18g0483	strong similarity to formaldehyde dismutase like protein An07g07160 - Aspergillus niger	5e-57	BX572599_	product: "zinc-containing dehydrogenase"; Rhodopseudomonas palu	12.0	13.9	13.6	48.3	2e-81	01.05.01 C-compound and carbohydrate utilization	
Pc18g0499	strong similarity to alkane-inducible cytochrome P450 gene ALK1 - Yarrowia lipolytica	3e-87	AB010388_	gene: "ALK1"; product: "ALK1"; Yarrowia lipolytica gene for ALK1, c	51.6	56.9	152.0	236.0	1e-132	01.03.19 nucleotide transport	
Pc18g0553	similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans	2e-19	AP003010_	gene: "mlr6875"; product: "probable oxidoreductase"; Mesorhizobiun	208.3	169.9	310.5	462.7	4e-70	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc20g0142	strong similarity to purine permease with broad specificity uapC - Aspergillus nidulans	0.0	A56382	purine permease, broad specificity - Emericella nidulans	16.9	24.3	38.6	32.5	1e-52	01 METABOLISM	
Pc20g0179	strong similarity to high affinity glucose transporter HGT1 - Kluyveromyces lactis	1e-122	HGT1_KLU	HIGH-AFFINITY GLUCOSE TRANSPORTER.	36.1	16.7	32.1	40.0	1e-117	01.02 nitrogen and sulfur metabolism	
Pc20g0322	3-phosphoadenosine-5-phosphosulfate reductase ParA - Penicillium chrysogenum	1e-180	AF227433_	gene: "ParA"; product: "3'-phosphoadenosine-5'-phosphosulfate redu	297.6	354.1	467.6	895.6	4e-80	01.05.07 C-compound, carbohydrate transport	
Pc20g0389	strong similarity to epoxide hydrolase hyl1 - Aspergillus niger	1e-140	ANI238459	gene: "hyl1"; product: "epoxide hydrolase"; Aspergillus niger hyl1 gen	64.2	95.1	196.8	236.3	1e-63	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc20g0403	strong similarity to quinate transport protein qutD - Aspergillus nidulans	1e-58	BX649605_	gene: "qutD"; product: "quinate permease, putative"; Aspergillus fum	458.9	93.3	242.0	605.9	1e-98	01.01.04 regulation of amino acid metabolism	
Pc20g0428	strong similarity to levodione reductase lvr - Corynebacterium aquaticum	4e-30	AE012980_	gene: "FabG"; product: "Dehydrogenases with different specificities (	186.3	220.3	287.3	508.8	2e-60	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc20g0663	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	1e-13	S49627	regulatory protein ARGR2 - yeast (Saccharomyces cerevisiae)	12.5	18.7	31.4	55.3	4e-81	01.05.07 C-compound, carbohydrate transport	
Pc20g0686	strong similarity to hypothetical short chain dehydrogenase SPCC736.13 - Schizosaccharom	7e-38	T41570	hypothetical protein SPCC736.13 - fission yeast (Schizosaccharomy	16.2	12.0	30.9	37.3	2e-73	01.02.01 nitrogen and sulfur utilization	
Pc20g0728	strong similarity to mitochondrial phosphate transport protein G7 - Glycine max	1e-117	TMA23853	gene: "pcp"; product: "putative mitochondrial phosphate carrier protei	135.3	264.5	851.0	647.4	1e-75	01.01.04 regulation of amino acid metabolism	
Pc20g0943	similarity to hypothetical ureidoglycolate hydrolase SPAC19G12.04 - Schizosaccharomyces p	9e-19	S42022	ureidoglycolate hydrolase (EC 3.5.3.19) - yeast (Saccharomyces cere	19.7	31.9	40.2	51.2	2e-61	01.05.01 C-compound and carbohydrate utilization	
Pc20g0960	similarity to transcription factor Aro80 - Saccharomyces cerevisiae	3e-23	S69704	hypothetical protein YDR421w - yeast (Saccharomyces cerevisiae)	14.5	12.0	39.4	33.0	1e-90	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc20g0993	similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans	6e-54	T48777	6-HYDROXY-D-NICOTINE OXIDASE related protein [imported] - Ne	13.4	12.0	67.8	47.5	1e-133	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis	
Pc20g1086	strong similarity to geranylgeranyl pyrophosphate synthase al-3 - Neurospora crassa	1e-59	MCI276129	gene: "carG"; product: "geranylgeranyl pyrophosphate synthase"; Mu	18.6	12.0	31.9	33.5	1e-62	01 METABOLISM	
Pc20g1203	strong similarity to sterol delta14,15-reductase erg-3 - Neurospora crassa	0.0	NHSTR2G	gene: "STR2"; N.haematococca STR2 gene	153.4	89.9	113.9	218.8	1e-106	01.01 amino acid metabolism	
Pc20g1247	strong similarity to delta3-cis-delta2-trans-enoyl-CoA isomerase Eci1 - Saccharomyces cerev	7e-41	S50369	probable membrane protein YLR284c - yeast (Saccharomyces cerevi	84.2	118.2	153.3	360.8	1e-135	01 METABOLISM	
Pc20g1342	strong similarity to biotin synthesis enzyme like protein An15g01990 - Aspergillus niger	1e-121	AP003859_	gene: "OJ1033_B09.17"; product: "putative adenosylmethionine-8-an	226.3	193.1	372.1	568.6	0.0	01.05.01 C-compound and carbohydrate utilization	
Pc20g1350	strong similarity to very long-chain fatty acyl-CoA synthase Fat1 - Saccharomyces cerevisiae	1e-163	ACH50763	gene: "cefD1"; product: "isopenicillin N-CoA synthetase"; Acremoniu	54.7	25.9	45.7	143.7	1e-108	01.20 secondary metabolism	
Pc20g1351	strong similarity to methylcitrate synthase mcsA - Aspergillus nidulans	0.0	ANI249117	gene: "mcsA"; product: "methylcitrate synthase"; Aspergillus nidulan	254.2	229.7	319.8	460.0	5e-91	01.05 C-compound and carbohydrate metabolism	
Pc20g1396	strong similarity to anthranilate N-benzoyltransferase like protein An01g12130 - Aspergillus n	9e-10	AF466397_	gene: "DBNTBT"; product: "3'-N-debenzoyltaxol N-benzoyltransferas	38.2	20.1	41.1	51.0	1e-114	01.01.07 amino acid transport	
Pc20g1405	similarity to fructosamine-3-kinase FN3K - Homo sapiens	3e-27	NCB3E4_6	gene: "B3E4.080"; product: "conserved hypothetical protein"; Neuros	18.7	13.5	28.4	37.1	1e-102	01.01.10 amino acid degradation (catabolism)	
Pc20g1488	strong similarity to general amino acid permease Gap1 - Saccharomyces cerevisiae	1e-77	UFA30825	gene: "AAT1"; product: "amino acid transporter"; Uromyces fabae A	12.0	12.0	12.0	40.3	0.0	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis	
Pc20g1515	similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	5e-23	T40295	fructosyl amine - fission yeast (Schizosaccharomyces pombe)	55.1	103.0	116.2	217.3	9e-75	01.05.07 C-compound, carbohydrate transport	
Pc21g0096	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	0.0	AY495602_	gene: "PKS12"; product: "polyketide synthase"; Gibberella moniliform	81.0	16.6	138.1	116.3	1e-148	01.05.01.01 C-compound, carbohydrate catabolism	
Pc21g0173	strong similarity to quinate transport protein qutD - Aspergillus nidulans	2e-82	S08498	quinate transport protein - Emericella nidulans	49.8	36.5	73.7	75.1	1e-53	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g0255	strong similarity to hexokinase-like protein xprF - Aspergillus nidulans	0.0	ANI251893	gene: "xprF"; product: "hexokinase-like protein"; Aspergillus nidulans	335.0	664.0	1112.7	1368.2	0.0	01.01.01 amino acid biosynthesis	
Pc21g0309	strong similarity to meso-2,3-butanediol dehydrogenase like protein An14g05430 - Aspergillu	3e-42	F83629	probable short chain dehydrogenase PA0117 [imported] - Pseudomo	35.7	42.8	58.6	94.4	0		0
Pc21g0359	strong similarity to tryptophan synthase Trp5 - Saccharomyces cerevisiae	0.0	AF207903_	gene: "trpB"; product: "bifunctional tryptophan synthase TRPB"; Asp	207.2	197.1	395.3	400.4	1e-50	01.05.07 C-compound, carbohydrate transport	
Pc21g0415	similarity to cytosine deaminase codA - Escherichia coli	6e-26	AE016948_	product: "N-acyl-D-amino-acid deacylase family protein"; Enterococc	38.1	30.5	58.1	80.5	6e-80	01.01.04 regulation of amino acid metabolism	
Pc21g0458	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	9e-89	T41345	probable allantoate permease - fission yeast (Schizosaccharomyces p	30.0	27.4	50.2	104.0	4e-46	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g0505	weak similarity to positive regulator qa-1F - Neurospora crassa	2e-16	AY218847_	gene: "PRF"; product: "binuclear zinc transcription factor"; Nectria h	480.5	770.1	1169.9	973.6	2e-78	01.05.07 C-compound, carbohydrate transport	
Pc21g0811	similarity to developmental protein C-factor csgA - Myxococcus xanthus	2e-32	AG0388	probable short-chain dehydrogenase [imported] - Yersinia pestis (stra	12.0	14.8	14.1	33.2	2e-50	11.05.01 resistance proteins	
Pc21g0834	strong similarity to quinate transport protein qutD - Aspergillus nidulans [putative sequencing	2e-67	S08498	quinate transport protein - Emericella nidulans	46.2	28.1	56.1	102.3	2e-84	01.05.07 C-compound, carbohydrate transport	
Pc21g0960	strong similarity to esterase A gene EstA - Streptomyces chrysomallus	1e-101	AY052630_	gene: "cddB"; product: "lactone hydrolase"; Rhodococcus ruber strai	116.2	57.8	130.3	202.8	3e-92	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g0968	strong similarity to quinic acid permease QA-Y - Neurospora crassa	4e-86	G31277	quinate transport protein - Neurospora crassa (tentative sequence)	12.0	12.0	17.4	35.2	4e-95	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g0978	strong similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	0.0	AF035700_	product: "fructosyl amine:oxygen oxidoreductase"; Aspergillus fumig	12.0	12.0	30.7	43.3	0.0	01.05 C-compound and carbohydrate metabolism	
Pc21g0991	strong similarity to cytochrome P450 trichodiene oxygenase TRI4 - Fusarium sporotrichioides	1e-118	AY102602_	gene: "TRI4"; product: "cytochrome P450"; Fusarium culmorum strai	12.6	12.0	32.1	41.8	2e-66	01.01.10 amino acid degradation (catabolism)	
Pc21g1006	strong similarity to 1,4-alpha-glucan branching enzyme Glc3 - Saccharomyces cerevisiae	0.0	AB072730_	gene: "gbeA"; product: "glycogen branching enzyme"; Aspergillus or	219.6	159.0	370.4	388.0	1e-73	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	
Pc21g1023	strong similarity to salicylate hydroxylase nahG - Pseudomonas putida	4e-53	BX640431_	product: "putative monooxygenase"; Bordetella parapertussis strain 1	78.1	64.8	106.7	131.0	3e-46	01.05.01 C-compound and carbohydrate utilization	
Pc21g1025	strong similarity to pyridoxamine-phosphate oxidase Pdx3 - Saccharomyces cerevisiae	2e-36	S41301	pyridoxamine-phosphate oxidase (EC 1.4.3.5) - yeast (Saccharomyce	19.5	26.6	63.0	53.9	2e-51	01.04.07 phosphate transport	
Pc21g1059	strong similarity to carbonic anhydrase pca1 - Porphyridium purpureum	8e-55	AE011245_	gene: "icfA"; product: "Carbonic anhydrase"; Leptospira interrogans s	37.6	33.8	139.6	96.7	0		0
Pc21g1094	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	2e-71	T41345	probable allantoate permease - fission yeast (Schizosaccharomyces p	12.0	12.0	12.0	33.6	0		0
Pc21g1163	weak similarity to hypothetical polysaccharide synthase CPS1 - Filobasidiella neoformans [pu	1e-84	BX842682_	gene: "B13C5.060"; product: "putative protein"; Neurospora crassa D	12.0	12.0	43.7	34.9	1e-119	01.06.04 breakdown of lipids, fatty acids and isoprenoids	
Pc21g1178	strong similarity to 3-dehydroshikimate dehydratase qa-4 - Neurospora crassa	2e-57	BX649605_	gene: "qutC"; product: "3-dehydroshikimate dehydratase, putative"; A	12.0	12.0	12.0	32.6	1e-164	01.05.01.01 C-compound, carbohydrate catabolism	
Pc21g1211	strong similarity to triacylglycerol lipase Tgl2 - Saccharomyces cerevisiae	4e-40	SCTGL2_1	gene: "TGL2"; product: "triglyceride lipase"; S.cerevisiae TGL2 gene	56.5	53.5	75.4	121.7	5e-67	01.03 nucleotide metabolism	
Pc21g1367	strong similarity to enzyme with sugar transferase activity like protein An01g10930 - Aspergil	0.0	AB057788_	gene: "agdB"; product: "alpha-glucosidase B"; Aspergillus nidulans g	881.8	1205.8	3599.5	3336.1	3e-23	01.01.04 regulation of amino acid metabolism	
Pc21g1498	strong similarity to methionine adenosyltransferase regulatory beta subunit like protein An02g	3e-97	NCB10H4_	gene: "B10H4.170"; product: "related to methionine adenosyltransfera	36.9	44.8	84.3	101.6	4e-90	01.04 phosphate metabolism	
Pc21g1503	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	6e-06	SAJ10151_	gene: "pro1"; product: "PRO1 protein"; Sordaria macrospora pro1 ge	13.1	13.9	36.2	50.1	7e-81	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g1525	strong similarity to phosphate-repressible phosphate permease pho-4 - Neurospora crassa	2e-98	JQ0116	phosphate-repressible phosphate permease - Neurospora crassa	37.6	36.8	77.2	45.3	1e-143	01.04.01 phosphate utilization	
Pc21g1545	strong similarity to cytochrome P450 monooxygenase P450I - Gibberella fujikuroi	8e-85	GFP450I_1	gene: "P450I"; product: "cytochrome P450 monooxygenase"; Gibber	344.1	281.2	1420.2	617.7	1e-112	01.02.01.09.99 other catabolism of nitrogenous compounds	
Pc21g1597	strong similarity to cytosolic exopolyphosphatase Ppx1 - Saccharomyces cerevisiae	4e-24	T38544	probable exopolyphosphatase - fission yeast (Schizosaccharomyces	31.2	29.5	54.8	83.5	1e-124	01.01.01.15.03 biosynthesis of leucine	
Pc21g1603	strong similarity to dimethylaniline monooxygenase like protein An09g05690 - Aspergillus nig	3e-94	NC93G11_	gene: "93G11.170"; product: "related to flavin-containing monooxyge	21.5	23.5	38.0	62.1	0.0	01 METABOLISM	
Pc21g1759	strong similarity to acyl-CoA dehydrogenase like protein An17g01150 - Aspergillus niger	0.0	NCB10H4_	gene: "B10H4.130"; product: "conserved hypothetical protein"; Neur	529.8	553.1	838.7	1248.7	1e-120	01.05.01 C-compound and carbohydrate utilization	
Pc21g1779	strong similarity to glutathione synthase Gsh2 - Saccharomyces cerevisiae	2e-81	AF397211_	gene: "HME2"; product: "glutathione synthetase"; Pichia angusta glut	181.7	244.5	349.9	532.6	0		0
Pc21g1781	strong similarity to flavocytochrome b2 L-lactate dehydrogenase CYB2 - Pichia anomala	1e-62	S06600	L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast	18.0	24.0	34.3	55.5	1e-77	01.01 amino acid metabolism	
Pc21g1819	strong similarity to alpha-glucuronidase aguA - Aspergillus niger	0.0	ANI290451	gene: "aguA"; product: "alpha-glucuronidase"; Aspergillus niger aguA	12.0	12.0	14.2	40.7	0.0	01.01.01 amino acid biosynthesis	
Pc21g1879	strong similarity to hypothetical protein An02g09790 - Aspergillus niger	1e-139	T39195	probable amino acid permease - fission yeast (Schizosaccharomyces	90.8	123.2	286.5	367.5	1e-36	99 UNCLASSIFIED PROTEINS	
Pc21g1936	sulfate permease SutA - Penicillium chrysogenum	0.0	AF163975_	gene: "sutA"; product: "SutA"; Penicillium chrysogenum SutA (sutA)	34.2	12.0	38.5	51.4	1e-80	01.01.99 other amino acid metabolism activities	
Pc21g2040	strong similarity to alpha-galactosidase aglC - Aspergillus niger	0.0	ANI251873	gene: "aglC"; product: "alpha-galactosidase C"; Aspergillus niger aglC	15.6	18.6	27.6	37.7	0.0	01.20.37.03 biosynthesis of peptide antibiotics	
Pc21g2138	isopenicillin N synthase ips PcbC - Penicillium chrysogenum	0.0	S04441	isopenicillin N synthase (EC 1.14.11.-) ips [similarity] - Penicillium ch	1312.0	2381.9	5107.0	5111.8	1e-158	13 REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT	
Pc21g2139	alpha-aminoadipyl-cysteinyl-valine synthetase pcbAB acvA - Penicillium chrysogenum [putati	0.0	YGPLV8	alpha-aminoadipyl-cysteinyl-valine synthetase (EC 6.-.-.-) - Penicilliur	1098.0	2060.0	4345.2	4557.4	1e-66	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g2154	strong similarity to lipase lip1 - Geotrichum candidum	1e-103	NCB23G1_	gene: "B23G1.090"; product: "related to cholinesterase"; Neurospora	12.0	12.4	27.8	53.8	1e-134	01 METABOLISM	
Pc21g2181	strong similarity to levodione reductase lvr - Corynebacterium aquaticum	1e-110	AFA12H2_	gene: "AfA12H2.17c"; product: "putative 3-oxoacyl-[acyl-carrier prote	79.3	82.3	154.4	241.3	1e-90	01 METABOLISM	
Pc21g2243	strong similarity to p-nitrobenzyl esterase pnbA - Bacillus subtilis	7e-33	YLI249751	gene: "lip3"; product: "carboxylesterase/lipase type B"; Yarrowia lipol	12.0	12.0	42.4	50.6	1e-104	01 METABOLISM	
Pc21g2255	strong similarity to hydroxymethylbilane synthase Hem3 - Saccharomyces cerevisiae [putative	1e-57	CAC38F10	gene: "Ca38F10.02"; product: "Porphobilinogen deaminase"; C.albic	15.0	12.0	34.8	40.5	1e-102	01.02.01 nitrogen and sulfur utilization	
Pc21g2266	strong similarity to aldehydereductase ALR - Rattus norvegicus	6e-73	AY207463_	gene: "Akr1a4"; product: "aldehyde reductase"; Mus musculus aldeh	12.0	12.0	12.0	41.6	2e-93	01 METABOLISM	
Pc21g2359	strong similarity to cyanamide hydratase - Myrothecium verrucaria	6e-46	S56194	hypothetical protein YFL061w - yeast (Saccharomyces cerevisiae)	193.0	191.7	411.6	800.9	6e-84	01 METABOLISM	
Pc21g2365	strong similarity to D-lactate dehydrogenase ldhA - Escherichia coli	1e-127	BX842680_	gene: "90C4.110"; product: "related to D-lactate dehydrogenase"; Ne	82.9	87.7	121.8	189.9	3e-64	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g0016	strong similarity to protein with stereoselective transaminase activity like protein An04g08630	3e-66	MLO67211	gene: "msi247"; product: "PUTATIVE BRANCHED-CHAIN AMINO A	53.5	29.8	55.3	105.9	3e-74	01.05.07 C-compound, carbohydrate transport	
Pc22g0024	similarity to short-chain alcohol dehydrogenase adhA - Aspergillus parasiticus	8e-15	AF396778_	gene: "bacC"; product: "BacC"; Bacillus subtilis strain A1/3 bacilysin	85.6	84.3	74.2	273.0	1e-163	01 METABOLISM	
Pc22g0052	strong similarity to carnitine acyl carnitine carrier acuH - Aspergillus nidulans	1e-134	ENAJ1156	gene: "acuH"; product: "carnitine/acyl carnitine carrier"; Emericella n	94.1	47.1	112.8	107.9	1e-126	01.01 amino acid metabolism	
Pc22g0096	strong similarity to acetoacetyl-CoA synthase acsA - Sinorhizobium meliloti	0.0	NC15E11_	gene: "15E11.130"; product: "related to acetoacetyl-CoA synthetase"	35.6	71.6	80.2	160.1	1e-126	01.01 amino acid metabolism	
Pc22g0097	strong similarity to glutamate decarboxylase GAD1 - Arabidopsis thaliana	0.0	JC7915	glutamate decarboxylase (EC 4.1.1.15) - Aspergillus oryzae	54.2	61.9	161.9	205.6	3e-70	01 METABOLISM	
Pc22g0097	strong similarity to glutamate decarboxylase GAD1 - Arabidopsis thaliana	0.0	JC7915	glutamate decarboxylase (EC 4.1.1.15) - Aspergillus oryzae	54.2	61.9	161.9	205.6	4e-99	01.01.10 amino acid degradation (catabolism)	
Pc22g0100	strong similarity to nitrilase NIT1 - Arabidopsis thaliana	1e-144	AB078872_	gene: "NITA"; product: "hypothetical nitrilase-like protein"; Aspergillu	26.8	37.2	83.2	91.6	1e-70	01.05.07 C-compound, carbohydrate transport	
Pc22g0175	strong similarity to hypothetical amidase - Schizosaccharomyces pombe	2e-74	OSJN0019	gene: "OSJNBb0006L01.6"; Oryza sativa genomic DNA, chromosor	12.0	12.0	12.0	32.5	5e-90	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	
Pc22g0197	strong similarity to carnitine acylcarnitine translocase like protein An08g10550 - Aspergillus r	2e-57	CNS09S49	DNA centromeric region sequence from BAC DP26B06, DP34F04, D	31.8	38.4	66.7	137.0	7e-97	01.05 C-compound and carbohydrate metabolism	
Pc22g0231	strong similarity to 3,4-dihydroxy-2-butanone 4-phosphate synthase Rib3 - Saccharomyces c	5e-72	AF430214_	product: "3,4-dihydroxy-2-butanone 4-phosphate synthase"; Magnap	41.5	35.0	57.7	71.5	2e-66	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g0357	strong similarity to benzyl alcohol dehydrogenase areB - Acinetobacter sp.	5e-65	AE007890_	gene: "AGR_pAT_280"; product: "AGR_pAT_280p"; Agrobacterium	33.5	34.9	55.4	81.7	0.0	01.01 amino acid metabolism	
Pc22g0368	strong similarity to NADPH-dependent beta-ketoacyl reductase RhlG - Pseudomonas aerugir	1e-53	BX572608_	gene: "rhlG"; product: "putative beta-ketoacyl reductase"; Rhodopseu	161.8	130.5	370.5	460.7	9e-50	01.04.07 phosphate transport	
Pc22g0374	strong similarity to gamma-Glutamyltranspeptidase - Pseudomonas aeruginosa	0.0	NC9G6_26	gene: "9G6.280"; product: "related to lincomycin-condensing protein	55.3	88.1	129.9	193.3	1e-155	01.04.01 phosphate utilization	
Pc22g0576	strong similarity to H+-biotin symporter Vht1 - Saccharomyces cerevisiae	2e-82	S51956	probable membrane protein YAL067c - yeast (Saccharomyces cerevi	81.2	79.4	97.1	287.2	4e-82	01.05.07 C-compound, carbohydrate transport	
Pc22g0761	strong similarity to phytase phyA3 - Aspergillus fumigatus	2e-57	AX799096_	Sequence 2 from Patent WO03054199.	97.7	92.5	149.6	230.6	1e-131	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis	
Pc22g0787	strong similarity to maltose transport protein Mal31 - Saccharomyces cerevisiae	0.0	AB044389_	gene: "malP"; product: "maltose permease"; Aspergillus oryzae malP	417.6	121.0	810.4	1132.6	0.0	02.11 electron transport and membrane-associated energy conservation	

Pc22g0903	strong similarity to 3-oxoacyl-(acyl-carrier-protein) synthase like protein An02g14220 - Asper	1e-143	AF021234_	gene: "cem-1"; product: "3-oxoacyl-[acyl-carrier-protein]-synthase"; N	53.6	51.6	84.1	111.2	6e-64	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g0940	strong similarity to aryl-alcohol oxidase precursor aao - Pleurotus eryngii	1e-160	CNS07TIX	DNA centromeric region sequence from BAC DP15B03, DP38F06 o	12.0	12.0	13.1	33.0	3e-66	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis	
Pc22g0948	strong similarity to 2-keto-3-deoxygluconate oxidoreductase kduD - Erwinia chrysanthemi	1e-40	TACID3_9	gene: "Ta0747"; product: "glucose 1-dehydrogenase related protein";	63.3	35.6	59.4	99.6	6e-55	01.02.01 nitrogen and sulfur utilization	
Pc22g0956	strong similarity to cyclopropane-fatty-acyl-phospholipid like protein An02g04530 - Aspergillu	1e-36	AP005035_	gene: "cfa"; product: "putative cyclopropane fatty acid synthase"; Str	59.2	23.5	71.2	131.1	2e-72	01.06.10 regulation of lipid, fatty-acid and isoprenoid metabolism	
Pc22g1148	strong similarity to 2-nitropropane dioxygenase ncd-2 - Neurospora crassa	8e-55	T46693	probable 2-nitropropane dioxygenase (EC 1.13.11.32) precursor [imp	187.5	248.9	405.9	622.9	0.0	01.04 phosphate metabolism	
Pc22g1204	strong similarity to protein involved in fatty acid regulation like protein An04g07120 - Aspergill	3e-48	AE017009_	product: "Nitroreductase family protein"; Bacillus cereus ATCC 1457	51.2	65.8	78.0	161.0	9e-73	01.01.04 regulation of amino acid metabolism	
Pc22g1235	strong similarity to extracellular alpha-glucosidase aglU - Aspergillus niger	0.0	JC4217	alpha-glucosidase (EC 3.2.1.20) - Aspergillus oryzae	70.2	70.3	297.0	214.2	3e-55	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc22g1236	strong similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	0.0	AF155808_	gene: "amyR"; product: "unknown"; Aspergillus niger (amyR) gene, c	121.5	83.0	353.7	458.8	1e-76	01.05 C-compound and carbohydrate metabolism	
Pc22g1270	strong similarity to hypothetical sugar transporter encoded by DRA0271 - Deinococcus radio	7e-96	SPAPB1E7	gene: "SPAPB1E7.08c"; S.pombe chromosome I BAC pB1E7.	29.9	25.3	36.4	56.3	1e-129	01.01 amino acid metabolism	
Pc22g1339	strong similarity to alcohol dehydrogenase like protein An02g02060 - Aspergillus niger	8e-41	AE017006_	product: "Alcohol dehydrogenase"; Bacillus cereus ATCC 14579 sec	258.1	301.5	529.1	917.1	4e-78	01.05.07 C-compound, carbohydrate transport	
Pc22g1365	strong similarity to 2,2-dialkylglycine decarboxylase structural protein dgdA - Pseudomonas c	1e-171	AY093612_	gene: "DGD1"; product: "dialkylglycine decarboxylase"; Mycosphaere	12.0	12.0	20.6	37.9	1e-130	01 METABOLISM	
Pc22g1453	strong similarity to maltose transport protein Mal31 - Saccharomyces cerevisiae	1e-96	BX842681_	gene: "B13N4.080"; product: "probable maltose permease"; Neurosp	76.4	60.4	94.5	159.0	7e-94	01.05.01 C-compound and carbohydrate utilization	
Pc22g1490	phenylacetyl-CoA ligase pclA - Penicillium chrysogenum	0.0	PCPHCOA	gene: "pclA"; product: "phenylacetyl-CoA ligase"; Penicillium chrysog	108.5	140.0	222.5	381.6	1e-100	01.05.01 C-compound and carbohydrate utilization	
Pc22g1539	strong similarity to alpha-glucan synthase mok1p - Schizosaccharomyces pombe	0.0	T43731	cell wall alpha-glucan synthase (EC 2.4.1.-) mok1 - fission yeast (Sch	69.5	35.9	101.0	149.1	1e-82	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	
Pc22g1651	strong similarity to isoamyl alcohol oxidase mreA - Aspergillus oryzae	0.0	AB078977_	gene: "mreB"; product: "probable alcohol oxidase"; Aspergillus oryza	118.0	112.8	182.5	242.2	1e-127	01 METABOLISM	
Pc22g1937	strong similarity to biotin-apoprotein ligase Bpl1 - Saccharomyces cerevisiae [putative sequer	1e-111	S64646	biotin-[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15) [validated] - yeas	82.2	86.3	111.3	174.8	1e-75	01 METABOLISM	
Pc22g2027	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	2e-94	SCO93911	gene: "SCO4383"; "4CL-2"; "SCD10.15"; product: "4-coumarate:CoA	111.8	173.9	186.3	458.8	0.0	01.05 C-compound and carbohydrate metabolism	
Pc22g2037	strong similarity to carnitine racemase like protein An03g03550 - Aspergillus niger	6e-40	AP005945_	gene: "fadB"; product: "enoyl CoA hydratase"; Bradyrhizobium japoni	12.0	12.0	12.0	43.3	1e-126	01.01.01 amino acid biosynthesis	
Pc22g2212	strong similarity to 4-alpha-glucanotransferase amylo-1,6-glucosidase Gdb1 - Saccharomyc	0.0	S59841	4-alpha-glucanotransferase / amylo-1,6-glucosidase homolog YPR18	126.0	175.2	750.7	460.1	8e-61	01.04.07 phosphate transport	
Pc22g2251	strong similarity to branched-chain amino acid aminotransferase bcaT - Lactococcus lactis	5e-81	AF157629_	gene: "TOXF"; product: "putative branched-chain amino acid aminotr	140.9	173.4	442.5	370.7	1e-157	01.05 C-compound and carbohydrate metabolism	
Pc22g2334	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	3e-84	T41604	probable membrane transport protein - fission yeast (Schizosaccharo	12.0	12.0	12.0	46.1	0		0
Pc22g2337	strong similarity to aldehyde dehydrogenase aldh3 - Homo sapiens	8e-98	AF016452_	gene: "T05H4.13"; product: "Hypothetical protein T05H4.13b"; Caen	188.1	110.5	162.9	275.9	4e-79	01.01.01.01 assimilation of ammonia, biosynthesis of the glutamate group	
Pc22g2370	weak similarity to fructosyl amine oxygen oxidoreductase - Aspergillus fumigatus	1e-04	AFU82830	product: "fructosyl amine: oxygen oxidoreductase"; Aspergillus fumig	12.4	15.1	32.4	52.0	1e-45	01.05 C-compound and carbohydrate metabolism	
Pc22g2371	strong similarity to pyrroline-5-carboxylate reductase P5CR - Zalerion arboricola	2e-55	JC4830	pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Zalerion arboricola	12.0	14.4	25.3	37.3	1e-124	01.05.01 C-compound and carbohydrate utilization	
Pc22g2397	strong similarity to hypothetical phosphoglycerate mutase YKR043c - Saccharomyces cerevi	2e-45	S38115	hypothetical protein YKR043c - yeast (Saccharomyces cerevisiae)	44.0	36.1	101.0	123.7	4e-83	01.05.01 C-compound and carbohydrate utilization	
Pc22g2413	strong similarity to L-lactate 2-monooxygenase LA2M - Mycobacterium smegmati	1e-106	SPAPB1A1	gene: "SPAPB1A11.03"; S.pombe chromosome I BAC pB1A11.	106.8	73.2	219.3	451.4	1e-116	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc22g2487	strong similarity to 6-hydroxy-d-nicotine oxidase 6-HDNO - Arthrobacter oxidans	4e-51	B95997	probable oxidoreductase, oxygen dependent, FAD-dependent protein	83.1	109.4	160.4	230.3	3e-95	01 METABOLISM	
Pc22g2515	strong similarity to acyl CoA dehydrogenase aidB - Escherichia coli	4e-81	NC2E4_2	gene: "2E4.020"; product: "conserved hypothetical protein"; Neurosp	46.2	17.5	96.9	189.3	5e-61	01.01.10.01.03 degradation of arginine	
Pc22g2516	strong similarity to chitinase 1 precursor cts1 - Coccidioides immitis	6e-97	AF529207_	gene: "chiB"; product: "endochitinase"; Botryotinia fuckeliana endoch	156.3	145.3	356.8	443.3	1e-121	02.19 metabolism of energy reserves (e.g. glycogen, trehalose)	
Pc12g1462	strong similarity to flavohemoglobin Fhp - Alcaligenes eutrophus	1e-104	AB016807_	product: "flavohemoglobin"; Fusarium oxysporum mRNA for flavoher	148.3	150.1	243.0	430.4	7e-42	01.01.01.01.02.01 biosynthesis of proline	
Pc16g0422	strong similarity to trehlose metabolism factor Pmu1 - Saccharomyces cerevisiae	2e-32	T18237	conserved hypothetical protein - yeast (Candida albicans)	31.5	30.8	34.8	64.8	1e-109	01 METABOLISM	
Pc20g0200	strong similarity to 3-oxoadipate enol-lactone hydrolase catD - Pseudomonas sp.	1e-113	NCB13B3_	gene: "B13B3.090"; product: "related to 3-OXOADIPATE ENOL-LAC	12.0	12.0	20.2	49.2	1e-100	01.03 nucleotide metabolism	
Pc22g0366	strong similarity to isocitrate lyase acuD - Aspergillus nidulans	0.0	AY442291_	Aspergillus fumigatus isocitrate lyase (icl) gene, complete cds.	276.0	155.8	456.4	509.8	1e-122	03.01.05 DNA recombination and DNA repair	
Pc22g1415	similarity to transaldolase talB - Synechocystis sp.	4e-25	AY144980_	product: "TAL1"; Saccharomyces castellii clone Contig2026 TAL1 g	34.7	41.3	59.7	130.1	3e-26	01.05.01.01 C-compound, carbohydrate catabolism	
Pc13g0053	similarity to helicase Pif1 - Saccharomyces cerevisiae	5e-15	T47241	RRM3/PIF1 helicase homolog - fission yeast (Schizosaccharomyces	37.6	22.9	59.7	55.0	1e-73	01.04 phosphate metabolism	
Pc13g0650	similarity to adaptive response regulatory protein Ada - Escherichia coli	5e-19	F91016	O6-methylguanine-DNA methyltransferase [imported] - Escherichia c	12.5	12.0	29.7	44.5	1e-120	03.01.05 DNA recombination and DNA repair	
Pc16g1385	similarity to dis1-suppressing protein kinase dsk1p - Schizosaccharomyces pombe	3e-12	S28282	hypothetical protein B0464.5 - Caenorhabditis elegans	55.7	39.2	86.9	83.8	0.0	03.01.05.01 DNA repair	
Pc21g1193	strong similarity to protein DLH1 - Candida albicans	1e-116	A38214	meiosis-specific recombination protein DMC1 [validated] - yeast (Sac	119.2	89.8	186.2	240.2	8e-68	01.04 phosphate metabolism	
Pc22g2255	strong similarity to DNA photolyase phr1 - Trichoderma harzianum	0.0	THA00996	gene: "phr1"; product: "DNA photolyase"; Trichoderma harzianum ph	14.7	12.0	43.0	29.9	4e-21	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc06g0024	weak similarity to SR protein kinase Sky1 - Saccharomyces cerevisiae	4e-29	A47726	dis1-suppressing protein kinase dsk1 - fission yeast (Schizosaccharo	26.7	12.0	38.6	34.3	6e-75	04 TRANSCRIPTION	
Pc06g0185	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	1e-31	CNS09S49	DNA centromeric region sequence from BAC DP26B06, DP34F04, D	27.1	15.0	31.1	32.7	8e-38	04.05.01.04 transcriptional control	
Pc06g0203	similarity to developmental control protein like protein An09g01040 - Aspergillus niger	2e-06	AE003420_	gene: "EG:BACR42I17.11"; product: "CG11398-PA"; Drosophila me	108.3	80.1	228.5	221.9	5e-79	01.06.01.07.11 tetracyclic and pentacyclic triterpenes (cholesterin, steroids and hopanoids) biosynthesis	
Pc13g0658	strong similarity to root-specific homeotic protein like protein An14g00520 - Aspergillus niger	3e-15	BX842620_	gene: "B11E5.180"; product: "hypothetical protein"; Neurospora cras	12.0	12.0	28.2	41.1	0		0
Pc13g0944	strong similarity to transcription factor like protein An02g06940 - Aspergillus niger	7e-15	BC055035_	gene: "Tcfcp2l3"; product: "Tcfcp2l3 protein"; Mus musculus transcr	112.1	101.6	251.6	238.0	1e-90	01.01.04 regulation of amino acid metabolism	
Pc13g0989	weak similarity to cercosporin resistance protein crg1 - Cercospora nicotianae	0	0	0	12.0	12.0	19.7	43.0	1e-107	01.01.04 regulation of amino acid metabolism	
Pc13g1444	strong similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	3e-29	CT1A_FUS	CUTINASE TRANSCRIPTION FACTOR 1 ALPHA.	12.0	13.3	13.1	29.9	3e-21	01.01.04 regulation of amino acid metabolism	
Pc14g0002	weak similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	4e-24	NC5E6_27	gene: "5E6.310"; product: "related to nitrate assimilation regulatory pr	85.6	132.7	153.2	343.6	7e-31	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc14g0098	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	1e-06	T41718	hypothetical fungal Zn(2)-Cys(6) zinc-finger protein - fission yeast (S	44.2	69.4	153.7	182.8	5e-77	04.05.01.04 transcriptional control	
Pc14g0137	similarity to transcription factor Upc2 - Saccharomyces cerevisiae	6e-08	S61580	probable membrane protein YDR213w - yeast (Saccharomyces cerev	94.7	144.9	235.0	320.1	0		0
Pc15g0121	similarity to transcription regulator 2 of pai operon paiB - Bacillus subtilis	2e-26	AP002994_	gene: "mll0013"; product: "transcriptional regulator"; Mesorhizobium	88.3	83.5	174.2	169.7	1e-87	01.01.04 regulation of amino acid metabolism	
Pc16g0022	similarity to cutinase transcription factor alpha CTF1a - Fusarium solani	2e-14	NCB11N2_	gene: "B11N2.030"; product: "probable CUTINASE TRANSCRIPTIC	12.0	12.0	16.2	40.3	2e-81	01.01.04 regulation of amino acid metabolism	
Pc16g0107	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	4e-43	BX908809_	gene: "29E8.250"; product: "conserved hypothetical protein"; Neuros	28.5	25.4	38.9	52.5	3e-80	04.05.01.04 transcriptional control	
Pc16g0910	strong similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	3e-35	A41696	regulatory protein nit-4 - Neurospora crassa	18.1	19.6	66.0	62.3	9e-90	01.01.04 regulation of amino acid metabolism	
Pc16g0913	similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	5e-11	AY027529_	product: "Ste12-like transcription factor"; Neurospora crassa Ste12-li	27.4	30.2	50.2	77.7	1e-31	01.01.04 regulation of amino acid metabolism	
Pc18g0109	weak similarity to protein PRIB - Lentinus edodes	0	0	0	40.1	34.8	57.9	77.2	2e-18	01.01.04 regulation of amino acid metabolism	
Pc18g0315	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces p	1e-08	T37604	probable transcription activator - fission yeast (Schizosaccharomyces	20.3	30.1	44.9	82.4	4e-37	01.01.04 regulation of amino acid metabolism	
Pc20g0175	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	9e-04	S61587	transcription activator LYS14 - yeast (Saccharomyces cerevisiae)	24.3	18.2	37.9	39.3	1e-103	01.03.13 regulation of nucleotide metabolism	
Pc20g0654	weak similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	8e-64	AJ582911_	Aspergillus fumigatus regA gene for transcription factor RegA,	42.1	45.2	64.6	121.8	5e-95	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc20g0657	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	6e-15	T40521	hypothetical protein SPBC530.05 - fission yeast (Schizosaccharomyc	13.2	12.0	14.1	24.2	2e-97	01.01.04 regulation of amino acid metabolism	
Pc20g0744	similarity to protein Srb8 - Saccharomyces cerevisiae	2e-24	S74293	SRB8 protein - yeast (Saccharomyces cerevisiae)	12.0	12.0	20.4	27.5	6e-90	01.01.04 regulation of amino acid metabolism	
Pc20g1213	weak similarity to transcription activator Put3 - Saccharomyces cerevisiae	2e-35	T38690	probable regulatory protein - fission yeast (Schizosaccharomyces por	12.0	12.0	13.2	33.3	0		0
Pc20g1487	strong similarity to hypothetical transcriptional regulator SPCC417.09c - Schizosaccharomyc	1e-130	ANAJ3459	gene: "prnA"; product: "PrnA protein"; Aspergillus nidulans prnD, prn	19.5	27.1	62.1	78.6	5e-75	01.04 phosphate metabolism	
Pc20g1506	similarity to aflatoxin biosynthesis regulator aflR - Aspergillus flavus	6e-05	AF441421_	gene: "aflR"; product: "AFLR"; Aspergillus nomius isolate BN013P A	32.3	26.4	47.1	70.4	0		0
Pc21g0093	similarity to SR protein kinase Sky1 - Saccharomyces cerevisiae	7e-27	C84553	probable protein kinase [imported] - Arabidopsis thaliana	17.6	12.0	14.4	28.4	8e-58	01.01.04 regulation of amino acid metabolism	
Pc21g0939	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora cra	0	0	0	31.0	22.3	66.2	78.3	2e-82	04 TRANSCRIPTION	
Pc21g0942	similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	4e-15	SPAPB1A1	gene: "SPAPB1A11.04c"; S.pombe chromosome I BAC pB1A11.	20.5	23.6	38.7	77.8	1e-106	03.01.99 other DNA processing	
Pc21g1749	strong similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	0.0	S61908	DNA-binding protein amdA - Emericella nidulans	45.6	40.9	59.1	83.9	0		0
Pc21g1774	strong similarity to helicase-like transcription factor - Homo sapiens	1e-107	ATAB5245	product: "helicase-like transcription factor-like protein"; Arabidopsis t	32.4	16.0	28.4	28.7	1e-36	01.02.04 regulation of nitrogen and sulphur utilization	
Pc21g1957	similarity to cutinase transcription factor beta CTF1b - Fusarium solani	5e-24	BX897674_	gene: "B2N18.280"; product: "conserved hypothetical protein"; Neuro	24.1	40.0	41.8	86.5	1e-73	01.04 phosphate metabolism	
Pc22g0048	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	4e-15	NCB9B15_	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa D	38.3	40.5	84.6	87.3	7e-85	01.01.04 regulation of amino acid metabolism	
Pc22g0180	strong similarity to SR protein kinase Sky1 - Saccharomyces cerevisiae	2e-26	T04655	protein kinase homolog F8D20.10 - Arabidopsis thaliana	12.0	12.0	24.9	33.1	0.0	99 UNCLASSIFIED PROTEINS	
Pc22g0217	weak similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	4e-12	S54779	purine utilization positive regulator - Emericella nidulans	12.0	12.0	17.0	42.6	1e-142	04.03.99 other tRNA-transcription activities	
Pc22g1233	weak similarity to transcription activator Put3 - Saccharomyces cerevisiae	6e-23	SPAC1399	gene: "SPAC1399.05c"; S.pombe chromosome II cosmid c1399.	100.6	199.7	245.8	424.6	2e-69	01.01.04 regulation of amino acid metabolism	
Pc22g1600	strong similarity to Sen1 like protein An12g10480 - Aspergillus niger [putative sequencing err	5e-81	AY325141_	product: "Ab1-133"; Rattus norvegicus Ab1-133 mRNA, complete co	21.1	18.5	43.7	48.2	1e-51	01.06.99 other lipid, fatty-acid and isoprenoid metabolism activities	
Pc22g1621	similarity to hypothetical transcription factor Aro80 - Saccharomyces cerevisiae	9e-85	BX649607_	gene: "nirA"; product: "nitrogen assimilation transcription regulator, pu	12.0	12.0	20.6	36.8	1e-135	01.05.01.01.09 aerobic aromate catabolism	
Pc24g0054	weak similarity to transcription activator Upc2 - Saccharomyces cerevisiae	8e-06	S61580	probable membrane protein YDR213w - yeast (Saccharomyces cerev	15.2	12.0	21.5	28.7	1e-162	01.20.50 catabolism of secondary metabolites	
Pc22g2529	strong similarity to protein phosphatase methylesterase Ppe1 - Saccharomyces cerevisiae	1e-116	BX842629_	gene: "B20J13.050"; product: "related to ribosomal protein YmS2, mi	20.1	16.5	33.9	37.2	1e-168	03 CELL CYCLE AND DNA PROCESSING	
Pc06g0009	strong similarity to hypothetical membrane dipeptidase - Schizosaccharomyces pombe	1e-141	BX842620_	gene: "B11E5.370"; product: "related to membrane dipeptidase"; Ne	88.5	79.7	157.9	174.0	1e-122	05.04 translation	
Pc12g0985	strong similarity to calpain nCL-3 like protein An11g02950 - Aspergillus niger	1e-152	NC123A4_	gene: "123A4.270"; product: "related to micromolar calcium activated	45.1	41.6	143.5	70.2	1e-104	01.05.01 C-compound and carbohydrate utilization	
Pc12g1053	strong similarity to multicatalytic endopeptidase regulator like protein An11g04890 - Aspergill	1e-134	BX842627_	gene: "B8J22.150"; product: "related to GTP-binding protein 2"; Neu	138.8	127.0	221.4	268.6	0.0	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc12g1109	similarity to alpha-1,6-mannosyltransferase Hoc1 - Saccharomyces cerevisiae	2e-49	AF374353_	product: "putative mannosyltransferase"; Paracoccidioides brasiliensi	12.0	12.0	14.3	48.5	1e-136	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc12g1468	strong similarity to hypothetical lysosomal pepstatin insensitive protease CLN2 - Canis lupus	0.0	AFU57847	gene: "tpp1"; product: "tripeptidylpeptidase 1"; Aspergillus fumigatus	23.4	16.4	51.1	84.4	4e-68	01 METABOLISM	
Pc13g0356	strong similarity to dipeptidyl-peptidase V DPP V - Aspergillus fumigatus	0.0	AF125190_	product: "alanyl dipeptidyl peptidase"; Aspergillus oryzae alanyl dipep	165.5	60.7	115.0	555.4	1e-116	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc15g0011	weak similarity to subunit 13 of glutathione S-transferase GTK1 - Rattus norvegicus	1e-10	T27747	hypothetical protein ZK1320.1 - Caenorhabditis elegans	58.1	15.1	38.3	119.2	6e-82	05 PROTEIN SYNTHESIS	
Pc16g1106	strong similarity to histidine kinase nik-1 - Neurospora crassa	0.0	T18359	nik-1 protein - Neurospora crassa	47.9	53.0	149.8	125.1	1e-49	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc16g1306	strong similarity to cyclophilin cypB - Aspergillus nidulans	6e-53	CSZPA	peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccha	1089.8	1734.7	2509.7	2502.4	2e-96	06.04 protein targeting, sorting and translocation	
Pc18g0079	strong similarity to glutathione S-transferase like protein An02g06560 - Aspergillus niger	1e-116	AF425746_	gene: "gstA"; product: "theta class glutathione S-transferase"; Emeri	372.3	823.3	985.7	1419.0	0		0
Pc20g0642	strong similarity to erythrocyte splice form 1 of ankyrin like protein An12g05680 - Aspergillus	1e-21	AE2149	hypothetical protein all2748 [imported] - Nostoc sp. (strain PCC 7120	23.4	23.3	56.5	83.2	1e-136	01.05.01 C-compound and carbohydrate utilization	
Pc20g1514	strong similarity to secreted serine protease 19 kDa CS antigen CS-Ag - Coccidioides immiti	1e-33	AFAJ2026_	gene: "rasp f 13"; product: "rAsp f 13"; Aspergillus fumigatus mRNA	817.8	1129.1	2074.1	2320.3	1e-60	01.04 phosphate metabolism	
Pc21g0230	strong similarity to aminonitrophenyl propanediol resistance protein Anp1 - Saccharomyces c	1e-155	BX897674_	gene: "B2N18.080"; product: "probable ANP1 protein"; Neurospora c	76.9	70.5	144.2	184.1	9e-95	11.01 stress response	
Pc21g2006	similarity to protein kinase AFC1 - Arabidopsis thaliana	4e-19	T04655	protein kinase homolog F8D20.10 - Arabidopsis thaliana	119.4	58.2	179.2	253.0	3e-86	13.11 cellular sensing and response	
Pc21g2364	similarity to glutathione S-transferase Gtt1 - Saccharomyces cerevisiae	9e-34	AE011876_	gene: "gstA"; product: "glutathione S-transferase"; Xanthomonas axo	58.1	39.8	54.5	113.8	6e-76	01.04 phosphate metabolism	

Pc22g0808	strong similarity to actin interacting protein like protein An02g14620 - Aspergillus niger	1e-175	BT002525_	product: "Unknown protein"; Arabidopsis thaliana Unknown protein n	206.0	234.9	421.0	472.8	4e-61	06.07.99 other protein modifications	
Pc22g0853	weak similarity to cdc25C associated protein kinase c-tak1 - Homo sapiens	2e-09	AP006568_	Gloeobacter violaceus PCC 7421 DNA, complete genome, section 1/	133.2	186.7	302.7	397.1	8e-46	20 SYSTEMIC REGULATION OF / INTERACTION WITH ENVIRONMENT	
Pc22g0985	weak similarity to pyroglutamyl-peptidase I PGPI - Pyrococcus furiosus	2e-14	AK003373_	Mus musculus 18-day embryo whole body cDNA, RIKEN full-length (	38.4	50.3	88.9	108.6	3e-34	02.11 electron transport and membrane-associated energy conservation	
Pc22g1165	similarity to glutathione S-transferase omega - Sus scrofa	9e-22	ZMA01043	gene: "gst6"; product: "GST6 protein"; Zea mays mRNA for glutathic	17.7	17.3	64.2	63.9	5e-88	01.01 amino acid metabolism	
Pc22g1457	strong similarity to protein disulfide isomerase A pdiA - Aspergillus niger	8e-34	S57942	protein disulfide-isomerase (EC 5.3.4.1) - Aspergillus niger	407.2	182.8	823.1	669.0	3e-93	06.07 protein modification	
Pc22g1718	strong similarity to amidohydrolase like protein An02g00990 - Aspergillus niger	0.0	BX649605_	product: "peptidase, putative"; Aspergillus fumigatus BAC pilot proje	32.0	43.7	107.8	144.4	2e-87	06.04 protein targeting, sorting and translocation	
Pc22g1902	strong similarity to metalloprotease like protein An04g01980 - Aspergillus niger	0.0	BX842618_	gene: "B13M13.060"; product: "conserved hypothetical protein"; Neu	66.1	78.1	134.3	147.7	1e-59	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc24g0298	strong similarity to erythrocyte splice form 1 of ankyrin like protein An12g05680 - Aspergillus	5e-33	AY084207_	gene: "CG10011"; product: "SD03956p"; Drosophila melanogaster S	12.8	16.5	27.0	38.8	1e-103	01.01.07 amino acid transport	
Pc12g0024	strong similarity to aminotriazole resistance protein Atr1 - Saccharomyces cerevisiae	1e-55	BX649605_	product: "transporter, putative"; Aspergillus fumigatus BAC pilot proje	16.8	12.0	21.3	27.9	0.0	10.05 transmembrane signal transduction	
Pc12g0837	strong similarity to peptide transport protein Ptr2 - Saccharomyces cerevisiae	1e-115	AY187281_	product: "di/tri peptide transporter 2"; Phaeosphaeria nodorum di/tri p	25.9	15.7	24.9	36.0	2e-48	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc12g1238	strong similarity to anion transporter YNL275w - Saccharomyces cerevisiae	1e-130	BX842620_	gene: "B11E5.170"; product: "related to chloride-bicarbonate anion ex	12.0	12.0	51.6	43.4	9e-53	01.05.07 C-compound, carbohydrate transport	
Pc13g0429	strong similarity to ferrioxamine B permease Sit1 - Saccharomyces cerevisiae	1e-135	S50524	hypothetical protein YEL065w - yeast (Saccharomyces cerevisiae)	58.4	52.6	77.1	115.5	1e-62	01.06.13 lipid and fatty-acid transport	
Pc13g1366	strong similarity to multidrug resistance protein Hol1 - Saccharomyces cerevisiae	1e-155	T39346	probable major facilitator family multi-drug resistance protein - fission	31.9	24.8	67.2	68.7	2e-50	01.05.07 C-compound, carbohydrate transport	
Pc13g1382	similarity to phosphatidylinositol-phosphatidylcholine transfer protein Sec14 - Saccharomyces	8e-17	BX908789_	gene: "B13D24.190"; product: "probable phosphatidylinositol/phosph	53.3	31.1	100.8	115.2	7e-43	08.16 extracellular transport, exocytosis and secretion	
Pc14g0161	strong similarity to multidrug resistance protein Hol1 - Saccharomyces cerevisiae	2e-34	S63386	HOL1 protein - yeast (Saccharomyces cerevisiae)	87.7	63.7	196.1	153.7	1e-88	99 UNCLASSIFIED PROTEINS	
Pc16g0345	strong similarity to hypothetical conserved protein CAD21291.1 - Neurospora crassa	1e-126	NCG15G9_	gene: "G15G9.040"; product: "conserved hypothetical protein"; Neur	17.7	13.7	19.8	27.6	1e-41	08.19 cellular import	
Pc16g0578	similarity to inhibitor of endosome-lysosome fusion DotA - Legionella pneumophila	2e-24	S50468	hypothetical protein YER010c - yeast (Saccharomyces cerevisiae)	48.9	38.8	56.1	83.4	0.0	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS	
Pc16g0640	similarity to high affinity copper transporter ctr4p - Schizosaccharomyces pombe	8e-27	PAN30311	gene: "ctr3"; product: "high affinity copper transporter"; Podospora a	110.3	77.0	175.1	321.0	0.0	01.06.13 lipid and fatty-acid transport	
Pc16g0951	strong similarity to multidrug resistance protein like protein An08g02330 - Aspergillus niger [p	0.0	AY246696_	Alternaria brassicae ABC transporter (Atr1) gene, complete cds;	24.5	23.9	59.9	82.1	7e-95	08.13 vacuolar transport	
Pc16g1147	strong similarity to ATP-binding cassette multidrug transport protein atrB - Aspergillus nidula	0.0	AB060639_	gene: "PMR5"; product: "ABC transporter PMR5"; Penicillium digitatu	73.8	65.5	249.8	116.6	2e-52	01.05.07 C-compound, carbohydrate transport	
Pc16g1182	strong similarity to vacuolar H(+) Ca(2+) exchanger Vcx1 - Saccharomyces cerevisiae	2e-57	T41141	probable caCA proton/calcium exchanger - fission yeast (Schizosacc	17.4	12.8	26.9	33.8	0.0	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc16g1351	similarity to multidrug resistance protein Hol1 - Saccharomyces cerevisiae	1e-33	T39346	probable major facilitator family multi-drug resistance protein - fission	12.0	12.0	24.7	26.9	0.0	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc20g0122	strong similarity to multidrug resistance protein mdr1 - Aspergillus flavus	0.0	T30882	multidrug resistance protein 1 - Aspergillus flavus	93.2	125.5	274.7	144.1	0.0	01.06.13 lipid and fatty-acid transport	
Pc20g0977	strong similarity to multidrug resistance protein atrD - Aspergillus nidulans [putative sequenc	0.0	AF291822_	gene: "atrD"; product: "multidrug resistance protein MDR"; Trichoph	12.0	12.0	12.0	24.6	0.0	01 METABOLISM	
Pc20g1226	strong similarity to ATP-binding cassette multidrug transport protein atrB - Aspergillus nidula	0.0	T43022	ATP-binding multidrug cassette transport protein - Botryotinia fuckelia	12.4	30.3	51.8	25.5	2e-44	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc20g1340	strong similarity to P-type ATPase ENA1 - Schwanniomyces occidentalis	0.0	NCR24352	gene: "ena-1"; product: "putative sodium P-type ATPase"; Neurospo	12.0	12.0	18.4	33.7	0.0	14.04.03.03 pheromone response, mating-type determination, sex-specific proteins	
Pc20g1394	strong similarity to siderophore-iron transporter for enterobactin Enb1 - Saccharomyces cere	1e-133	AY131330_	gene: "mirB"; product: "major facilitator MIRB"; Emericella nidulans m	149.7	171.6	178.2	601.1	4e-87	03.03 cell cycle	
Pc20g1553	strong similarity to oligopeptide transporter Opt1 - Saccharomyces cerevisiae	1e-173	T38497	hypothetical protein SPAC29B12.10c - fission yeast (Schizosacchard	24.6	26.1	38.6	56.2	2e-82	11.05.01.01 antibiotic resistance	
Pc21g0209	similarity to kinesin Kif21b - Mus musculus	4e-17	AF155117_	product: "NY-REN-62 antigen"; Homo sapiens NY-REN-62 antigen m	108.7	145.8	382.2	378.3	2e-94	08.13 vacuolar transport	
Pc21g0707	strong similarity to ethionine resistance protein Erc1 - Saccharomyces cerevisiae	1e-120	AFA12H2_	gene: "AfA12H2.11c"; product: "hypothetical protein"; Aspergillus fu	16.3	14.7	25.1	38.6	2e-42	01.05.07 C-compound, carbohydrate transport	
Pc21g2026	similarity to vacuolar H(+) Ca(2+) exchanger Vcx1 - Saccharomyces cerevisiae	2e-22	AF053229_	gene: "cax"; product: "calcium/proton exchanger"; Neurospora crass	28.5	27.0	37.0	61.1	4e-98	04 TRANSCRIPTION	
Pc21g2076	strong similarity to hypothetical protein B15I20.50 - Neurospora crassa	1e-95	T51035	hypothetical protein B15I20.50 [imported] - Neurospora crassa	87.8	122.7	176.4	236.0	1e-56	01.05.07 C-compound, carbohydrate transport	
Pc21g2191	strong similarity to kinesin light chain like protein An19g00300 - Aspergillus niger	5e-36	AY392413_	Streptomyces clavuligerus plasmid pSCL2 clone contig3.73, partial	28.9	21.2	28.7	70.2	3e-79	13.01.01.99 homeostasis of other cations	
Pc22g0453	similarity to fluconazole resistance transporter Flr1 - Saccharomyces cerevisiae	1e-24	T39346	probable major facilitator family multi-drug resistance protein - fission	18.7	19.4	34.3	56.2	6e-56	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc22g0466	strong similarity to iron and manganese transporter Ccc1 - Saccharomyces cerevisiae	6e-37	S43453	CCC1 protein - yeast (Saccharomyces cerevisiae)	12.8	12.9	37.5	30.9	1e-31	01.05.07 C-compound, carbohydrate transport	
Pc22g1553	strong similarity to tetracyclin resistance protein like protein An15g02680 - Aspergillus niger	1e-19	T37692	probable transport protein - fission yeast (Schizosaccharomyces pom	36.6	42.6	55.5	99.7	0		0
Pc22g2414	similarity to membrane protein Tpo2 - Saccharomyces cerevisiae [truncated ORF][putative ps	6e-18	T41018	probable membrane transporter - fission yeast (Schizosaccharomyce	12.0	16.4	27.9	27.6	0		0
Pc12g0080	similarity to integral membrane protein PTH11 - Magnaporthe grisea	1e-22	AF329397_	gene: "pth"; product: "integral membrane protein"; Blumeria graminis	35.9	34.9	83.4	89.3	9e-95	04.05.01.04 transcriptional control	
Pc12g0307	similarity to integral membrane protein PTH11 - Magnaporthe grisea	4e-23	AF119670_	gene: "PTH11"; product: "integral membrane protein"; Magnaporthe	65.6	83.8	170.9	133.3	1e-60	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc12g0556	similarity to vegetative incompatibility factor het-e1 - Podospora anserina [putative sequencing	1e-30	AF323583_	gene: "het-e"; product: "beta transducin-like protein HET-E2C*4"; Po	22.8	16.7	64.9	63.7	1e-169	99 UNCLASSIFIED PROTEINS	
Pc13g0282	strong similarity to retinal short-chain dehydrogenase reductase like protein An18g05090 - As	1e-79	NCB17B1_	gene: "B17B1.060"; product: "related to a retinal short-chain dehydro	12.0	12.5	16.3	31.2	5e-73	01.05.07 C-compound, carbohydrate transport	
Pc13g0470	strong similarity to nonhemolytic phospholipase like protein An01g14940 - Aspergillus niger	1e-174	AX952974_	unnamed ORF; Sequence 2 from Patent WO03097825.	281.8	455.8	880.7	1279.0	5e-77	01.04 phosphate metabolism	
Pc13g1270	strong similarity to glucose permease Rgt2 - Saccharomyces cerevisiae	1e-156	NC13E11_	gene: "13E11.140"; product: "probable sugar transporter"; Neurospo	379.8	243.9	230.5	462.6	4e-59	01.04.04 regulation of phosphate utilization	
Pc16g0366	weak similarity to serine protein kinase SRPK1 - Homo sapiens	2e-25	NCB1D14_	gene: "B1D14.120"; product: "probable dis1-suppressing protein kina	95.5	88.0	159.7	201.2	1e-130	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc21g0004	strong similarity to histidine kinase like protein An10g00250 - Aspergillus niger	1e-110	AY456015_	gene: "HHK12"; product: "putative histidine kinase HHK12p"; Cochli	12.0	12.0	22.1	29.9	1e-135	10.05 transmembrane signal transduction	
Pc21g1891	strong similarity to beta transducin-like protein like protein An01g01380 - Aspergillus niger	3e-20	BC043394_	product: "ANKRD17 protein"; Homo sapiens ankyrin repeat domain 1	27.7	17.2	34.4	37.5	1e-148	04.05.01.04 transcriptional control	
Pc22g1565	strong similarity to peptide pheromone a-factor receptor Ste3 - Saccharomyces cerevisiae	1e-35	AF309805_	gene: "ste3"; product: "putative a-factor pheromone receptor Ste3a";	23.0	14.4	53.1	78.3	5e-72	02.11 electron transport and membrane-associated energy conservation	
Pc06g0089	strong similarity to heat shock protein Hsp104 - Saccharomyces cerevisiae	0.0	AY229978_	product: "heat shock protein CLPA"; Paracoccidioides brasiliensis he	211.6	269.2	461.4	321.7	7e-67	01.03 nucleotide metabolism	
Pc12g1110	strong similarity to antioxidant protein like protein An11g07650 - Aspergillus niger	2e-71	AF312927_	gene: "TSA1"; product: "putative thiol-specific antioxidant protein Tsa	374.6	462.6	771.5	737.2	0		0
Pc13g0707	weak similarity to 2-hydroxyisoflavone reductase IFRH - Arabidopsis thaliana	2e-12	AB045984_	Verticillium dahliae mRNA from tomato pathotype-specific DNA fragn	31.0	29.3	51.7	77.2	0		0
Pc13g1361	strong similarity to capsular associated protein CAP10 - Filobasidiella neoformans	8e-48	AF144574_	gene: "CAP10"; product: "capsular associated protein"; Filobasidiella	74.5	97.4	157.5	194.6	0		0
Pc13g1381	strong similarity to capsular associated protein CAP10 - Filobasidiella neoformans	1e-53	AF144574_	gene: "CAP10"; product: "capsular associated protein"; Filobasidiella	64.1	25.2	85.4	81.6	1e-108	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc16g0569	similarity to protease inhibitor like protein An08g01700 - Aspergillus niger	0	0	0	66.1	145.2	376.8	199.0	0.0	01.06.13 lipid and fatty-acid transport	
Pc16g1217	strong similarity to cytochrome P450 pisatin demethylase PDAT9 - Nectria haematococca	6e-48	NCB14A6_	gene: "B14A6.030"; product: "probable benzoate 4-monooxygenase c	122.0	98.0	331.3	400.9	7e-46	01.04.07 phosphate transport	
Pc16g1291	strong similarity to ABC transporter CDR4 - Candida albicans	0.0	T30541	ABC1 transport protein - rice blast fungus	602.5	440.1	1101.3	1238.3	2e-88	11.01 stress response	
Pc16g1389	strong similarity to hypothetical membrane transport protein SPAC3H1.06c - Schizosacchar(	1e-78	AY220913_	gene: "comD"; product: "ComD"; Dictyostelium discoideum ComD (c	12.0	12.0	17.4	30.4	8e-54	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc16g1422	manganese superoxide dismutase AAC36583 - Penicillium chrysogenum	1e-116	AF026523_	product: "manganese superoxide dismutase"; Penicillium chrysogenu	42.5	15.2	30.0	46.3	4e-62	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc16g1437	strong similarity to hypothetical membrane transport protein SPAC3H1.06c - Schizosacchar(	3e-52	AF448056_	gene: "dotC"; product: "putative dothistromin transporter"; Mycospha	18.5	13.0	34.3	59.7	1e-101	01.01.01.07 biosynthesis of the aspartate family	
Pc18g0178	strong similarity to glutathione peroxidase Hyr1 - Saccharomyces cerevisiae	8e-63	BX842620_	gene: "B11E5.410"; product: "probable glutathione peroxidase"; Neu	280.7	254.1	384.3	509.8	0		0
Pc20g0666	strong similarity to D-amino-acid oxidase DAO - Fusarium solani	1e-37	AF309689_	product: "putative D-amino acid oxidase G6G8.6"; Neurospora crassa	29.8	24.8	63.2	79.5	5e-26	01.03.04 pyrimidine nucleotide metabolism	
Pc21g0271	similarity to cytochrome P450 pisatin demethylase like protein An02g00150 - Aspergillus nige	0	0	0	12.0	12.0	29.5	39.9	5e-68	11.07 detoxification	
Pc21g0611	strong similarity to thioredoxin - Aspergillus nidulans	4e-48	A49888	thioredoxin - Penicillium chrysogenum	192.2	291.2	632.9	720.3	2e-99	01 METABOLISM	
Pc21g1088	similarity to 7-aminocholesterol resistance protein Rta1 - Saccharomyces cerevisiae	2e-14	NCG15D1_	gene: "G15D1.020"; product: "conserved hypothetical protein"; Neur	347.4	175.0	872.2	572.7	7e-88	13.01.01.03 homeostasis of protons	
Pc22g1332	strong similarity to cytochrome P450 52A4 - Candida maltosa	7e-85	JS0203	cytochrome P450 52A1, alkane-inducible - yeast (Candida tropicalis)	66.3	48.0	95.1	137.9	2e-51	13.01 ionic homeostasis	
Pc06g0064	similarity to Na+ H+ antiporter NapA - Enterococcus hirae	4e-37	AF441858_	gene: "SSC1"; product: "sodium-hydrogen antiporter"; Filobasidiella	18.1	12.0	28.7	37.3	2e-88	01.02.01.07 nitric oxide biosynthesis	
Pc13g0603	strong similarity to Na+ H+-exchanging protein like protein An14g01710 - Aspergillus niger	2e-50	AF441858_	gene: "SSC1"; product: "sodium-hydrogen antiporter"; Filobasidiella	26.1	27.7	46.3	64.2	4e-18	01.07.10 transport of vitamins, cofactors, and prosthetic groups	
Pc21g0877	strong similarity to serine threonine-specific protein kinase Hal4 - Saccharomyces cerevisiae	4e-43	T38473	probable serine/threonine-specific protein kinase (EC 2.7.1.-) - fission	20.0	18.2	62.5	35.8	1e-168	13.01.01.03 homeostasis of protons	
Pc22g1461	similarity to copper transport protein like protein An08g00370 - Aspergillus niger	2e-07	AY166608_	gene: "tahA"; product: "copper chaperone TahA"; Trametes versicolo	23.6	48.4	93.8	74.4	0		0
Pc22g2253	strong similarity to K+ H+ exchanger Kha1 - Saccharomyces cerevisiae	1e-129	T50062	Probable K+/H+-antiporter [imported] - fission yeast (Schizosaccharo	143.3	195.6	384.3	421.5	1e-137	02.11.05 accessory proteins of electron transport and membrane-associated energy conservation	
Pc21g1458	weak similarity to blastomyces yeast phase-specific protein 1 bys1 - Ajellomyces dermatitidis	8e-27	NCB24G2(	gene: "B24G20.140"; product: "related to blastomyces yeast phase-s	520.7	340.6	944.1	1598.8	5e-75	02 ENERGY	
Pc22g2019	Pc22g20190 peroxin-1 PEX1 - Penicillium chrysogenum	0.0	AF233276_	gene: "PEX1"; product: "peroxin-1"; Penicillium chrysogenum peroxi	227.5	132.6	198.8	261.5	0		0
Pc16g0016	strong similarity to PRG3 protein like protein An15g07360 - Aspergillus niger	2e-92	CNS07TIX	DNA centromeric region sequence from BAC DP15B03, DP38F06 of	12.0	12.0	14.9	45.6	0		0
Pc22g0726	strong similarity to hypothetical neutral amino acid permease - Neurospora crassa	1e-119	S47892	neutral amino acid permease - Neurospora crassa	17.4	13.3	21.2	47.0	0		0
Pc06g0007	strong similarity to hypothetical protein contig12.tfa_800cg - Aspergillus fumigatus	0	0	0	101.4	39.1	118.9	125.5	0		0
Pc06g0008	strong similarity to penicillolysin - Penicillium citrinum	1e-129	S47635	penicillolysin - Penicillium citrinum	44.8	18.5	121.0	125.7	0		0
Pc06g0063	strong similarity to hypothetical protein An08g09090 - Aspergillus niger	2e-49	BX842620_	gene: "B11E5.130"; product: "hypothetical protein"; Neurospora cras	53.4	62.4	83.5	137.9	1e-64	01.01.01.01.02.05 biosynthesis of glutamate	
Pc06g0140	strong similarity to hypothetical protein SPAC1039.06 - Schizosaccharomyces pombe	1e-47	T50056	hypothetical protein SPAC1039.06 [imported] - fission yeast (Schizos	12.0	12.0	12.0	41.3	0		0
Pc06g0157	strong similarity to hypothetical protein - Chromobacterium violaceum	2e-30	AE016910_	Chromobacterium violaceum ATCC 12472 section 1 of 16 of the	12.0	12.0	28.9	27.0	0		0
Pc06g0184	weak similarity to hypothetical protein PA4177 - Pseudomonas aeruginosa	4e-04	D83123	hypothetical protein PA4177 [imported] - Pseudomonas aeruginosa (s	14.3	15.8	33.6	48.7	0		0
Pc06g0201	weak similarity to hypothetical protein contig1492_0.tfa_2370cg - Aspergillus fumigatus	0	0	0	12.0	12.0	23.5	27.9	0		0
Pc06g0201	weak similarity to hypothetical protein contig1492_0.tfa_2370cg - Aspergillus fumigatus	0	0	0	12.0	12.0	23.5	27.9	0		0
Pc06g0202	similarity to hypothetical protein An12g02590 - Aspergillus niger	0	0	0	12.0	12.0	56.7	41.4	0		0
Pc06g0240	hypothetical protein	0	0	0	240.6	188.8	342.1	463.7	0		0
Pc08g0001	strong similarity to hypothetical protein mg05551.1 - Magnaporthe grisea	0	0	0	17.4	20.3	21.0	58.7	1e-33	03.03.01.01.11 mitosis	
Pc12g0091	weak similarity to hypothetical protein B8J22.030 - Neurospora crassa	3e-09	BX842627_	gene: "B8J22.030"; product: "conserved hypothetical protein"; Neurc	19.9	24.4	38.8	56.2	4e-66	01 METABOLISM	
Pc12g0101	strong similarity to hypothetical protein An15g03240 - Aspergillus niger	0	0	0	57.4	69.3	136.4	81.3	1e-55	99 UNCLASSIFIED PROTEINS	
Pc12g0117	strong similarity to hypothetical protein contig31_part_ii.tfa_1450cg - Aspergillus fumigatus	5e-72	T51067	hypothetical protein B2A19.10 [imported] - Neurospora crassa	145.4	92.3	183.8	187.3	1e-70	01.04 phosphate metabolism	
Pc12g0176	similarity to hypothetical protein ba0ab028h05lp1 - Kluyveromyces lactis	7e-17	S46119	probable purine nucleotide-binding protein YBR242w - yeast (Saccha	58.1	58.0	122.9	155.5	0		0
Pc12g0178	strong similarity to hypothetical protein An09g02520 - Aspergillus niger	1e-09	AY437641_	gene: "ST1"; product: "serine/threonine kinase"; Leptosphaeria macu	120.2	148.9	277.1	252.5	1e-125	02.11.05 accessory proteins of electron transport and membrane-associated energy conservation	
Pc12g0186	strong similarity to hypothetical protein contig1496_0.tfa_730wg - Aspergillus fumigatus	0	0	0	25.5	39.9	59.1	92.3	0		0
Pc12g0187	strong similarity to hypothetical protein ncu09357.1 - Neurospora crassa	4e-77	AE017268_	product: "stage V sporulation protein K"; Bacillus cereus ATCC 1098	12.0	12.0	22.0	30.9	0		0
Pc12g0220	strong similarity to hypothetical protein An15g04720 - Aspergillus niger	0	0	0	12.1	16.1	28.1	39.3	6e-83	98 CLASSIFICATION NOT YET CLEAR-CUT	

Pc12g0224	hypothetical protein	0	0	0	12.0	12.0	15.9	29.6	7e-72	01 METABOLISM	
Pc12g0267	strong similarity to hypothetical protein mg05066.1 - Magnaporthe grisea	1e-32	BX640440_	product: "putative aldolase"; Bordetella bronchiseptica strain RB50, c	12.0	12.0	12.2	42.8	0		0
Pc12g0296	strong similarity to hypothetical protein 1384_scaffold_6.tfa_150cg - Fusarium graminearum	7e-13	AY228175_	product: "putative arylamine N-acetyltransferase"; Streptomyces mur	18.9	24.6	82.8	77.8	0		0
Pc12g0362	similarity to hypothetical protein contig_1_165_scaffold_14.tfa_80wg - Aspergillus nidulans	0	0	0	12.0	12.0	34.5	38.7	0		0
Pc12g0380	strong similarity to hypothetical protein - Penicillium chrysogenum	5e-28	AB091505_	product: "hypothetical protein"; Penicillium chrysogenum mRNA for h	12.0	12.0	22.4	29.2	1e-63	01 METABOLISM	
Pc12g0604	strong similarity to hypothetical protein An07g02930 - Aspergillus niger	0	0	0	30.6	31.8	123.4	109.8	9e-32	01 METABOLISM	
Pc12g0630	strong similarity to hypothetical oxidoreductase of the short-chain dehydrogenase reductase f	1e-51	E87298	hypothetical protein CC0398 [imported] - Caulobacter crescentus	27.1	36.6	62.9	55.6	0		0
Pc12g0689	strong similarity to hypothetical isochorismatase Ta0729 - Thermoplasma acidophilum	6e-22	TACID3_8	gene: "Ta0729"; product: "conserved hypothetical protein"; Thermop	314.5	325.8	726.1	984.1	0		0
Pc12g0694	strong similarity to hypothetical protein An01g09800 - Aspergillus niger	7e-86	ENAC133_	product: "ORF"; Emericella nidulans cosmid SW06E08, complete se	25.9	18.4	31.7	53.1	1e-103	11.01 stress response	
Pc12g0696	strong similarity to hypothetical protein contig1477_1.tfa_810wg - Aspergillus fumigatus	0	0	0	93.7	93.8	293.9	256.7	4e-79	03.01.05 DNA recombination and DNA repair	
Pc12g0792	strong similarity to hypothetical protein SPCC757.02c - Schizosaccharomyces pombe	5e-60	T41593	hypothetical protein SPCC757.02c - fission yeast (Schizosaccharomy	12.0	12.0	44.1	56.7	0		0
Pc12g0800	strong similarity to sirtuin type 5 SIRT5 - Homo sapiens	2e-41	AE010224_	gene: "PF1154"; product: "transcriptional regulatory protein, sir2"; Py	94.9	84.7	98.0	172.5	0		0
Pc12g0819	strong similarity to hypothetical protein contig1492_0.tfa_2200wg - Aspergillus fumigatus	4e-09	NCB11N2_	gene: "B11N2.100"; product: "putative protein"; Neurospora crassa D	22.9	19.0	63.7	44.8	3e-58	01.01.04 regulation of amino acid metabolism	
Pc12g0861	strong similarity to hypothetical conserved protein 3H10.120 - Neurospora crassa	9e-96	NC3H10_1	gene: "3H10.120"; product: "conserved hypothetical protein"; Neuros	24.7	34.2	83.3	93.8	0		0
Pc12g0870	weak similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	3e-07	ANU56099	gene: "facB"; product: "FacB"; Aspergillus niger putative DNA bindir	69.5	63.7	138.1	148.2	1e-148	04.05.01.04 transcriptional control	
Pc12g0872	strong similarity to hypothetical protein HI0753 - Synechocystis sp.	6e-66	AE012994_	gene: "TTE0217"; product: "conserved hypothetical protein"; Thermo	12.0	12.0	21.8	27.9	1e-58	01.01.01 amino acid biosynthesis	
Pc12g0873	strong similarity to conserved hypothetical protein - Xanthomonas axonopodis	1e-79	AE012042_	gene: "XAC3928"; product: "conserved hypothetical protein"; Xantho	827.9	670.2	2649.0	2984.8	2e-72	01.06.01.05 fatty acid biosynthesis	
Pc12g0900	strong similarity to hypothetical protein contig1496_7.tfa_220cg - Aspergillus fumigatus	8e-38	AE016924_	Chromobacterium violaceum ATCC 12472 section 15 of 16 of the	38.8	62.4	100.9	102.2	5e-43	01.02 nitrogen and sulfur metabolism	
Pc12g0917	similarity to hypothetical protein SMb20006 - Sinorhizobium meliloti	1e-32	AE016778_	product: "oxidoreductase, FAD-binding"; Pseudomonas putida KT24	63.9	56.5	164.3	190.9	0		0
Pc12g0945	similarity to conserved hypothetical protein - Bacillus anthracis	1e-12	AE017030_	product: "conserved hypothetical protein"; Bacillus anthracis str. Ame	70.0	89.5	131.0	207.3	0		0
Pc12g0956	similarity to hypothetical protein An17g00600 - Aspergillus niger	0	0	0	24.2	16.1	29.8	39.8	0		0
Pc12g1011	strong similarity to hypothetical protein contig_1_86_scaffold_5.tfa_140wg - Aspergillus nidu	0	0	0	17.5	12.0	73.0	50.5	3e-73	01.02.01.07 nitric oxide biosynthesis	
Pc12g1062	strong similarity to hypothetical protein contig1496_0.tfa_1440wg - Aspergillus fumigatus	0	0	0	39.2	39.6	77.0	88.8	5e-40	01.01.04 regulation of amino acid metabolism	
Pc12g1074	similarity to hypothetical protein 1168_scaffold_2.tfa_590cg - Fusarium graminearum	4e-12	AY437641_	gene: "ST1"; product: "serine/threonine kinase"; Leptosphaeria macu	36.8	21.1	46.6	47.1	0		0
Pc12g1115	weak similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyce	7e-06	S48917	probable regulatory protein YHR178w - yeast (Saccharomyces cerevi	18.9	38.9	44.8	60.4	1e-155	99 UNCLASSIFIED PROTEINS	
Pc12g1135	hypothetical protein	0	0	0	58.3	60.5	310.6	143.2	9e-27	01.01.01.01.02 biosynthesis of the glutamate group (proline, hydroxyprolin, arginine, glutamine, glutamate)	
Pc12g1245	strong similarity to hypothetical protein contig1490_3.tfa_450cg - Aspergillus fumigatus	6e-48	AE016921_	Chromobacterium violaceum ATCC 12472 section 12 of 16 of the	50.1	37.2	71.3	77.0	1e-61	99 UNCLASSIFIED PROTEINS	
Pc12g1247	strong similarity to hypothetical protein 1141_scaffold_2.tfa_370wg - Fusarium graminearum	4e-30	NC80A10_	gene: "80A10.200"; product: "conserved hypothetical protein"; Neuro	12.0	12.0	46.3	43.8	3e-71	01.05 C-compound and carbohydrate metabolism	
Pc12g1275	similarity to hypothetical protein YPL067c - Saccharomyces cerevisiae	7e-12	S60923	hypothetical protein YPL067c - yeast (Saccharomyces cerevisiae)	107.5	63.8	156.2	137.7	0		0
Pc12g1320	strong similarity to hypothetical protein contig46_part_ii.tfa_3260wg - Aspergillus fumigatus	2e-72	AE012994_	gene: "TTE0212"; product: "predicted sugar phosphate isomerase";	466.4	540.0	863.9	1413.8	0		0
Pc12g1451	strong similarity to hypothetical protein contig_1_55_scaffold_3.tfa_710cg - Aspergillus nidul	5e-63	AE016790_	product: "polysaccharide deacetylase family protein"; Pseudomonas	12.0	12.0	14.1	35.0	0		0
Pc12g1456	hypothetical protein	0	0	0	104.5	102.4	407.6	503.0	0		0
Pc12g1470	similarity to hypothetical protein contig_1_122_scaffold_9.tfa_160wg - Aspergillus nidulans	0	0	0	549.8	285.9	970.7	1130.0	0.0	01.06.13 lipid and fatty-acid transport	
Pc12g1477	hypothetical protein	0	0	0	17.9	12.0	47.3	43.8	0		0
Pc12g1585	strong similarity to hypothetical protein An12g05670 - Aspergillus niger	0.0	S77690	probable membrane protein YOL075c - yeast (Saccharomyces cerev	18.4	19.2	31.5	56.4	0		0
Pc13g0023	strong similarity to hypothetical protein An18g00170 - Aspergillus niger	0	0	0	44.4	66.9	111.9	133.1	0		0
Pc13g0055	similarity to hypothetical protein ncu01851.1 - Neurospora crassa	0	0	0	12.2	12.0	16.8	27.1	4e-93	01 METABOLISM	
Pc13g0066	weak similarity to hypothetical protein BAB55393.1 - Homo sapiens	0	0	0	36.2	23.3	55.0	91.3	1e-144	11.01 stress response	
Pc13g0153	strong similarity to hypothetical protein contig589.tfa_450wg - Aspergillus fumigatus	9e-52	S57117	probable aldehyde reductase (EC 1.1.1.-) YJR096w - yeast (Sacchar	34.2	42.7	67.9	123.3	0		0
Pc13g0206	similarity to hypothetical protein SPCC757.02c - Schizosaccharomyces pombe	2e-37	NCB9B11_	gene: "B9B11.170"; product: "conserved hypothetical protein"; Neuro	12.0	12.0	12.0	26.5	3e-78	01.05.01 C-compound and carbohydrate utilization	
Pc13g0236	hypothetical protein	0	0	0	12.0	12.0	12.0	24.8	0		0
Pc13g0367	strong similarity to hypothetical protein contig31_part_i.tfa_1050wg - Aspergillus fumigatus	5e-30	AB009053_	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQB2.	162.5	182.1	337.2	333.1	0		0
Pc13g0395	strong similarity to hypothetical protein An12g00900 - Aspergillus niger	0	0	0	20.9	17.5	32.0	36.8	6e-38	10.01 intracellular signalling	
Pc13g0426	strong similarity to hypothetical protein An15g04720 - Aspergillus niger	0	0	0	71.8	62.0	111.1	132.0	0		0
Pc13g0471	strong similarity to hypothetical protein An05g00690 - Aspergillus niger	4e-05	BC057529_	gene: "supt5h"; product: "supt5h protein"; Danio rerio suppressor of T	364.7	417.0	820.4	513.0	0		0
Pc13g0476	strong similarity to hypothetical protein An08g01950 - Aspergillus niger	2e-97	AE015942_	gene: "CTC01793"; product: "transcriptional regulator"; Clostridium t	96.4	105.3	344.5	325.6	9e-57	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc13g0480	strong similarity to hypothetical protein An05g00625 - Aspergillus niger	6e-04	BC041788_	product: "Similar to RIKEN cDNA 1110025J15 gene"; Homo sapiens	114.3	73.8	172.0	155.8	0		0
Pc13g0481	strong similarity to hypothetical protein contig_1_100_scaffold_7.tfa_370wg - Aspergillus nid	7e-32	BC038340_	product: "dehydrogenase/reductase (SDR family) member 8"; Mus m	43.2	18.6	66.8	121.0	1e-126	30.16 mitochondrion	
Pc13g0491	hypothetical protein	0	0	0	12.0	14.5	35.1	32.2	0		0
Pc13g0558	strong similarity to hypothetical protein mg06134.1 - Magnaporthe grisea	3e-49	T40474	hypothetical protein SPBC4B4.02c - fission yeast (Schizosaccharom	71.9	74.1	121.8	172.5	0		0
Pc13g0619	similarity to hypothetical intracellular protease amidase related enzyme of the ThiJ family CA(	2e-16	G97247	intracellular protease/amidase related enzyme (ThiJ family) [imported	34.9	23.4	85.3	71.0	0		0
Pc13g0635	strong similarity to hypothetical protein contig1477_1.tfa_530wg - Aspergillus fumigatus	7e-06	T38995	hypothetical protein SPAC637.03 - fission yeast (Schizosaccharomyc	332.5	302.0	451.1	633.5	2e-89	01.02.01 nitrogen and sulfur utilization	
Pc13g0727	strong similarity to hypothetical protein contig1495_2.tfa_590cg - Aspergillus fumigatus	8e-19	BX640416_	product: "conserved hypothetical protein"; Bordetella pertussis strain	31.2	52.6	66.9	120.7	0		0
Pc13g0743	strong similarity to hypothetical protein contig1488_2.tfa_760cg - Aspergillus fumigatus	1e-104	BX842618_	gene: "B13M13.090"; product: "conserved hypothetical protein"; Neu	57.5	37.2	106.8	226.3	1e-127	99 UNCLASSIFIED PROTEINS	
Pc13g0747	strong similarity to hypothetical protein An12g02830 - Aspergillus niger	0	0	0	12.0	13.9	32.6	51.0	1e-151	40 SUBCELLULAR LOCALISATION	
Pc13g0795	similarity to hypothetical protein YER080w - Saccharomyces cerevisiae	2e-13	S50583	hypothetical protein YER080w - yeast (Saccharomyces cerevisiae)	26.6	16.5	30.3	37.1	2e-40	99 UNCLASSIFIED PROTEINS	
Pc13g0896	strong similarity to hypothetical protein SPBC354.08c - Schizosaccharomyces pombe	1e-116	T40288	hypothetical protein SPBC354.08c - fission yeast (Schizosaccharomy	137.0	114.1	227.9	246.0	0		0
Pc13g0995	weak similarity to hypothetical protein YGL079w - Saccharomyces cerevisiae	8e-22	NCB9B11_	gene: "B9B11.220"; product: "conserved hypothetical protein"; Neuro	26.4	37.8	97.2	79.1	0		0
Pc13g1023	hypothetical protein	0	0	0	55.6	85.8	117.1	98.9	0		0
Pc13g1096	hypothetical protein	0	0	0	27.1	28.3	63.4	72.8	0		0
Pc13g1112	weak similarity to hypothetical protein mg10737.1 - Magnaporthe grisea	0	0	0	12.0	17.7	18.5	36.8	6e-35	99 UNCLASSIFIED PROTEINS	
Pc13g1121	strong similarity to hypothetical protein An02g02460 - Aspergillus niger	3e-04	AY228175_	gene: "kinU"; product: "LanU-like protein"; Streptomyces murayamae	40.3	68.1	122.3	159.2	1e-76	01.02.04 regulation of nitrogen and sulphur utilization	
Pc13g1127	weak similarity to hypothetical protein YER182w - Saccharomyces cerevisiae	2e-06	AX119091_	unnamed ORF; Sequence 255 from Patent WO0129221.	12.0	17.2	26.9	49.5	2e-62	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc13g1187	strong similarity to DCG1-like protein, putative - Aspergillus fumigatus	4e-80	BX649606_	product: "DCG1-like protein, putative"; Aspergillus fumigatus BAC pil	19.1	23.1	30.9	46.9	7e-96	01.01 amino acid metabolism	
Pc13g1223	strong similarity to hypothetical conserved protein SPAC11H11.03c - Schizosaccharomyces	5e-84	BX649606_	product: "smr family protein, putative"; Aspergillus fumigatus BAC pil	180.1	169.4	254.6	346.7	0		0
Pc13g1314	strong similarity to hypothetical protein gi_19075788 - Schizosaccharomyces pombe	1e-115	T41346	probable glutamate-1-semialdehyde aminotransferase - fission yeast	34.3	61.9	76.1	135.3	1e-52	99 UNCLASSIFIED PROTEINS	
Pc13g1339	hypothetical protein	0	0	0	50.0	44.7	161.3	85.0	3e-37	01.03 nucleotide metabolism	
Pc13g1340	strong similarity to hypothetical protein SPAC1039.06 - Schizosaccharomyces pombe	7e-51	T50056	hypothetical protein SPAC1039.06 [imported] - fission yeast (Schizos	46.9	53.3	97.5	114.4	0		0
Pc13g1380	strong similarity to hypothetical protein 1348_scaffold_5.tfa_420cg - Fusarium graminearum	6e-56	T49704	hypothetical protein B23L21.170 [imported] - Neurospora crassa	83.6	52.2	127.2	180.1	0		0
Pc13g1411	strong similarity to hypothetical protein An15g05550 - Aspergillus niger	0	0	0	18.4	18.8	29.3	46.6	2e-95	11.05.01 resistance proteins	
Pc13g1419	strong similarity to hypothetical protein contig61.tfa_890cg - Aspergillus fumigatus	0	0	0	77.6	93.7	280.1	199.9	0		0
Pc13g1430	similarity to hypothetical beta-lactamase XF1621 - Xylella fastidiosa	2e-74	NC104H10	gene: "104H10.010"; product: "conserved hypothetical protein"; Neu	77.1	49.1	120.9	116.3	2e-43	99 UNCLASSIFIED PROTEINS	
Pc13g1476	weak similarity to hypothetical protein B2O8.260 - Neurospora crassa	0	0	0	25.2	25.1	91.7	88.9	0		0
Pc13g1497	strong similarity to hypothetical protein ncu04039.1 - Neurospora crassa	2e-22	BX897678_	gene: "B10H18.160"; product: "conserved hypothetical protein"; Neu	49.1	50.3	164.6	225.2	8e-53	01.03 nucleotide metabolism	
Pc13g1523	strong similarity to hypothetical protein An15g02470 - Aspergillus niger	0	0	0	51.4	90.5	122.1	126.9	0		0
Pc14g0023	strong similarity to ketoreductase krd - Zygosaccharomyces rouxii	1e-52	T38902	probable cinnamoyl-coa reductase - fission yeast (Schizosaccharomy	12.0	12.0	12.0	24.9	1e-102	01 METABOLISM	
Pc14g0073	similarity to hypothetical protein encoded by SMc00431 - Sinorhizobium meliloti	1e-13	AP005085_	gene: "VPA0515"; product: "hypothetical protein"; Vibrio parahaemol	12.0	12.0	28.4	22.1	1e-62	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc14g0127	strong similarity to hypothetical 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase BH2000 - Ba	6e-55	BC009403_	product: "Unknown (protein for MGC:15165)"; Homo sapiens, clone I	269.1	364.3	481.4	807.0	1e-78	01.01.01.15 biosynthesis of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine	
Pc14g0196	strong similarity to hypothetical protein contig_1_98_scaffold_6.tfa_1140wg - Aspergillus nid	3e-18	U94886_1	Brachyspira hyodysenteriae ACP reductase (fabG), acyl carrier	167.7	157.2	202.0	513.5	6e-33	47.03.01.01.01.99 other brain areas	
Pc15g0010	strong similarity to hypothetical protein An02g03640 - Aspergillus niger	1e-17	AE014397_	gene: "BR0950"; product: "oxidoreductase, putative"; Brucella suis 1	100.3	124.8	238.2	330.5	1e-51	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc15g0063	weak similarity to hypothetical protein SPBC31F10.02 - Schizosaccharomyces pombe	8e-10	CEC25H3_	gene: "C25H3.3"; product: "Hypothetical protein C25H3.3"; Caenorh	145.4	121.4	172.3	374.7	3e-62	01 METABOLISM	
Pc15g0090	similarity to hypothetical short chain alcohol dehydrogenase cta - Cucumis sativus	3e-17	AE003507_	gene: "scu"; product: "CG7113-PA"; Drosophila melanogaster chron	39.8	12.0	34.1	75.7	0		0
Pc15g0101	strong similarity to hypothetical protein F49E12.10 - Caenorhabditis elegans	6e-36	T22443	hypothetical protein F49E12.9 - Caenorhabditis elegans	43.7	15.2	18.4	118.4	0		0
Pc15g0134	weak similarity to hypothetical protein An05g00060 - Aspergillus niger	0	0	0	14.9	18.8	44.0	33.7	8e-81	01.01.99 other amino acid metabolism activities	
Pc15g0141	strong similarity to hypothetical protein An08g08410 - Aspergillus niger	0	0	0	66.0	45.0	87.2	114.0	6e-82	01.04 phosphate metabolism	
Pc15g0182	strong similarity to hypothetical oxidoreductase PA0147 - Pseudomonas aeruginosa	3e-63	C83628	probable oxidoreductase PA0147 [imported] - Pseudomonas aerugin	12.0	20.0	26.0	47.5	2e-55	01.03 nucleotide metabolism	
Pc15g0210	strong similarity to hypothetical protein encoded by CG16717 - Drosophila melanogaster	4e-32	AE003551_	product: "CG16717-PA"; Drosophila melanogaster chromosome 3L,	16.3	12.0	33.3	28.7	2e-12	99 UNCLASSIFIED PROTEINS	
Pc16g0013	strong similarity to ketoreductase krd - Zygosaccharomyces rouxii	8e-55	T38902	probable cinnamoyl-coa reductase - fission yeast (Schizosaccharomy	32.0	44.7	112.4	90.4	0		0
Pc16g0026	weak similarity to hypothetical protein YGR273c - Saccharomyces cerevisiae	8e-04	T39810	hypothetical protein SPBC19C7.04c - fission yeast (Schizosaccharon	66.9	32.2	85.9	167.9	0		0
Pc16g0029	similarity to hypothetical protein BAB52928.1 - Mesorhizobium loti	3e-10	BX572599_	product: "conserved unknown protein"; Rhodopseudomonas palustris	12.0	12.0	13.3	32.7	0		0
Pc16g0033	strong similarity to hypothetical protein An10g00180 - Aspergillus niger	0	0	0	12.0	12.0	15.4	26.9	2e-53	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc16g0043	strong similarity to hypothetical protein contig1490_3.tfa_790cg - Aspergillus fumigatus	1e-12	S76925	hypothetical protein - Synechocystis sp. (strain PCC 6803)	12.0	12.0	19.8	25.7	0		0

Pc16g0071	strong similarity to hypothetical protein contig50.tfa_130wg - Aspergillus fumigatus	1e-32	BC054138_	product: "Unknown (protein for MGC:63829)"; Danio rerio cDNA clor		69.2	19.1	78.4	98.0	0		0
Pc16g0090	strong similarity to hypothetical protein contig10.tfa_380cg - Aspergillus fumigatus	0	0		0	68.6	13.4	129.5	92.2	0		0
Pc16g0303	strong similarity to hypothetical protein contig1492_0.tfa_6350cg - Aspergillus fumigatus	1e-179	AB110615_	gene: "sdn1"; product: "saponin hydrolase precursor"; Neocosmospo		16.1	12.0	71.3	49.6	0		0
Pc16g0371	strong similarity to hypothetical protein An17g00600 - Aspergillus niger	0	0		0	47.2	23.4	112.4	72.1	0		0
Pc16g0444	strong similarity to hypothetical protein mg01514.1 - Magnaporthe grisea	0	0		0	41.4	93.8	155.6	78.8	0		0
Pc16g0497	strong similarity to hypothetical protein 1A9.40 - Neurospora crassa	1e-107	T48700	hypothetical protein 1A9.40 [imported] - Neurospora crassa		28.2	15.8	83.1	74.4	0		0
Pc16g0509	strong similarity to hypothetical protein contig46_part_i.tfa_950wg - Aspergillus fumigatus	7e-70	AE015942_	gene: "CTC01794"; product: "transcriptional regulator"; Clostridium t		49.8	66.1	130.6	160.2	0		0
Pc16g0573	strong similarity to hypothetical protein encoded by SMb20234 - Sinorhizobium meliloti	6e-58	A95870	hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) r		15.5	12.0	24.6	26.1	0		0
Pc16g0611	similarity to hypothetical protein contig46_part_i.tfa_930cg - Aspergillus fumigatus	0	0		0	16.2	12.0	29.7	36.7	3e-82	01.05.07 C-compound, carbohydrate transport	
Pc16g0616	weak similarity to hypothetical serine-rich protein SPCC1322.10 - Schizosaccharomyces pon	5e-06	T40941	hypothetical serine-rich protein - fission yeast (Schizosaccharomyces		1639.3	2079.8	3349.4	3181.9	0		0
Pc16g0741	strong similarity to hypothetical protein 1323_scaffold_5.tfa_330wg - Fusarium graminearum	1e-103	T51198	related to myo-inositol transport protein ITR1 [imported] - Neurospora		255.4	184.8	1059.9	670.9	0		0
Pc16g0769	strong similarity to hypothetical protein An04g03340 - Aspergillus niger	0	0		0	83.8	54.2	180.4	155.6	0.0	99 UNCLASSIFIED PROTEINS	
Pc16g0802	strong similarity to hypothetical protein SCF91.02c - Streptomyces coelicolor	1e-175	SCO93910	gene: "SCO0642"; "SCF91.02c"; product: "conserved hypothetical pr		81.6	108.2	189.1	243.9	8e-58	01.05 C-compound and carbohydrate metabolism	
Pc16g0805	strong similarity to hypothetical protein - Streptomyces avermitilis	0.0	AP005048_	product: "hypothetical protein"; Streptomyces avermitilis genomic DN		19.9	24.0	33.2	84.2	1e-99	01.05 C-compound and carbohydrate metabolism	
Pc16g0823	strong similarity to hypothetical myoinositol-dehydrogenase spcB - Streptomyces spectabilis	1e-35	AF170704_	gene: "spcB"; product: "SpcB"; Streptomyces spectabilis SpcC (spc		71.4	66.2	173.9	218.0	0		0
Pc16g0914	strong similarity to hypothetical protein PA5145 - Pseudomonas aeruginosa	1e-123	BX897675_	gene: "B2E7.160"; product: "conserved hypothetical protein"; Neuros		160.6	182.6	194.3	381.7	0		0
Pc16g0950	strong similarity to hypothetical protein 1244_scaffold_3.tfa_50cg - Fusarium graminearum	1e-06	AF451898_	gene: "orf126"; product: "tetracyclin-resistance protein"; Heliothis zea		27.6	17.7	50.4	92.8	0		0
Pc16g0969	strong similarity to hypothetical protein contig50.tfa_290cg - Aspergillus fumigatus	0	0		0	64.0	64.4	90.6	135.3	0.0	99 UNCLASSIFIED PROTEINS	
Pc16g1003	hypothetical protein	0	0		0	27.2	32.5	75.6	102.8	0		0
Pc16g1069	strong similarity to hypothetical protein YIR007w - Saccharomyces cerevisiae	1e-150	S50878	hypothetical protein YIR007w - yeast (Saccharomyces cerevisiae)		93.4	27.2	165.5	198.2	0		0
Pc16g1132	strong similarity to hypothetical protein contig1490_3.tfa_1270wg - Aspergillus fumigatus	0	0		0	63.9	34.2	169.1	197.6	0		0
Pc16g1139	strong similarity to hypothetical protein contig_1_116_scaffold_8.tfa_60wg - Aspergillus nidu	0	0		0	12.0	12.0	36.9	38.1	0		0
Pc16g1140	strong similarity to hypothetical protein ncu05317.1 - Neurospora crassa [putative sequencin	3e-07	T52364	hypothetical protein B11E6.130 [imported] - Neurospora crassa		12.0	12.0	44.3	38.0	0		0
Pc16g1160	strong similarity to hypothetical protein contig46_part_ii.tfa_1620wg - Aspergillus fumigatus	0	0		0	25.3	12.2	36.9	53.4	0		0
Pc16g1220	similarity to hypothetical protein AAM35689.1 - Xanthomonas axonopodis	1e-15	AP006577_	Gloeobacter violaceus PCC 7421 DNA, complete genome, section 10		27.2	12.0	18.7	24.8	0		0
Pc16g1242	weak similarity to hypothetical protein An01g07060 - Aspergillus niger	0	0		0	12.0	12.0	23.1	49.8	0		0
Pc16g1300	strong similarity to hypothetical protein contig1492_0.tfa_6240cg - Aspergillus fumigatus	2e-48	AP003004_	gene: "mll4579"; product: "2-haloalkanoic acid dehalogenase"; Meso		27.4	42.9	70.1	74.6	1e-72	01.04 phosphate metabolism	
Pc16g1321	strong similarity to hypothetical protein contig46_part_ii.tfa_1200wg - Aspergillus fumigatus	0	0		0	12.0	12.0	27.2	42.0	0		0
Pc16g1343	weak similarity to hypothetical protein An01g12910 - Aspergillus niger	4e-06	AF421215_	gene: "snf"; product: "protein kinase SNF"; Colletotrichum gloeospori		45.7	47.8	122.1	116.2	8e-40	01.05.01.01 C-compound, carbohydrate catabolism	
Pc16g1377	similarity to hypothetical protein contig46_part_ii.tfa_1100wg - Aspergillus fumigatus	0	0		0	259.1	162.0	462.8	372.9	0		0
Pc16g1428	strong similarity to hypothetical protein contig5_part_i.tfa_940wg - Aspergillus fumigatus	5e-16	AF409109_	product: "14.5 kDa bacteriolytic enzyme"; Dermatophagoides pterony		12.0	12.0	53.9	58.9	0		0
Pc16g1443	similarity to hypothetical protein contig1477_1.tfa_1040wg - Aspergillus fumigatus	0	0		0	50.1	77.1	176.0	159.1	0		0
Pc16g1465	strong similarity to hypothetical protein contig_1_139_scaffold_11.tfa_640wg - Aspergillus ni	0	0		0	821.8	442.1	1648.8	2938.4	0		0
Pc16g1483	similarity to hypothetical protein contig46_part_ii.tfa_2020cg - Aspergillus fumigatus	0	0		0	24.5	42.2	83.6	37.2	0		0
Pc16g1529	similarity to hypothetical protein An08g01250 - Aspergillus niger	0	0		0	149.6	150.5	363.0	385.8	0		0
Pc16g1530	similarity to hypothetical protein 1367_scaffold_6.tfa_40cg - Fusarium graminearum	0	0		0	325.9	311.3	556.0	678.9	0		0
Pc16g1532	strong similarity to hypothetical protein An12g10330 - Aspergillus niger	0	0		0	16.4	19.4	40.7	45.9	0		0
Pc16g1533	similarity to hypothetical protein ncu05318.1 - Neurospora crassa	0	0		0	201.6	204.5	414.7	532.7	0		0
Pc16g1537	weak similarity to hypothetical protein An03g00300 - Aspergillus niger	0	0		0	22.3	16.3	49.0	41.8	0		0
Pc16g1540	strong similarity to hypothetical protein An12g10730 - Aspergillus niger	8e-44	AC115592_	product: "hypothetical protein"; Dictyostelium discoideum chromosor		364.2	655.1	958.4	966.1	0		0
Pc17g0019	hypothetical protein	0	0		0	152.0	118.1	478.4	427.2	0		0
Pc18g0013	similarity to integral membrane protein PTH11 - Magnaporthe grisea [putative sequencing err	1e-16	NC94C8_2	gene: "94C8.020"; product: "related to integral membrane protein PTI		43.9	106.2	152.6	88.0	1e-118	01.01.01 amino acid biosynthesis	
Pc18g0014	strong similarity to hypothetical conserved protein 99H12.80 - Neurospora crassa	3e-93	BX649605_	product: "hypothetical protein, conserved"; Aspergillus fumigatus BA(		72.4	141.3	228.4	309.4	0		0
Pc18g0031	strong similarity to hypothetical protein CP0630 - Chlamydophila pneumoniae	1e-114	NCB13B3_	gene: "B13B3.110"; product: "conserved hypothetical protein"; Neurc		12.0	12.0	12.0	34.1	0		0
Pc18g0036	strong similarity to hypothetical protein contig336.tfa_290wg - Aspergillus fumigatus [putative	0	0		0	12.0	12.0	27.5	26.4	1e-51	01.03 nucleotide metabolism	
Pc18g0051	similarity to hypothetical phosphoglycerate mutase SPAC5H10.03 - Schizosaccharomyces p	2e-20	NC49D12_	gene: "49D12.140"; product: "conserved hypothetical protein"; Neurc		12.0	12.0	14.5	45.2	1e-110	40.30 prokaryotic cell membrane (inner membrane of gram - bacteria)	
Pc18g0108	strong similarity to hypothetical UDP-glucose 4-epimerase - Alcaligenes eutrophus	4e-63	BX649607_	product: "possible epimerase"; Aspergillus fumigatus BAC pilot proje		16.6	22.2	27.0	56.1	0.0	01.05.01.01 C-compound, carbohydrate catabolism	
Pc18g0130	similarity to hypothetical protein Aut4 - Saccharomyces cerevisiae	2e-19	S19366	hypothetical protein YCL038c - yeast (Saccharomyces cerevisiae)		166.0	241.1	381.6	696.5	2e-50	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc18g0131	strong similarity to hypothetical beta-hexosamidase A precursor BH0675 - Bacillus halodurar	4e-91	AP004604_	gene: "OB3206"; product: "beta-N-acetylhexosaminidase (beta-hexos		131.4	173.2	283.8	363.7	0		0
Pc18g0132	strong similarity to hypothetical protein contig_1_172_scaffold_16.tfa_550cg - Aspergillus ni(	2e-55	AF061253_	gene: "GST1"; product: "glutathione S-transferase"; Botryotinia fuck(		563.9	677.7	1417.0	1418.4	0		0
Pc18g0184	strong similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae	4e-75	AF359360_	gene: "OrfF"; product: "putative methyltransferase"; Fusarium sporot		802.0	768.7	2089.2	2059.1	9e-45	03.03.01.01.11 mitosis	
Pc18g0248	strong similarity to hypothetical protein contig_1_66_scaffold_4.tfa_40cg - Aspergillus nidula	0	0		0	12.0	13.3	32.8	47.0	5e-70	01 METABOLISM	
Pc18g0268	strong similarity to hypothetical protein contig5_part_ii.tfa_60cg - Aspergillus fumigatus	6e-30	AB109765_	Aspergillus kawachii cwpB gene for hypothetical protein, complete		1790.1	2021.9	4539.9	3792.0	4e-73	04.05.01.04 transcriptional control	
Pc18g0278	strong similarity to hypothetical protein contig1488_2.tfa_1170cg - Aspergillus fumigatus	8e-81	AF312927_	gene: "TSA1"; product: "putative thiol-specific antioxidant protein Tsa		1291.4	1846.8	3341.5	3891.4	1e-167	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS	
Pc18g0284	strong similarity to hypothetical protein contig_1_10_scaffold_1.tfa_200cg - Aspergillus nidul	5e-24	AP002994_	gene: "mll0013"; product: "transcriptional regulator"; Mesorhizobium		15.7	23.3	37.9	51.9	1e-38	05.01 ribosome biogenesis	
Pc18g0305	strong similarity to hypothetical protein contig_1_167_scaffold_14.tfa_30wg - Aspergillus nid	2e-44	NTG1_MU	SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER		89.6	58.3	107.2	224.1	9e-49	99 UNCLASSIFIED PROTEINS	
Pc18g0533	strong similarity to hypothetical protein contig248.tfa_180wg - Aspergillus fumigatus	4e-31	CAL39049	gene: "rps21"; product: "ribosomal protein S21"; Candida albicans m		59.4	50.8	86.2	120.1	1e-77	01.03.01.01 purine nucleotide catabolism	
Pc18g0594	weak similarity to hypothetical protein T17H3.1 - Arabidopsis thaliana	1e-05	AY045812_	gene: "At1g27510"; product: "unknown protein"; Arabidopsis thaliana		12.8	12.0	27.7	34.6	1e-116	08.16 extracellular transport, exocytosis and secretion	
Pc20g0059	strong similarity to hypothetical protein ncu01441.1 - Neurospora crassa	1e-64	NCB20D17	gene: "B20D17.150"; product: "probable inosine triphosphate pyroph(		200.8	168.7	291.2	342.6	0		0
Pc20g0088	strong similarity to hypothetical protein SPBC27B12.12c - Schizosaccharomyces pombe	1e-115	SPAB4539	gene: "pi066"; product: "probable membrane protein YOL130w"; Sch		73.3	74.3	150.1	103.2	0		0
Pc20g0143	strong similarity to hypothetical protein An12g06840 - Aspergillus niger	0	0		0	101.4	81.0	148.5	171.2	0		0
Pc20g0188	strong similarity to hypothetical protein SC9B2.03 - Streptomyces coelicolor	1e-169	T35899	hypothetical protein SC9B2.03 - Streptomyces coelicolor		16.0	16.5	52.4	76.6	0		0
Pc20g0202	strong similarity to hypothetical protein mg01347.1 - Magnaporthe grisea	7e-43	NC80A10_	gene: "80A10.320"; product: "conserved hypothetical protein"; Neurc		26.1	28.2	70.6	60.9	8e-91	01.01.04 regulation of amino acid metabolism	
Pc20g0210	strong similarity to hypothetical protein An02g13400 - Aspergillus niger	0	0		0	12.0	12.0	32.2	34.3	5e-23	04 TRANSCRIPTION	
Pc20g0238	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces p	6e-10	T49482	hypothetical protein B14D6.340 [imported] - Neurospora crassa		15.0	12.0	15.0	24.5	0		0
Pc20g0351	strong similarity to hypothetical protein contig_1_51_scaffold_3.tfa_1450cg - Aspergillus nid	2e-14	AX885834_	unnamed ORF; Sequence 1697 from Patent EP1033401.		127.6	166.3	589.7	344.5	0		0
Pc20g0362	similarity to integral membrane protein PTH11 - Magnaporthe grisea	5e-20	NCB7H23_	gene: "B7H23.130"; product: "related to L-fucose permease"; Neuros		12.0	12.0	18.4	36.1	9e-43	06.13 proteolytic degradation	
Pc20g0391	weak similarity to hypothetical protein YBR246w - Saccharomyces cerevisiae	8e-39	CNS09S4	DNA centromeric region sequence from BAC DP26B06, DP34F04, D		19.2	20.6	115.1	54.7	1e-56	01.04 phosphate metabolism	
Pc20g0406	similarity to DNA-directed RNA polymerase II largest chain - Mastigamoeba invertens	2e-23	T31670	DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - Mastig		40.6	12.0	52.9	47.2	3e-85	01 METABOLISM	
Pc20g0455	strong similarity to hypothetical protein An01g12010 - Aspergillus niger	5e-19	C86394	protein T24P13.14 [imported] - Arabidopsis thaliana		16.8	12.0	17.3	27.0	8e-82	01 METABOLISM	
Pc20g0501	strong similarity to hypothetical 3-hydroxyacyl-CoA-dehydrogenase hcd - Gibberella zeae	7e-34	AB088352_	gene: "hcd"; product: "putative 3-hydroxyacyl-CoA-dehydrogenase";		61.7	72.5	99.6	208.5	0		0
Pc20g0672	strong similarity to hypothetical homolog of prokaryotic 2-hydroxyhepta-2,4-diene-1,7-dioate is	2e-55	T50353	homolog to prokaryotic 2-hydroxyhepta-2,4-diene-1,7-dioate isomeras		91.5	108.1	101.1	234.9	1e-111	01.04 phosphate metabolism	
Pc20g0875	similarity to hypothetical gag protein - Oryza sativa	2e-10	T18349	probable gag protein - rice blast fungus gypsy retroelement		60.1	100.5	135.2	128.6	0		0
Pc20g0951	similarity to hypothetical protein An11g01250 - Aspergillus niger	9e-10	A49865	protein-tyrosine kinase (EC 2.7.1.112) matk, long splice form - humar		12.0	12.0	26.0	51.0	4e-39	08.16 extracellular transport, exocytosis and secretion	
Pc20g0989	strong similarity to hypothetical protein An16g07980 - Aspergillus niger	0	0		0	12.0	12.0	32.3	34.4	0		0
Pc20g1006	strong similarity to hypothetical protein SPBC12C2.09c - Schizosaccharomyces pombe	5e-44	AC006733_	gene: "Y32H12A.5"; product: "Hypothetical protein Y32H12A.5"; Ca(		12.0	12.0	25.8	37.3	1e-76	40.10 nucleus	
Pc20g1076	weak similarity to hypothetical protein B2I10.080 - Neurospora crassa	0	0		0	78.6	46.6	132.1	164.8	8e-73	01.01.01.07.06 biosynthesis of lysine	
Pc20g1108	weak similarity to hypothetical transcription factor btd - Schizosaccharomyces pombe	9e-13	NC80A10_	gene: "80A10.010"; product: "related to transcriptional activator CMR		12.1	14.3	19.7	31.6	3e-78	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc20g1157	strong similarity to hypothetical protein YJL055w - Saccharomyces cerevisiae	2e-63	NC7F4_33	gene: "7F4.340"; product: "conserved hypothetical protein"; Neurosp		167.6	156.1	277.7	337.3	0		0
Pc20g1269	strong similarity to hypothetical protein BAB09014.1 - Arabidopsis thaliana	1e-93	BX842620_	gene: "B11E5.400"; product: "conserved hypothetical protein"; Neurc		37.4	36.7	135.6	113.7	0		0
Pc20g1273	similarity to hypothetical protein An12g07270 - Aspergillus niger	0	0		0	12.0	12.0	24.1	44.7	0		0
Pc20g1286	similarity to hypothetical protein contig_1_119_scaffold_9.tfa_20cg - Aspergillus nidulans	0	0		0	19.5	13.4	19.4	27.5	2e-96	01 METABOLISM	
Pc20g1287	strong similarity to hypothetical protein contig1485_1.tfa_290cg - Aspergillus fumigatus	0	0		0	22.7	20.3	42.2	77.8	8e-58	04 TRANSCRIPTION	
Pc20g1341	strong similarity to hypothetical protein contig_1_110_scaffold_8.tfa_570wg - Aspergillus nid	5e-55	G72004	8-amino-7-oxononanoate synthase (EC 2.3.1.47) - Chlamydophila pn		137.9	87.8	167.6	229.3	1e-111	01 METABOLISM	
Pc20g1393	weak similarity to hypothetical protein An12g03400 - Aspergillus niger	2e-04	AK016708_	Mus musculus adult male testis cDNA, RIKEN full-length enriched lib		129.9	103.4	450.5	299.9	0		0
Pc20g1397	strong similarity to hypothetical UDP-glucose,sterol transferase gstA - Aspergillus oryzae	0.0	AB078723_	gene: "gstA"; product: "UDP-glucose,sterol transferase"; Aspergillus		28.4	27.4	53.4	70.7	0		0
Pc20g1404	strong similarity to hypothetical mixed-linked glucanase precursor related protein MLG1 - Neu	1e-76	T39920	probable glucanase precursor - fission yeast (Schizosaccharomyces		37.5	28.5	57.7	66.9	6e-51	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc20g1428	similarity to hypothetical protein An02g04060 - Aspergillus niger	0	0		0	277.7	189.3	462.6	461.4	0		0
Pc20g1484	similarity to hypothetical monocarboxylate permease Esbp6 - Saccharomyces cerevisiae	2e-25	AY236409_	gene: "mct"; product: "monocarboxylate transporter-like protein"; Em		77.2	54.3	247.6	255.4	2e-55	01.06.04 breakdown of lipids, fatty acids and isoprenoids	
Pc20g1493	strong similarity to hypothetical protein An04g09900 - Aspergillus niger [putative sequencing	0	0		0	32.7	14.7	43.0	80.5	5e-25	03.01.09.05 DNA conformation modification (e.g. chromatin)	
Pc20g1538	strong similarity to hypothetical protein contig14.tfa_260wg - Aspergillus fumigatus	7e-20	A71213	alanine-tRNA ligase truncated homolog PH1969 - Pyrococcus horiko		42.9	57.4	95.6	150.8	0		0
Pc20g1546	strong similarity to hypothetical protein CAB92029.2 - Neurospora crassa	2e-34	NCB9J10_	gene: "B9J10.220"; product: "hypothetical protein"; Neurospora cras		134.9	82.8	116.6	177.3	1e-113	01 METABOLISM	

Pc20g155	strong similarity to hypothetical protein contig1492_0.tfa_3030cg - Aspergillus fumigatus	4e-62	MUKAD	lysozyme (EC 3.2.1.17) - fungus (Chalara sp.)	12.6	12.3	39.0	52.6	0		0
Pc20g155	strong similarity to hypothetical protein contig1492_0.tfa_3060wg - Aspergillus fumigatus	1e-150	NCB3E4_1	gene: "B3E4.200"; product: "related to guanine deaminase"; Neurosp	12.0	12.0	27.7	36.3	5e-47	99 UNCLASSIFIED PROTEINS	
Pc20g156	strong similarity to hypothetical protein contig_1_100_scaffold_7.tfa_390cg - Aspergillus nidu	1e-06	AP005945_	gene: "bll2936"; Bradyrhizobium japonicum USDA 110 DNA, comple	12.0	12.0	12.0	41.2	9e-84	04.05.01.04 transcriptional control	
Pc20g156	strong similarity to hypothetical protein An13g01790 - Aspergillus niger	1e-15	AP004334_	gene: "P0455H11.102"; product: "unknown protein"; Oryza sativa (ja	12.0	12.0	21.1	33.2	6e-76	01.05 C-compound and carbohydrate metabolism	
Pc20g157	strong similarity to hypothetical protein mg10764.1 - Magnaporthe grisea	4e-15	S36336	probable transcription factor PLZF - human	37.1	18.4	36.4	36.1	2e-41	01.04.07 phosphate transport	
Pc21g0151	strong similarity to hypothetical protein contig31_part_ii.tfa_2650cg - Aspergillus fumigatus	4e-38	G72391	conserved hypothetical protein - Thermotoga maritima (strain MSB8)	71.0	110.1	145.8	207.1	0		0
Pc21g016	strong similarity to hypothetical membrane protein YOL119c - Saccharomyces cerevisiae	3e-80	NCB23B1	gene: "B23B10.030"; product: "related to monocarboxylate transporte	12.0	12.0	33.7	23.9	0		0
Pc21g023	weak similarity to hypothetical protein T24H10.2 - Caenorhabditis elegans	4e-11	AF361222_	gene: "jlbA"; product: "JUN-like bZIP transcription factor"; Emericella	524.6	660.9	3263.0	1231.9	0		0
Pc21g026	weak similarity to hypothetical protein An15g05860 - Aspergillus niger	0	0	0	12.0	12.0	31.7	19.7	0		0
Pc21g042	strong similarity to hypothetical protein An14g06630 - Aspergillus niger	0	0	0	83.2	76.6	146.4	165.9	5e-83	99 UNCLASSIFIED PROTEINS	
Pc21g0491	strong similarity to hypothetical protein CAD28442.1 - Aspergillus fumigatus	2e-69	BX649606_	product: "hypothetical protein, conserved"; Aspergillus fumigatus BA	42.1	27.4	51.1	67.5	3e-23	01.01 amino acid metabolism	
Pc21g060	similarity to hypothetical membrane domain protein involved in signal transduction AAL22257	3e-11	AE008856_	gene: "STM3388"; product: "putative membrane domain protein invol	12.0	12.0	45.3	41.0	0		0
Pc21g061	similarity to hypothetical conserved protein ynaD - Bacillus subtilis	2e-11	NC80A10_	gene: "80A10.200"; product: "conserved hypothetical protein"; Neur	14.4	12.0	52.2	69.7	0		0
Pc21g069	strong similarity to hypothetical protein An02g04420 - Aspergillus niger	0	0	0	12.6	12.0	38.9	44.6	0		0
Pc21g083	similarity to hypothetical protein An14g06230 - Aspergillus niger	5e-11	BX842620_	gene: "B11E5.090"; product: "conserved hypothetical protein"; Neur	12.0	12.1	29.0	27.5	0		0
Pc21g0901	hypothetical protein	0	0	0	24.7	14.2	64.2	47.1	0		0
Pc21g0917	strong similarity to hypothetical protein CC0533 - Caulobacter crescentus	1e-108	D87315	conserved hypothetical protein CC0533 [imported] - Caulobacter cres	184.9	198.2	391.2	488.1	0		0
Pc21g095	weak similarity to hypothetical protein An01g06790 - Aspergillus niger	0	0	0	34.5	14.5	35.6	47.1	8e-88	99 UNCLASSIFIED PROTEINS	
Pc21g098	strong similarity to hypothetical protein contig_1_158_scaffold_13.tfa_200wg - Aspergillus ni	9e-15	AX196125_	Sequence 197 from Patent WO0151639.	24.7	20.5	89.7	72.4	0		0
Pc21g098	strong similarity to hypothetical protein contig1477_1.tfa_1650wg - Aspergillus fumigatus [pu	3e-24	AP005024_	product: "hypothetical protein"; Streptomyces avermitilis genomic DN	19.4	22.8	68.0	63.4	0		0
Pc21g104	similarity to hypothetical protein contig_1_46_scaffold_3.tfa_20cg - Aspergillus nidulans	0	0	0	13.4	12.0	25.3	37.4	0		0
Pc21g104	strong similarity to hypothetical protein contig_1_150_scaffold_12.tfa_180cg - Aspergillus ni	5e-09	AF067182_	gene: "idi-2"; product: "IDI-2 precursor"; Podospora anserina IDI-2 pr	17.3	22.9	37.7	50.8	5e-65	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc21g1057	strong similarity to hypothetical protein An15g07820 - Aspergillus niger	0	0	0	65.3	51.2	119.8	203.2	3e-83	01.01.04 regulation of amino acid metabolism	
Pc21g108	similarity to MINDBOMB - Homo sapiens	5e-18	AY147849_	gene: "MIB"; product: "MINDBOMB"; Homo sapiens MINDBOMB (M	236.8	140.4	542.3	324.2	0		0
Pc21g109	strong similarity to hypothetical regulator protein CAB16735.1 - Schizosaccharomyces pomb	2e-40	T38690	probable regulatory protein - fission yeast (Schizosaccharomyces pom	12.0	18.7	48.6	48.8	6e-94	01.05.01 C-compound and carbohydrate utilization	
Pc21g109	similarity to hypothetical protein contig_1_26_scaffold_2.tfa_360cg - Aspergillus nidulans	0	0	0	15.9	27.5	53.5	70.1	0		0
Pc21g121	strong similarity to hypothetical oxidoreductase SPAC977.14c - Schizosaccharomyces pomb	1e-116	AY072188_	gene: "At1g18270"; product: "unknown protein"; Arabidopsis thaliana	12.0	12.0	13.7	36.8	2e-47	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g1247	weak similarity to heterokaryon incompatibility protein het-6 - Neurospora crassa	0	0	0	12.0	12.0	38.3	49.4	0		0
Pc21g126	strong similarity to hypothetical protein 1465_scaffold_9.tfa_470wg - Fusarium graminearum	9e-36	C82643	daunorubicin C-13 ketoreductase XF1741 [imported] - Xylella fastidio	585.3	599.2	2024.5	2102.3	0		0
Pc21g130	hypothetical protein	0	0	0	12.0	12.7	19.4	37.7	0		0
Pc21g139	strong similarity to hypothetical protein - Gloeobacter violaceus	4e-30	AP006569_	Gloeobacter violaceus PCC 7421 DNA, complete genome, section 2/	19.1	17.3	64.3	79.2	0		0
Pc21g1411	strong similarity to hypothetical protein mg06620.1 - Magnaporthe grisea	0	0	0	216.3	122.0	181.3	267.0	5e-55	13.11 cellular sensing and response	
Pc21g145	strong similarity to hypothetical protein contig_1_41_scaffold_2.tfa_40cg - Aspergillus nidula	0	0	0	16.9	15.6	33.6	58.9	0		0
Pc21g146	strong similarity to hypothetical protein YDR196c - Saccharomyces cerevisiae	5e-42	S52703	hypothetical protein YDR196c - yeast (Saccharomyces cerevisiae)	53.1	62.7	82.4	175.9	1e-50	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	
Pc21g146	strong similarity to hypothetical protein An09g02950 - Aspergillus niger	4e-07	T50951	hypothetical protein B24P7.60 [imported] - Neurospora crassa	23.9	18.0	54.3	50.2	0		0
Pc21g154	weak similarity to hypothetical UbiE COQ5 family methlytransferase - Caulobacter crescentu	2e-06	AP005943_	gene: "ubiE"; product: "ubiquinone/menaquinone biosynthesis methyl	769.1	614.6	3302.2	1796.0	0		0
Pc21g156	strong similarity to cyanovirin-N like protein An01g05960 - Aspergillus niger	1e-04	NC43E3_4	gene: "43E3.40"; product: "hypothetical protein"; Neurospora crassa	1076.2	1439.8	3096.1	2699.3	0		0
Pc21g1581	strong similarity to hypothetical protein contig1495_1.tfa_1490wg - Aspergillus fumigatus	0	0	0	37.7	40.9	69.1	83.6	0		0
Pc21g1637	strong similarity to hypothetical protein An09g05240 - Aspergillus niger	2e-38	BX842620_	gene: "B11E5.340"; product: "putative protein"; Neurospora crassa	18.2	14.9	37.0	33.3	0		0
Pc21g168	strong similarity to hypothetical protein ybiU - Escherichia coli	9e-61	E64819	ybiU protein - Escherichia coli (strain K-12)	12.4	12.7	35.0	55.0	0		0
Pc21g173	similarity to hypothetical protein SC4B10.22 - Streptomyces coelicolor	1e-13	SCO9391	gene: "SCO7121"; "SC4B10.22"; product: "putative secreted protein"	16.5	17.3	23.7	62.7	2e-90	01.05.01 C-compound and carbohydrate utilization	
Pc21g182	weak similarity to hypothetical protein An17g00620 - Aspergillus niger	0	0	0	14.4	12.0	14.8	31.6	0		0
Pc21g186	strong similarity to hypothetical protein mg06182.1 - Magnaporthe grisea	1e-96	T52133	potassium channel beta subunit homolog [imported] - Arabidopsis tha	227.5	268.8	477.4	618.9	2e-68	01 METABOLISM	
Pc21g186	similarity to hypothetical protein CC3654 - Caulobacter crescentus	5e-18	AP005943_	gene: "bll2446"; Bradyrhizobium japonicum USDA 110 DNA, comple	12.0	12.0	41.6	55.5	0		0
Pc21g197	strong similarity to hypothetical protein contig31_part_ii.tfa_3670wg - Aspergillus fumigatus	1e-09	AD1155	conserved hypothetical proteins homolog lmo0644 [imported] - Listeri	79.3	98.3	160.0	155.7	1e-111	01.03.16 polynucleotide degradation	
Pc21g200	strong similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae	1e-39	AF359361_	gene: "OrfF"; product: "methyltransferase"; Gibberella zeae strain GZ	14.2	12.0	43.3	65.7	0		0
Pc21g201	strong similarity to hypothetical protein contig1492_0.tfa_3170cg - Aspergillus fumigatus	7e-92	NCB11B2	gene: "B11B23.050"; product: "related to lariat-debranching enzyme"	31.2	23.0	55.0	60.0	0		0
Pc21g214	similarity to hypothetical protein An09g03770 - Aspergillus niger	0	0	0	12.0	12.0	22.5	41.3	0		0
Pc21g214	hypothetical protein	0	0	0	27.9	22.1	90.9	55.5	0		0
Pc21g218	hypothetical protein	0	0	0	12.0	12.0	14.4	36.1	0		0
Pc21g219	weak similarity to hypothetical protein contig_1_149_scaffold_12.tfa_40cg - Aspergillus nidul	0	0	0	19.8	14.1	19.5	53.1	5e-38	01.01.04 regulation of amino acid metabolism	
Pc21g221	strong similarity to hypothetical protein 1316_scaffold_4.tfa_360cg - Fusarium graminearum	5e-08	AY057845_	product: "unknown"; Zymomonas mobilis strain ZM4 plasmid 1, com	141.5	44.6	55.5	184.3	0		0
Pc21g228	strong similarity to transcription regulator alcR - Aspergillus nidulans	0.0	ALCR_EM	REGULATORY PROTEIN ALCR.	108.0	112.8	142.8	295.0	1e-86	08.16.03 Type I protein secretion system (ABC-type transport systems)	
Pc21g229	weak similarity to hypothetical glutathione S-transferase BAB68404.1 - Gibberella fujikuroi	8e-07	AB071861_	product: "putative glutathione S-transferase"; Gibberella fujikuroi mR	16.0	13.0	53.3	28.4	0		0
Pc21g230	strong similarity to hypothetical protein contig46_part_ii.tfa_2310cg - Aspergillus fumigatus	7e-66	BX897679_	gene: "B2C22.090"; product: "probable positive effector protein GCN	46.9	69.5	224.5	150.7	3e-21	03.01.99 other DNA processing	
Pc21g235	strong similarity to hypothetical protein CAD21381.1 - Neurospora crassa	8e-28	NC123A4_	gene: "123A4.300"; product: "conserved hypothetical protein"; Neur	257.9	352.7	572.3	1016.9	0		0
Pc21g239	similarity to protease synthase and sporulation negative regulatory protein pai1 - Enterococcu	1e-18	AE016956_	product: "protease synthase and sporulation negative regulatory prote	12.6	12.0	26.5	41.0	0		0
Pc22g004	weak similarity to hypothetical protein T1G12.10 - Arabidopsis thaliana	1e-06	T40752	hypothetical protein SPBC8D2.07c - fission yeast (Schizosaccharom	37.0	36.7	70.8	91.4	0		0
Pc22g005	strong similarity to hypothetical conserved protein PA2682 - Pseudomonas aeruginosa	1e-56	D83310	conserved hypothetical protein PA2682 [imported] - Pseudomonas ae	39.8	73.5	129.0	169.4	1e-170	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc22g006	strong similarity to hypothetical protein CC0533 - Caulobacter crescentus	1e-95	D87315	conserved hypothetical protein CC0533 [imported] - Caulobacter cres	12.8	12.0	28.6	30.4	0		0
Pc22g018	weak similarity to ankyrin AAC37208.1 - Drosophila melanogaster	1e-28	T13940	ankyrin - fruit fly (Drosophila melanogaster)	51.1	32.0	148.4	140.0	7e-72	01.02.99 other nitrogen and sulfur metabolism activities	
Pc22g019	similarity to hypothetical protein contig1492_0.tfa_5060wg - Aspergillus fumigatus	0	0	0	226.6	199.7	440.8	530.4	0		0
Pc22g034	strong similarity to hypothetical protein aq_928 - Aquifex aeolicus	3e-67	G90073	conserved hypothetical protein SA2448 [imported] - Staphylococcus	19.9	12.0	21.5	35.7	1e-71	03.03.01 mitotic cell cycle and cell cycle control	
Pc22g046	strong similarity to hypothetical protein contig12.tfa_1670wg - Aspergillus fumigatus	0	0	0	54.7	84.6	112.7	111.6	0		0
Pc22g062	similarity to hypothetical AAA-ATPase AAR34299.1 - Geobacter sulfurreducens	3e-16	AE017210_	product: "ATPase, AAA family"; Geobacter sulfurreducens PCA, se	12.0	12.0	31.3	40.1	0		0
Pc22g065	similarity to hypothetical protein 1193_scaffold_2.tfa_450wg - Fusarium graminearum	4e-07	T45428	hypothetical protein MLCB637.35c [imported] - Mycobacterium leprae	12.0	12.0	38.6	56.7	0		0
Pc22g0681	strong similarity to hypothetical protein ydcF - Escherichia coli	1e-38	E85737	hypothetical protein ydcF [imported] - Escherichia coli (strain O157_	45.6	25.1	54.2	57.5	0		0
Pc22g074	strong similarity to hypothetical protein An11g09420 - Aspergillus niger	0	0	0	12.0	12.0	32.5	38.3	0		0
Pc22g075	similarity to hypothetical protein contig202.tfa_130cg - Aspergillus fumigatus	0	0	0	98.1	75.0	146.2	206.7	2e-21	01.01.01 amino acid biosynthesis	
Pc22g076	similarity to hypothetical protein DRB0099 - Deinococcus radiodurans	2e-16	A75629	hypothetical protein - Deinococcus radiodurans (strain R1)	15.5	12.0	36.8	50.9	2e-51	01 METABOLISM	
Pc22g076	weak similarity to hypothetical thiosulfate sulfurtransferase - Pseudomonas aeruginosa	1e-125	F83319	probable thiosulfate sulfurtransferase PA2603 [imported] - Pseudom	60.2	94.3	120.0	262.3	0		0
Pc22g082	strong similarity to hypothetical protein - Danio rerio	2e-33	BC066536_	product: "Unknown (protein for MGC:76849)"; Danio rerio cDNA clo	12.6	12.0	44.9	50.6	0		0
Pc22g082	hypothetical protein	0	0	0	25.3	16.9	37.0	34.6	0		0
Pc22g0881	strong similarity to hypothetical protein An02g14010 - Aspergillus niger	0	0	0	37.3	37.8	135.2	97.5	1e-141	99 UNCLASSIFIED PROTEINS	
Pc22g0897	weak similarity to hypothetical protein all7165 - Nostoc sp.	3e-04	F96014	conserved hypothetical protein SMb20675 [imported] - Sinorhizobium	84.5	133.3	317.4	403.9	2e-57	01 METABOLISM	
Pc22g094	strong similarity to hypothetical protein T16K5.230 - Arabidopsis thaliana	8e-39	AE016941_	product: "conserved hypothetical protein"; Bacteroides thetaiotaomicr	12.0	12.0	12.0	26.4	0		0
Pc22g128	similarity to hypothetical protein F24K9.9 - Arabidopsis thaliana	2e-09	T02539	hypothetical protein At2g37730 [imported] - Arabidopsis thaliana	159.2	159.3	197.9	385.3	1e-104	03.01.03 DNA synthesis and replication	
Pc22g1357	hypothetical protein	0	0	0	12.0	12.0	12.0	29.2	4e-23	01.01.07 amino acid transport	
Pc22g140	strong similarity to hypothetical double strand break catalysing AtSPO11-1 - Arabidopsis thal	2e-37	T48781	MEIOTIC RECOMBINATION PROTEIN REC12 related protein [imp	12.0	12.0	40.8	30.1	2e-84	01.02.01 nitrogen and sulfur utilization	
Pc22g141	strong similarity to hypothetical membrane protein YOL092w - Saccharomyces cerevisiae	1e-48	S57377	probable membrane protein YOL092w - yeast (Saccharomyces cerev	47.5	37.9	63.7	76.0	0		0
Pc22g1427	strong similarity to hypothetical protein contig5_part_ii.tfa_390wg - Aspergillus fumigatus	4e-99	BX572599_	product: "possible 2-nitropropane dioxygenase"; Rhodopseudomona	231.2	118.9	318.6	333.5	1e-102	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc22g145	strong similarity to hypothetical protein An07g01270 - Aspergillus niger	0	0	0	12.0	19.8	34.7	32.2	0.0	99 UNCLASSIFIED PROTEINS	
Pc22g156	similarity to hypothetical membrane protein YPR147c - Saccharomyces cerevisiae	6e-21	S69034	probable membrane protein YPR147c - yeast (Saccharomyces cerev	15.2	12.0	24.7	30.7	1e-19	04.05.01.04 transcriptional control	
Pc22g166	strong similarity to hypothetical membrane protein YIL067c - Saccharomyces cerevisiae	1e-121	NC5F3_22	gene: "5F3.220"; product: "conserved hypothetical protein"; Neurosp	56.5	65.2	91.9	163.1	0		0
Pc22g172	strong similarity to hypothetical protein 1185_scaffold_2.tfa_260wg - Fusarium graminearum	6e-11	AP002994_	gene: "mll0013"; product: "transcriptional regulator"; Mesorhizobium	13.2	23.1	37.0	61.9	0		0
Pc22g1771	strong similarity to hypothetical protein An11g02090 - Aspergillus niger	1e-35	NCB19A17	gene: "B19A17.170"; product: "hypothetical protein"; Neurospora cra	22.4	12.0	47.0	38.6	0		0
Pc22g1957	weak similarity to hypothetical protein An07g04490 - Aspergillus niger	0	0	0	46.9	74.7	94.4	171.3	1e-70	01.06.99 other lipid, fatty-acid and isoprenoid metabolism activities	
Pc22g201	weak similarity to hypothetical protein An13g02200 - Aspergillus niger	0	0	0	20.8	19.3	26.6	42.3	0		0
Pc22g205	weak similarity to hypothetical RNA polymerase II transcription factor Upc2 - Saccharomyces	4e-05	S51451	probable membrane protein YLR228c - yeast (Saccharomyces cerevi	18.2	20.2	41.4	75.6	1e-83	01.06.04 breakdown of lipids, fatty acids and isoprenoids	
Pc22g207	strong similarity to hypothetical protein An14g03100 - Aspergillus niger	0	0	0	26.6	23.5	52.4	61.7	1e-125	01 METABOLISM	
Pc22g210	strong similarity to hypothetical protein contig31_part_i.tfa_2380cg - Aspergillus fumigatus [p	6e-13	AE016911_	Chromobacterium violaceum ATCC 12472 section 2 of 16 of the	18.8	23.4	24.2	70.4	0		0
Pc22g214	strong similarity to hypothetical protein mg06547.1 - Magnaporthe grisea	1e-142	AV32375_	gene: "ttuC'"; product: "tartrate dehydrogenase"; Agrobacterium vitis	47.8	36.4	45.9	82.1	0		0

Pc22g216(	similarity to hypothetical protein contig_1_18_scaffold_1.tfa_110wg - Aspergillus nidulans	0	0	0	22.1	12.0	47.9	51.6	0	0
Pc22g217(	strong similarity to hypothetical protein contig1490_3.tfa_1220cg - Aspergillus fumigatus	8e-24	NCB13H1ξ	gene: "B13H18.210"; product: "related to G protein coupled receptor	30.7	33.4	61.7	112.0	1e-29	99 UNCLASSIFIED PROTEINS
Pc22g2231	hypothetical protein	0	0	0	12.0	12.0	24.9	32.8	0	0
Pc22g230ξ	strong similarity to hypothetical protein An12g07700 - Aspergillus niger	5e-07	AE015943_	gene: "CTC02163"; product: "ethanolamine utilization protein (transcı	16.3	16.9	31.3	46.5	0	0
Pc22g231ξ	strong similarity to hypothetical protein An03g06340 - Aspergillus niger	0	0	0	12.0	12.0	21.6	43.0	0	0
Pc22g2321	strong similarity to hypothetical protein An03g06370 - Aspergillus niger	0	0	0	12.0	12.0	16.8	28.9	1e-64	03.03.01 mitotic cell cycle and cell cycle control
Pc22g239:	strong similarity to hypothetical protein ncu07110.1 - Neurospora crassa	0	0	0	25.0	33.5	53.9	66.7	0	0
Pc22g241ξ	strong similarity to hypothetical protein contig42.tfa_50wg - Aspergillus fumigatus	4e-65	AP006575_	Gloeobacter violaceus PCC 7421 DNA, complete genome, section 8/	20.1	26.0	43.9	58.5	3e-39	01 METABOLISM
Pc22g241ɩ	strong similarity to hypothetical protein An18g01930 - Aspergillus niger	0	0	0	14.2	19.0	36.4	26.5	0	0
Pc22g242ɩ	weak similarity to hypothetical isochorismatase Ta0729 - Thermoplasma acidophilum	1e-22	AE016863_	product: "isochorismatase family protein"; Pseudomonas syringae pv	67.3	75.6	201.6	242.6	0	0
Pc22g249ɩ	weak similarity to hypothetical protein AAM35689.1 - Xanthomonas axonopodis	3e-13	BX649607_	product: "hypothetical protein, conserved"; Aspergillus fumigatus BA(	12.0	12.0	26.5	30.9	0	0
Pc22g252ɩ	similarity to hypothetical protein An18g06380 - Aspergillus niger	0	0	0	13.6	12.0	34.3	41.6	0	0
Pc22g255ɩ	strong similarity to hypothetical protein contig1497_2.tfa_50wg - Aspergillus fumigatus	0	0	0	484.2	567.4	1130.3	1145.9	0	0
Pc23g005(	strong similarity to hypothetical protein An07g04950 - Aspergillus niger [putative sequencing	4e-06	AY258009_	product: "Orf17"; Streptomyces clavuligerus clavulanic acid biosynth	12.0	12.0	39.4	20.1	0	0

Supplementary Table 14. K-mean cluster 6

@=Values given are the average of three independent experiments

orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels @				FunCat (auto)		
		p-value	Gene code	description	WIS - PAA	WIS + PAA	DS - PAA	DS + PAA	pval	category	
Pc06g00170	weak similarity to gentisate 1,2-dioxygenases GDO - Pseudomonas alcaligenes	0.0	BX649605_118	product: "salicylate hydroxylase, putative"; Aspergillus fumigatus B.	19.8	90.8	134.1	31.6	2e-98	01.05.01 C-compound and carbohydrate utilization	
Pc12g01540	strong similarity to sulfate permease SutB - Penicillium chrysogenum	0.0	AF163974_1	gene: "sutB"; product: "sulfate permease SutB"; Penicillium chrysog	15.1	12.0	33.8	12.0	1e-106	01.05.01 C-compound and carbohydrate utilization	
Pc12g06430	strong similarity to precursor of alpha-amylase A - Aspergillus niger	6e-96	AOTAAG1_1	A.oryzae Taka-amylase A (Taa-G1) gene, complete cds.	112.7	12.0	106.7	59.6	7e-87	01.05.01.01.01 sugar, glucoside, polyol and carboxylate catabolism	
Pc12g07100	strong similarity to alcohol dehydrogenase adhIII - Aspergillus nidulans	1e-157	ADH1_ASPFL	ALCOHOL DEHYDROGENASE I (EC 1.1.1.1).	24.1	12.0	147.8	30.4	0		0
Pc12g12910	strong similarity to endo-alpha-1,5-arabinanase abnA - Aspergillus niger	4e-52	A27981_1	gene: "abnA"; product: "endo 1,5-alpha-arabinase"; A.niger abnA ge	49.9	22.7	48.8	30.2	3e-62	01.05.07 C-compound, carbohydrate transport	
Pc13g05340	weak similarity to cell wall synthesis protein KRE9 - Candida albicans	6e-04	AF064252_1	gene: "KNH1"; product: "Knh1p"; Candida glabrata Knh1p (KNH1) g	47.4	12.0	52.3	12.0	0.0	01.03 nucleotide metabolism	
Pc13g07200	strong similarity to carboxylic acid transport protein Jen1 - Saccharomyces cerevisiae	0.0	AF500226_1	gene: "JEN1"; product: "carboxylic acid transport protein"; Metarhiz	51.0	15.3	102.8	58.5	0.0	01.05.07 C-compound, carbohydrate transport	
Pc13g07630	strong similarity to IMP dehydrogenase IMH3 - Candida albicans	0.0	IMH3_CANAL	PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE	596.8	48.4	420.6	206.8	1e-107	01.03.04 pyrimidine nucleotide metabolism	
Pc13g13280	strong similarity to carnitine acetyl transferase facC - Aspergillus nidulans	0.0	BX649605_112	gene: "facC"; product: "carnitine acetyl transferase, putative"; Aspe	252.6	181.5	523.9	230.3	0		0
Pc13g13450	strong similarity to purine-cytosine permease pcpl3 - Kluyveromyces marxianus	8e-61	KMA011419_1	gene: "pcpl3"; product: "purine-cytosine permease, putative"; Kluyv	27.9	12.0	30.5	12.0	1e-163	03.01.03 DNA synthesis and replication	
Pc16g03600	strong similarity to phosphinothricin acetyltransferase like protein An04g09830 - Aspergillus niger	2e-08	NCB13B3_5	gene: "B13B3.050"; product: "conserved hypothetical protein"; Neur	12.0	12.0	46.7	12.0	1e-127	01.01.01.15.03 biosynthesis of leucine	
Pc16g04000	strong similarity to DNA polymerase lambda POL lambda - Homo sapiens [putative pseudogene]	9e-64	BC055597_1	product: "Unknown (protein for MGC:66320)"; Danio rerio cDNA clon	45.6	24.1	56.2	25.1	0		0
Pc16g07560	strong similarity to long-chain acyl-CoA dehydrogenase like protein An04g03290 - Aspergillus niger	1e-178	AY033936_1	product: "probable acyl-CoA dehydrogenase"; Glomus intraradices p	375.9	156.2	291.8	143.1	0.0	01.05.01.01 C-compound, carbohydrate catabolism	
Pc16g10900	strong similarity to beta-fructofuranosidase precursor suc1 - Aspergillus niger	0.0	ASY289046_1	gene: "sft"; product: "fructosyltransferase"; Aspergillus sydowii mRN	30.0	12.0	23.6	12.0	0.0	01.05.01 C-compound and carbohydrate utilization	
Pc20g10170	strong similarity to beta-glucosidase 1 bgl1 - Aspergillus aculeatus	0.0	TR09580_1	gene: "bgl1"; product: "beta-D-glucoside glucohydrolase"; Trichoder	91.7	35.6	69.0	26.6	4e-75	01.05.07 C-compound, carbohydrate transport	
Pc20g14200	strong similarity to beta-glucan synthesis associated protein Kre6 - Saccharomyces cerevisiae	1e-144	AY371293_1	Pneumocystis carinii beta-1,6-glucan synthetase (KRE6) mRNA,	14.4	12.0	27.2	12.0	1e-47	01.05.07 C-compound, carbohydrate transport	
Pc20g15720	strong similarity to high affinity hexose transporter Hxt1 - Saccharomyces cerevisiae	1e-89	NC13E11_7	gene: "13E11.140"; product: "probable sugar transporter"; Neurospo	46.8	22.9	39.7	29.2	1e-41	01.01.10.05.02 degradation of cysteine	
Pc21g01210	similarity to hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	2e-22	T41145	probable amine transporter - fission yeast (Schizosaccharomyces p	192.1	28.1	95.6	12.0	3e-65	01 METABOLISM	
Pc21g04760	strong similarity to cysteine dioxygenase CDO1 - Rattus norvegicus	2e-29	BC060414_1	gene: "MGC68656"; product: "MGC68656 protein"; Xenopus laevis I	109.5	23.1	157.7	78.2	0		0
Pc21g10870	strong similarity to fatty-acyl-CoA synthase beta chain fas1p - Schizosaccharomyces pombe	0.0	S37178	fatty-acyl-CoA synthase (EC 2.3.1.86) beta chain - yeast (Candida a	202.5	106.7	281.6	140.2	5e-46	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc21g12820	strong similarity to 3-dehydroshikimate dehydratase qa-4 - Neurospora crassa	1e-89	BX649605_32	gene: "qutC"; product: "3-dehydroshikimate dehydratase, putative";	223.3	63.6	943.2	312.9	0		0
Pc21g12830	strong similarity to hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	9e-38	T41145	probable amine transporter - fission yeast (Schizosaccharomyces p	83.1	20.6	156.9	93.6	1e-101	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g15430	strong similarity to dimethylallyltryptophan synthase dmaW - Claviceps purpurea	2e-56	AY259838_1	gene: "dmaW"; product: "L-tryptophan dimethylallyl transferase"; N	883.9	595.2	2123.9	823.6	0.0	01.20.37.03 biosynthesis of peptide antibiotics	
Pc21g15470	similarity to mitochondrial 25-hydroxyvitamin D3 24-hydroxylase cP450cc24 - Gallus gallus	6e-15	AL138805_1	gene: "CYP24"; product: "dJ1075G21.1 (cytochrome P450, subfamil	241.7	115.5	742.6	98.6	1e-38	01.04 phosphate metabolism	
Pc21g15480	strong similarity to cyclic peptide AM-toxin synthase like protein An03g00650 - Aspergillus niger	0.0	MAPEPSYNT_1	gene: "pesA"; product: "peptide synthetase"; Metarhizium anisopliae	562.2	207.4	1488.2	162.2	0		0
Pc21g15780	strong similarity to chitinase precursor chit33 - Trichoderma harzianum [putative sequencing error]	1e-104	AF510393_1	gene: "CTS4"; product: "chitinase 4"; Coccidioides immitis chitinase	26.8	12.0	41.3	12.0	1e-105	01.05.01 C-compound and carbohydrate utilization	
Pc21g16420	strong similarity to scytalone dehydratase - Pyricularia oryzae	8e-62	U95042_1	gene: "arp1"; product: "scytalone dehydratase"; Aspergillus fumigatu	80.0	18.9	93.2	43.0	0.0	01.04 phosphate metabolism	
Pc21g22820	strong similarity to alcohol dehydrogenase alcA - Aspergillus nidulans	1e-169	A29054	alcohol dehydrogenase (EC 1.1.1.1) - Emericella nidulans	181.5	71.8	313.9	156.7	0.0	01.05.01.01 C-compound, carbohydrate catabolism	
Pc21g23200	strong similarity to extracellular alpha-glucosidase aglU - Aspergillus niger	0.0	NCX4G11_13	gene: "X4G11.130"; product: "related to alpha-glucosidase b"; Neur	221.5	44.1	133.8	37.9	1e-112	01 METABOLISM	
Pc21g23540	strong similarity to xylosidase xlnD - Aspergillus niger	0.0	JC7966	xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Talaromyces emersonii	12.0	12.0	27.1	12.0	1e-168	01.05.01 C-compound and carbohydrate utilization	
Pc22g01100	strong similarity to chitinase 1 precursor cts1 - Coccidioides immitis	1e-158	AY271350_1	gene: "ChiB"; product: "chitinase"; Aspergillus fumigatus strain YJ-	431.0	589.8	3604.3	848.1	3e-73	01.05.07 C-compound, carbohydrate transport	
Pc22g01850	glucan 1,4-alpha-glucosidase BAC8255 - Penicillium chrysogenum	0.0	AB091510_1	product: "glucoamylase"; Penicillium chrysogenum mRNA for gluco	18.6	12.0	31.9	12.5	0		0
Pc22g04640	strong similarity to high affinity glucose transporter HGT1 - Kluyveromyces lactis	1e-130	AF168613_2	gene: "hxtA"; product: "hexose transporter protein"; Aspergillus par	38.8	12.0	31.5	12.0	0.0	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc22g05490	weak similarity to 2-haloacid halidohydrolase IVa - Burkholderia cepacia	9e-36	NCB11N2_26	gene: "B11N2.300"; product: "conserved hypothetical protein"; Neur	59.3	15.6	50.6	16.6	2e-78	01.05.07 C-compound, carbohydrate transport	
Pc22g07130	strong similarity to 4-hydroxyphenylpyruvate dioxygenase HPPD - Mycosphaerella graminicola	1e-124	HPPD_MYCGR	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (EC 1.13.11.27)	182.1	36.8	106.1	51.9	1e-104	01.05 C-compound and carbohydrate metabolism	
Pc22g07470	strong similarity to hexose transporter Hxt13 - Saccharomyces cerevisiae	9e-82	NC13E11_7	gene: "13E11.140"; product: "probable sugar transporter"; Neurospo	14.8	12.0	228.5	12.0	0.0	01.05 C-compound and carbohydrate metabolism	
Pc22g08420	strong similarity to brown 2 protein abr2 - Aspergillus fumigatus	0.0	AF104823_1	gene: "abr2"; product: "brown 2"; Aspergillus fumigatus brown 2 (ab	34.0	12.0	82.1	12.0	9e-96	01.02.01.09.99 other catabolism of nitrogenous compounds	
Pc22g13330	strong similarity to glycerol kinase GK - Mus musculus	1e-139	AK076631_1	Mus musculus adult male testis cDNA, RIKEN full-length enriched li	39.5	12.0	291.7	51.5	1e-139	03.03.02 meiosis	
Pc22g16830	strong similarity to lactone-specific esterase estf1 - Pseudomonas fluorescens	2e-71	F83383	probable flavin-binding monooxygenase PA2097 [imported] - Pseudo	91.8	34.2	66.6	39.1	1e-114	01.02.01 nitrogen and sulfur utilization	
Pc22g19920	weak similarity to 35.6K acid phosphatase - Aspergillus nidulans	3e-36	NCB21J21_12	gene: "B21J21.280"; product: "related to meiosis-specific protein ND	86.1	26.9	228.3	20.7	2e-86	01.05 C-compound and carbohydrate metabolism	
Pc22g20960	strong similarity to urate oxidase uaz - Aspergillus flavus	1e-143	A38097	urate oxidase (EC 1.7.3.3) - Aspergillus flavus	107.1	97.3	318.0	96.2	9e-60	01 METABOLISM	
Pc22g22650	strong similarity to androgen-inducible aldehyde reductase aiar - Rattus norvegicus	3e-32	HSA271799_1	gene: "AFAR2"; product: "aflatoxin B1 aldehyde reductase 2"; Hom	48.1	38.4	151.4	56.9	5e-91	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc22g23820	strong similarity to lipase LipP - Pseudomonas sp.	6e-31	AF034088_1	gene: "lipP"; product: "lipase"; Pseudomonas sp. B11-1 lipase (lipP	120.3	110.1	183.9	58.1	1e-66	01 METABOLISM	
Pc22g24730	strong similarity to delta-12 fatty acid desaturase - Mortierella alpina	1e-93	BX649605_129	gene: "odeA"; product: "oleate delta-12 desaturase"; Aspergillus fur	55.0	12.0	30.4	17.8	0		0
Pc22g24830	strong similarity to carboxyphosphonoenolpyruvate phosphonomutase bcpA - Streptomyces hygroscopicus	1e-155	ANI567910_1	gene: "oahA"; product: "oxaloacetate acetylhydrolase"; Aspergillus	364.5	76.6	3298.0	375.2	1e-137	01.04 phosphate metabolism	
Pc10g00010	weak similarity to kinesin-related protein kLPA - Aspergillus nidulans	0	0	0	292.0	100.0	539.8	319.6	0		0
Pc22g23660	strong similarity to Swe1 regulating protein kinase Hsl1 - Saccharomyces cerevisiae	3e-93	KLA555232_1	gene: "hsl1"; product: "protein kinase"; Kluyveromyces lactis hsl1 g	35.1	12.0	107.0	12.0	4e-29	04.05.01.04 transcriptional control	
Pc14g01250	strong similarity to gene expression regulator like protein An12g00680 - Aspergillus niger	0	0	0	34.4	23.1	83.2	37.1	3e-88	01.01.04 regulation of amino acid metabolism	
Pc16g09610	strong similarity to protein abaA - Aspergillus nidulans	0.0	A32434	abaA protein - Emericella nidulans	22.6	12.0	63.5	12.0	0		0
Pc21g05320	similarity to cutinase transcription factor beta CTF1b - Fusarium solani	3e-42	CT1B_FUSSO	CUTINASE TRANSCRIPTION FACTOR 1 BETA.	29.0	15.0	66.9	12.0	7e-29	06.01 protein folding and stabilization	
Pc22g06240	weak similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	2e-14	BX842622_15	gene: "B15B3.150"; product: "related to general repressor of transcri	41.3	23.9	65.3	31.9	0.0	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc12g03440	strong similarity to heat-shock protein hsp30 - Aspergillus nidulans	1e-25	AB126868_1	gene: "hsp30"; product: "heat shock protein 30"; Aspergillus oryzae	87.7	58.5	139.2	47.8	2e-90	06.07 protein modification	
Pc20g15570	similarity to lysosomal protease CLN2 - Rattus norvegicus	1e-159	AB084899_1	gene: "aorO"; product: "aorsin"; Aspergillus oryzae aorO gene for a	86.3	59.3	201.2	39.1	1e-98	08.13 vacuolar transport	
Pc21g14160	alkaline serine protease AAM33821 - Penicillium chrysogenum	1e-175	AF321100_1	product: "alkaline serine protease"; Penicillium chrysogenum alkalin	110.4	76.4	510.7	143.0	7e-93	08.13 vacuolar transport	
Pc21g02740	strong similarity to vacuolar H(+) Ca(2+) exchanger Vcx1 - Saccharomyces cerevisiae	8e-57	T41141	probable caCA proton/calcium exchanger - fission yeast (Schizosac	245.6	170.1	290.2	125.5	0		0
Pc21g02750	strong similarity to vacuolar H(+) Ca(2+) exchanger Vcx1 - Saccharomyces cerevisiae	1e-39	AF053229_1	gene: "cax"; product: "calcium/proton exchanger"; Neurospora cras	153.6	85.8	151.2	61.9	1e-153	01.05 C-compound and carbohydrate metabolism	
Pc21g09650	weak similarity to ecto-ATPase c-cam105 - Rattus norvegicus	0	0	0	23.1	12.0	66.6	12.3	1e-160	08.19 cellular import	
Pc21g16380	strong similarity to cell surface ferroxidase precursor Fet3 - Saccharomyces cerevisiae	0.0	AF116901_1	gene: "abr1"; product: "brown 1"; Aspergillus fumigatus brown 1 (ab	31.3	12.0	61.5	12.0	2e-95	03.03.01 mitotic cell cycle and cell cycle control	
Pc22g06520	weak similarity to potassium transport protein Trk2 - Saccharomyces cerevisiae	2e-47	SOC290453_1	gene: "trk1"; product: "high-affinity potassium uptake transporter"; S	12.0	12.0	33.7	12.0	0		0
Pc12g02730	strong similarity to vegetative incompatibility factor het-e1 - Podospora anserina [putative sequencing error]	1e-158	AF323585_1	gene: "het-d"; product: "beta transducin-like protein HET-D2Y"; Pod	54.5	33.6	60.4	18.7	0		0
Pc12g05710	weak similarity to chemoattractant receptor CAR1 - Dictyostelium discoideum	2e-69	NCB13H18_19	gene: "B13H18.210"; product: "related to G protein coupled receptor	12.3	12.0	47.0	12.9	0		0
Pc12g07300	weak similarity to cyanovirin-N CV-N - Nostoc ellipsosporum	2e-12	NC43E3_4	gene: "43E3.40"; product: "hypothetical protein"; Neurospora crassa	28.6	13.3	25.0	12.0	0		0
Pc12g08290	similarity to antifungal protein precursor paf - Penicillium chrysogenum	1e-32	AX597412_1	unnamed ORF; Sequence 1 from Patent WO02090384.	525.5	51.7	354.5	32.1	4e-62	11.07 detoxification	
Pc13g03440	strong similarity to capsular associated protein CAP10 - Filobasidiella neoformans	1e-46	AF144574_1	gene: "CAP10"; product: "capsular associated protein"; Filobasidiel	29.9	31.2	58.3	21.5	0.0	40.08 Golgi	
Pc13g12500	weak similarity to nitrosoguanidine resistance factor Sng1 - Saccharomyces cerevisiae	7e-07	S53920	SNG1 protein - yeast (Saccharomyces cerevisiae)	12.0	12.0	42.0	12.0	1e-69	01 METABOLISM	
Pc15g01490	strong similarity to copper resistance-associated P-type ATPase CRP1 - Candida albicans	0.0	AF193508_1	gene: "CRP1"; product: "copper resistance-associated P-type ATPa	19.1	13.0	44.1	17.1	4e-54	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc18g02620	strong similarity to cyanide hydratase Cht - Gloeocercospora sorghi	1e-140	AY325811_1	gene: "CyhAB"; product: "cyanide hydratase"; Alternaria brassicicol	12.0	12.0	28.3	12.0	3e-58	11.07 detoxification	
Pc20g01760	strong similarity to cercosporin transporter CFP - Cercospora kikuchii	1e-137	AF238225_1	gene: "Bcmfs1"; product: "DHA14-like major facilitator"; Botryotinia	44.8	12.0	42.8	12.0	7e-97	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc20g14340	similarity to hypothetical 7-aminocholesterol resistance protein Rta1 - Saccharomyces cerevisiae	2e-21	S64536	7-aminocholesterol resistance protein RTA1 - yeast (Saccharomyce	17.4	27.8	81.8	12.0	9e-61	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc21g09770	strong similarity to pisatin demethylase PDA6-1 - Nectria haematococca	2e-55	S34286	pisatin demethylase PDA6-1 - fungus (Nectria haematococca)	144.9	52.0	208.9	57.9	2e-48	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc21g09810	strong similarity to hypothetical membrane transport protein SPAC3H1.06c - Schizosaccharomyces pombe	3e-32	AF186391_1	gene: "mfs1.1"; product: "Mfs1.1"; Coprinus cinereus Mfs1.1 (mfs1.	12.8	12.0	38.3	12.0	1e-72	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g15420	strong similarity to cercosporin transporter CFP - Cercospora kikuchii	1e-153	AF238225_1	gene: "Bcmfs1"; product: "DHA14-like major facilitator"; Botryotinia	1629.0	807.3	2564.7	668.8	1e-125	02.11 electron transport and membrane-associated energy conservation	
Pc21g16330	strong similarity to hypothetical cytochrome P450 monooxygenase p450-4 - Gibberella fujikuroi	1e-105	AF279808_3	gene: "paxP"; product: "cytochrome P450 monooxygenase"; Penic	28.4	15.3	113.9	27.3	1e-175	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc22g23460	similarity to ferric cupric reductase Fre2 - Saccharomyces cerevisiae	0.0	BX842622_23	gene: "B15B3.230"; product: "conserved hypothetical protein"; Neur	804.8	265.1	508.0	336.3	1e-170	01.03 nucleotide metabolism	
Pc21g03870	similarity to ankyrin 3 (splice form 3) - Mus musculus	3e-31	T42714	ankyrin 3, splice form 2 - mouse	34.0	24.9	95.6	46.2	2e-38	01.05 C-compound and carbohydrate metabolism	
Pc06g00210	strong similarity to secretory component IDGF - Sarcophaga peregrina	1e-138	NC5F3_11	gene: "5F3.110"; product: "related to cecr1 protein"; Neurospora cra	41.4	17.7	100.6	12.4	0		0
Pc06g01530	similarity to hypothetical protein 4 - Streptomyces coelicolor	2e-30	AC117176_51	product: "similar to Homo sapiens (Human). HSCARG"; Dictyosteli	33.9	24.4	56.0	12.0	0		0
Pc06g02040	similarity to hypothetical protein 15_scaffold_1.tfa_520cg - Fusarium graminearum	0	0	0	276.5	144.0	622.8	87.7	0		0
Pc06g02050	strong similarity to hypothetical protein An08g11990 - Aspergillus niger	0	0	0	97.3	22.5	619.0	40.2	0		0
Pc06g02070	weak similarity to hypothetical protein contig46_part_ii.tfa_1990wg - Aspergillus fumigatus	0	0	0	39.9	12.0	509.5	21.9	0		0
Pc06g02070	weak similarity to hypothetical protein contig46_part_ii.tfa_1990wg - Aspergillus fumigatus	0	0	0	39.9	12.0	509.5	21.9	0		0
Pc06g02080	weak similarity to hypothetical protein An06g02320 - Aspergillus niger	0	0	0	12.0	12.0	61.3	12.0	0		0
Pc06g02080	weak similarity to hypothetical protein An06g02320 - Aspergillus niger	0	0	0	12.0	12.0	61.3	12.0	0		0
Pc06g02090	hypothetical protein	0	0	0	12.0	12.0	63.9	12.0	0		0
Pc06g02100	hypothetical protein	0	0	0	93.9	52.8	387.8	66.2	0.0	03.01.05.01 DNA repair	
Pc09g00160	hypothetical protein	0	0	0	868.8	245.0	579.3	158.4	0		0
Pc12g02720	weak similarity to NAD+ ADP-ribosyltransferase PPOL - Homo sapiens	0.0	AY347573_1	product: "poly(ADP)-ribose polymerase"; Emericella nidulans poly(A	15.7	12.0	25.5	12.0	2e-46	01.03 nucleotide metabolism	
Pc12g02850	weak similarity to hypothetical protein - Aspergillus fumigatus	7e-09	BX649606_42	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot proj	32.3	13.7	37.7	22.1	0		0
Pc12g02930	strong similarity to oxidoreductase like protein An09g01260 - Aspergillus niger	2e-18	AE003435_50	product: "CG4020-PA"; Drosophila melanogaster chromosome X se	12.0	12.0	24.5	12.0	0		0
Pc12g03260	similarity to hypothetical protein An16g07330 - Aspergillus niger	0	0	0	61.5	16.1	147.2	12.0	0		0
Pc12g06450	strong similarity to hypothetical protein contig_1_55_scaffold_3.tfa_110cg - Aspergillus nidulans	0	0	0	12.0	12.0	99.8	22.7	0		0
Pc12g06460	strong similarity to hypothetical protein contig28.tfa_310cg - Aspergillus fumigatus	0	0	0	12.0	12.0	123.8	17.3	2e-57	01.04 phosphate metabolism	
Pc12g06880	hypothetical protein	0	0	0	117.0	24.4	288.0	112.6	0		0
Pc12g06900	strong similarity to hypothetical protein An08g11790 - Aspergillus niger	0	0	0	24.4	12.0	47.7	24.9	2e-26	03.03.01.01.11 mitosis	
Pc12g07740	similarity to hypothetical protein contig_1_129_scaffold_10.tfa_800wg - Aspergillus nidulans	0	0	0	86.4	56.3	92.2	30.6	0		0
Pc12g09800	strong similarity to hypothetical protein SPAC637.13c - Schizosaccharomyces pombe	1e-40	T39005	hypothetical protein SPAC637.13c - fission yeast (Schizosaccharon	140.5	158.8	219.7	72.7	0		0
Pc12g10150	strong similarity to hypothetical protein An01g11250 - Aspergillus niger	0	0	0	27.0	15.4	39.0	13.4	0		0
Pc12g12350	hypothetical protein	0	0	0	40.9	37.5	58.6	12.0	6e-54	01.05.01.01.02 polysaccharide degradation	
Pc12g13160	strong similarity to hypothetical mixed-linked glucanase precursor related protein MLG1 - Neurospora crassa	4e-69	U81606_1	gene: "MLG1"; product: "mixed-linked glucanase precursor"; Cochli	84.0	32.7	67.1	14.2	0		0
Pc12g13430	strong similarity to hypothetical protein B2J23.120 - Neurospora crassa	1e-132	NCB2J23_12	gene: "B2J23.120"; product: "conserved hypothetical protein"; Neur	24.4	12.0	39.6	14.9	0		0
Pc12g13940	strong similarity to hypothetical protein contig_1_41_scaffold_2.tfa_160wg - Aspergillus nidulans	0	0	0	12.0	12.0	57.7	12.0	0		0
Pc12g14130	similarity to hypothetical protein Atu4302 - Agrobacterium tumefaciens	3e-14	AP005951_40	gene: "blr4383"; Bradyrhizobium japonicum USDA 110 DNA, compl	16.1	12.0	105.5	12.0	0		0
Pc12g14960	similarity to hypothetical protein An08g06730 - Aspergillus niger	8e-06	BX649606_119	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot proj	141.5	17.8	216.4	12.0	2e-72	01.04 phosphate metabolism	
Pc12g15480	strong similarity to hypothetical protein contig_1_93_scaffold_6.tfa_720cg - Aspergillus nidulans	9e-08	AP005348_63	gene: "VVA0976"; product: "Rhs family protein"; Vibrio vulnificus YJ	12.0	12.0	25.0	12.0	1e-120	13.01 ionic homeostasis	
Pc12g15660	similarity to hypothetical protein 1168_scaffold_2.tfa_590cg - Fusarium graminearum	9e-05	AY144182_1	gene: "PPCK2"; product: "phosphoenolpyruvate carboxylase kinase"	17.8	17.6	26.2	12.0	0		0
Pc13g00880	strong similarity to ceruloplasmin - Danio rerio	7e-66	BC064000_1	gene: "cp"; product: "ceruloplasmin"; Danio rerio ceruloplasmin, mF	63.6	13.5	158.3	12.0	2e-99	14.04.03.05 sporulation and germination	
Pc13g02150	weak similarity to hypothetical protein An11g05870 - Aspergillus niger [putative pseudogene]	0	0	0	23.2	12.0	116.2	24.9	0		0
Pc13g06170	similarity to pyoverdine biosynthesis protein PvcA - Pseudomonas aeruginosa	2e-19	AF002222_1	gene: "pvcA"; product: "PvcA"; Pseudomonas aeruginosa pyoverdin	57.4	33.2	164.7	56.9	1e-53	06.13 proteolytic degradation	
Pc13g06950	weak similarity to hypothetical protein B12F1.100 - Neurospora crassa	5e-26	NCG65A3_12	gene: "G65A3.110"; product: "conserved hypothetical protein"; Neu	60.1	34.6	67.5	31.3	0		0

Pc13g09460	similarity to zonadhesin - Mus musculus	2e-18	T42215	zonadhesin - mouse	772.1	730.7	2458.2	646.9	0	0
Pc13g11090	hypothetical protein	0	0	0	12.0	12.0	30.1	12.0	0	0
Pc13g13860	strong similarity to hypothetical protein contig_1_79_scaffold_5.tfa_170wg - Aspergillus nidulans	0	0	0	22.0	17.2	42.0	18.1	3e-40	01 METABOLISM
Pc13g13920	hypothetical protein	0	0	0	25.0	15.4	38.2	12.0	0	0
Pc13g14650	strong similarity to hypothetical protein 1166_scaffold_2.tfa_100wg - Fusarium graminearum	2e-11	AE016944_40	product: "phosphoglycolate phosphatase"; Bacteroides thetaiotaomi	12.0	12.0	42.0	13.7	0	0
Pc13g15620	strong similarity to hypothetical protein An09g04440 - Aspergillus niger	2e-17	NC80A10_14	gene: "80A10.140"; product: "hypothetical protein"; Neurospora cra	67.4	39.0	76.6	28.5	0	0
Pc13g15630	strong similarity to hypothetical protein An09g04380 - Aspergillus niger	0	0	0	81.7	20.3	59.3	22.7	0	0
Pc13g15650	similarity to hypothetical protein contig61.tfa_1600cg - Aspergillus fumigatus	0	0	0	441.5	184.3	473.0	189.3	1e-112	99 UNCLASSIFIED PROTEINS
Pc13g16010	weak similarity to spore-wall fungal hydrophobin dewA - Aspergillus nidulans	6e-07	S67924	spore-wall fungal hydrophobin DewA - Emericella nidulans	55.7	12.0	58.6	12.0	1e-87	06.13 proteolytic degradation
Pc14g00580	strong similarity to hypothetical membrane protein YDL237w - Saccharomyces cerevisiae	2e-26	S67801	probable membrane protein YDL237w - yeast (Saccharomyces cere	249.9	149.9	245.9	111.6	0	0
Pc15g00470	weak similarity to hypothetical protein UNC-89 - Caenorhabditis elegans	2e-06	AE003576_35	product: "CG33196-PB"; Drosophila melanogaster chromosome 2L	30.7	12.0	30.1	12.0	0	0
Pc15g02120	weak similarity to hypothetical protein SCF34.07 - Streptomyces coelicolor	0.0	AY505013_1	gene: "rhmA"; product: "alpha-L-rhamnosidase A"; Thermomicrobia	38.2	17.5	63.0	39.6	0	0
Pc16g00180	strong similarity to hypothetical protein contig10.tfa_220cg - Aspergillus fumigatus	3e-11	AP006581_119	Gloeobacter violaceus PCC 7421 DNA, complete genome, section 1	18.1	12.0	68.0	12.0	0	0
Pc16g04550	hypothetical protein	0	0	0	25.8	12.0	109.3	12.0	0	0
Pc16g04840	hypothetical protein	0	0	0	85.7	12.0	143.1	12.0	0	0
Pc16g05400	weak similarity to hypothetical protein contig49.tfa_1510wg - Aspergillus fumigatus	0	0	0	16.3	12.0	29.6	12.0	0	0
Pc16g06660	weak similarity to hypothetical protein encoded by CG4090 - Drosophila melanogaster	0	0	0	155.8	207.4	469.0	12.0	0	0
Pc16g06690	similarity to spore-wall fungal hydrophobin dewA - Aspergillus nidulans	7e-14	S67924	spore-wall fungal hydrophobin DewA - Emericella nidulans	70.6	27.0	57.5	13.0	0	0
Pc16g08570	strong similarity to hypothetical protein An01g02040 - Aspergillus niger [putative sequencing error]	0	0	0	27.4	12.0	39.1	12.0	6e-43	01.20 secondary metabolism
Pc16g08820	similarity to hypothetical protein contig_1_7_scaffold_1.tfa_740cg - Aspergillus nidulans	0	0	0	105.5	42.1	74.0	53.7	1e-40	99 UNCLASSIFIED PROTEINS
Pc16g10190	strong similarity to hypothetical glutathione-S-transferase SPCC965.07c - Schizosaccharomyces pombe	5e-42	T41222	probable glutathione s-transferase - fission yeast (Schizosaccharom	12.0	12.0	26.4	12.0	0	0
Pc16g11150	strong similarity to hypothetical protein contig_1_135_scaffold_11.tfa_750wg - Aspergillus nidulans	9e-09	T41383	hypothetical protein SPCC550.08 - fission yeast (Schizosaccharomy	121.4	30.9	92.7	23.9	1e-86	04.05.01.04 transcriptional control
Pc16g11310	strong similarity to allergen rAsp f 4 - Aspergillus fumigatus	4e-75	AFRASPF4_1	gene: "rasp f 4"; product: "rAsp f 4"; Aspergillus fumigatus mRNA fo	14.0	12.0	25.5	12.0	0	0
Pc16g12230	strong similarity to hypothetical protein contig46_part_ii.tfa_240wg - Aspergillus fumigatus	1e-151	BX649607_4	product: "zinc finger protein, putative"; Aspergillus fumigatus BAC pi	105.0	93.0	142.2	64.3	0	0
Pc16g13260	similarity to hypothetical protein An01g10940 - Aspergillus niger	0	0	0	67.0	39.2	97.3	12.0	0	0
Pc16g13330	similarity to hypothetical protein An15g07090 - Aspergillus niger	0	0	0	556.9	770.5	1407.2	458.4	1e-96	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc16g13500	weak similarity to integral membrane protein PTH11 from patent WO9913094-A2 - Magnaporthe grisea	7e-09	AF119670_1	gene: "PTH11"; product: "integral membrane protein"; Magnaporthe	24.0	28.0	60.3	14.5	0	0
Pc18g03220	strong similarity to hypothetical protein contig1490_3.tfa_900cg - Aspergillus fumigatus	8e-51	I39975	sarcosine oxidase (EC 1.5.3.1) - Bacillus sp.	50.8	44.0	76.9	30.3	2e-81	99 UNCLASSIFIED PROTEINS
Pc18g04570	weak similarity to hypothetical protein C0390w - Plasmodium falciparum	2e-13	T18435	hypothetical protein C0390w - malaria parasite (Plasmodium falcipar	342.2	58.3	780.3	17.0	0	0
Pc18g06050	similarity to hypothetical protein SPAC15A10.09c - Schizosaccharomyces pombe	2e-16	NCB11H24_7	gene: "B11H24.070"; product: "conserved hypothetical protein"; Neu	49.3	37.7	85.3	33.4	0	0
Pc20g00930	strong similarity to hypothetical protein An17g02060 - Aspergillus niger	0	0	0	25.3	15.9	61.4	31.1	0	0
Pc20g02790	weak similarity to hypothetical protein contig1487_1.tfa_1190cg - Aspergillus fumigatus	0	0	0	57.4	25.2	66.9	20.9	5e-54	01.07.10 transport of vitamins, cofactors, and prosthetic groups
Pc20g05380	hypothetical protein	0	0	0	1298.5	195.6	2737.3	338.7	1e-45	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM
Pc20g05740	strong similarity to superoxide dismutase (Cu-Zn) 4-2 - Caenorhabditis elegans	1e-32	JE0098	superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4-2 - Caenorhabditis ele	164.5	16.9	430.7	21.8	0	0
Pc20g08040	strong similarity to hypothetical protein contig1487_1.tfa_410wg - Aspergillus fumigatus	5e-31	S69582	hypothetical protein YDR527w - yeast (Saccharomyces cerevisiae)	51.0	46.2	69.2	26.5	0	0
Pc20g09950	strong similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae	9e-80	AF359360_1	gene: "OrfF"; product: "putative methyltransferase"; Fusarium sporo	12.0	12.0	34.1	12.0	0	0
Pc20g10640	similarity to hypothetical protein An08g09690 - Aspergillus niger	0	0	0	37.8	13.0	37.6	22.8	0	0
Pc20g11480	hypothetical protein	0	0	0	581.1	358.3	778.7	315.2	0	0
Pc20g11490	hypothetical protein	0	0	0	290.8	327.8	651.4	119.7	2e-44	01.01.10 amino acid degradation (catabolism)
Pc20g13710	weak similarity to hypothetical protein - lasmodium falciparum	4e-08	PFMAL3P7_35	gene: "MAL3P7.34"; "PFC1015c"; product: "hypothetical protein"; F	47.8	12.0	54.5	12.0	0	0
Pc20g15160	strong similarity to hypothetical amidase Z37509 - Saccharomyces cerevisiae	1e-106	S50309	hypothetical protein (MEL4 3' region) - yeast (Saccharomyces cerev	16.3	32.4	41.8	16.3	2e-78	06.04 protein targeting, sorting and translocation
Pc21g00950	similarity to hypothetical protein contig_1_168_scaffold_14.tfa_260wg - Aspergillus nidulans	0	0	0	700.0	148.6	436.1	328.0	2e-69	11.07 detoxification
Pc21g02340	similarity to hypothetical protein contig127.tfa_140cg - Aspergillus fumigatus	7e-13	AY075446_1	gene: "CG17419"; product: "RE06111p"; Drosophila melanogaster R	12.0	12.0	50.4	12.0	9e-91	04.05.01.04 transcriptional control
Pc21g03010	strong similarity to molasses resistency protein Rtm1 - Saccharomyces cerevisiae	5e-32	S59140	RTM1 protein - yeast (Saccharomyces cerevisiae) (strain FL100)	104.9	94.0	612.4	89.7	7e-83	99 UNCLASSIFIED PROTEINS
Pc21g06630	similarity to hypothetical protein contig12.tfa_950wg - Aspergillus fumigatus	1e-10	T48778	hypothetical protein 13E11.260 [imported] - Neurospora crassa	12.0	12.0	27.1	12.0	0	0
Pc21g06950	strong similarity to hypothetical protein YML079w - Saccharomyces cerevisiae	5e-41	NC123A4_27	gene: "123A4.290"; product: "conserved hypothetical protein"; Neur	52.4	13.7	397.0	56.9	0	0
Pc21g07580	weak similarity to hypothetical protein An04g09900 - Aspergillus niger	0	0	0	26.0	12.0	25.7	12.0	0	0
Pc21g08140	strong similarity to hypothetical protein contig_1_107_scaffold_7.tfa_1090cg - Aspergillus nidulans	6e-09	AE008818_5	gene: "STM2587"; product: "Gifsy-1 prophage protein"; Salmonella	171.8	34.0	229.4	65.3	0	0
Pc21g08370	similarity to hypothetical protein An11g07840 - Aspergillus niger	4e-04	BX908811_15	gene: "H4H7.150"; product: "conserved hypothetical protein"; Neurc	19.3	12.0	25.5	12.0	2e-26	01.01.01.01.02 biosynthesis of the glutamate group (proline, hydroxyprolin, arginine, glutamine, glutamate)
Pc21g08460	strong similarity to hypothetical protein contig1492_0.tfa_2410wg - Aspergillus fumigatus	0	0	0	456.3	185.4	595.9	446.8	0	0
Pc21g08470	similarity to hypothetical protein 1465_scaffold_9.tfa_210wg - Fusarium graminearum	2e-13	NC80A10_20	gene: "80A10.200"; product: "conserved hypothetical protein"; Neur	44.3	20.8	41.2	25.9	0	0
Pc21g09590	strong similarity to hypothetical protein contig5_part_ii.tfa_220cg - Aspergillus fumigatus	0	0	0	116.3	12.0	57.4	56.9	0	0
Pc21g09640	similarity to hypothetical protein ncu05632.1 - Neurospora crassa	0	0	0	15.8	12.0	65.6	21.5	0	0
Pc21g10690	strong similarity to hypothetical protein contig1488_2.tfa_1690cg - Aspergillus fumigatus	0	0	0	80.2	38.4	69.3	45.2	1e-154	01.20.37.03 biosynthesis of peptide antibiotics
Pc21g12310	hypothetical protein	0	0	0	710.5	516.4	1304.5	588.6	0	0
Pc21g12840	strong similarity to hypothetical protein contig_1_153_scaffold_12.tfa_490wg - Aspergillus nidulans	3e-96	MAPEPSYNT_1	gene: "pesA"; product: "peptide synthetase"; Metarhizium anisoplia	258.6	54.7	235.3	84.8	1e-141	14.04.03.05 sporulation and germination
Pc21g14100	strong similarity to hypothetical protein An14g02980 - Aspergillus niger	0	0	0	36.6	14.5	72.2	12.0	0	0
Pc21g15320	similarity to pyoverdine biosynthesis protein PvcA - Pseudomonas aeruginosa	2e-23	H83363	pyoverdine biosynthesis protein PvcA PA2254 [imported] - Pseudom	12.7	12.0	92.4	12.0	0	0
Pc21g16130	similarity to hypothetical protein contig1495_1.tfa_1320wg - Aspergillus fumigatus	0	0	0	171.9	107.3	337.2	36.4	2e-44	03.03.01 mitotic cell cycle and cell cycle control
Pc21g16440	strong similarity to hypothetical yellowish-green 1 ayg1 - Aspergillus fumigatus	1e-161	AF116902_1	gene: "ayg1"; product: "yellowish-green 1"; Aspergillus fumigatus ye	53.4	12.0	55.5	33.7	0	0
Pc21g18070	weak similarity to suppressor of cdc25 mutations Tfs1 - Saccharomyces cerevisiae	3e-06	S18843	TFS1 protein - yeast (Saccharomyces cerevisiae)	61.6	57.6	118.2	19.9	7e-53	01.03 nucleotide metabolism
Pc21g20790	strong similarity to hypothetical precursor of spore coat protein sp96 - Neurospora crassa	5e-43	T51044	related to spore coat protein SP96 precursor [imported] - Neurospora	55.4	12.0	59.7	12.0	0	0
Pc22g00460	strong similarity to hypothetical protein An06g01070 - Aspergillus niger	6e-19	BC045017_1	product: "Similar to RIKEN cDNA 3732409C05 gene"; Xenopus laev	62.9	67.2	227.7	87.9	0	0
Pc22g02820	strong similarity to hypothetical protein contig12.tfa_1430wg - Aspergillus fumigatus	0	0	0	545.8	113.5	527.4	445.7	7e-66	11.05.01 resistance proteins
Pc22g07700	strong similarity to hypothetical protein SCF91.02c - Streptomyces coelicolor	1e-154	SCO939106_93	gene: "SCO0642"; "SCF91.02c"; product: "conserved hypothetical p	12.5	13.7	27.2	12.0	0	0
Pc22g07760	strong similarity to hypothetical protein 1194_scaffold_2.tfa_330wg - Fusarium graminearum	7e-67	NC1A9_4	gene: "1A9.050"; product: "conserved hypothetical protein"; Neuros	20.9	12.0	40.9	16.0	4e-44	01.05 C-compound and carbohydrate metabolism
Pc22g08820	hypothetical protein	0	0	0	33.1	12.9	88.4	21.5	0	0
Pc22g12780	weak similarity to hypothetical myoinositol-dehydrogenase spcB - Streptomyces spectabilis	2e-09	D71201	hypothetical protein PH1881 - Pyrococcus horikoshii	55.6	18.7	44.1	21.6	0	0
Pc22g14300	similarity to hypothetical protein An02g09010 - Aspergillus niger	3e-05	AY184388_1	gene: "Muc6"; product: "MUC6"; Mus musculus MUC6 (Muc6) gene	132.4	22.1	390.3	12.0	3e-71	06.04 protein targeting, sorting and translocation
Pc22g17040	hypothetical protein	0	0	0	129.0	17.5	243.9	12.0	3e-29	13.07 cell adhesion
Pc22g17420	strong similarity to hypothetical protein contig_1_153_scaffold_12.tfa_500cg - Aspergillus nidulans	2e-10	AY195855_1	product: "ankyrin repeat protein E4_2"; Synthetic construct ankyrin	42.0	12.5	69.1	12.0	0	0
Pc22g17690	strong similarity to rAsp f 7 - Aspergillus fumigatus	2e-30	AFAJ3315_1	gene: "rasp f 7"; product: "rAsp f 7"; Aspergillus fumigatus mRNA fo	961.9	802.6	1740.9	855.0	0	0
Pc22g21690	hypothetical protein	0	0	0	38.5	12.0	48.2	17.8	1e-145	01.20.05.11 biosynthesis of polyketides
Pc22g22540	strong similarity to hypothetical protein contig_1_7_scaffold_1.tfa_90cg - Aspergillus nidulans	0	0	0	46.0	24.0	44.7	12.0	0	0
Pc22g22580	strong similarity to hypothetical protein contig_1_153_scaffold_12.tfa_490wg - Aspergillus nidulans	2e-92	AF469045_1	gene: "tex1"; product: "nonribosomal peptide synthetase"; Hypocre	12.0	12.0	33.1	12.0	2e-66	01.05 C-compound and carbohydrate metabolism
Pc22g22620	weak similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae	1e-09	AY437642_2	Leptosphaeria maculans ATP binding cassette transporter (ABCt4) a	12.0	12.0	50.6	12.0	0	0
Pc22g22810	strong similarity to sulphydryl oxidase Sox from patent EP565172-A1 - Aspergillus niger	1e-129	A78767_1	unnamed ORF; Sequence 1 from Patent EP0565172.	517.8	311.8	645.2	55.5	0	0
Pc22g22920	strong similarity to hypothetical protein contig_1_153_scaffold_12.tfa_50wg - Aspergillus nidulans	0	0	0	12.0	12.0	33.2	12.0	0	0
Pc22g24690	weak similarity to hypothetical protein mlr2143 - Mesorhizobium loti	1e-07	AL646075_14	gene: "RSc3377"; "RS02651"; product: "CONSERVED HYPOTHETI	24.5	44.4	203.4	23.7	0	0
Pc22g24750	similarity to hypothetical protein B8J22.030 - Neurospora crassa	6e-18	BX842627_2	gene: "B8J22.030"; product: "conserved hypothetical protein"; Neur	12.0	12.0	95.7	12.0	0	0
Pc22g24850	similarity to hypothetical protein B8J22.030 - Neurospora crassa	7e-13	BX842627_2	gene: "B8J22.030"; product: "conserved hypothetical protein"; Neur	35.5	47.0	217.0	18.3	0	0
Pc22g25460	hypothetical protein	0	0	0	574.7	36.9	1275.2	188.0	0	0
Pc22g26260	hypothetical protein	0	0	0	47.9	15.5	63.8	12.4	0	0
Pc23g00740	weak similarity to protein CG33196-PB - Drosophila melanogaster [truncated ORF]	3e-05	AE003576_35	product: "CG33196-PB"; Drosophila melanogaster chromosome 2L	308.4	109.1	644.5	379.8	0	0
Pc24g00300	hypothetical protein	0	0	0	32.6	12.7	43.7	14.5	3e-94	03.03.01.01.09 G2/M transition of mitotic cell cycle
Pc24g00920	hypothetical protein	0	0	0	307.9	70.3	231.1	42.9	0	0
Pc24g01580	weak similarity to polycystic kidney disease 1-like 3 - Mus musculus	8e-10	AY164486_1	gene: "Pkd1l3"; product: "polycystic kidney disease 1-like 3"; Mus	69.2	14.6	41.9	13.1	0	0

Supplementary Table 15. K-mean cluster 7

@=Values given are the average of three independent experiments

orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels @				FunCat (auto)		
		p-value	Gene code	description	WIS - PAA	WIS + PAA	DS - PAA	DS + PAA	pval	category	
Pc12g020	strong similarity to glucose transporter rco-3 - Neurospora crassa	1e-151	BX842632_4	gene: "B5K2.040"; product: "RCO3-probable glucose transporter"; Neurospora crass	2281.3	1010.5	113.3	87.6	3e-84	01.05.07 C-compound, carbohydrate transport	
Pc12g108	strong similarity to endo 1,5-alpha-arabinanase abnA - Aspergillus niger	7e-82	ABNA_ASPNG	ARABINAN ENDO-1,5-ALPHA-L-ARABINOSIDASE A PRECURSOR (EC 3.2.1.99) (	1101.3	1179.8	133.8	12.0	7e-94	01.05.07 C-compound, carbohydrate transport	
Pc15g000	strong similarity to sugar transporter Sut2 - Pichia stipitis	2e-44	S50708	hexose transport protein HXT9 - yeast (Saccharomyces cerevisiae)	780.3	199.3	12.0	13.5	0		0
Pc15g000	strong similarity to hexose transporter ght2p - Schizosaccharomyces pombe	0.0	AY081847_1	gene: "mstC"; product: "monosaccharide transporter"; Aspergillus niger monosaccha	760.9	250.7	189.9	52.1	1e-107	01 METABOLISM	
Pc16g131	strong similarity to hypothetical glucan beta-1,3 exoglucanase exgS - Aspergillus phoenicis	0.0	BX649607_83	gene: "exgO"; product: "exo-1,3-beta-D-glucanase, putative"; Aspergillus fumigatus E	238.8	107.6	76.0	28.7	0		0
Pc16g150	strong similarity to chitinase chiC - Aspergillus nidulans	1e-101	AJ617333_1	product: "chitin binding protein"; Pichia acaciae plasmid pPac1-2 ORF1, ORF2, ORF	74.8	55.4	12.0	12.0	1e-102	01.05.01 C-compound and carbohydrate utilization	
Pc18g001	weak similarity to isoflavone reductase IFR - Medicago sativa	1e-173	ENI344256_1	gene: "cipA"; product: "CipA protein"; Emericella nidulans cipA gene	212.6	187.5	21.9	23.0	0		0
Pc18g006	strong similarity to acetate kinase like protein An02g06420 - Aspergillus niger	1e-123	BX842635_4	gene: "B12J7.040"; product: "related to acetate kinase"; Neurospora crassa DNA lin	106.3	61.5	34.5	12.0	0		0
Pc18g042	similarity to gentamicin resistance gene like protein An08g01130 - Aspergillus niger	0	0	0	212.7	239.1	75.5	38.1	1e-126	01 METABOLISM	
Pc20g026	strong similarity to glutaminase A gtaA - Aspergillus oryzae	0.0	AB029553_1	gene: "gtaA"; product: "glutaminase A"; Emericella nidulans gtaA gene for glutaminas	1177.7	1257.7	246.6	12.0	1e-169	13 REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT	
Pc21g078	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	0.0	AY254381_1	Emericella nidulans adenylate-forming enzyme (afeA) gene, complete	274.7	116.8	23.7	17.0	1e-163	13 REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT	
Pc21g111	strong similarity to triacylglycerol lipase lipI - Geotrichum candidum	1e-120	BX842680_30	gene: "90C4.300"; product: "related to cholinesterase precursor"; Neurospora crass	462.5	190.0	258.1	23.2	6e-90	01.05.07 C-compound, carbohydrate transport	
Pc21g131	strong similarity to cholinesterase 1 ChE1 - Branchiostoma floridae	8e-48	BC058815_1	Mus musculus hypothetical protein LOC234669, mRNA (cDNA clone	263.0	236.1	96.0	30.1	2e-78	01.05.07 C-compound, carbohydrate transport	
Pc21g140	strong similarity to hexose transporter Hxt2 - Saccharomyces cerevisiae	1e-170	AY081849_1	gene: "mstE"; product: "monosaccharide transporter"; Aspergillus niger monosaccha	387.7	127.7	12.0	12.0	6e-82	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc21g197	strong similarity to high-affinity glucose transporter HGT1 - Kluyveromyces lactis	0.0	THA269534_1	gene: "gtt1"; product: "glucose transporter"; Trichoderma harzianum mRNA for gluco	367.8	98.4	12.0	12.0	1e-111	01.01.01 amino acid biosynthesis	
Pc21g215	strong similarity to glucose transporter rco-3 - Neurospora crassa	1e-126	AMMST1_1	gene: "AmMst-1"; product: "AmMst-1"; A.muscaria mRNA for monosaccharide trans	665.7	166.9	88.1	29.8	4e-79	01.05.07 C-compound, carbohydrate transport	
Pc22g009	strong similarity to tryptophan synthase Trp5 - Saccharomyces cerevisiae	3e-94	A32959	tryptophan synthase (EC 4.2.1.20) - Neurospora crassa	238.9	333.9	17.7	14.6	1e-171	01.01.01 amino acid biosynthesis	
Pc22g030	strong similarity to sugar transporter Sut2 - Pichia stipitis	1e-164	NC13E11_7	gene: "13E11.140"; product: "probable sugar transporter"; Neurospora crassa DNA	1109.3	428.5	42.1	19.7	4e-78	01.01 amino acid metabolism	
Pc22g094	similarity to nonribosomal peptide synthase MxaA - Stigmatella aurantiaca	9e-31	AY495593_1	gene: "PKS3"; product: "polyketide synthase"; Gibberella moniliformis polyketide synt	696.1	129.9	108.3	21.4	3e-51	01.03.16 polynucleotide degradation	
Pc22g122	strong similarity to choline permease Hnm1 - Saccharomyces cerevisiae	2e-51	ENI131668_1	gene: "gabA"; product: "GABA permease"; Emericella nidulans gabA gene	139.6	85.9	100.2	12.0	3e-51	01.03.16 polynucleotide degradation	
Pc09g000	strong similarity to ribonuclease H 3-5 exonuclease like protein An11g03420 - Aspergillus niger	4e-17	AY080843_1	gene: "At5g67240"; product: "unknown protein"; Arabidopsis thaliana unknown protei	364.1	316.2	53.3	51.0	1e-70	04.05.01.04 transcriptional control	
Pc09g000	strong similarity to ribonuclease H 3-5 exonuclease like protein An11g03420 - Aspergillus niger	4e-17	AY080843_1	gene: "At5g67240"; product: "unknown protein"; Arabidopsis thaliana unknown protei	364.1	316.2	53.3	51.0	1e-158	04 TRANSCRIPTION	
Pc06g004	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	1e-134	AF533070_1	gene: "brlA"; product: "BRLA"; Aspergillus parasiticus BRLA (brlA) gene, complete c	299.2	306.6	69.6	22.2	0.0	10.01.01 unspecified signal transduction	
Pc06g013	similarity to copper homeostasis protein Cup9 - Saccharomyces cerevisiae	2e-09	AF170065_1	product: "meis2"; Danio rerio meis2 mRNA, complete cds.	362.6	439.7	76.3	58.2	0.0	10.01.01 unspecified signal transduction	
Pc06g021	strong similarity to retrotransposon Tto1 - Nicotiana tabacum	1e-135	AP002538_10	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P04	801.6	934.0	267.7	82.9	1e-115	04 TRANSCRIPTION	
Pc06g021	strong similarity to retrotransposon Tto1 - Nicotiana tabacum	1e-135	AP002538_10	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P04	801.6	934.0	267.7	82.9	3e-21	04 TRANSCRIPTION	
Pc12g045	weak similarity to Wilms tumor susceptibility protein WT1 - Homo sapiens	9e-50	NCB13O20_2	gene: "B13O20.050"; product: "related to finger protein AZF1"; Neurospora crassa D	175.3	70.9	53.0	17.4	0		0
Pc12g165	weak similarity to bZIP transcription factor Yap3 - Saccharomyces cerevisiae	4e-40	BX842630_4	gene: "B13D15.040"; product: "hypothetical protein"; Neurospora crassa DNA linkag	941.4	823.2	152.1	111.8	3e-26	04 TRANSCRIPTION	
Pc13g155	weak similarity to hypothetical transcription factor CAD37059.1 - Neurospora crassa	8e-09	BX649606_48	product: "possible zinc finger protein"; Aspergillus fumigatus BAC pilot project superc	164.3	108.2	40.6	17.6	0.0	10.01.01 unspecified signal transduction	
Pc22g041	similarity to 13.7 kD subunit of DNA-directed RNA polymerase I Rpa12 - Saccharomyces cerevisiae	1e-11	A48107	DNA-directed RNA polymerase (EC 2.7.7.6) I chain A12.2 - yeast (Saccharomyces	111.3	72.4	32.0	14.6	0		0
Pc24g019	strong similarity to retrotransposon Tto1 - Nicotiana tabacum	1e-123	AC079889_11	gene: "OSJNBa0092M19.11"; product: "gag-pol polyprotein"; Oryza sativa chromoso	391.1	395.6	125.5	47.5	1e-41	03.03.05.03 cell cycle dependent actin filament reorganization	
Pc06g000	strong similarity to aspergillopepsin II precursor (acid proteinase A) - Aspergillus niger	7e-64	A41025	aspergillopepsin II (EC 3.4.23.19) precursor - Aspergillus niger (var. macrosporus)	438.8	67.6	114.2	21.2	6e-39	06.04 protein targeting, sorting and translocation	
Pc12g075	similarity to cofilin Cof1 - Saccharomyces cerevisiae	1e-21	NCB2O8_27	gene: "B2O8.270"; product: "related to cofilin"; Neurospora crassa DNA linkage grou	474.3	84.7	31.4	12.0	1e-86	06.13 proteolytic degradation	
Pc16g150	similarity to ankyrin like protein An11g03610 - Aspergillus niger	4e-09	AE017257_17	product: "ankyrin repeat domain protein"; Wolbachia endosymbiont of Drosophila me	82.4	75.0	12.0	12.0	1e-54	01.05.07 C-compound, carbohydrate transport	
Pc21g023	strong similarity to aspergillopepsin apnS - Aspergillus phoenicis	8e-93	AF439995_1	product: "pepsin-type protease"; Talaromyces emersonii pepsin-type protease gene,	100.5	56.7	15.0	12.0	0		0
Pc21g130	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae	0.0	AJ515522_1	Zygosaccharomyces bailii ffz1 gene for fructose facilitator.	556.4	192.9	12.0	12.0	0		0
Pc21g227	strong similarity to integral membrane protein like protein An04g06980 - Aspergillus niger	8e-08	BX649605_15	product: "integral membrane protein, putative"; Aspergillus fumigatus BAC pilot proje	239.7	51.1	18.4	12.0	2e-54	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc20g070	strong similarity to 1,4-beta-D-arabinoxylan arabinofuranohydrolase axhA - Aspergillus niger	1e-133	ANAXHA_1	gene: "axhA"; product: "(1,4)-beta-D-arabinoxylan arabinofuranohydrolase"; A.niger	179.9	108.3	24.1	12.0	1e-106	13.11.03.07 pheromone response	
Pc22g235	strong similarity to cercosporin transporter CFP - Cercospora kikuchii	1e-175	AF238225_1	gene: "Bcmfs1"; product: "DHA14-like major facilitator"; Botryotinia fuckeliana DHA1	874.3	712.6	373.5	42.5	0		0
Pc12g164	strong similarity to cell polarity protein tea1p - Schizosaccharomyces pombe	0.0	AJ622827_1	gene: "teaA"; product: "kelch-domain protein"; Emericella nidulans teaA gene for kelc	668.5	482.1	130.8	86.4	0		0
Pc21g183	strong similarity to rodletless protein rodA - Aspergillus nidulans	7e-39	AFHYDROP_1	gene: "HYP1"; product: "hydrophobin"; Aspergillus fumigatus hydrophobin (HYP1) ge	436.9	126.4	107.0	37.3	0		0
Pc21g237	similarity to rodletless protein rodA - Aspergillus nidulans	1e-11	A40323	Rodletless protein - Emericella nidulans	1516.4	809.8	620.5	35.9	0		0
Pc22g142	strong similarity to rodletless protein rodA - Aspergillus nidulans	4e-50	AFHYDROP_1	gene: "HYP1"; product: "hydrophobin"; Aspergillus fumigatus hydrophobin (HYP1) ge	1500.1	395.1	77.3	14.1	1e-160	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc16g149	strong similarity to retrotransposable element like protein An08g11510 - Aspergillus niger [putative sequenc	0	0	0	157.2	82.0	34.0	19.4	0		0
Pc16g094	similarity to ankyrin ANK1 - Homo sapiens	5e-32	A35049	ankyrin 1, erythrocyte splice form 2 - human	211.4	244.1	12.0	12.0	8e-55	01.04.07 phosphate transport	
Pc22g139	strong similarity to transmembrane protein PTH11 - Magnaporthe grisea	6e-28	NCB7H23_13	gene: "B7H23.130"; product: "related to L-fucose permease"; Neurospora crassa DN	122.5	146.2	53.7	12.0	1e-26	01.05.07 C-compound, carbohydrate transport	
Pc06g017	strong similarity to hypothetical transport protein YCR023c - Saccharomyces cerevisiae	2e-69	S19434	probable transport protein YCR023c - yeast (Saccharomyces cerevisiae)	1399.9	1208.9	151.2	146.9	0		0
Pc15g017	similarity to hypothetical membrane protein YMR088c - Saccharomyces cerevisiae	1e-18	CNS07TIX_2	DNA centromeric region sequence from BAC DP15B03, DP38F06 of chromosome 5	616.6	182.5	248.2	12.0	0		0
Pc01g000	weak similarity to hypothetical protein An12g08820 - Aspergillus niger	0	0	0	339.2	344.1	121.5	12.0	0		0
Pc04g000	similarity to hypothetical protein contig1492_0.tfa_2370cg - Aspergillus fumigatus	0	0	0	837.0	295.2	276.4	32.4	0		0
Pc06g002	similarity to hypothetical protein B2O8.260 - Neurospora crassa	3e-07	NCB2O8_14	gene: "B2O8.140"; product: "conserved hypothetical protein"; Neurospora crassa DN	213.9	100.7	12.0	12.0	0		0
Pc06g003	strong similarity to hypothetical protein contig1493_1.tfa_1830wg - Aspergillus fumigatus	7e-10	BX321860_127	product: "putative death on curing protein"; Nitrosomonas europaea ATCC 19718, co	457.2	156.1	43.4	12.0	0		0
Pc06g003	strong similarity to hypothetical protein An01g10620 - Aspergillus niger	0	0	0	238.6	135.1	65.7	12.9	1e-50	01.05 C-compound and carbohydrate metabolism	
Pc06g004	weak similarity to hypothetical protein contig46_part_i.tfa_580wg - Aspergillus fumigatus	0	0	0	512.9	781.4	150.2	37.5	0		0
Pc06g008	strong similarity to splicing coactivator subunit like protein An01g13270 - Aspergillus niger [truncated ORF]	2e-21	NC68B2_1	gene: "68B2.020"; product: "related to glucan 1, 4-alpha-glucosidase"; Neurospora c	294.6	196.6	104.8	42.0	1e-49	04.03.06 tRNA modification	
Pc06g011	similarity to hypothetical protein 1460_scaffold_8.tfa_310cg - Fusarium graminearum	2e-06	NCB10C3_2	gene: "B10C3.020"; product: "hypothetical protein"; Neurospora crassa DNA linkage	263.1	44.6	43.5	22.1	0		0
Pc06g016	strong similarity to hypothetical protein contig_1_14_scaffold_1.tfa_170cg - Aspergillus nidulans	6e-47	S48907	probable purine nucleotide-binding protein YHR168w - yeast (Saccharomyces cerevi	695.8	516.7	131.0	80.0	1e-138	99 UNCLASSIFIED PROTEINS	
Pc06g017	hypothetical protein	0	0	0	108.1	80.9	12.0	12.0	0		0
Pc09g000	similarity to hypothetical protein YER080w - Saccharomyces cerevisiae	2e-15	S50583	hypothetical protein YER080w - yeast (Saccharomyces cerevisiae)	157.2	152.7	12.0	12.0	2e-65	14.04 cell differentiation	
Pc09g000	hypothetical protein	0	0	0	75.3	117.7	12.0	12.0	0		0
Pc09g000	weak similarity to hypothetical protein BAB55393.1 - Homo sapiens	2e-07	BC001705_1	Homo sapiens serine active site containing 1, mRNA (cDNA clone	1197.6	924.8	12.0	12.0	2e-69	01.04 phosphate metabolism	
Pc09g001	weak similarity to hypothetical protein - Plasmodium falciparum [truncated ORF]	6e-06	PFA929354_65	gene: "PFE1535w"; product: "hypothetical protein"; Plasmodium falciparum strain 3D	1222.8	1118.4	12.0	12.0	0		0
Pc12g004	strong similarity to hypothetical protein An09g02520 - Aspergillus niger	5e-09	AY437641_1	gene: "ST1"; product: "serine/threonine kinase"; Leptosphaeria maculans serine/thre	225.6	73.2	47.6	24.6	4e-78	01.05.01.01.01 sugar, glucoside, polyol and carboxylate catabolism	
Pc12g006	similarity to hypothetical protein CC3092 - Caulobacter crescentus	2e-54	NCB8P8_4	gene: "B8P8.040"; product: "conserved hypothetical protein"; Neurospora crassa DN	1974.2	2466.3	181.8	109.0	0		0
Pc12g013	strong similarity to hypothetical protein contig31_part_ii.tfa_1360wg - Aspergillus fumigatus	5e-14	AE016938_2	product: "endo-1,4-beta-xylanase D precursor"; Bacteroides thetaiotaomicron VPI-54	1049.5	1447.0	279.8	54.5	0		0
Pc12g029	hypothetical protein	0	0	0	424.5	119.3	179.4	22.6	0		0
Pc12g090	similarity to hypothetical protein SPAC1420.01c - Schizosaccharomyces pombe [putative sequencing erro	2e-13	T37664	hypothetical protein SPAC1420.01c SPAC56E4.08c - fission yeast (Schizosaccharo	357.3	242.5	92.4	48.5	0		0
Pc12g118	strong similarity to hypothetical protein An02g05760 - Aspergillus niger	0	0	0	292.6	108.8	19.1	21.1	2e-80	04.05.01.04 transcriptional control	
Pc12g121	similarity to hypothetical protein 9G6.360 - Neurospora crassa	3e-21	BX649607_60	product: "hypothetical protein, conserved"; Aspergillus fumigatus BAC pilot project su	129.3	125.8	26.4	12.0	0		0
Pc12g121	strong similarity to hypothetical zinc-finger protein flbC - Aspergillus nidulans	5e-97	AF083468_1	gene: "flbC"; product: "putative zinc finger protein"; Emericella nidulans putative zinc	103.4	57.4	24.0	14.2	5e-44	20.25.01.03 hearing	
Pc13g010	strong similarity to hypothetical protein An14g02490 - Aspergillus niger	0	0	0	150.5	168.9	41.6	27.2	8e-58	01.01.04 regulation of amino acid metabolism	
Pc13g025	similarity to cellulosomal scaffoldin anchoring protein C - Acetivibrio cellulolyticus	4e-19	AY221113_1	gene: "scaC"; product: "cellulosomal scaffoldin anchoring protein C"; Acetivibrio cell	236.9	137.6	22.4	15.4	4e-83	10.01.01 unspecified signal transduction	
Pc13g031	strong similarity to myb-like DNA binding protein flbD - Aspergillus nidulans	1e-75	EN19882_1	gene: "flbD"; product: "FlbD"; Emericella nidulans DNA binding protein FlbD (flbD) g	279.3	219.4	69.7	31.6	0		0
Pc13g034	similarity to hypothetical MAP3K protein kinase-like protein MLD14.3 - Arabidopsis thaliana	2e-46	NCB11H24_8	gene: "B11H24.090"; product: "conserved hypothetical protein"; Neurospora crassa	252.4	53.4	68.1	14.0	0		0
Pc13g044	similarity to hypothetical protein contig_1_105_scaffold_7.tfa_350cg - Aspergillus nidulans	0	0	0	150.1	117.1	45.4	22.5	0		0
Pc13g048	hypothetical protein	0	0	0	228.0	92.8	47.1	28.7	1e-116	01.05 C-compound and carbohydrate metabolism	
Pc13g073	strong similarity to hypothetical protein An04g02250 - Aspergillus niger	0	0	0	244.7	291.0	67.5	50.1	0		0
Pc13g073	strong similarity to hypothetical protein contig_1_93_scaffold_6.tfa_580cg - Aspergillus nidulans	1e-45	BX294142_8	gene: "pel"; product: "pectate lyase"; Pirellula sp. strain 1 complete genome; segmen	72.4	195.1	19.6	22.8	0		0
Pc13g081	similarity to hypothetical protein An04g03210 - Aspergillus niger	0	0	0	76.4	47.3	12.0	12.0	0		0
Pc13g098	strong similarity to hypothetical protein An02g07340 - Aspergillus niger	3e-11	AP006582_94	Gloeobacter violaceus PCC 7421 DNA, complete genome, section 15/16;	150.8	88.2	41.2	20.3	0		0
Pc13g142	strong similarity to hypothetical protein contig_1_6_scaffold_1.tfa_280wg - Aspergillus nidulans	0	0	0	312.7	208.0	12.0	12.0	0		0
Pc14g015	strong similarity to hypothetical protein An18g06400 - Aspergillus niger	2e-09	AP004602_110	gene: "OB2740"; product: "hypothetical conserved protein"; Oceanobacillus iheyensi	81.7	68.0	12.0	12.4	0		0
Pc15g002	strong similarity to hypothetical protein 1196_scaffold_3.tfa_500cg - Fusarium graminearum	0	0	0	449.9	316.9	200.3	49.8	0		0
Pc15g017	hypothetical protein	0	0	0	569.5	185.9	296.2	18.3	3e-94	01.04 phosphate metabolism	
Pc16g025	hypothetical protein	0	0	0	155.5	148.4	88.2	20.4	1e-45	03.03 cell cycle	
Pc16g051	strong similarity to hypothetical protein 1142_scaffold_2.tfa_40cg - Fusarium graminearum	5e-18	T48202	protein kinase AK22 (EC 2.7.1.-) - Arabidopsis thaliana	75.2	78.5	12.0	12.0	2e-54	01.05.01 C-compound and carbohydrate utilization	
Pc16g058	similarity to surface layer protein - Bacillus cereus	2e-21	AE017195_61	product: "surface layer protein"; Bacillus cereus ATCC 10987 plasmid pBc10987, co	134.8	63.4	21.0	12.0	1e-109	01.04 phosphate metabolism	

Pc16g071	similarity to hypothetical protein YCR010c - Saccharomyces cerevisiae	3e-17	S31258	probable membrane protein FUN34 - yeast (Saccharomyces cerevisiae)	97.6	99.9	57.3	12.0	4e-29	01.04.04 regulation of phosphate utilization
Pc16g085	similarity to hypothetical protein ncu02885.1 - Neurospora crassa	2e-12	TCU74762_1	gene: "tcrk1"; product: "cdc2-related protein kinase 1"; Trypanosoma cruzi cdc2-rela	315.9	262.8	14.3	14.3	0	0
Pc16g087	strong similarity to Pcl-like cyclin pclA - Aspergillus nidulans	1e-102	ANI272133_1	gene: "pclA"; product: "cyclin"; Aspergillus nidulans pclA gene for cyclin	361.6	210.0	64.2	12.0	0	0
Pc16g098	hypothetical protein	0	0	0	260.4	103.5	87.5	24.4	0	0
Pc16g125	strong similarity to hypothetical protein An13g01540 - Aspergillus niger	0	0	0	95.2	68.3	12.0	12.0	3e-50	01.05 C-compound and carbohydrate metabolism
Pc16g145	weak similarity to cyanovirin-N CV-N - Nostoc ellipsosporum	0	0	0	134.0	243.9	32.3	12.0	1e-46	01.04 phosphate metabolism
Pc16g150	strong similarity to hypothetical protein ncu05319.1 - Neurospora crassa	4e-12	T29861	hypothetical protein F10G2.5 - Caenorhabditis elegans	174.2	157.1	12.0	12.0	0	0
Pc17g000	hypothetical protein	0	0	0	133.5	24.0	12.0	12.0	0	0
Pc17g003	hypothetical protein	0	0	0	358.2	413.7	111.0	13.6	0	0
Pc18g015	hypothetical protein	0	0	0	781.6	1175.4	667.3	83.1	0	0
Pc18g017	hypothetical protein	0	0	0	736.8	826.2	104.1	12.0	0	0
Pc18g020	strong similarity to hypothetical protein contig1471_1.tfa_1190cg - Aspergillus fumigatus	0	0	0	372.2	280.9	12.0	12.0	0	0
Pc18g027	strong similarity to hypothetical protein contig1488_2.tfa_1200wg - Aspergillus fumigatus	2e-05	T31670	DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - Mastigamoeba inverten	244.9	133.8	30.8	23.3	0	0
Pc18g030	weak similarity to integral membrane protein PTH11 - Magnaporthe grisea	5e-09	NCB7H23_13	gene: "B7H23.130"; product: "related to L-fucose permease"; Neurospora crassa DN	311.1	276.0	165.1	19.2	0	0
Pc18g031	strong similarity to hypothetical protein mg00375.1 - Magnaporthe grisea	8e-82	AY157839_1	gene: "gluB"; product: "beta-1,3-glucanase B"; Lysobacter enzymogenes strain N4-7	1069.6	612.0	299.0	26.8	0	0
Pc18g032	weak similarity to hypothetical protein mlr2143 - Mesorhizobium loti	2e-06	AP002999_29	gene: "mlr2143"; Mesorhizobium loti DNA, complete genome, section 6/21.	491.4	270.4	132.8	29.3	0	0
Pc18g045	weak similarity to hypothetical protein An04g07540 - Aspergillus niger	0	0	0	252.2	147.9	354.9	12.0	0	0
Pc18g052	strong similarity to hypothetical protein 53H1.090 - Neurospora crassa	3e-25	BX842633_9	gene: "53H1.090"; product: "hypothetical protein"; Neurospora crassa DNA linkage g	99.9	64.9	12.7	12.0	0	0
Pc20g016	similarity to hypothetical protein An07g02230 - Aspergillus niger	0	0	0	829.2	617.2	118.2	37.6	0	0
Pc20g020	strong similarity to hypothetical protein contig1487_1.tfa_1460cg - Aspergillus fumigatus	0	0	0	633.5	462.2	225.7	64.0	1e-136	99 UNCLASSIFIED PROTEINS
Pc20g026	hypothetical protein	0	0	0	93.4	52.8	12.0	12.0	3e-35	99 UNCLASSIFIED PROTEINS
Pc20g027	strong similarity to hypothetical membrane protein YPR157w - Saccharomyces cerevisiae	1e-54	S61141	probable membrane protein YPR157w - yeast (Saccharomyces cerevisiae)	507.2	259.3	100.5	14.3	0	0
Pc20g070	similarity to hypothetical Ydr124wp-like protein - Pneumocystis carinii	6e-18	AF309805_4	product: "Ydr124wp-like protein"; Pneumocystis carinii f. sp. carinii glutathione synth	1380.0	1037.4	501.9	180.7	2e-76	30.04 cytoskeleton
Pc20g070	strong similarity to hypothetical protein contig1487_1.tfa_2180cg - Aspergillus fumigatus	0	0	0	184.4	147.1	63.7	26.6	0	0
Pc20g078	strong similarity to hypothetical protein contig_1_60_scaffold_4.tfa_40wg - Aspergillus nidulans	6e-27	BX649607_5	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot project supercontig;	128.7	96.4	12.0	12.0	2e-65	04.05.01.04 transcriptional control
Pc20g092	weak similarity to hypothetical integral membrane protein SC10B7.28 - Streptomyces coelicolor	1e-101	BX842629_33	gene: "B20J13.330"; product: "conserved hypothetical protein"; Neurospora crassa	456.9	283.2	66.9	91.5	0	0
Pc20g128	similarity to hypothetical protein An08g12140 - Aspergillus niger	1e-05	BC064665_1	gene: "zgc:63970"; product: "hypothetical protein MGC63970"; Danio rerio hypotheti	226.1	210.1	89.7	12.0	0	0
Pc21g010	similarity to hypothetical protein ncu01891.1 - Neurospora crassa	0	0	0	229.6	127.9	12.0	12.0	0	0
Pc21g010	weak similarity to hypothetical protein An07g04500 - Aspergillus niger	0	0	0	219.8	205.3	56.5	28.5	0	0
Pc21g032	similarity to hypothetical protein contig_1_187_scaffold_29.tfa_20cg - Aspergillus nidulans	0	0	0	362.2	267.2	56.0	25.5	2e-75	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc21g053	hypothetical protein	0	0	0	1059.8	777.3	866.9	40.4	0	0
Pc21g066	strong similarity to mono- and diacylglycerol lipase precursor - Penicillium camembertii	1e-156	JQ1188	mono- and diacylglycerol lipase (EC 3.1.1.-) precursor - Penicillium camembertii	1937.4	925.4	114.9	475.3	0	0
Pc21g073	strong similarity to hypothetical protein An18g02150 - Aspergillus niger	9e-20	BX908807_3	gene: "B13B7.030"; product: "putative protein"; Neurospora crassa DNA linkage grou	340.8	334.7	71.3	59.6	4e-57	01.05 C-compound and carbohydrate metabolism
Pc21g086	weak similarity to hypothetical transcription regulator SPCC4F11.01 - Schizosaccharomyces pombe	2e-38	NCB11C21_4	gene: "B11C21.040"; product: "conserved hypothetical protein"; Neurospora crassa	584.0	695.0	546.9	60.1	0	0
Pc21g091	strong similarity to hypothetical protein contig42.tfa_1900cg - Aspergillus fumigatus	8e-14	T39896	probable nucleic acid-binding protein - fission yeast (Schizosaccharomyces pombe)	219.9	151.1	50.5	18.2	5e-28	01.05 C-compound and carbohydrate metabolism
Pc21g150	hypothetical protein [putative pseudogene]	0	0	0	79.9	53.0	14.2	12.0	0	0
Pc21g186	strong similarity to hypothetical protein B1D4.110 - Neurospora crassa	5e-35	BX908788_9	gene: "B23N11.090"; product: "conserved hypothetical protein"; Neurospora crassa	836.8	1004.2	215.5	135.0	2e-55	01 METABOLISM
Pc21g188	similarity to hypothetical protein An02g09830 - Aspergillus niger	4e-05	T30886	integumentary mucin B.1 - African clawed frog (fragment)	62.7	87.4	14.4	12.0	1e-77	01.20.17.03 biosynthesis of amines
Pc21g206	strong similarity to cDNA GS1 - Homo sapiens [putative sequencing error]	6e-46	T40833	haloacid dehalogenase-like hydrolase - fission yeast (Schizosaccharomyces pombe)	589.8	680.2	47.7	54.8	0	0
Pc21g220	strong similarity to hypothetical protein contig_1_153_scaffold_12.tfa_510wg - Aspergillus nidulans	4e-65	AFU293806_1	gene: "tyr1"; product: "tyrosinase"; Aspergillus fumigatus tyr1 gene for tyrosinase, ex	224.0	90.6	79.0	12.0	0	0
Pc21g221	strong similarity to hypothetical protein An16g00290 - Aspergillus niger	2e-12	NCB19A17_10	gene: "B19A17.100"; product: "hypothetical protein"; Neurospora crassa DNA linkag	78.4	49.1	12.0	12.0	7e-64	01.04 phosphate metabolism
Pc21g229	weak similarity to hypothetical protein An01g11580 - Aspergillus niger	0	0	0	126.0	160.8	12.0	12.0	0.0	99 UNCLASSIFIED PROTEINS
Pc22g019	strong similarity to hypothetical protein An09g02520 - Aspergillus niger	3e-12	AY437641_1	gene: "ST1"; product: "serine/threonine kinase"; Leptosphaeria maculans serine/thre	421.9	202.0	67.3	26.5	0	0
Pc22g063	strong similarity to hypothetical membrane protein YNL279w - Saccharomyces cerevisiae	2e-60	S63253	probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae)	275.9	210.5	12.0	12.0	0	0
Pc22g132	hypothetical protein	0	0	0	85.5	70.9	13.6	16.7	0	0
Pc22g160	strong similarity to hypothetical protein contig5_part_ii.tfa_1430wg - Aspergillus fumigatus	0	0	0	364.4	375.6	256.4	46.9	0	0
Pc22g165	hypothetical protein	0	0	0	182.6	114.7	12.0	12.0	5e-49	25.05.15 myogenesis
Pc22g178	strong similarity to hypothetical protein contig40.tfa_650cg - Aspergillus fumigatus	0	0	0	1426.5	1249.7	338.0	197.2	0	0
Pc22g185	weak similarity to polycystic kidney disease 1-like 3 - Mus musculus	7e-09	AY164486_1	gene: "Pkd1l3"; product: "polycystic kidney disease 1-like 3"; Mus musculus polycys	380.5	235.4	171.1	34.9	8e-42	25.05.10 late embryonic development
Pc22g244	similarity to hypothetical protein An12g08820 - Aspergillus niger	0	0	0	322.0	305.3	128.1	46.7	0	0
Pc22g254	strong similarity to hypothetical protein An01g05100 - Aspergillus niger	1e-04	T09108	RNA binding protein, 24K, chloroplast - spinach (fragment)	119.1	52.9	22.4	12.0	1e-42	99 UNCLASSIFIED PROTEINS
Pc22g265	hypothetical protein	0	0	0	486.2	176.7	20.1	12.0	0	0
Pc22g271	similarity to hypothetical Ydr124wp-like protein - Pneumocystis carinii	3e-19	AF309805_4	product: "Ydr124wp-like protein"; Pneumocystis carinii f. sp. carinii glutathione synth	326.2	331.0	12.0	12.0	0	0
Pc23g003	strong similarity to hypothetical protein 1103_scaffold_1.tfa_190cg - Fusarium graminearum	0	0	0	449.9	222.6	65.9	27.3	0	0
Pc23g003	hypothetical protein	0	0	0	12.0	12.0	12.0	15.5	0	0
Pc24g006	similarity to hypothetical protein An15g05640 - Aspergillus niger	0	0	0	975.2	403.9	12.0	12.0	0	0
Pc24g007	strong similarity to hypothetical protein An02g07830 - Aspergillus niger	0	0	0	460.0	103.1	14.0	65.9	0	0
Pc24g008	hypothetical protein	0	0	0	720.7	20.9	12.0	12.0	0	0
Pc24g008	strong similarity to hypothetical protein An11g09490 - Aspergillus niger	0	0	0	330.8	12.0	12.0	12.0	0	0
Pc24g008	hypothetical protein	0	0	0	83.0	12.0	12.0	12.0	0	0
Pc24g014	strong similarity to hypothetical protein An11g09490 - Aspergillus niger	0	0	0	239.0	12.0	12.0	12.0	0	0
Pc24g016	hypothetical protein	0	0	0	1761.1	13.0	22.1	12.0	0	0
Pc24g016	hypothetical protein	0	0	0	236.2	14.3	28.4	17.2	0	0
Pc24g025	hypothetical protein	0	0	0	125.7	97.4	36.2	12.0	0	0
Pc24g027	hypothetical protein	0	0	0	982.9	198.9	91.2	28.8	0	0
Pc36g000	weak similarity to hypothetical membrane protein YIL151c - Saccharomyces cerevisiae	0	0	0	750.5	100.7	83.0	63.1	0	0

Supplementary Table 16. K-mean cluster 8

@=Values given are the average of three independent experiments

orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels @				FunCat (auto)	
		p-value	Gene code	description	WIS - PAA	WIS + PAA	DS - PAA	DS + PAA	pval	category
Pc06g00430	strong similarity to ribonuclease T2 precursor rntB - Aspergillus oryzae	3e-89	JU0205	ribonuclease T2 (EC 3.1.27.1) precursor - Aspergillus oryzae	239.8	359.6	129.3	61.5		01.05 C-compound and carbohydrate metabolism
Pc06g00800	strong similarity to 1,3,6,8-tetrahydroxynaphthalene reductase like protein An07g01830 - Aspergillus niger	7e-39	BX640445_60	product: "probable short-chain dehydrogenase"; Bordetella br	114.8	160.5	106.2	51.4	3e-39	01.04.07 phosphate transport
Pc06g01310	strong similarity to brown 2 protein abr2 - Aspergillus fumigatus [putative sequencing error]	1e-161	ANI305224_1	gene: "tilA"; product: "laccase"; Aspergillus nidulans tilA ger	14.2	24.9	12.0	12.0	1e-54	01.05.04 regulation of C-compound and carbohydrate utilization
Pc06g01490	strong similarity to hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	6e-30	T41145	probable amine transporter - fission yeast (Schizosaccharomy	57.4	41.2	14.2	12.0	1e-177	01.05 C-compound and carbohydrate metabolism
Pc12g00230	strong similarity to tartrate transport protein ttuB - Agrobacterium vitis	2e-93	NC80A10_5	gene: "80A10.050"; product: "conserved hypothetical protein"	710.7	233.2	119.3	163.9	9e-73	01.05.07 C-compound, carbohydrate transport
Pc12g01730	strong similarity to 3-hydroxy-3-methylglutaryl-CoA synthase Erg13 - Saccharomyces cerevisiae	1e-159	T49718	probable hydroxymethylglutaryl-CoA synthase [imported] - Ne	42.2	20.0	18.8	12.0	0.0	01.05.01 C-compound and carbohydrate utilization
Pc12g04160	strong similarity to mitochondrial carrier protein Rim2 - Saccharomyces cerevisiae	8e-74	S36081	probable carrier protein RIM2, mitochondrial - yeast (Sacchar	83.7	69.2	39.5	25.6	1e-169	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc12g05400	strong similarity to citrate synthase citA - Aspergillus niger	0.0	ANI243204_1	gene: "citA"; product: "citrate synthase"; Aspergilluse niger c	665.6	586.5	417.2	266.8	0.0	01.05.01 C-compound and carbohydrate utilization
Pc12g05520	strong similarity to long-chain-fatty-acid--CoA ligase Faa2 - Saccharomyces cerevisiae	0.0	NCB13I18_11	gene: "B13I18.110"; product: "related to long-chain-fatty-acid-	366.5	169.8	224.3	235.2	0	0
Pc12g09360	strong similarity to phosphoenolpyruvate carboxykinase KlPck1 - Kluyveromyces lactis	0.0	AY049067_1	gene: "acuF"; product: "phosphoenolpyruvate carboxykinase"	465.4	439.0	559.4	210.6	1e-167	13 REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT
Pc12g09440	strong similarity to precursor of liver carboxylesterase like protein An12g05840 - Aspergillus niger	0	0	0	578.8	618.6	225.2	184.3	1e-161	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis
Pc12g13400	strong similarity to cephalosporin esterase - Rhodosporidium toruloides	1e-129	BX842634_28	gene: "B16B8.280"; product: "related to triacylglycerol lipase	159.5	214.3	104.2	68.3	0.0	04.01.04 rRNA processing
Pc12g15520	strong similarity to aureobasidin-resistance protein aurA - Aspergillus nidulans	0.0	AF076691_1	gene: "aurA"; product: "aureobasidin-resistance protein"; Em	325.9	314.7	143.2	128.7	1e-101	98 CLASSIFICATION NOT YET CLEAR-CUT
Pc12g15620	strong similarity to exosome complex exonuclease Rrp6 - Saccharomyces cerevisiae	1e-147	BX908789_27	gene: "B13D24.270"; product: "related to nucleolar 100K poly	104.4	99.1	77.5	41.8	6e-70	01.04 phosphate metabolism
Pc13g02420	strong similarity to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase hpcH - Escherichia coli	5e-63	BX649605_29	product: "2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase"; A	70.1	31.0	48.2	51.6	5e-37	01.03.16.01 RNA degradation
Pc13g02870	similarity to SR-protein-specific kinase SRPK2 - Mus musculus	1e-18	MMU92456_1	product: "WW domain binding protein 6"; Mus musculus WV	57.8	44.0	23.1	17.3	0.0	01 METABOLISM
Pc13g03230	weak similarity to thermostable nuclease Tnase nuch - Staphylococcus hyicus	5e-31	T39827	probable nuclease - fission yeast (Schizosaccharomyces por	94.9	108.2	43.8	75.0	0.0	01.05 C-compound and carbohydrate metabolism
Pc13g03920	strong similarity to acetyl-CoA carboxylase SPAC56E4.04c - Schizosaccharomyces pombe	0.0	S60200	acetyl-CoA carboxylase (EC 6.4.1.2) - smut fungus (Ustilago	505.1	462.6	379.1	192.6	3e-43	01 METABOLISM
Pc13g04510	strong similarity to NADP-dependent malate dehydrogenase mdh - Homo sapiens	0.0	AF529885_1	gene: "maeA"; product: "NADP-dependent malic enzyme"; A	97.9	98.2	81.3	33.4	1e-83	01.01.01 amino acid biosynthesis
Pc13g05050	weak similarity to methyl sterol oxidase Erg25 - Saccharomyces cerevisiae	2e-08	AF346734_1	product: "sterol 4-alpha-methyl-oxidase"; Arabidopsis thaliana	103.2	12.0	12.0	12.0	3e-38	01.02 nitrogen and sulfur metabolism
Pc13g06360	strong similarity to salt tolerance protein Met22 - Saccharomyces cerevisiae	8e-50	NCB15B24_7	gene: "B15B24.060"; product: "related to 3'(2'), 5'-BISPHOSP	65.9	49.1	32.8	24.6	0	0
Pc13g06790	weak similarity to 3-oxoadipate enol-lactone hydrolase part of the dual specificity protein pcaL - Rhodococcus opacus	2e-08	B87548	hypothetical protein CC2411 [imported] - Caulobacter crescer	113.5	259.2	66.9	90.9	0.0	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis
Pc13g08100	similarity to cutinase precursor cutA - Fusarium solani	9e-26	AF326784_1	gene: "cut1"; product: "cutinase"; Blumeria graminis cutinas	126.5	14.0	13.3	35.2	1e-105	01 METABOLISM
Pc13g08690	strong similarity to lovastatin diketide synthase lovF - Aspergillus terreus	0.0	AY495595_1	gene: "PKS5"; product: "polyketide synthase"; Gibberella mo	61.9	33.2	41.6	14.4	4e-20	01.01.04 regulation of amino acid metabolism
Pc13g09520	strong similarity to chitinase 1 precursor cts1 - Coccidioides immitis	1e-158	END063_1	gene: "chiB"; product: "chitinase"; Aspergillus nidulans chiB	1005.2	551.9	512.2	261.0	0	0
Pc13g10310	similarity to sterigmatocystin synthesis transcription regulator aflR - Aspergillus nidulans	1e-06	AF549411_2	gene: "gsp"; product: "unknown"; Glarea lozoyensis polyketi	645.5	638.9	660.1	91.2	2e-95	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc13g13110	strong similarity to hypothetical endoglucanase IV - Trichoderma reesei	5e-99	BX649606_3	product: "endoglucanase, putative"; Aspergillus fumigatus BA	120.8	70.1	40.5	57.4	1e-154	13 REGULATION OF / INTERACTION WITH CELLULAR ENVIRONMENT
Pc13g13170	strong similarity to delta-12 fatty acid desaturase - Mortierella alpina	0.0	AY267349_1	gene: "odeA"; product: "oleate delta-12 desaturase"; Aspergi	1303.5	1202.6	928.3	535.2	6e-74	01.05.04 regulation of C-compound and carbohydrate utilization
Pc13g15360	strong similarity to extracellular triacylglycerol lipase Lip1 - Candida rugosa	1e-59	S23448	triacylglycerol lipase (EC 3.1.1.3) - yeast (Candida rugosa)	69.8	123.5	121.5	37.2	5e-57	01 METABOLISM
Pc13g15980	strong similarity to hexose transporter Hxt2 - Saccharomyces cerevisiae	1e-156	S69591	sugar transport protein STP1 - yeast (Saccharomyces cerevis	330.1	157.9	177.9	273.9	1e-71	01.01.04 regulation of amino acid metabolism
Pc14g00740	strong similarity to fatty-acyl-CoA synthase beta chain fas1p - Schizosaccharomyces pombe	0.0	S15999	fatty-acyl-CoA synthase (EC 2.3.1.86) beta chain - yeast (Ya	878.2	835.0	618.3	366.5	1e-141	03.01.05.01 DNA repair
Pc14g00920	similarity to transcription factor Gal4 - Saccharomyces cerevisiae	2e-11	AY218847_1	gene: "PRF"; product: "binuclear zinc transcription factor"; N	79.0	76.6	26.8	24.6	1e-146	01.25.07 extracellular ester compounds degradation
Pc14g01820	strong similarity to polynucleotide kinase-3-phosphatase PNKP - Homo sapiens	7e-69	T38242	probable phosphatase - fission yeast (Schizosaccharomyces	55.6	63.5	34.4	25.1	2e-47	01 METABOLISM
Pc16g00640	strong similarity to triacylglycerol lipase Lip4 - Candida rugosa	1e-125	JN0552	triacylglycerol lipase (EC 3.1.1.3) 4 precursor - yeast (Candid	40.1	51.2	63.4	18.7	1e-108	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc16g00700	weak similarity to acetyl-hydrolase chnC - Acinetobacter sp.	2e-57	BX649606_74	product: "esterase/lipase/thioesterase family protein, putative'	37.1	12.0	12.0	12.0	0.0	01.05 C-compound and carbohydrate metabolism
Pc16g00720	strong similarity to cytochrome P450 protein like protein An03g06720 - Aspergillus niger	1e-82	AF155773_16	gene: "FUM15"; product: "Fum15p"; Gibberella moniliformis f	28.5	12.0	12.0	12.0	8e-54	01.05.07 C-compound, carbohydrate transport
Pc16g01790	strong similarity to glycerol-3-phosphate dehydrogenase like protein An08g00210 - Aspergillus niger	0.0	T49652	glycerol-3-phosphate dehydrogenase precursor related protein	694.2	977.7	350.7	477.0	1e-173	01 METABOLISM
Pc16g02680	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	2e-60	T41604	probable membrane transport protein - fission yeast (Schizos	100.0	180.0	79.8	76.9	5e-38	01.05.01.01 C-compound, carbohydrate catabolism
Pc16g03670	strong similarity to phenylalanine ammonia-lyase Pal - Rhodosporidium toruloides	1e-109	AX366860_1	unnamed ORF; Sequence 12 from Patent WO0208402.	42.0	107.0	20.8	12.0	0	0
Pc16g07140	weak similarity to isoflavone reductase IFR - Medicago sativa	6e-14	AB045984_1	Verticillium dahliae mRNA from tomato pathotype-specific DN	160.1	134.2	46.8	43.1	7e-44	01.01.01 amino acid biosynthesis
Pc16g07600	weak similarity to hypothetical oxidoreductase PA5309 - Pseudomonas aeruginosa	7e-34	NC5F3_10	gene: "5F3.100"; product: "conserved hypothetical protein"; N	40.3	12.0	12.1	12.0	0.0	06.10 assembly of protein complexes
Pc16g08560	strong similarity to acyl CoA reductase like protein An14g04760 - Aspergillus niger	2e-20	BC044166_1	product: "Similar to RIKEN cDNA 3732409C05 gene"; Danio	230.6	189.5	257.2	72.2	2e-25	01.05.01.01.09 aerobic aromate catabolism
Pc16g08980	weak similarity to 1,3-beta-glucanosyltransferase gel1 - Aspergillus fumigatus	0.0	AF121133_1	gene: "ENGL1"; product: "beta(1-3)endoglucanase"; Aspergil	142.3	31.6	64.5	12.0	2e-62	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc16g09880	similarity to salicylate hydroxylase sal - Pseudomonas putida	1e-36	BX640445_156	product: "putative monooxygenase"; Bordetella bronchiseptic	223.3	85.8	63.4	32.2	0.0	01.05.01 C-compound and carbohydrate utilization
Pc16g11410	similarity to triacylglycerol lipase gehA - Propionibacterium acnes	6e-30	AP005047_47	product: "putative secreted lipase"; Streptomyces avermitilis (	247.9	291.3	78.3	63.1	2e-98	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc16g11870	strong similarity to alpha,alpha-trehalase treA - Aspergillus nidulans	0.0	T18304	acid trehalase homolog - Emericella nidulans	710.2	259.9	427.9	298.4	1e-91	01.01 amino acid metabolism
Pc16g12090	strong similarity to fatty-acid subterminal hydroxylase P450foxy - Fusarium oxysporum	2e-78	AB078738_1	gene: "CYP505A3"; product: "fatty acid hydroxylase"; Asper	717.6	822.4	672.1	289.8	0.0	01 METABOLISM
Pc16g13170	strong similarity to agmatinase like protein An14g05960 - Aspergillus niger	1e-148	NCB13A5_2	gene: "B13A5.050"; product: "conserved hypothetical protein"	60.9	69.0	18.1	18.3	2e-69	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis
Pc16g14170	strong similarity to mannosyl-oligosaccharide 1,2-alpha-mannosidase like protein An01g12550 - Aspergillus niger	0.0	S58766	mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.	138.6	95.2	81.5	15.4	0	0
Pc16g14460	strong similarity to CDPdiacylglycerol--inositol 3-phosphatidyltransferase - Rattus norvegicus	2e-93	NCB1D14_2	gene: "B1D14.020"; product: "related to CDP diacylglycerol-in	231.9	222.5	120.1	85.2	1e-111	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc16g14950	strong similarity to esterase like protein An05g02280 - Aspergillus niger	3e-20	CNS07TIX_49	DNA centromeric region sequence from BAC DP15B03, DP38	34.5	32.2	12.0	12.0	1e-110	01.05 C-compound and carbohydrate metabolism
Pc18g00240	strong similarity to precursor of linoleate diol synthase - Gaeumannomyces graminis	0.0	AY502073_1	gene: "ppoA"; product: "psi producing oxygenase"; Emericel	139.2	315.4	210.4	97.3	5e-64	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc18g02640	strong similarity to beta-galactosidase like protein An02g00610 - Aspergillus niger [putative sequencing error]	0.0	BX842629_35	gene: "B20J13.350"; product: "conserved hypothetical protein	638.2	490.6	173.6	159.9	0	0
Pc18g02880	strong similarity to NAD-dependent D-arabinitol dehydrogenase ard - Candida tropicalis	2e-54	AF458074_1	product: "putative oxidoreductase"; Aspergillus nidulans puta	2176.2	2099.6	850.0	639.4	1e-162	11.07.01 detoxification involving cytochrome P450
Pc18g06380	strong similarity to mutanase mutA - Penicillium purpurogenum	1e-152	AF214481_1	gene: "mutA"; product: "mutanase"; Penicillium purporogenu	310.1	221.7	108.7	90.3	6e-99	01.01.01 amino acid biosynthesis
Pc20g01290	strong similarity to Fe(II)-dependent sulfonate alpha-ketoglutarate dioxygenase YLL057c - Saccharomyces cerevisiae	6e-69	S50963	hypothetical protein YLL057c - yeast (Saccharomyces cerevis	773.6	766.2	209.9	168.6	6e-99	01 METABOLISM
Pc20g01660	strong similarity to ribose-phosphate pyrophosphokinase Prps1 - Saccharomyces cerevisiae	1e-75	S30558	ribose-phosphate diphosphokinase (EC 2.7.6.1) PRPS1 - yea	474.0	447.3	358.5	207.4	1e-179	01.02.01.07 nitric oxide biosynthesis
Pc20g02250	similarity to chitinase - Chelonus sp.	1e-122	AY039007_1	gene: "Chi1"; product: "extracellular chitinase"; Blumeria gra	395.5	189.3	223.2	45.6	0	0
Pc20g04310	strong similarity to fatty acid omega-hydroxylase CYP505 - Fusarium oxysporum	0.0	AB078738_1	gene: "CYP505A3"; product: "fatty acid hydroxylase"; Asper	87.0	42.4	39.7	39.9	1e-180	01.04 phosphate metabolism
Pc20g07360	strong similarity to choline monooxygenase like protein An04g09810 - Aspergillus niger	2e-12	G70946	probable dioxygenase (EC 1.14.-.-) Rieske iron-sulfur compor	33.3	15.0	20.0	12.0	0	0
Pc20g07880	strong similarity to phosphatidylinositol-4-phosphate 5-kinase - Schizosaccharomyces pombe	1e-149	T38001	probable phosphatidylinositol-4-phosphate 5-kinase - fission y	97.8	74.6	48.3	36.2	1e-87	01.05.07 C-compound, carbohydrate transport
Pc20g10530	weak similarity to pentalenene synthase - Streptomyces sp.	0	0	0	45.6	31.5	20.5	38.0	2e-83	98 CLASSIFICATION NOT YET CLEAR-CUT
Pc20g10820	strong similarity to glucose transporter rco-3 - Neurospora crassa	1e-143	BX842632_4	gene: "B5K2.040"; product: "RCO3-probable glucose transpor	53.4	12.0	12.0	12.0	8e-76	01.03 nucleotide metabolism
Pc20g12210	similarity to gluconate transport-inducing protein gti1p - Schizosaccharomyces pombe	4e-25	S50452	hypothetical protein YEL007w - yeast (Saccharomyces cerev	218.7	220.5	126.1	95.9	2e-88	01.05.01 C-compound and carbohydrate utilization
Pc20g12360	strong similarity to protein involved in glycosylphosphatidylinositol biosynthesis Gpi13 - Saccharomyces cerevisiae	1e-151	S64782	probable membrane protein YLL031c - yeast (Saccharomyces	62.8	59.7	36.3	28.6	1e-40	01 METABOLISM
Pc20g13440	strong similarity to isoamyl alcohol oxidase mreA - Aspergillus oryzae	1e-177	NC94C8_4	gene: "94C8.040"; product: "probable isoamyl alcohol oxidase	96.1	56.1	31.9	16.4	7e-65	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc20g13460	weak similarity to methyl sterol oxidase Erg25 - Saccharomyces cerevisiae	3e-08	AE016793_188	product: "conserved hypothetical protein"; Pseudomonas puti	95.7	12.0	12.0	12.0	0.0	01 METABOLISM
Pc21g01050	strong similarity to NAD-dependent D-arabinitol dehydrogenase ard - Candida tropicalis	1e-153	AY387591_1	gene: "arbD"; product: "D-arabinitol dehydrogenase"; Emeric	727.7	573.8	355.3	162.7	0.0	01.20.37.03 biosynthesis of peptide antibiotics
Pc21g01060	strong similarity to 3-methylcrotonyl-CoA carboxylase (MCC) biotin-containing alpha subunit MCCA - Homo sapiens	0.0	AY387592_1	gene: "mccA"; product: "3-methylcrotonyl-CoA carboxylase b	258.7	207.6	110.1	189.4	4e-57	01.04.07 phosphate transport
Pc21g01710	strong similarity to peptide synthase like protein An04g06260 - Aspergillus niger	0.0	AF469045_1	gene: "tex1"; product: "nonribosomal peptide synthetase"; H	47.9	27.7	46.0	12.0	0	0
Pc21g02510	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	1e-128	BX908809_43	gene: "29E8.430"; product: "related to nicotinamide mononuc	267.2	248.8	119.1	178.3	1e-102	13.11.01 photoperception and response
Pc21g02590	weak similarity to nitrate reductase (NADPH) niaD - Aspergillus niger	0	0	0	21.5	47.5	32.9	12.4	3e-64	02.11 electron transport and membrane-associated energy conservation
Pc21g02950	strong similarity to hypothetical phosphatidic acid-preferring phospholipase A1 B14D6.220 - Neurospora crassa	0.0	T49470	phosphatidic acid-preferring phospholipase A1 related protein	108.4	94.4	52.3	55.7	4e-83	01.03.16 polynucleotide degradation
Pc21g03180	similarity to thioredoxin - Gallus gallus	1e-122	NC17E5_25	gene: "17E5.270"; product: "conserved hypothetical protein";	298.3	467.5	174.4	202.6	0.0	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis
Pc21g03380	strong similarity to mRNA turnover 4 protein Mrt4 - Saccharomyces cerevisiae	2e-58	T39330	probable 60S acidic ribosomal protein - fission yeast (Schizos	230.2	216.7	177.9	104.1	1e-94	01.05.01 C-compound and carbohydrate utilization
Pc21g05070	strong similarity to polyketide synthase like protein An09g01860 - Aspergillus niger	0.0	AY495622_1	gene: "PKS17"; product: "polyketide synthase"; Botryotinia fu	71.6	69.0	65.5	29.9	1e-153	01.04.04 regulation of phosphate utilization
Pc21g06250	similarity to alpha-1,6-mannosyltransferase Hoc1 - Saccharomyces cerevisiae	3e-27	SPAC1006_5	gene: "och1"; "SPAC1006.05c"; S.pombe chromosome I cos	95.9	29.4	36.7	56.3	1e-75	03.03.01.03 cell cycle checkpoints (checkpoints of morphogenesis, DNA-damage,-replication, mitotic phase and spindle)
Pc21g06470	strong similarity to cyclin-dependent protein kinase Pho85 - Saccharomyces cerevisiae	0.0	T49815	related to multifunctional cyclin-dependent kinase PHO85 [im	1300.1	1220.4	838.5	534.7	2e-44	01 METABOLISM
Pc21g07220	strong similarity to methylase Spb1 - Saccharomyces cerevisiae	0.0	T37754	pmt2 methyltransferase - fission yeast (Schizosaccharomyce	158.3	118.6	114.2	47.3	0	0
Pc21g09740	similarity to lipase LipP - Pseudomonas sp.	8e-20	F84000	carboxylesterase BH2806 [imported] - Bacillus halodurans (st	52.1	38.3	53.9	18.9	4e-84	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc21g13950	strong similarity to aspergillopepsin II - Aspergillus niger	6e-39	AF439998_1	product: "pepstatin-insensitive acid protease"; Talaromyces e	55.6	16.3	28.6	12.0	0	0
Pc21g15720	similarity to alkaline ceramidase Ypc1 - Saccharomyces cerevisiae	6e-28	NCB7F18_4	gene: "B7F18.050"; product: "conserved hypothetical protein"	64.2	47.9	28.8	26.9	0.0	01.04 phosphate metabolism
Pc21g16900	weak similarity to methyl sterol oxidase Erg25 - Saccharomyces cerevisiae	3e-05	E87456	sterol desaturase family protein [imported] - Caulobacter cres	97.5	44.4	29.9	23.6	2e-94	01.05.01 C-compound and carbohydrate utilization
Pc21g17940	strong similarity to eIF2-alpha specific protein kinase Gcn2 - Saccharomyces cerevisiae	0.0	NCB10H4_7	gene: "B10H4.070"; product: "cpc-3 protein"; Neurospora cras	270.5	217.7	151.2	101.6	6e-75	01.05.07 C-compound, carbohydrate transport
Pc21g18830	strong similarity to fatty acid elongase Fen1 - Saccharomyces cerevisiae	1e-120	NC7F4_14	gene: "7F4.130"; product: "probable fatty acid elongase (FEN	908.8	947.1	474.0	444.7	1e-121	01 METABOLISM
Pc21g19660	strong similarity to high affinity glucose transporter HGT1 - Kluyveromyces lactis	2e-56	AY444343_1	gene: "hxt1"; product: "glucose transporter"; Hypocrea jecorir	78.9	63.1	52.6	26.2	8e-70	01.01 amino acid metabolism
Pc21g22010	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	9e-78	AP005036_223	product: "putative 4-coumarate:CoA ligase"; Streptomyces av	50.8	45.3	22.0	12.0	3e-95	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc21g22770	strong similarity to choline permease Hnm1 - Saccharomyces cerevisiae	4e-53	S11175	choline transport protein - yeast (Saccharomyces cerevisiae)	59.9	19.4	12.0	12.0	2e-88	01.05 C-compound and carbohydrate metabolism
Pc21g22790	similarity to cytochrome P450 monooxygenase TRI4 - Myrothecium roridum	2e-22	AV38478_1	gene: "cyp110A2"; product: "cytochrome P450"; Anabaena va	72.7	26.3	19.6	12.0	0	0
Pc21g23190	strong similarity to sorbitol dehydrogenase SDH - Rattus norvegicus	0.0	AB116938_1	gene: "xdhB"; product: "xylitol dehydrogenase"; Aspergillus o	358.6	165.3	225.0	154.5	1e-101	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc22g03700	similarity to methyl chloride transferase AAC72357.1 - Batis maritima	6e-17	AF387791_1	gene: "tmt1"; product: "thiol methyltransferase 1"; Brassica c	229.3	418.6	161.2	132.6	4e-77	01.05.01 C-compound and carbohydrate utilization
Pc22g04610	strong similarity to fatty-acid subterminal hydroxylase P450foxy - Fusarium oxysporum	3e-71	AB078738_1	gene: "CYP505A3"; product: "fatty acid hydroxylase"; Asper	294.3	192.5	70.3	54.0	1e-119	01.05 C-compound and carbohydrate metabolism
Pc22g05190	strong similarity to gluconokinase gntV - Escherichia coli	2e-49	BX842635_14	gene: "B12J7.140"; product: "related to thermoresistant gluco	421.2	217.7	117.9	133.1	4e-83	01.01.04 regulation of amino acid metabolism
Pc22g06040	strong similarity to mannose-1-phosphate guanyltransferase like protein An04g04990 - Aspergillus niger	0.0	U89991_1	gene: "MPG1"; product: "mannose-1-phosphate guanylyltrans	973.4	757.3	450.3	462.8	1e-137	01.06 lipid, fatty-acid and isoprenoid metabolism
Pc22g06450	similarity to thiamine-repressible protein thi1p - Schizosaccharomyces pombe	1e-18	S41962	thiamin repressible genes regulatory protein thi1 [imported] - f	430.0	459.9	267.0	224.4	2e-96	01.05.01 C-compound and carbohydrate utilization
Pc22g06820	strong similarity to peroxisomal acetyl-CoA C-acyltransferase POT1 - Yarrowia lipolytica	1e-119	S36838	acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - ye	475.3	194.3	244.3	157.4	0	0
Pc22g07010	strong similarity to alpha 1,2 galactosyltransferase gma12p - Schizosaccharomyces pombe	1e-74	NCB14D6_53	gene: "B14D6.530"; product: "related to alpha-1, 2-galactosyl	80.9	39.9	65.2	43.2	9e-63	01.01.01.11 biosynthesis of the cysteine-aromatic group
Pc22g07490	weak similarity to zeaxanthin epoxidase ABA2 - Nicotiana plumbaginifolia	2e-14	NCB8G12_30	gene: "B8G12.280"; product: "related to oxygenase"; Neuros	61.5	38.1	33.5	12.0	0.0	02.11 electron transport and membrane-associated energy conservation
Pc22g09490	strong similarity to carbonyl reductase (NADPH) S1 - Candida magnoliae	4e-31	JC7338	carbonyl reductase (NADPH2) (EC 1.1.1.184) - Candida magr	74.1	58.4	36.7	69.4	1e-103	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis
Pc22g09610	strong similarity to FAD dependent L-sorbose dehydrogenase - Gluconobacter oxydans	1e-54	AL646074_194	gene: "betA"; "RSc3345"; "RS02583"; product: "PUTATIVE C	40.1	38.5	12.0	22.7	9e-85	01.05.07 C-compound, carbohydrate transport
Pc22g09640	strong similarity to chalcone synthase Gchs2 - Gerbera hybrida	4e-30	C75587	probable chalcone synthase - Deinococcus radiodurans (strai	29.4	15.3	12.0	12.0	0.0	02.11 electron transport and membrane-associated energy conservation
Pc22g09740	strong similarity to high-affinity glucose transporter HGT1 - Kluyveromyces lactis	7e-71	ANI251561_1	gene: "mstA"; product: "MSTA protein"; Aspergillus nidulans	185.5	76.2	30.7	37.6	0.0	01.05 C-compound and carbohydrate metabolism
Pc22g10020	strong similarity to alcohol dehydrogenase alkJ - Pseudomonas oleovorans	1e-169	SCO939121_176	gene: "SCO4829"; "SC2A6.14"; product: "putative oxidoreduc	682.6	1153.4	306.8	231.3	0.0	01 METABOLISM
Pc22g10030	strong similarity to betaine-aldehyde dehydrogenase betB - Escherichia coli	1e-154	ECU73857_33	gene: "betB"; product: "betaine-aldehyde dehydrogenase"; E	373.4	568.7	212.3	232.8	6e-95	01.05.01 C-compound and carbohydrate utilization
Pc22g12200	strong similarity to alpha 1,2-mannosidase IC - Homo sapiens	1e-141	NCB14A6_31	gene: "B14A6.310"; product: "probable class I alpha-mannosi	24.5	25.0	23.1	12.0	0	0
Pc22g12340	strong similarity to extracellular alpha-amylase amyA amyB - Aspergillus niger	0.0	ALAS3	alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae	161.1	52.2	58.3	67.7	0.0	01.03.01.03 purine nucleotide anabolism
Pc22g17150	weak similarity to 2-haloacid halidohydrolase IVa - Burkholderia cepacia	3e-04	SCO939116_165	gene: "SCO3446"; "SCE46.03c"; product: "putative dehaloger	190.8	164.6	94.5	94.0	5e-42	01.04.01 phosphate utilization
Pc22g17720	strong similarity to ribonucleotide reductase like protein An04g01080 - Aspergillus niger	0.0	WMBY3L	ribonucleoside-diphosphate reductase (EC 1.17.4.1) 3 large c	378.0	327.8	269.9	161.1	1e-62	01.05.01 C-compound and carbohydrate utilization
Pc22g18680	strong similarity to glycosylphosphatidylinositol-anchored beta(1-3)glucanosyltransferase gel3 - Aspergillus fumigatus	0.0	AF208040_1	gene: "GEL3"; product: "beta (1-3) glucanosyltransferase Gel	41.1	17.6	12.0	12.0	1e-81	01.05.07 C-compound, carbohydrate transport

Pc22g18690	weak similarity to alpha-1,6-mannosyltransferase Hoc1 - Saccharomyces cerevisiae [truncated ORF]	4e-19	AF374353_1	product: "putative mannosyltransferase"; Paracoccidioides bra	61.4	35.3	18.3	22.7	7e-92	01.05 C-compound and carbohydrate metabolism
Pc22g24680	strong similarity to high-affinity glucose transporter HGT1 - Kluyveromyces lactis	1e-172	AY444343_1	gene: "hxt1"; product: "glucose transporter"; Hypocrea jecorin	1352.7	1579.5	1824.5	735.6	8e-84	01.01.10 amino acid degradation (catabolism)
Pc22g24890	strong similarity to pectate lyase plyA - Aspergillus niger	1e-119	ANI276331_1	gene: "plyA"; product: "pectate lyase A"; Aspergillus niger str	29.8	21.8	12.0	12.0	0.0	01.05 C-compound and carbohydrate metabolism
Pc22g24900	similarity to salicylate 1-monooxygenase sal1 - Pseudomonas putida	8e-19	AD2770	salicylate hydroxylase [imported] - Agrobacterium tumefacien	50.1	101.6	18.8	30.1	2e-67	01.03 nucleotide metabolism
Pc22g25050	strong similarity to myo-inositol-1-phosphate synthase like protein An10g00530 - Aspergillus niger	0.0	NC100H1_10	gene: "100H1.120"; product: "probable myo-inositol 1-phosph	1199.8	1383.4	616.9	498.9	0	0
Pc22g25560	strong similarity to dUTP pyrophosphatase DUT1 - Candida albicans	2e-49	BX842627_10	gene: "B8J22.110"; product: "probable dUTP pyrophosphatas	494.1	415.7	261.2	163.3	0	0
Pc24g02480	similarity to 35.6K acid phosphatase - Aspergillus nidulans	7e-21	PC08104_1	gene: "phoG"; product: "PHOG"; Penicillium chrysogenum P	27.3	35.2	12.0	12.0	1e-86	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups
Pc24g02480	similarity to 35.6K acid phosphatase - Aspergillus nidulans	7e-21	PC08104_1	gene: "phoG"; product: "PHOG"; Penicillium chrysogenum P	27.3	35.2	12.0	12.0	1e-107	04 TRANSCRIPTION
Pc20g14590	strong similarity to assembly factor of cytochrome c oxidase Cox11 - Saccharomyces cerevisiae	1e-62	NCB13I18_14	gene: "B13I18.140"; product: "probable cytochrome-c oxidase	938.1	987.5	263.9	322.6	4e-28	01.03.01 purine nucleotide metabolism
Pc21g17100	strong similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	1e-123	S61908	DNA-binding protein amdA - Emericella nidulans	160.1	94.7	69.3	73.1	1e-166	05.01 ribosome biogenesis
Pc21g19380	strong similarity to mitochondrial ATP synthase subunit 9 oliC31 - Aspergillus nidulans	8e-31	LWNCA	H+-transporting two-sector ATPase (EC 3.6.3.14) lipid-binding	1539.4	1552.1	726.9	354.8	2e-55	02.11 electron transport and membrane-associated energy conservation
Pc22g11690	strong similarity to mitochondrial ribosomal protein Nam9 - Saccharomyces cerevisiae	4e-46	S55146	probable ribosomal protein S4 precursor, mitochondrial - yeas	144.0	143.1	99.1	57.5	0.0	05.04 translation
Pc49g00030	H+-transporting two-sector ATPase protein 6 - Penicillium chrysogenum	2e-99	S42271	H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - I	36.0	33.4	12.5	12.0	0.0	01.06.10 regulation of lipid, fatty-acid and isoprenoid metabolism
Pc12g01650	strong similarity to ras pathway interacting protein moe1p - Schizosaccharomyces pombe	1e-151	SPAC637_7	gene: "SPAC637.07"; "moe1"; S.pombe chromosome I cosm	805.8	789.5	557.5	238.9	7e-70	01.04 phosphate metabolism
Pc12g03120	strong similarity to regulator protein Sin3 - Saccharomyces cerevisiae	0.0	BX842632_7	gene: "B5K2.070"; product: "related to transcription regulatory	126.5	118.1	75.6	50.0	1e-74	99 UNCLASSIFIED PROTEINS
Pc12g07790	weak similarity to hypothetical serine threonine protein phosphatase topA - Fervidobacterium islandicum	3e-11	S50713	probable phosphoesterase (EC 3.1.-.-) YNL217w - yeast (Sac	199.3	186.4	91.2	103.9	1e-157	01.04 phosphate metabolism
Pc12g08830	strong similarity to nucleolin protein like protein An11g06190 - Aspergillus niger	2e-14	T38810	hypothetical protein SPAC4F10.06 - fission yeast (Schizosac	51.5	46.4	36.6	17.7	2e-94	01.04 phosphate metabolism
Pc12g12830	strong similarity to extragenic suppressor of the bimD6 mutation sudD - Aspergillus nidulans	0.0	AF013590_1	gene: "sudD"; product: "extragenic suppressor of the bimD6 r	130.2	131.2	88.0	46.5	4e-88	01.04 phosphate metabolism
Pc12g12920	similarity to dis1-suppressing protein kinase dsk1p - Schizosaccharomyces pombe	8e-18	NCB1D14_12	gene: "B1D14.120"; product: "probable dis1-suppressing prot	35.2	13.7	13.1	14.8	1e-175	04.05.01.04 transcriptional control
Pc13g02340	strong similarity to protein kinase of the MAP kinase kinase 2 Mkk2 - Saccharomyces cerevisiae [truncated ORF][putative sequencing	1e-166	AY452723_1	Podospora anserina chromosome 7 MAP kinase kinase 1 (M	487.1	379.2	181.0	188.2	1e-53	01.05 C-compound and carbohydrate metabolism
Pc13g08850	similarity to protein involved in silencing Sas10 - Saccharomyces cerevisiae	1e-43	T40331	hypothetical protein SPBC3B8.09 - fission yeast (Schizosacc	90.9	72.5	79.7	31.7	9e-90	01.04 phosphate metabolism
Pc13g10160	weak similarity to replication protein cdc23p - Schizosaccharomyces pombe	5e-68	BX897676_13	gene: "B8I24.130"; product: "related to replication protein CDC	45.5	48.2	25.3	22.4	0.0	03.01.01 cellular DNA uptake
Pc13g10330	strong similarity to meiosis control kinase ran1p - Schizosaccharomyces pombe	2e-94	FS53329_1	product: "Ran1-like protein kinase"; Fusarium solani Ran1-lik	446.7	303.6	220.5	121.9	0	0
Pc13g11700	strong similarity to cullin 1 - Homo sapiens	0.0	BX649606_39	gene: "culA"; product: "scf complex protein, putative"; Asper	254.5	239.5	136.2	97.0	1e-131	03.01.05 DNA recombination and DNA repair
Pc13g12210	similarity to cell division control protein cdc14p - Schizosaccharomyces pombe	6e-96	BX649606_61	product: "cell division control protein cdc14, putative"; Asperg	194.0	151.0	102.4	66.6	1e-74	01.04 phosphate metabolism
Pc13g13180	strong similarity to protein Rad57 - Saccharomyces cerevisiae	1e-121	BX649605_128	product: "rad57 protein, putative"; Aspergillus fumigatus BAC	71.4	65.8	41.5	30.9	0.0	01.05.04 regulation of C-compound and carbohydrate utilization
Pc16g07130	similarity to dis1-suppressing protein kinase dsk1p - Schizosaccharomyces pombe	2e-10	SPBC530_14	gene: "dsk1"; "SPBC530.14c"; S.pombe chromosome II cos	65.4	56.0	24.0	18.6	0.0	03.03 cell cycle
Pc16g09180	strong similarity to ADA and SAGA histone acetyltransferase subunint Ada3 - Saccharomyces cerevisiae	8e-32	SCADA3A_1	gene: "ADA3"; product: "alteration/deficiency in activation 3 p	31.6	18.0	12.0	12.0	6e-61	01.05.04 regulation of C-compound and carbohydrate utilization
Pc16g14970	strong similarity to hypothetical tubulin alpha-2 chain tubB - Aspergillus nidulans	0.0	S13337	tubulin alpha-2 chain - Emericella nidulans	26.0	19.4	12.0	12.0	4e-82	01.04 phosphate metabolism
Pc18g00860	weak similarity to suppressor of tom1 protein Mpt4 - Saccharomyces cerevisiae	3e-09	S48511	MPT4 protein - yeast (Saccharomyces cerevisiae)	780.9	1063.0	487.5	202.6	1e-161	03.01.05 DNA recombination and DNA repair
Pc18g01560	strong similarity to guanine nucleotide-releasing factor Lte1 - Saccharomyces cerevisiae	1e-135	AY365418_10	product: "LTE1-like protein"; Epichloe festucae clone BAC 0(	398.9	307.8	166.3	144.3	0.0	03.03.01 mitotic cell cycle and cell cycle control
Pc18g01820	similarity to ATP-dependent DNA helicase II 86 KD subunit G22P2 - Homo sapiens	2e-84	SPBC543_3	gene: "SPBC543.03c"; S.pombe chromosome II cosmid c54	385.7	267.9	103.3	90.6	4e-53	01.04 phosphate metabolism
Pc20g00750	strong similarity to centromere microtubule-binding protein Cbf5 - Saccharomyces cerevisiae	0.0	CBF5_ASPFU	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (C	679.1	698.1	435.2	335.8	1e-66	04.05.05.01.10 regulation of splicing
Pc20g05050	strong similarity to small protein-tyrosine-phosphatase stp1p - Schizosaccharomyces pombe	1e-31	A38148	protein-tyrosine-phosphatase (EC 3.1.3.48), low molecular we	177.1	205.5	125.2	95.0	1e-108	03.01.09.05 DNA conformation modification (e.g. chromatin)
Pc20g06960	strong similarity to fizzy-related protein Fzr1 - Mus musculus	0.0	BX842618_15	gene: "B13M13.150"; product: "probable FZR protein (fizzy-re	76.8	70.3	38.1	34.7	2e-81	03.01.03 DNA synthesis and replication
Pc20g08240	strong similarity to protein Rsc1 - Saccharomyces cerevisiae	1e-140	CNS09S4S_87	DNA centromeric region sequence from BAC DP26B06, DP34	106.7	101.0	60.0	49.2	5e-90	01.04 phosphate metabolism
Pc20g08490	weak similarity to DNA polymerase kappa TRF4 - Homo sapiens	2e-15	BT002764_1	gene: "At5g53770"; product: "unknown protein"; Arabidopsis t	353.3	355.0	198.2	156.1	4e-87	03.01.03 DNA synthesis and replication
Pc20g10270	strong similarity to protein kinase functional homolog of cdc2 nimX - Aspergillus nidulans	1e-145	CC2_EMENI	CELL DIVISION CONTROL PROTEIN 2 (EC 2.7.1.-) (CYCLIN	27.2	28.8	29.8	12.0	7e-38	03.01.09.05 DNA conformation modification (e.g. chromatin)
Pc20g14580	strong similarity to replication factor C 38-kDa subunit RFC3 - Homo sapiens	1e-160	NCB14D6_46	gene: "B14D6.460"; product: "probable replication factor C 38	135.5	134.3	65.6	72.2	1e-136	03.03.01 mitotic cell cycle and cell cycle control
Pc21g01490	strong similarity to suppressor of the septation mutant cdc11 sce3p - Schizosaccharomyces pombe	2e-27	T45516	probable RNA-binding protein sce3 - fission yeast (Schizosac	172.3	148.8	112.8	48.5	2e-67	14.10.02.02.01 apoptotic mitochondrial changes
Pc21g01980	strong similarity to cohesin subunit XSA1 - Xenopus laevis	1e-167	NC3H10_5	gene: "3H10.050"; product: "related to nuclear protein SA-1";	73.3	59.8	36.5	34.4	5e-68	03.01.03 DNA synthesis and replication
Pc21g02020	similarity to lethal(2)denticleless l(2)dtl - Drosophila melanogaster	1e-111	T48835	lethal(2)denticleless related protein [imported] - Neurospora c	96.5	90.6	47.4	40.1	1e-100	03.01.03 DNA synthesis and replication
Pc21g04330	strong similarity to cell division control protein cdc18p - Schizosaccharomyces pombe	7e-55	A40726	cell division control protein CDC18+ - fission yeast (Schizosa	43.0	29.2	20.7	18.1	2e-72	05 PROTEIN SYNTHESIS
Pc21g04620	strong similarity to DNA polymerase kappa TRF4 - Homo sapiens	2e-42	S62544	hypothetical protein SPAC12G12.13c - fission yeast (Schizos	49.3	35.8	32.3	16.6	0.0	03.01.03 DNA synthesis and replication
Pc21g07340	strong similarity to spi1-GTPase binding protein sbp1p - Schizosaccharomyces pombe	1e-49	BX908807_2	gene: "B13B7.020"; product: "probable spi1-GTP-binding prot	811.3	868.6	670.0	362.2	8e-67	03.01.03 DNA synthesis and replication
Pc21g11310	strong similarity to DNA polymerase II subunit-B Dpb2 - Saccharomyces cerevisiae	0.0	NC80A10_25	gene: "80A10.250"; product: "related to DNA directed DNA po	69.5	62.0	36.6	25.7	0.0	03.01.03 DNA synthesis and replication
Pc21g14450	strong similarity to replication factor C subunit ARFC3 - Arxula adeninivorans	1e-149	NCB13B3_18	gene: "B13B3.180"; product: "related to replication factor C cl	152.5	145.8	80.9	67.2	7e-93	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM
Pc21g15650	strong similarity to cell division protein nda4p - Schizosaccharomyces pombe	0.0	NC123A4_6	gene: "123A4.060"; product: "probable cell division control pro	222.7	169.7	97.7	100.6	3e-92	01.05 C-compound and carbohydrate metabolism
Pc22g00760	strong similarity to class II inner centromere protein like protein An08g08590 - Aspergillus niger	6e-16	CE33058_1	gene: "unc-89"; product: "UNC-89"; Caenorhabditis elegans U	198.5	167.7	96.9	85.0	0.0	03.01.09.05 DNA conformation modification (e.g. chromatin)
Pc22g01220	similarity to G T mismatch-specific thymine-DNA glycosylase TDG - Homo sapiens	9e-21	T41658	hypothetical protein SPCC965.05c - fission yeast (Schizosac	77.1	71.0	40.0	22.4	8e-98	03.03.01 mitotic cell cycle and cell cycle control
Pc22g03590	strong similarity to Isw2 - Saccharomyces cerevisiae	0.0	S67208	hypothetical protein YOR304w - yeast (Saccharomyces cerev	271.9	235.3	150.6	109.9	2e-37	06.07.03 modification by phosphorylation, dephosphorylation
Pc22g05300	strong similarity to cyclin B nimE - Aspergillus nidulans	0.0	S22694	cyclin B - Emericella nidulans	281.3	245.9	175.2	117.6	3e-60	01.03.16.01 RNA degradation
Pc22g06390	weak similarity to cell division control protein Cdc31 - Saccharomyces cerevisiae	1e-31	S47549	cell division control protein CDC31 - yeast (Saccharomyces c	187.2	162.9	79.6	77.8	4e-66	04 TRANSCRIPTION
Pc22g08880	strong similarity to RNA binding protein nrd1p - Schizosaccharomyces pombe	1e-128	S65196	probable membrane protein YPL184c - yeast (Saccharomyce	225.0	160.6	91.0	46.8	1e-107	04 TRANSCRIPTION
Pc22g09870	weak similarity to DNA polymerase V Pol5 - Saccharomyces cerevisiae [truncated ORF]	4e-55	BX842631_3	gene: "B1O14.030"; product: "related to DNA polymerase V";	150.6	133.8	102.4	54.4	3e-73	03.01.05 DNA recombination and DNA repair
Pc22g09880	strong similarity to DNA polymerase V Pol5 - Saccharomyces cerevisiae [truncated ORF]	1e-74	BX842631_3	gene: "B1O14.030"; product: "related to DNA polymerase V";	60.8	52.4	40.2	26.2	3e-76	03 CELL CYCLE AND DNA PROCESSING
Pc22g18050	strong similarity to Rad52 homologue MUS11 - Neurospora crassa	1e-123	AY032591_1	gene: "radC"; product: "RADC"; Aspergillus nidulans RADC (	36.3	27.4	12.0	12.0	0.0	03.01.03 DNA synthesis and replication
Pc22g18920	strong similarity to Dom34p-interacting protein like protein An04g01900 - Aspergillus niger	0.0	NCB11N2_16	gene: "B11N2.160"; product: "conserved hypothetical protein"	61.4	52.1	64.9	26.2	8e-29	03 CELL CYCLE AND DNA PROCESSING
Pc22g21010	strong similarity to polymerase I Pol1 - Saccharomyces cerevisiae	0.0	DJZPA	DNA-directed DNA polymerase (EC 2.7.7.7) alpha - fission ye	320.3	262.1	159.6	155.8	6e-57	04 TRANSCRIPTION
Pc23g00440	similarity to protein required for accurate chromosome transmission Chl12 - Saccharomyces cerevisiae	5e-08	S50340	CHL12 protein - yeast (Saccharomyces cerevisiae)	40.4	37.1	12.9	12.0	1e-109	01.01.04 regulation of amino acid metabolism
Pc04g00010	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	4e-37	A28913	regulatory protein brlA - Emericella nidulans	12.0	12.0	12.0	12.0	3e-38	04.05.05 mRNA processing (splicing, 5'-, 3'-end processing)
Pc06g01270	weak similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	1e-137	T51029	related to pathway-specific nitrogen regulator [imported] - Neu	426.4	335.9	112.8	100.3	2e-66	01.01.04 regulation of amino acid metabolism
Pc12g03020	strong similarity to SMAD interacting protein like protein An16g07230 - Aspergillus niger	2e-52	AF236664_1	gene: "hzfA"; product: "hypothetical zinc-finger protein"; Asp	103.6	102.4	59.0	44.1	3e-88	04.05.01.04 transcriptional control
Pc12g10710	similarity to transcription activator Put3 - Saccharomyces cerevisiae	4e-10	A39792	transcription activator PUT3 - yeast (Saccharomyces cerevisi	90.6	79.7	27.2	35.1	0.0	01.04 phosphate metabolism
Pc12g11050	strong similarity to hypothetical zinc-finger protein - Schizosaccharomyces pombe	2e-69	NC49D12_20	gene: "49D12.200"; product: "conserved hypothetical protein"	282.1	280.8	172.7	122.2	4e-72	01.01.04 regulation of amino acid metabolism
Pc12g11400	strong similarity to subunit of transcription initiation factor TFIID like protein An11g05530 - Aspergillus niger	1e-149	S62469	probable transcription initiation factor tfiid subunit - fission yea	333.3	272.3	173.8	107.4	3e-96	04 TRANSCRIPTION
Pc12g14900	similarity to zinc-finger protein CZF1 - Candida albicans	5e-09	AY190521_1	gene: "MPP1"; product: "ZnII/2cys6 transcription factor"; Pic	52.8	46.8	24.8	34.1	6e-37	01.05.04 regulation of C-compound and carbohydrate utilization
Pc12g15680	similarity to DNA binding regulatory protein amdX - Aspergillus nidulans	1e-11	SCRGM1_1	gene: "RGM1"; product: "proline-rich zinc finger protein"; S.c	137.0	104.1	83.7	40.0	3e-84	01.01.04 regulation of amino acid metabolism
Pc12g15760	similarity to nuclear polyadenylated RNA-binding protein Nab3 - Saccharomyces cerevisiae	3e-18	T38767	probable RNA-binding protein - fission yeast (Schizosaccharo	83.1	57.7	46.9	24.4	2e-31	01.01.04 regulation of amino acid metabolism
Pc12g16580	strong similarity to zinc-finger transcription factor Rdr1 - Saccharomyces cerevisiae	2e-85	S67292	probable membrane protein YOR380w - yeast (Saccharomyce	343.2	378.4	52.5	98.1	8e-25	01.01.04 regulation of amino acid metabolism
Pc13g01970	similarity to RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	6e-06	NCR238440_1	gene: "pro1"; product: "PRO1"; Neurospora crassa pro1 gene	180.6	178.7	96.6	83.2	5e-55	03.03.01 mitotic cell cycle and cell cycle control
Pc13g02260	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	9e-06	T41718	hypothetical fungal Zn(2)-Cys(6) zinc-finger protein - fission ye	89.4	50.3	42.5	33.7	7e-36	01.03.01 purine nucleotide metabolism
Pc13g02830	strong similarity to protein Sof1 - Saccharomyces cerevisiae	1e-155	T49318	probable SOF1 protein [imported] - Neurospora crassa	191.1	163.9	134.4	72.6	0	0
Pc13g04110	strong similarity to 14.2 kD subunit of DNA-directed RNA polymerase II Rpb9 - Saccharomyces cerevisiae	7e-29	RNBY29	DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB9 - y	448.0	416.8	206.9	185.5	2e-50	03.03.01 mitotic cell cycle and cell cycle control
Pc13g04600	strong similarity to transcription elongation factor like protein An05g00780 - Aspergillus niger	7e-06	T40079	hypothetical protein SPBC29A3.08 - fission yeast (Schizosac	58.2	54.2	27.7	23.6	1e-107	04 TRANSCRIPTION
Pc13g04920	strong similarity to transcription factor involved in differentiation stuA - Aspergillus nidulans	1e-143	ENSTUA_1	gene: "StuA"; product: "cell pattern formation-associated prot	255.5	192.5	125.3	69.0	1e-107	01.04 phosphate metabolism
Pc13g09500	similarity to transcription factor Swi5 - Saccharomyces cerevisiae	3e-22	T39062	hypothetical zinc-finger protein - fission yeast (Schizosacchar	305.3	251.1	166.3	89.0	3e-87	04 TRANSCRIPTION
Pc13g10360	strong similarity to pre-mRNA splicing modulating serine threonine kinase prp4p - Schizosaccharomyces pombe	1e-116	T11720	mRNA splicing-associated serine-threonine protein kinase (E(	205.2	157.2	109.0	70.9	0	0
Pc13g14480	strong similarity to ATP dependent RNA helicase Spb4 - Saccharomyces cerevisiae	1e-160	NCB9B11_20	gene: "B9B11.200"; product: "related to RNA helicase SPB4"	46.7	32.3	47.5	20.7	2e-41	11.05.05 virulence, disease factors
Pc13g15780	strong similarity to prodos protein like protein An09g03980 - Aspergillus niger	1e-08	AK057383_1	unnamed ORF; Homo sapiens cDNA FLJ32821 fis, clone TE	52.8	51.1	20.6	29.1	3e-71	04.01.01 rRNA synthesis
Pc15g01260	strong similarity to Ran-GTPase-activating protein 1 rna1p - Schizosaccharomyces pombe	8e-81	S37691	ran GTPase activating protein 1 - fission yeast (Schizosaccha	107.6	102.2	82.2	42.3	1e-38	04.05.01.04 transcriptional control
Pc16g01890	weak similarity to transcription initiation factor Rrn6 - Saccharomyces cerevisiae	4e-11	NCB24N11_8	gene: "B24N11.080"; product: "hypothetical protein"; Neuros	51.4	40.7	29.9	17.5	7e-71	10.01 intracellular signalling
Pc16g04210	strong similarity to homeobox protein like protein An08g02580 - Aspergillus niger	4e-08	MMU89343_1	gene: "Lhx4"; product: "LIM-homeobox protein"; Mus musculu	843.5	592.0	363.7	202.0	4e-62	04.05.01.04 transcriptional control
Pc16g04390	strong similarity to transcription factor fet5p - Schizosaccharomyces pombe	1e-103	BX842634_8	gene: "B16B8.080"; product: "conserved hypothetical protein"	170.3	156.8	88.3	59.7	0.0	04 TRANSCRIPTION
Pc16g06560	strong similarity to transcriptional activator glcD - Aspergillus nidulans	6e-76	AF320978_1	gene: "glcd"; product: "GLCD gamma"; Aspergillus nidulans G	174.0	102.7	82.1	52.2	1e-92	04.05.01.04 transcriptional control
Pc16g07450	strong similarity to CCAAT-binding transcription factor CBF - Homo sapiens [putative sequencing error]	1e-144	T38813	hypothetical protein SPAC4F10.09c - fission yeast (Schizosa	73.5	69.3	33.7	21.9	5e-38	04 TRANSCRIPTION
Pc16g10300	strong similarity to transcription factor like protein An01g04370 - Aspergillus niger	6e-42	T37676	zinc-finger protein - fission yeast (Schizosaccharomyces pom	58.6	106.5	49.7	39.2	0.0	04.05.01 mRNA synthesis
Pc16g10310	strong similarity to 23 kD subunit of DNA-directed RNA polymerase I,II,III Rpo26 - Saccharomyces cerevisiae	3e-31	RNBYR6	DNA-directed RNA polymerase (EC 2.7.7.6) chain RPO26 - y	402.7	483.4	345.1	231.6	2e-47	01.02.04 regulation of nitrogen and sulphur utilization
Pc16g10890	strong similarity to RNA helicase 1 HRH1 - Homo sapiens	1e-172	S35546	ATP-dependent RNA helicase - fission yeast (Schizosacchar	44.2	40.9	33.5	15.9	2e-44	04 TRANSCRIPTION
Pc16g11730	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	5e-09	T49729	zinc finger protein 1 homolog [imported] - Neurospora crassa	219.1	161.9	119.7	80.8	4e-43	04.05.01.04 transcriptional control
Pc16g11930	strong similarity to TATA-binding protein-associated phosphoprotein Dr1 - Homo sapiens	2e-36	BX842622_20	gene: "B15B3.200"; product: "related to TBP-binding represso	281.7	281.3	173.5	130.2	0.0	04 TRANSCRIPTION
Pc16g13800	strong similarity to large subunit of transcription initation factor TFIIA like protein An01g12770 - Aspergillus niger	5e-25	T40052	probable transcription initiation factor IIA large subunit - fission	74.8	48.8	41.7	21.1	5e-34	01.01.04 regulation of amino acid metabolism
Pc16g13990	strong similarity to largest subunit of DNA-directed RNA polymerase II rpb1p - Schizosaccharomyces pombe	0.0	RNFF2L	DNA-directed RNA polymerase (EC 2.7.7.6) II 215K chain [va	380.4	337.9	195.0	129.8	1e-74	04.05.01.04 transcriptional control
Pc16g14350	similarity to hypothetical transcriptional regulator FCR1 - Candida albicans	7e-13	AF057038_1	gene: "FCR1"; product: "zinc cluster transcription factor Fcr1p	58.8	25.1	23.9	13.5	1e-115	99 UNCLASSIFIED PROTEINS
Pc18g00800	strong similarity to transcription factor ZFM1 - Homo sapiens	1e-164	NC94C8_6	gene: "94C8.060"; product: "related to branch point bridging p	245.1	226.6	148.0	89.7	1e-101	04 TRANSCRIPTION
Pc18g02410	similarity to protein involved in ribosome biogenesis Kri1 - Saccharomyces cerevisiae	1e-32	T11615	hypothetical protein SPAC22G7.05 - fission yeast (Schizosac	71.0	71.3	80.8	37.5	4e-40	01.01.04 regulation of amino acid metabolism
Pc18g03520	weak similarity to C2H2-type zinc finger protein Mhy1p - Yarrowia lipolytica	7e-53	FSU61841_1	gene: "gbp"; product: "cutinase G-box binding protein"; Fusa	303.1	191.8	149.4	64.1	3e-77	04.01.04 rRNA processing
Pc18g04480	similarity to transcription factor Ume6 - Saccharomyces cerevisiae	1e-157	ENI519682_1	gene: "rosA"; product: "repressor of sexual development"; As	437.9	229.9	157.0	148.6	6e-51	01.04 phosphate metabolism
Pc20g00320	similarity to component of the U3 small nucleolar ribonucleoprotein Mpp10 - Saccharomyces cerevisiae	4e-40	S55189	hypothetical protein YJR002w - yeast (Saccharomyces cerevi	80.5	72.2	67.3	30.8	4e-86	04 TRANSCRIPTION
Pc20g00650	strong similarity to hnf-3 forkhead transcription factor sep1p - Schizosaccharomyces pombe	8e-30	JC6500	hnf-3/forkhead transcription factor homolog sep1 - fission yeas	96.3	66.7	36.8	38.2	1e-163	01.01.04 regulation of amino acid metabolism
Pc20g06400	strong similarity to Cys2-His2 zinc finger transcription factor ACEI - Hypocrea jecorina	1e-165	AY072919_1	product: "zinc finger transcription factor ACE I"; Talaromyces	838.7	772.8	611.2	373.9	2e-21	01.02.04 regulation of nitrogen and sulphur utilization
Pc20g06460	weak similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	0.0	AF272849_1	product: "nitrogen regulatory protein OTam"; Aspergillus oryza	304.9	366.7	179.5	168.9	1e-148	05.07 translational control
Pc20g11000	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa [putative sequencing error]	0	0	0	124.9	107.3	55.9	53.0	0.0	04.05.01 mRNA synthesis
Pc20g11660	strong similarity to mitochondrial mRNA processing protein Pet127 - Saccharomyces cerevisiae	1e-122	NC65E11_7	gene: "65E11.070"; product: "related to PET127"; Neurospora	71.9	61.1	51.4	26.7	6e-35	04.05.05 mRNA processing (splicing, 5'-, 3'-end processing)
Pc20g12310	strong similarity to DEAH-box RNA helicase Dhr1 - Saccharomyces cerevisiae	0.0	NC99H12_11	gene: "99H12.110"; product: "conserved hypothetical protein"	94.2	74.6	70.1	35.1	1e-112	01.03.16.01 RNA degradation
Pc20g12320	strong similarity to splicing coactivator subunit like protein An15g01170 - Aspergillus niger	1e-04	T46237	hypothetical protein T9C5.190 - Arabidopsis thaliana	79.1	81.7	48.3	31.9	2e-70	01 METABOLISM
Pc20g12340	strong similarity to RNA binding protein like protein An15g01180 - Aspergillus niger	1e-105	BC024218_1	product: "Unknown (protein for MGC:11163)"; Homo sapiens,	148.3	92.5	84.9	30.2	0.0	04.01.04 rRNA processing
Pc20g14170	strong similarity to glucose repression mediator protein Ssn6 - Saccharomyces cerevisiae	1e-146	NCB17B1_3	gene: "B17B1.030"; product: "related to TPR-containing prote	167.8	140.7	145.4	67.0	1e-111	04 TRANSCRIPTION
Pc21g02010	strong similarity to ribosomal RNA processing protein Rrp5 - Saccharomyces cerevisiae	0.0	T40847	probable rRNA biogenesis protein - fission yeast (Schizosacc	230.4	199.6	140.1	89.9	9e-45	04 TRANSCRIPTION
Pc21g04980	strong similarity to calcineurin responsive zinc-finger transcription factor like protein An13g00370 - Aspergillus niger	3e-41	BX842634_16	gene: "B16B8.160"; product: "related to zinc finger protein cro	85.5	44.4	51.2	22.2	1e-18	01.01.04 regulation of amino acid metabolism
Pc21g05130	strong similarity to 13.6 kD subunit of DNA-directed RNA polymerase II Rpb11 - Saccharomyces cerevisiae	1e-24	S58933	DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB11 -	303.8	249.8	134.3	119.8	1e-74	29 TRANSPOSABLE ELEMENTS, VIRAL AND PLASMID PROTEINS
Pc21g05540	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	1e-116	ENI294750_1	gene: "ARCA"; product: "ARCA protein"; Emericella nidulans	169.6	125.2	97.8	52.9	0.0	04.05.05 mRNA processing (splicing, 5'-, 3'-end processing)
Pc21g05640	GATA transcription factor sreP - Penicillium chrysogenum	0.0	JC6170	GATA-transcription factor - Penicillium chrysogenum	221.4	169.5	122.1	76.1	8e-71	01.05 C-compound and carbohydrate metabolism
Pc21g06700	strong similarity to ATP dependent RNA helicase and pre-mRNA splicing factor Prp43 - Saccharomyces cerevisiae	0.0	T49573	probable ATP-binding protein PRP16 [imported] - Neurospora	354.8	314.8	202.7	110.2	1e-108	04 TRANSCRIPTION

Pc21g07940	strong similarity to transcription factor like protein An14g04590 - Aspergillus niger	1e-79	AX513585_1	unnamed ORF; Sequence 22 from Patent WO02059324.	171.8	142.0	85.8	66.3	0		0
Pc21g11090	strong similarity to zinc-finger transcription factor like protein An16g08800 - Aspergillus niger	2e-21	NCB13H18_21	gene: "B13H18.230"; product: "hypothetical protein"; Neuros	231.6	258.0	230.6	115.2	9e-34	05 PROTEIN SYNTHESIS	
Pc21g13260	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	1e-15	NC5E6_17	gene: "5E6.190"; product: "related to ARCA protein"; Neuros	48.0	26.8	23.4	36.6	2e-35	01.01.04 regulation of amino acid metabolism	
Pc21g20940	similarity to hypothetical spliceosome associated protein Spf31 - Homo sapiens	3e-52	AFA12H2_5	gene: "AfA12H2.05c"; product: "hypothetical DNA j domain c	142.9	133.4	81.0	65.2	0.0	04.05 mRNA transcription	
Pc21g21680	strong similarity to hypothetical C6 hypothetical protein CAD37146.1 - Aspergillus fumigatus	1e-47	AFA12H2_8	gene: "AfA12H2.08c"; product: "hypothetical protein"; Asper	71.9	63.8	42.1	16.3	2e-28	29 TRANSPOSABLE ELEMENTS, VIRAL AND PLASMID PROTEINS	
Pc22g02150	strong similarity to DNA RNA helicase Hfm1 - Saccharomyces cerevisiae	1e-170	S61610	HFM1 protein - yeast (Saccharomyces cerevisiae)	49.6	41.3	26.6	17.3	0		0
Pc22g03450	weak similarity to U1 snRNP protein C - Homo sapiens	2e-19	NC12F11_22	gene: "12F11.220"; product: "related to U1 SMALL NUCLEAF	95.1	97.2	40.0	30.4	9e-46	03 CELL CYCLE AND DNA PROCESSING	
Pc22g13510	weak similarity to 49 kD subunit of DNA-directed RNA polymerase I Rpa49 - Saccharomyces cerevisiae	4e-08	T38536	probable DNA-directed RNA polymerase (EC 2.7.7.6) I 49K cl	68.2	58.2	63.2	30.1	1e-141	05.07 translational control	
Pc22g13920	strong similarity to hypothetical transcription factor BAB47239.1 - Aspergillus oryzae	1e-131	AB052971_1	product: "putative transcriptional activator"; Aspergillus nidula	37.4	44.7	24.5	20.3	5e-55	04 TRANSCRIPTION	
Pc22g14170	strong similarity to tRNA Met processing protein Gcd14 - Saccharomyces cerevisiae	2e-96	NC21D9_6	gene: "21D9.070"; product: "related to GCN4 translational rep	46.0	38.6	35.2	18.4	1e-162	03.03.01 mitotic cell cycle and cell cycle control	
Pc22g16890	strong similarity to essential nucleolar protein Nop77 - Saccharomyces cerevisiae	1e-101	T40511	ribosomal processing, rna binding, nucleolar pro tein - fission	150.1	135.7	129.4	51.5	0.0	04.01.01 rRNA synthesis	
Pc22g20820	strong similarity to transcription adaptor Ada2 - Saccharomyces cerevisiae	1e-167	BX908808_2	gene: "G21B4.020"; product: "related to transcription adaptor	254.0	265.0	119.6	104.7	1e-77	40.10 nucleus	
Pc22g21540	strong similarity to RNA polymerase I transcription factor RRN3 - Homo sapiens	3e-86	BX842627_22	gene: "B8J22.220"; product: "related to RNA Polymerase I Tr	256.9	215.8	157.3	91.9	0.0	10.01.01 unspecified signal transduction	
Pc22g27040	strong similarity to XFIN like protein An04g05060 - Aspergillus niger	3e-31	NCB11B23_15	gene: "B11B23.150"; product: "conserved hypothetical protein	30.3	30.3	12.0	18.8	0.0	10.01.01 unspecified signal transduction	
Pc24g01560	weak similarity to retrotransposon Tto1 - Nicotiana tabacum	1e-132	T02206	hypothetical protein - common tobacco retrotransposon Tto1	44.7	73.7	33.1	28.7	1e-169	05.04 translation	
Pc24g01930	weak similarity to retrotransposon Tto1 - Nicotiana tabacum	1e-136	T02206	hypothetical protein - common tobacco retrotransposon Tto1	298.7	940.7	164.8	136.7	1e-171	04.03.01 tRNA synthesis	
Pc12g16540	strong similarity to cytosolic aspartate--tRNA ligase Dps1 - Saccharomyces cerevisiae	1e-147	SYBYDC	aspartate-tRNA ligase (EC 6.1.1.12), cytosolic [validated] - ye	1371.1	1554.0	734.8	763.0	0.0	05.04 translation	
Pc13g02680	strong similarity to glutamine--tRNA ligase - Saccharomyces cerevisiae	0.0	SYBYQT	glutamine-tRNA ligase (EC 6.1.1.18) - yeast (Saccharomyces	193.6	178.2	130.8	73.8	1e-157	04.05.01.04 transcriptional control	
Pc13g07040	strong similarity to translation initiation factor eIF-3 subunit like protein An14g01030 - Aspergillus niger	1e-159	T38786	translation intiation factor eif-3 - fission yeast (Schizosacchar	522.1	550.3	380.9	239.9	1e-100	05.04 translation	
Pc16g02320	strong similarity to conserved eukaryotic protein involved in ribosome biogenesis Erb1 - Saccharomyces cerevisiae	0.0	S54549	probable membrane protein YMR049c - yeast (Saccharomyce	231.1	180.2	154.8	76.0	1e-116	01.03.16.01 RNA degradation	
Pc16g05590	strong similarity to eukaryotic initiation factor 3H1 subunit TIF3H1 - Arabidopsis thaliana	4e-58	OSJN00130_13	gene: "OSJNBb0006N15.13"; Oryza sativa genomic DNA, ch	317.6	308.1	207.0	125.6	5e-63	05.04 translation	
Pc16g09030	strong similarity to polyadenylate-binding protein Pabp - Saccharomyces cerevisiae	0.0	ENU70731_1	gene: "fabM"; product: "putative poly(A)-binding protein FabM	490.4	408.0	422.4	188.1	1e-103	03.03.01 mitotic cell cycle and cell cycle control	
Pc16g10350	strong similarity to translation initiation factor eIF-3 - Schizosaccharomyces pombe	0.0	T39716	translation initiation factor eIF-3 subunit [imported] - fission ye	45.7	49.9	35.7	15.3	0.0	05.04 translation	
Pc20g08010	strong similarity to translation initiation factor 3 complex protein like protein An11g10630 - Aspergillus niger	1e-141	T40476	hypothetical protein SPBC4B4.04 - fission yeast (Schizosacc	277.4	284.0	314.2	148.1	9e-61	01.04 phosphate metabolism	
Pc20g09480	strong similarity to valine--tRNA ligase cyt-20 - Neurospora crassa	0.0	A41251	valine-tRNA ligase (EC 6.1.1.9) - Neurospora crassa	359.7	407.1	271.8	186.2	3e-42	03.03.01 mitotic cell cycle and cell cycle control	
Pc21g05120	strong similarity to poly(A)-specific ribonuclease Pan1 - Saccharomyces cerevisiae	9e-65	S48440	poly(A)-specific ribonuclease (EC 3.1.13.4) - yeast (Saccharo	99.8	85.3	68.8	37.2	7e-60	05.04 translation	
Pc21g08420	strong similarity to mitochondrial ribosomal protein of the large subunit Yml35 - Saccharomyces cerevisiae	5e-82	BX842620_10	gene: "B11E5.100"; product: "related to ribosomal protein Ym	175.2	156.9	118.1	78.0	2e-33	04.05.01.04 transcriptional control	
Pc21g23710	strong similarity to gamma subunit of translation elongation factor eEF-1 - Homo sapiens	2e-36	AB056105_1	gene: "ef-1 gamma"; product: "elongation factor-1 gamma"; C	1123.8	1708.7	941.1	679.7	1e-101	01.04 phosphate metabolism	
Pc22g17020	strong similarity to nucleolar protein gar2p - Schizosaccharomyces pombe	2e-32	AF465933_1	product: "RNA binding protein"; Elaeis oleifera RNA binding p	192.0	184.2	128.4	50.0	2e-94	06.01 protein folding and stabilization	
Pc12g00100	strong similarity to protein kinase like protein An15g03140 - Aspergillus niger	0.0	AY456071_1	gene: "RIM15"; product: "putative response regulator receiver	369.6	268.4	167.6	110.6	5e-99	06.13 proteolytic degradation	
Pc12g01320	strong similarity to protein precursor Bcs1 - Saccharomyces cerevisiae	1e-114	T49717	related to BCS1 protein precursor [imported] - Neurospora cra	51.4	44.8	40.8	21.4	4e-36	06.07 protein modification	
Pc12g04620	strong similarity to aspartic proteinase Yps3 - Saccharomyces cerevisiae	1e-165	AB044078_1	gene: "opsB"; product: "aspartic protease"; Aspergillus oryza	51.8	50.0	20.3	13.5	0.0	01.03.16.01 RNA degradation	
Pc12g08030	similarity to autophagy modulator Agp12 - Saccharomyces cerevisiae	4e-14	S46093	probable membrane protein YBR217w - yeast (Saccharomyce	27.1	24.6	12.0	15.6	0.0	06.07 protein modification	
Pc12g10670	strong similarity to dnaK-type molecular chaperone bipA - Aspergillus niger	0.0	T43723	dnaK-type molecular chaperone bipA [imported] - Aspergillus	1317.9	938.5	658.5	532.8	3e-62	01.05.01.01.99 other C-compound, carbohydrate catabolism	
Pc12g12880	strong similarity to ubiquitin specific protease like protein An02g01420 - Aspergillus niger	1e-87	S46636	hypothetical protein YJL197w - yeast (Saccharomyces cerevi	50.3	52.3	27.6	16.8	5e-48	04 TRANSCRIPTION	
Pc12g13910	strong similarity to spermidine spermine N(1)-acetyltransferase like protein An14g03030 - Aspergillus niger	2e-31	SPAC1002_7	gene: "ats1"; "SPAC1002.07c"; product: "N-acetyltransferase	145.6	136.8	48.8	35.0	5e-52	05 PROTEIN SYNTHESIS	
Pc12g14240	strong similarity to small GTPase like protein An14g02260 - Aspergillus niger	1e-52	RYL2_YARLI	RAS-LIKE GTP-BINDING PROTEIN RYL2.	215.0	134.0	87.2	83.6	0.0	06.04 protein targeting, sorting and translocation	
Pc12g14810	strong similarity to zuotin Zuo1 - Saccharomyces cerevisiae	1e-123	T50972	probable zuotin [imported] - Neurospora crassa	426.8	413.5	368.4	206.4	7e-42	06.04 protein targeting, sorting and translocation	
Pc12g16530	strong similarity to coatomer gamma subunit 2 copg2 - Homo sapiens	0.0	BX842630_6	gene: "B13D15.060"; product: "related to coatomer gamma-2	1527.1	1289.2	415.1	313.5	5e-25	05 PROTEIN SYNTHESIS	
Pc13g01450	strong similarity to SCF ubiquitin ligase (E3) F-box subunit FBL3 - Homo sapiens	1e-40	AK044693_1	Mus musculus adult retina cDNA, RIKEN full-length enriched	398.5	312.7	245.8	137.5	1e-180	06.07 protein modification	
Pc13g15850	strong similarity to heat shock protein hsp30 - Aspergillus nidulans	2e-52	AB126868_1	gene: "hsp30"; product: "heat shock protein 30"; Aspergillus	35.1	29.4	22.9	12.3	2e-74	06.04 protein targeting, sorting and translocation	
Pc14g00640	strong similarity to nuclear protein Enp1 - Saccharomyces cerevisiae	1e-85	T39410	hypothetical protein SPBC13G1.09 - fission yeast (Schizosac	202.5	163.3	182.3	87.5	1e-150	06.04 protein targeting, sorting and translocation	
Pc16g04240	strong similarity to nuclear localization protein Npl6 - Saccharomyces cerevisiae	9e-38	T40924	nuclear localization protein - fission yeast (Schizosaccharomy	265.3	158.8	102.3	60.3	8e-73	01.04 phosphate metabolism	
Pc16g06000	strong similarity to mitochondrial import protein Mpi1 - Saccharomyces cerevisiae	1e-149	AY212507_1	gene: "tim44"; product: "mitochondrial inner membrane transl	230.4	218.7	142.0	108.9	0.0	06.04 protein targeting, sorting and translocation	
Pc16g11990	similarity to cdc25C associated protein kinase like protein An18g01800 - Aspergillus niger	4e-09	G89287	protein H39E23.1 [imported] - Caenorhabditis elegans	29.6	12.0	15.1	12.3	1e-174	06.04 protein targeting, sorting and translocation	
Pc16g14760	strong similarity to karyopherin beta Kap95 - Saccharomyces cerevisiae	0.0	AY303543_1	gene: "KapB"; product: "putative karyopherin/importin beta-1"	295.6	277.0	173.9	105.5	0		0
Pc16g15440	weak similarity to ankyrin Ank2 - Homo sapiens	8e-54	A55575	ankyrin 3, long splice form - human	176.3	290.0	190.6	55.2	1e-97	01.04 phosphate metabolism	
Pc18g03700	similarity to receptor tyrosine kinase CCK-2 like protein An13g01560 - Aspergillus niger [putative pseudogene]	0	0		48.7	37.6	20.6	15.4	0		0
Pc18g04790	strong similarity to dual-specificity phosphatase mp1p - Schizosaccharomyces pombe	1e-26	T39517	dual-specificity MAP kinase phosphatase (EC 3.1.3.-) - fissio	202.6	120.7	82.9	55.6	1e-79	06.01 protein folding and stabilization	
Pc20g09730	similarity to glutamyl endoprotease polypeptide like protein An11g07120 - Aspergillus niger	0	0		56.2	47.0	12.0	26.6	2e-64	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc20g10240	strong similarity to serine-type carboxypeptidase precursor cpdS - Aspergillus phoenicis	0.0	S78072	serine-type carboxypeptidase (EC 3.4.16.-) I - Aspergillus nig	139.1	94.9	57.5	17.3	0.0	03 CELL CYCLE AND DNA PROCESSING	
Pc20g11320	weak similarity to ankyrin 2 Ank2 - Drosophila melanogaster	3e-11	AE017257_215	product: "ankyrin repeat domain protein"; Wolbachia endosyn	66.1	36.2	17.2	12.0	0.0	06.04 protein targeting, sorting and translocation	
Pc20g12430	strong similarity to protein required for accurate mitotic chromosome segregation Cse1 - Saccharomyces cerevisiae	0.0	NCB16M17_1	gene: "B16M17.010"; product: "probable mportin-alpha export	460.2	430.1	303.6	201.6	3e-42	04 TRANSCRIPTION	
Pc20g15310	strong similarity to RAN-binding protein Kap123 - Saccharomyces cerevisiae	1e-167	T39449	probable importin beta-4 subunit - fission yeast (Schizosacch	792.5	581.1	537.7	264.2	1e-120	01.04 phosphate metabolism	
Pc21g09710	strong similarity to ADP-ribosylation factor-like protein Arl1 - Saccharomyces cerevisiae	6e-29	AK009226_1	Mus musculus adult male tongue cDNA, RIKEN full-length en	25.5	49.8	18.2	12.8	3e-66	01.06.13 lipid and fatty-acid transport	
Pc21g14960	strong similarity to severin kinase - Dictyostelium discoideum	1e-157	NCB16M17_9	gene: "B16M17.090"; product: "related to Ste20-like kinase D	82.2	80.6	50.9	20.3	4e-43	04.05 mRNA transcription	
Pc21g16920	strong similarity to phosphatidylinositol-phosphatidylcholine transfer protein SEC14 - Yarrowia lipolytica	4e-29	BX908789_19	gene: "B13D24.190"; product: "probable phosphatidylinositol/	260.6	315.7	168.7	156.6	4e-45	06.04 protein targeting, sorting and translocation	
Pc21g23450	similarity to signal recognition particle chain Sec65 - Saccharomyces cerevisiae	1e-27	JC6516	signal recognition particle protein Sec65 - yeast (Yarrowia lipo	261.6	254.3	127.7	134.3	2e-38	06.04 protein targeting, sorting and translocation	
Pc22g02070	strong similarity to clathrin coat assembly protein CLAPS3 - Homo sapiens	6e-57	BX842596_1	Neurospora crassa DNA linkage group II BAC clone B10K17;	125.3	108.6	61.4	69.9	0.0	05 PROTEIN SYNTHESIS	
Pc22g07060	similarity to v-SNARE Vti1 - Saccharomyces cerevisiae	1e-24	T40349	vesicle transport v-snare protein - fission yeast (Schizosaccha	425.4	415.4	251.7	194.3	1e-112	08.13 vacuolar transport	
Pc22g13950	strong similarity to vacuolar aminopeptidase Ysci - Saccharomyces cerevisiae	1e-170	NCB13O20_13	gene: "B13O20.180"; product: "related to aminopeptidase ysc	815.1	768.1	404.3	392.2	1e-157	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc12g14430	strong similarity to vacuolar H(+) Ca(2+) exchanger Vcx1 - Saccharomyces cerevisiae	7e-82	AF053229_1	gene: "cax"; product: "calcium/proton exchanger"; Neurospo	252.5	118.6	195.7	88.3	1e-48	01.04.07 phosphate transport	
Pc12g16390	strong similarity to ABC-type vacuolar membrane protein hmt1p - Schizosaccharomyces pombe	1e-139	S25198	vacuolar membrane protein HMT1 - fission yeast (Schizosacc	91.7	101.7	53.6	37.7	3e-75	01.01 amino acid metabolism	
Pc15g01380	similarity to tetracyclin resistance protein tetA - Escherichia coli	1e-11	AB3073	tetracycline resistance protein [imported] - Agrobacterium tun	37.0	12.0	12.0	12.0	2e-54	01.05.07 C-compound, carbohydrate transport	
Pc16g03630	strong similarity to choline permease Hnm1 - Saccharomyces cerevisiae	1e-41	BX649605_108	gene: "gabA"; product: "GabA permease, putative"; Aspergill	54.2	12.0	22.0	18.5	1e-143	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS	
Pc16g12540	strong similarity to hypothetical transport protein YCR023c - Saccharomyces cerevisiae	0.0	BX649607_29	product: "possible transporter-like protein"; Aspergillus fumig	51.6	39.0	19.0	17.5	3e-43	08.19 cellular import	
Pc18g04170	strong similarity to ABC-type vacuolar membrane protein hmt1p - Schizosaccharomyces pombe	0.0	S25198	vacuolar membrane protein HMT1 - fission yeast (Schizosacc	1002.1	1034.4	716.9	400.7	1e-52	01.05.07 C-compound, carbohydrate transport	
Pc18g05180	strong similarity to high affinity copper transporter ctr4p - Schizosaccharomyces pombe	3e-39	PAN303117_1	gene: "ctr3"; product: "high affinity copper transporter"; Podo	312.4	198.1	98.6	106.3	0.0	01 METABOLISM	
Pc20g10660	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae	4e-90	BX649607_11	gene: "mdR"; product: "mfs-family multidrug resistance protei	55.9	36.1	22.6	13.9	4e-79	03.03.01.01 mitotic cell cycle	
Pc21g02720	strong similarity to calcium-transporting ATPase Pmc1 - Saccharomyces cerevisiae	0.0	NCB19A17_31	gene: "B19A17.310"; product: "putative calcium p-type ATPas	293.9	229.8	296.7	143.9	2e-57	04 TRANSCRIPTION	
Pc21g07990	weak similarity to kinesin Kif21b - Mus musculus	0.0	AY230423_1	gene: "KLP9"; product: "kinesin"; Botryotinia fuckeliana kine	109.2	83.5	48.9	27.8	1e-161	08.99 other intracellular transport activities	
Pc21g11550	strong similarity to GTP-binding protein rab4 - Homo sapiens	3e-47	T38030	ras-related protein - fission yeast (Schizosaccharomyces pon	177.1	125.1	75.2	78.5	0.0	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g13580	strong similarity to peptide transport protein Ptr2 - Saccharomyces cerevisiae	0.0	AY187281_1	product: "di/tri peptide transporter 2"; Phaeosphaeria nodorun	151.4	289.9	84.4	95.6	0.0	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g13720	ABC transporter sequence aa1 from patent WO200132904-A2 - Penicillium chrysogenum	0.0	AF071410_1	gene: "atrC"; product: "ATP-binding cassette multidrug transp	84.6	29.0	48.0	29.1	4e-96	13.01 ionic homeostasis	
Pc21g13720	Pc21g13720 ABC transporter sequence aa1 from patent WO200132904-A2 - Penicillium chrysogenum	0.0	AF071410_1	gene: "atrC"; product: "ATP-binding cassette multidrug transp	84.6	29.0	48.0	29.1	1e-149	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS	
Pc21g19890	strong similarity to Na(+) H(+) antiporter ZrSOD2-22 - Zygosaccharomyces rouxii	0.0	AY080962_2	gene: "25d9-2"; product: "Nha1p"; Aspergillus fumigatus Mvp	147.3	165.1	111.2	67.1	4e-49	01.05.07 C-compound, carbohydrate transport	
Pc21g20160	strong similarity to ABC-type vacuolar membrane protein hmt1p - Schizosaccharomyces pombe	0.0	S25198	vacuolar membrane protein HMT1 - fission yeast (Schizosacc	757.9	823.1	496.2	403.9	1e-134	67.04 ion transporters	
Pc21g20660	strong similarity to hypothetical amine transporter SPCC18.02 - Schizosaccharomyces pombe	1e-53	T41145	probable amine transporter - fission yeast (Schizosaccharomy	41.0	18.0	27.3	22.0	0.0	14.04.03.03 pheromone response, mating-type determination, sex-specific proteins	
Pc21g23380	strong similarity to mitochondrial tricarboxylate carrier - Rattus sp.	3e-94	S67168	probable membrane protein YOR271c - yeast (Saccharomyce	318.7	292.3	202.0	131.7	1e-105	08.13 vacuolar transport	
Pc21g23740	strong similarity to oligopeptide transporter Opt1 - Saccharomyces cerevisiae	1e-133	T38497	hypothetical protein SPAC29B12.10c - fission yeast (Schizos	56.2	66.0	37.4	31.7	6e-47	40.03 cytoplasm	
Pc22g09350	strong similarity to vacuolar H(+) Ca(2+) exchanger Vcx1 - Saccharomyces cerevisiae	3e-86	AF053229_1	gene: "cax"; product: "calcium/proton exchanger"; Neurospo	166.1	125.3	65.8	27.7	1e-100	01.04 phosphate metabolism	
Pc22g21840	weak similarity to transport protein Uso1 - Saccharomyces cerevisiae	3e-09	T18296	myosin heavy chain - Entamoeba histolytica	144.1	129.7	76.5	60.0	4e-27	06.07 protein modification	
Pc12g07850	strong similarity to neuronal protein kinase C PKC1B - Caenorhabditis elegans	1e-156	AF283107_1	product: "protein kinase C-like protein"; Blumeria graminis prc	75.1	65.1	43.7	26.5	1e-61	04.05.01.04 transcriptional control	
Pc16g09460	similarity to G protein alpha chain like protein An02g08000 - Aspergillus niger	2e-08	AF142058_1	gene: "ganA"; product: "G protein alpha subunit homolog Gar	26.9	20.9	12.0	12.0	3e-63	02.11 electron transport and membrane-associated energy conservation	
Pc20g13090	strong similarity to GTPase activating protein Gyp7 - Saccharomyces cerevisiae	0.0	NCB2F7_2	gene: "B2F7.020"; product: "probable GTPase activating prote	260.4	255.4	135.6	102.7	2e-70	01.04 phosphate metabolism	
Pc21g07360	strong similarity to G-protein beta subunit-interacting protein BDM-1 - Cryphonectria parasitica	4e-32	AF140555_1	gene: "bdm-1"; product: "phosducin"; Cryphonectria parasitica	87.9	68.1	43.8	40.5	0		0
Pc22g01860	similarity to stress activated protein kinase JNK3 - Rattus norvegicus	3e-14	AY437641_1	gene: "ST1"; product: "serine/threonine kinase"; Leptosphaer	27.7	25.1	12.0	12.0	0		0
Pc22g12210	strong similarity to integral membrane protein like protein An04g06980 - Aspergillus niger	2e-06	BX649605_15	product: "integral membrane protein, putative"; Aspergillus fu	113.0	85.9	96.9	12.0	0		0
Pc12g14800	weak similarity to kanamycin kinase - Enterococcus faecalis	0	0		43.7	12.0	22.1	12.0	0		0
Pc13g06780	similarity to integral membrane protein PTH11 - Magnaporthe grisea	1e-24	AF119672_1	gene: "PTH11"; product: "integral membrane protein"; Magna	31.3	105.2	12.0	12.0	4e-96	01.02.01.07 nitric oxide biosynthesis	
Pc16g12190	strong similarity to integral membrane protein PTH11 - Magnaporthe grisea	2e-30	NCB7H23_13	gene: "B7H23.130"; product: "related to L-fucose permease";	868.9	401.8	262.8	157.7	3e-67	01.05.07 C-compound, carbohydrate transport	
Pc20g08070	strong similarity to MAP kinase kinase EMK1 - Glomerella cingulata	1e-131	BGR304830_1	gene: "bek1"; product: "mitogen-activated protein kinase kina	128.2	112.9	87.7	49.5	1e-116	01.01.01.07 biosynthesis of the aspartate family	
Pc20g15050	strong similarity to hypothetical MFS multidrug efflux transporter - Schizosaccharomyces pombe	2e-41	ACH487683_1	gene: "cefT"; product: "multidrug resistant protein"; Acremon	537.3	598.4	406.9	161.3	0		0
Pc20g15540	strong similarity to D-amino-acid oxidase DAO - Fusarium solani	3e-35	T40989	probable d-amino acid oxidase - fission yeast (Schizosacchar	51.2	66.1	25.7	12.0	0		0
Pc21g01270	weak similarity to hard surface induced protein 3 chip3 - Glomerella cingulata	9e-91	BX897673_7	gene: "B13M15.070"; product: "related to hard surface induce	36.3	36.6	35.2	12.0	4e-15	01.05.07 C-compound, carbohydrate transport	
Pc21g06280	similarity to immunoreactive Antigen 2 Ag2 - Coccidioides immitis	1e-16	JC4589	immunoreactive protein precursor - Coccidioides immitis	493.2	30.4	35.5	57.1	0		0
Pc21g10610	similarity to cercosporin transporter CFP - Cercospora kikuchii [putative pseudogene]	1e-13	AF238225_1	gene: "Bcmfs1"; product: "DHA14-like major facilitator"; Botr	69.2	74.3	39.6	25.6	5e-84	01.01.99 other amino acid metabolism activities	
Pc21g13160	weak similarity to kanamycin kinase - Enterococcus faecalis	6e-04	PKSOJF	kanamycin kinase (EC 2.7.1.95) - Enterococcus faecalis plas	179.1	206.9	97.4	83.9	0		0
Pc22g00860	strong similarity to cytochrome-c peroxidase precursor Ccp1 - Saccharomyces cerevisiae	3e-72	AY363612_1	gene: "CCP1"; product: "mitochondrial cytochrome c peroxida	62.6	12.0	12.0	12.0	0		0
Pc22g05290	strong similarity to kanamycin kinase type like protein An15g02610 - Aspergillus niger	5e-04	AP005040_72	product: "hypothetical protein"; Streptomyces avermitilis gen	76.4	66.8	38.1	52.3	9e-46	67.28 drug transporters	
Pc22g06220	similarity to integral membrane protein PTH11 - Magnaporthe grisea	2e-13	AF119670_1	gene: "PTH11"; product: "integral membrane protein"; Magna	620.1	732.1	294.6	382.6	4e-76	13.01.01.99 homeostasis of other cations	
Pc22g09730	similarity to Pichia farinosa killer toxin resistance protein Pkr1 - Saccharomyces cerevisiae	4e-10	S54492	probable membrane protein YMR123w - yeast (Saccharomyc	149.2	178.3	73.2	87.1	5e-53	02.11 electron transport and membrane-associated energy conservation	
Pc12g15510	strong similarity to iron and manganese transporter Ccc1 - Saccharomyces cerevisiae	5e-37	S43453	CCC1 protein - yeast (Saccharomyces cerevisiae)	30.4	12.0	14.4	12.0	0.0	01 METABOLISM	
Pc12g16520	strong similarity to phosducin homolog Plp2 - Saccharomyces cerevisiae	6e-37	S67183	hypothetical protein YOR281c - yeast (Saccharomyces cerev	1338.3	1318.3	429.2	340.1	6e-68	01.05 C-compound and carbohydrate metabolism	
Pc13g12970	strong similarity to calcium-transporting ATPase Pmc1 - Saccharomyces cerevisiae	0.0	BX897676_11	gene: "B8I24.110"; product: "putative calcium P-type ATPase	50.3	46.1	32.0	13.1	1e-113	11.05.03 defense related proteins	
Pc16g12410	similarity to SUN family protein su1p - Schizosaccharomyces pombe	1e-118	BX649607_26	product: "SUN family protein, putative"; Aspergillus fumigatus	278.7	294.8	115.8	76.0	1e-112	01.20.35.02 biosynthesis of thyroids	
Pc20g05860	strong similarity to ferric cupric reductase Fre2 - Saccharomyces cerevisiae	1e-158	AF515629_1	gene: "freA"; product: "metalloreductase"; Emericella nidulans	66.4	13.6	28.4	23.9	4e-75	08 CELLULAR TRANSPORT AND TRANSPORT MECHANISMS	
Pc21g08040	similarity to ferric cupric reductase Fre2 - Saccharomyces cerevisiae	2e-31	AF515629_1	gene: "freA"; product: "metalloreductase"; Emericella nidulans	64.6	19.9	16.4	21.6	0		0
Pc21g08750	strong similarity to drainin phgA - Dictyostelium discoideum	4e-51	S62494	probable GTPase-activator protein of Rab-like small GTPases	101.3	89.7	88.0	43.9	2e-37	03.03.01 mitotic cell cycle and cell cycle control	
Pc22g21210	strong similarity to mucin like protein An02g02730 - Aspergillus niger	0	0		52.4	42.8	18.8	19.5	0		0
Pc13g15710	strong similarity to protein involved in actin distribution and bipolar budding Rsv167 - Saccharomyces cerevisiae	1e-138	NC5F3_6	gene: "5F3.060"; product: "probable RVS167 protein"; Neuro	277.9	294.2	208.3	143.9	2e-50	01.05 C-compound and carbohydrate metabolism	
Pc16g14270	similarity to heterokaryon incompatibility protein het-6 - Neurospora crassa	4e-11	NCB12N19_3	gene: "B12N19.040"; product: "related to heterokaryon incom	207.2	116.9	189.3	93.8	5e-87	01.05 C-compound and carbohydrate metabolism	
Pc20g03280	similarity to morphogenesis-related protein Msb1 - Saccharomyces cerevisiae	1e-19	S13759	morphogenesis-related protein MSB1 - yeast (Saccharomyce	81.8	43.4	33.6	26.1	4e-65	01.04 phosphate metabolism	
Pc21g11160	strong similarity to nuclear and nucleolar protein Nop14 - Saccharomyces cerevisiae	7e-97	T40394	conserved hypothetical protein SPBC3F6.04c - fission yeast (	74.8	71.2	55.7	28.2	3e-40	06.04 protein targeting, sorting and translocation	

Pc22g04120	weak similarity to MAPKK kinase nrc-1 - Neurospora crassa	2e-10	AY437641_1	gene: "ST1"; product: "serine/threonine kinase"; Leptosphaer	217.6	148.1	56.1	57.1	0.0	03.03.01 mitotic cell cycle and cell cycle control	
Pc12g15890	strong similarity to cAMP-independent repressor of ste11 expression ac2p - Schizosaccharomyces pombe	6e-46	S55723	camp independent regulatory protein - fission yeast (Schizosa	93.2	90.0	54.9	31.3	4e-40	01.04 phosphate metabolism	
Pc13g07910	strong similarity to protein pescadillo - Homo sapiens	0.0	BX842638_7	gene: "G17B7.070"; product: "related to pescadillo developme	107.0	80.1	85.7	34.4	1e-134	06.04 protein targeting, sorting and translocation	
Pc21g05960	weak similarity to glia maturation factor BmGMF - Brugia malayi	2e-14	T37877	cofilin/tropomyosin-type actin binding protein - fission yeast (S	31.1	36.6	12.0	19.7	0		0
Pc22g05200	strong similarity to embryogenesis protein H beta 58 - Mus musculus	1e-109	T38872	probable vacuolar sorting protein - fission yeast (Schizosacch	749.7	523.6	367.9	338.2	0		0
Pc06g02270	weak similarity to LTR-containing retrotransposable elements MARS1 - Ascobolus immersus	1e-04	S71892	RNA-directed DNA polymerase (EC 2.7.7.49) homolog Mars1	44.1	30.0	12.7	12.0	0		0
Pc06g02300	weak similarity to reverse transcriptase homolog - Bombyx mori	0	0	0	12.0	12.0	12.0	12.0	0		0
Pc12g02900	strong similarity to transposase Tan1 - Aspergillus niger [putative pseudogene]	1e-40	ENAC133_2	product: "ORF"; Emericella nidulans cosmid SW06E08, com	135.0	86.7	72.1	26.9	0.0	03.01.03 DNA synthesis and replication	
Pc12g03890	strong similarity to protein encoded by ORF1 of transposon Ant1 - Aspergillus niger	1e-134	AB072434_1	gene: "tnpA"; product: "putative transposase"; Aspergillus ory	117.0	110.3	46.2	49.9	0.0	03.01.03 DNA synthesis and replication	
Pc13g00330	strong similarity to LTR-containing retrotransposable elements MARS1 - Ascobolus immersus [putative pseudogene]	8e-59	S71892	RNA-directed DNA polymerase (EC 2.7.7.49) homolog Mars1	117.7	90.6	59.0	31.3	0		0
Pc16g15280	strong similarity to LTR-containing retrotransposable elements MARS1 - Ascobolus immersus [putative sequencing error]	4e-72	S71892	RNA-directed DNA polymerase (EC 2.7.7.49) homolog Mars1	128.6	110.1	158.3	60.7	3e-94	01.05.01 C-compound and carbohydrate utilization	
Pc18g02520	weak similarity to transposase of Tan1 - Aspergillus niger	8e-09	ENAC133_2	product: "ORF"; Emericella nidulans cosmid SW06E08, com	49.8	47.7	28.0	22.5	1e-121	03.01.05.03 DNA recombination	
Pc20g08660	strong similarity to transposase Tan1 - Aspergillus niger [putative pseudogene]	1e-157	ENAC133_2	product: "ORF"; Emericella nidulans cosmid SW06E08, com	23.9	12.0	12.0	12.0	6e-67	03 CELL CYCLE AND DNA PROCESSING	
Pc21g00540	similarity to transposase Minos-2 - Drosophila hydei	7e-77	AF282722_1	product: "transposase"; Fusarium oxysporum f. sp. melonis	100.8	88.5	47.5	56.2	1e-154	03.01.03 DNA synthesis and replication	
Pc20g01100	strong similarity to huntingtin interacting protein 1 HIF-1 - Homo sapiens	1e-115	T38490	hypothetical protein SPAC29B12.02c - fission yeast (Schizos	22.0	25.5	21.3	12.0	3e-73	06.04 protein targeting, sorting and translocation	
Pc21g14330	strong similarity to nucleolar protein like protein An16g01500 - Aspergillus niger	1e-146	T40814	probable nucleolar protein-NOL1-NOP2-sun family - fission ye	127.3	115.4	94.3	38.1	1e-62	04.05.05 mRNA processing (splicing, 5'-, 3'-end processing)	
Pc22g05040	strong similarity to component of the translocase of mitochondrial inner membrane Tim54 - Saccharomyces cerevisiae	5e-73	AF343072_1	gene: "tim54"; product: "TIM54"; Neurospora crassa TIM54 (t	102.5	95.6	64.4	42.7	7e-67	06.07 protein modification	
Pc12g05330	similarity to RNA processing factor Pcf11 - Saccharomyces cerevisiae	3e-67	T38863	hypothetical protein SPAC4G9.04c - fission yeast (Schizosac	95.8	96.0	65.1	47.8	6e-36	03.03.02 meiosis	
Pc12g16070	similarity to myosin heavy chain - Gallus gallus	1e-156	AF365926_1	product: "calmodulin-binding coil-coil protein"; Aspergillus nid	140.9	106.4	69.5	54.4	2e-53	06.07 protein modification	
Pc13g06070	strong similarity to nucleolar phosphoprotein like protein An14g00890 - Aspergillus niger	4e-05	SPAC11E3_3	gene: "pcs1"; "SPAC11E3.03"; S.pombe chromosome I cos	121.3	102.0	67.0	50.1	2e-52	40.03 cytoplasm	
Pc13g08720	similarity to myosin heavy chain - Gallus gallus	0.0	BX649605_22	product: "myosin heavy chain-like protein, putative"; Aspergil	105.0	97.6	67.6	42.8	0		0
Pc13g09040	strong similarity to myosin II heavy chain like protein An02g07380 - Aspergillus niger	2e-21	T39082	hypothetical protein SPAC7D4.04 - fission yeast (Schizosacc	120.8	78.7	39.1	36.3	2e-70	20.25.01.03 hearing	
Pc16g01090	similarity to hypothetical coiled-coil protein cgrA - Aspergillus nidulans	2e-17	AY008837_1	gene: "cgrA"; product: "CGRA"; Aspergillus fumigatus CGRA	245.7	246.8	202.4	114.2	0		0
Pc16g03390	similarity to poly(A)-binding protein interacting factor Pbp1 - Saccharomyces cerevisiae	1e-61	NCB15I20_7	gene: "B15I20.100"; product: "conserved hypothetical protein"	72.0	52.0	45.1	20.8	4e-82	03 CELL CYCLE AND DNA PROCESSING	
Pc18g02390	strong similarity to laminin A like protein An18g04250 - Aspergillus niger	0	0	0	71.4	71.9	40.5	16.6	1e-99	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc20g06990	strong similarity to chromosome segregation protein Smc1 - Saccharomyces cerevisiae	0.0	NC12F11_4	gene: "12F11.040"; product: "related to SMC1 protein"; Neur	207.5	173.5	98.7	101.8	3e-90	05 PROTEIN SYNTHESIS	
Pc21g08730	strong similarity to unconventional myosin heavy chain like protein An13g01180 - Aspergillus niger	2e-31	BC041628_1	product: "KIAA1010 protein"; Homo sapiens scaffold protein	105.1	93.8	52.8	42.0	2e-88	40.03 cytoplasm	
Pc21g19190	similarity to Golgi membrane protein Emp47 - Saccharomyces cerevisiae	3e-14	AY296117_1	Ixodes scapularis mannose-binding endoplasmic reticulum-G	300.1	266.2	150.0	159.6	1e-124	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc22g02290	similarity to nuclear pore complex associated protein TPR - Homo sapiens	0.0	BX897679_4	gene: "B2C22.040"; product: "related to nucleoprotein TPR";	231.6	234.6	160.5	116.3	7e-90	40.02 plasma membrane	
Pc24g02530	similarity to ankyrin Ank1 - Mus musculus	8e-24	S37431	ankyrin 2, neuronal long splice form - human	137.8	131.5	84.8	23.3	1e-110	01.06.13 lipid and fatty-acid transport	
Pc12g11760	strong similarity to high density lipoprotein-binding protein like protein An02g02410 - Aspergillus niger	2e-30	T40039	hypothetical protein SPAC9B6.13 - fission yeast (Schizosacc	182.6	185.5	109.3	89.1	9e-69	01.01.07 amino acid transport	
Pc12g12710	strong similarity to multidrug resistance ABC transporter like protein An02g04910 - Aspergillus niger	4e-82	AP004398_8	gene: "P0438G07.112-1"; product: "putative ABC transporter	92.9	186.2	29.0	26.6	7e-72	01.01.07 amino acid transport	
Pc15g01370	strong similarity to hypothetical neutral amino acid permease - Neurospora crassa	1e-119	S47892	neutral amino acid permease - Neurospora crassa	38.0	14.8	12.0	12.0	8e-67	08.19 cellular import	
Pc20g13430	strong similarity to hypothetical neutral amino acid permease - Neurospora crassa	5e-66	S47892	neutral amino acid permease - Neurospora crassa	42.8	36.8	15.5	18.2	3e-66	01.01.07 amino acid transport	
Pc21g08030	strong similarity to hypothetical plasma membrane iron permease - Schizosaccharomyces pombe	1e-100	CPU428490_1	gene: "cpit1"; product: "putative iron transferase"; Claviceps	29.3	12.0	13.1	12.0	9e-43	99 UNCLASSIFIED PROTEINS	
Pc22g06500	strong similarity to hypothetical neutral amino acid permease - Neurospora crassa	5e-59	S47892	neutral amino acid permease - Neurospora crassa	650.5	323.6	95.4	190.2	0		0
Pc03g00180	strong similarity to hypothetical Ydr124wp-like protein - Pneumocystis carinii	7e-21	AF309805_4	product: "Ydr124wp-like protein"; Pneumocystis carinii f. sp.	81.4	58.2	29.3	14.9	0		0
Pc03g00200	strong similarity to hypothetical protein An14g02320 - Aspergillus niger	0	0	0	35.3	39.2	37.5	13.6	3e-57	01.05 C-compound and carbohydrate metabolism	
Pc06g00410	hypothetical protein	0	0	0	115.8	141.8	51.6	35.1	6e-32	06.07 protein modification	
Pc06g00480	strong similarity to hypothetical protein contig46_part_ii.tfa_2410wg - Aspergillus fumigatus	1e-59	ENAC133_1	product: "ORF"; Emericella nidulans cosmid SW06E08, com	126.1	105.4	62.2	54.6	4e-98	30.04 cytoskeleton	
Pc06g00750	strong similarity to hypothetical protein An01g13240 - Aspergillus niger	4e-16	BX842597_14	Neurospora crassa DNA linkage group II BAC clone B22K18.	57.8	41.6	22.1	13.7	0		0
Pc06g00880	weak similarity to hypothetical protein An06g02110 - Aspergillus niger	7e-15	AK025859_1	unnamed ORF; Homo sapiens cDNA: FLJ22206 fis, clone HI	24.9	31.1	14.8	12.0	0		0
Pc06g01330	strong similarity to hypothetical protein contig202.tfa_250wg - Aspergillus fumigatus [putative pseudogene]	0	0	0	28.6	44.5	12.0	12.0	1e-112	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc06g01510	similarity to hypothetical protein AAM35689.1 - Xanthomonas axonopodis	4e-24	BX649607_31	product: "hypothetical protein, conserved"; Aspergillus fumiga	55.3	36.4	25.7	12.0	0		0
Pc06g01520	strong similarity to hypothetical protein 1323_scaffold_5.tfa_400cg - Fusarium graminearum	1e-76	AY102575_7	gene: "TRI11"; product: "trichothecene C-15 hydroxylase"; G	52.6	31.0	19.0	12.0	8e-41	06.01 protein folding and stabilization	
Pc06g01710	hypothetical protein	0	0	0	40.2	38.9	14.1	12.0	0		0
Pc06g01750	strong similarity to hypothetical protein contig46_part_ii.tfa_1580cg - Aspergillus fumigatus	6e-13	A81837	probable dnaJ-family protein NMA1461 [imported] - Neisseria	180.2	131.8	56.7	52.3	0		0
Pc06g01870	similarity to hypothetical protein CAD21276.1 - Neurospora crassa	3e-10	AF532169_1	gene: "esdC"; product: "ESDC"; Aspergillus nidulans ESDC	57.0	45.7	26.4	18.2	0		0
Pc06g01940	weak similarity to hypothetical protein ncu07834.1 - Neurospora crassa	0	0	0	57.7	38.5	28.7	31.7	0		0
Pc09g00090	hypothetical protein	0	0	0	34.3	27.1	12.0	12.0	0		0
Pc09g00170	hypothetical protein	0	0	0	110.5	43.3	29.8	27.3	4e-78	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc09g00180	strong similarity to hypothetical protein 1190_scaffold_2.tfa_540wg - Fusarium graminearum	0	0	0	38.2	34.2	17.8	15.6	0		0
Pc12g00510	strong similarity to hypothetical protein CAD21095.1 - Neurospora crassa	8e-57	BX842627_18	gene: "B8J22.180"; product: "related to calcium-independent	37.0	34.0	13.4	21.0	0		0
Pc12g00560	strong similarity to hypothetical verprolin related protein encoded by B24P7.40 - Neurospora crassa	1e-100	T50949	verprolin related protein [imported] - Neurospora crassa	1047.4	449.2	479.8	270.6	0		0
Pc12g00730	similarity to hypothetical protein contig1492_0.tfa_2140cg - Aspergillus fumigatus	0	0	0	57.1	47.7	19.2	14.3	0		0
Pc12g00750	similarity to hypothetical protein An09g03650 - Aspergillus niger	0	0	0	44.1	96.7	29.4	28.2	0		0
Pc12g00980	strong similarity to hypothetical 2,3-cyclic-nucleotide 3-phosphodiesterase related protein - Neurospora crassa	6e-22	NCB3E4_23	gene: "B3E4.310"; product: "related to 2', 3'-cyclic-nucleotide	108.0	97.5	42.4	25.1	0		0
Pc12g00990	strong similarity to hypothetical protein ncu09633.1 - Neurospora crassa	2e-32	T49617	hypothetical protein B3E4.300 [imported] - Neurospora crassa	41.4	39.1	13.4	12.0	1e-78	06.13 proteolytic degradation	
Pc12g01260	strong similarity to hypothetical bHLH transcription factor hpa3 - Aspergillus nidulans	4e-90	ENI269479_1	gene: "hpa3"; product: "putative bHLH transcription factor"; E	233.7	288.8	220.1	143.4	0		0
Pc12g01270	strong similarity to hypothetical protein contig_1_129_scaffold_10.tfa_1010cg - Aspergillus nidulans	7e-08	A49227	sialidase - Actinomyces viscosus	47.6	35.7	17.9	13.7	0		0
Pc12g01620	similarity to hypothetical C2H2-type zinc-finger protein - Schizosaccharomyces pombe	1e-18	T40660	hypothetical C2H2-type zinc-finger protein - fission yeast (Sch	171.8	159.2	110.5	71.5	0		0
Pc12g02490	similarity to hypothetical protein SPAC23H3.04 - Schizosaccharomyces pombe	4e-19	BX842682_15	gene: "B13C5.150"; product: "conserved hypothetical protein"	89.6	118.2	50.2	36.6	0		0
Pc12g02910	hypothetical protein	0	0	0	983.7	1044.6	575.7	240.9	0		0
Pc12g03000	strong similarity to hypothetical protein An16g07260 - Aspergillus niger	0	0	0	332.9	223.3	77.3	72.8	0		0
Pc12g03400	strong similarity to hypothetical protein B23L4.080 - Neurospora crassa	1e-43	BX842628_8	gene: "B23L4.080"; product: "conserved hypothetical protein"	207.7	202.0	87.4	54.1	0		0
Pc12g03590	weak similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus	4e-04	NCB14A6_15	gene: "B14A6.150"; product: "hypothetical protein"; Neurosp	60.4	27.9	40.6	21.2	0		0
Pc12g03720	similarity to hypothetical protein An09g06370 - Aspergillus niger	0	0	0	59.6	46.1	30.7	19.1	8e-58	01.01.07 amino acid transport	
Pc12g03820	hypothetical protein	0	0	0	57.3	12.0	16.6	12.0	0		0
Pc12g04190	strong similarity to hypothetical protein SPBC16A3.10 - Schizosaccharomyces pombe	1e-108	T39542	hypothetical protein SPBC16A3.10 - fission yeast (Schizosac	502.2	437.4	192.1	202.9	7e-70	03 CELL CYCLE AND DNA PROCESSING	
Pc12g04320	strong similarity to hypothetical protein An15g00400 - Aspergillus niger	1e-15	NCB20D17_4	gene: "B20D17.040"; product: "hypothetical protein"; Neuros	153.7	119.2	75.1	83.3	5e-89	99 UNCLASSIFIED PROTEINS	
Pc12g04630	strong similarity to hypothetical protein ncu00113.1 - Neurospora crassa	5e-75	YWBYM	tryptophan-tRNA ligase (EC 6.1.1.2), mitochondrial - yeast (S	33.7	12.5	16.7	15.5	0		0
Pc12g05070	similarity to hypothetical protein Fun19 - Saccharomyces cerevisiae	4e-42	BX842681_2	gene: "B13N4.020"; product: "conserved hypothetical protein"	627.0	571.6	250.8	175.5	0		0
Pc12g05150	strong similarity to hypothetical conserved protein B13I18.30 - Neurospora crassa	1e-148	NCB13I18_3	gene: "B13I18.30"; product: "conserved hypothetical protein";	247.6	215.3	123.6	127.5	0		0
Pc12g05500	similarity to hypothetical protein B13I18.100 - Neurospora crassa	1e-13	NCB13I18_10	gene: "B13I18.100"; product: "hypothetical protein"; Neurosp	430.8	219.2	172.4	125.9	6e-37	08.16 extracellular transport, exocytosis and secretion	
Pc12g06240	strong similarity to hypothetical protein An07g02740 - Aspergillus niger	0	0	0	42.6	40.6	28.5	18.4	0		0
Pc12g06480	strong similarity to hypothetical protein SPBC12C2.09c - Schizosaccharomyces pombe	1e-38	AE003739_24	product: "CG5315-PA"; "CG5315-PC"; Drosophila melanogas	48.2	39.3	19.1	20.8	3e-51	03.03.01 mitotic cell cycle and cell cycle control	
Pc12g06490	similarity to hypothetical protein contig_1_108_scaffold_7.tfa_130wg - Aspergillus nidulans [putative pseudogene]	0	0	0	36.9	18.3	18.5	12.0	0		0
Pc12g06770	strong similarity to hypothetical protein SPAC4F10.21 - Schizosaccharomyces pombe	1e-95	SPAC19B12_1	gene: "SPAC4F10.21"; "SPAC19B12.01"; S.pombe chromos	54.7	52.5	52.9	22.5	4e-82	14.10.02 apoptosis (type I programmed cell death)	
Pc12g06950	weak similarity to hypothetical protein PA2336 - Pseudomonas aeruginosa	2e-35	AP005021_230	product: "hypothetical protein"; Streptomyces avermitilis gen	29.3	31.0	14.6	14.5	0		0
Pc12g07160	strong similarity to hypothetical beta transducin-like protein het-e1 - Podospora anserina	6e-66	AF323585_1	gene: "het-d"; product: "beta transducin-like protein HET-D2Y	122.4	105.1	62.7	50.1	2e-59	10.05 transmembrane signal transduction	
Pc12g07360	strong similarity to hypothetical protein contig31_part_center.tfa_110wg - Aspergillus fumigatus	1e-34	T49641	nebula related protein [imported] - Neurospora crassa	254.6	179.2	211.7	91.0	0		0
Pc12g07590	strong similarity to hypothetical protein B5O22.250 - Neurospora crassa	0.0	T49643	hypothetical protein B5O22.250 [imported] - Neurospora crass	42.5	43.2	32.5	21.4	0		0
Pc12g07640	similarity to hypothetical protein An04g09580 - Aspergillus niger	0	0	0	48.0	27.3	21.6	21.4	3e-30	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc12g07780	strong similarity to hypothetical endo alpha-1,4 polygalactosaminidase precusor - Pseudomonas sp.	3e-65	NCB19A17_15	gene: "B19A17.150"; product: "hypothetical protein"; Neuros	41.9	33.1	12.0	12.0	0		0
Pc12g08130	similarity to DNA-directed RNA polymerase II largest chain - Mastigamoeba invertens	2e-12	T31670	DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain -	305.7	307.7	177.0	136.6	1e-156	04 TRANSCRIPTION	
Pc12g08280	strong similarity to hypothetical protein An07g01340 - Aspergillus niger	0	0	0	1629.5	767.9	1028.3	186.2	2e-58	01 METABOLISM	
Pc12g08420	similarity to hypothetical protein SPCC645.13 - Schizosaccharomyces pombe	2e-35	T41530	hypothetical protein SPCC645.13 - fission yeast (Schizosacc	160.4	139.3	81.1	59.1	2e-77	04.05 mRNA transcription	
Pc12g08960	weak similarity to hypothetical short chain dehydrogenase SPCC736.13 - Schizosaccharomyces pombe	1e-09	AY458632_11	product: "oxidoreductase, short-chain dehydrogenase/reducta	178.6	212.0	31.5	55.0	1e-42	01 METABOLISM	
Pc12g10310	strong similarity to hypothetical protein contig_1_32_scaffold_2.tfa_760wg - Aspergillus nidulans	1e-127	BX842627_8	gene: "B8J22.090"; product: "related to hnRNP protein E2";	216.2	195.9	158.8	97.7	0		0
Pc12g10460	strong similarity to hypothetical protein An11g04830 - Aspergillus niger	1e-06	AY164486_1	gene: "Pkd1l3"; product: "polycystic kidney disease 1-like 3";	72.7	66.9	36.1	28.8	0		0
Pc12g10790	hypothetical protein	0	0	0	40.7	32.6	12.0	12.0	0.0	06.13.01 cytoplasmic and nuclear degradation	
Pc12g10860	strong similarity to hypothetical protein An11g04410 - Aspergillus niger	0	0	0	268.4	232.2	116.0	112.2	5e-25	04.05 mRNA transcription	
Pc12g10930	strong similarity to hypothetical protein SPAC4F10.07c - Schizosaccharomyces pombe	1e-26	T38811	hypothetical protein SPAC4F10.07c - fission yeast (Schizosa	41.8	26.8	20.4	12.0	1e-42	01.05 C-compound and carbohydrate metabolism	
Pc12g10950	strong similarity to ssRNA-binding protein DdRBP1 - Dictyostelium discoideum	2e-30	T38159	probable RNA-binding protein - fission yeast (Schizosaccharo	134.4	128.5	87.2	56.6	1e-96	02.11.05 accessory proteins of electron transport and membrane-associated energy conservation	
Pc12g11180	strong similarity to hypothetical protein contig1496_7.tfa_160wg - Aspergillus fumigatus	4e-07	AF136223_1	product: "M3.4 protein"; Brassica napus M3.4 protein gene,	270.2	299.9	214.2	124.7	1e-126	20.25.16 immune response	
Pc12g11420	similarity to hypothetical AAA-ATPase AAR34299.1 - Geobacter sulfurreducens	5e-16	AE017145_167	product: "predicted ATPase (AAA-family)"; Helicobacter hepa	29.3	12.3	17.6	12.0	0		0
Pc12g12340	strong similarity to hypothetical protein contig_1_40_scaffold_2.tfa_50wg - Aspergillus nidulans	5e-61	AY033935_1	product: "annexin XIV-like protein"; Aspergillus niger annexin	176.7	201.2	140.3	91.7	0		0
Pc12g12550	similarity to hypothetical protein An02g05100 - Aspergillus niger	0	0	0	315.8	386.4	242.1	135.6	0		0
Pc12g12590	similarity to hypothetical protein An02g05120 - Aspergillus niger	0	0	0	44.2	12.0	23.8	12.0	0		0
Pc12g12600	weak similarity to hypothetical protein An02g05060 - Aspergillus niger [truncated ORF]	0	0	0	17.9	33.5	12.0	12.0	0		0
Pc12g12610	strong similarity to hypothetical protein An02g05060 - Aspergillus niger [truncated ORF]	0	0	0	20.1	42.2	12.0	12.0	3e-48	05.04 translation	
Pc12g12700	strong similarity to hypothetical protein contig31_part_ii.tfa_770wg - Aspergillus fumigatus	0	0	0	271.5	234.9	127.0	66.8	4e-45	99 UNCLASSIFIED PROTEINS	
Pc12g13050	strong similarity to hypothetical protein contig31_part_ii.tfa_980wg - Aspergillus fumigatus	1e-10	AE003584_29	product: "CG31671-PA"; Drosophila melanogaster chromoso	65.7	65.9	46.9	19.2	0		0
Pc12g13970	strong similarity to hypothetical protein An14g03160 - Aspergillus niger	1e-12	S30833	hypothetical protein YEL044w - yeast (Saccharomyces cerev	133.4	139.1	85.5	62.2	4e-35	03.03.01.01.11 mitosis	
Pc12g14230	weak similarity to hypothetical protein ncu09676.1 - Neurospora crassa	4e-08	NC64C2_21	gene: "64C2.220"; product: "conserved hypothetical protein";	83.8	73.5	38.8	38.8	0		0
Pc12g15320	similarity to hypothetical protein An08g04120 - Aspergillus niger	3e-07	AE014849_34	product: "hypothetical protein"; Plasmodium falciparum 3D7	295.8	157.9	137.5	72.8	4e-65	01.04 phosphate metabolism	
Pc12g15360	hypothetical protein	0	0	0	70.1	137.9	87.2	17.8	7e-41	06.13 proteolytic degradation	
Pc12g15460	similarity to hypothetical protein An09g02520 - Aspergillus niger	2e-12	AY437641_1	gene: "ST1"; product: "serine/threonine kinase"; Leptosphaer	71.7	84.5	46.3	33.7	0		0
Pc12g16140	strong similarity to essential protein like protein An16g02950 - Aspergillus niger	4e-27	T40010	hypothetical protein SPBC25H2.15 - fission yeast (Schizosac	138.4	139.4	110.0	63.0	0		0
Pc12g16210	strong similarity to hypothetical protein contig589.tfa_940cg - Aspergillus fumigatus	0	0	0	34.9	31.1	12.0	12.0	1e-40	01 METABOLISM	
Pc12g16410	weak similarity to hypothetical protein contig_1_79_scaffold_5.tfa_330wg - Aspergillus nidulans	0	0	0	594.7	606.7	317.5	174.1	1e-117	99 UNCLASSIFIED PROTEINS	
Pc12g16550	strong similarity to hypothetical phosphatidyl synthase SPAC22A12.08c - Schizosaccharomyces pombe	1e-106	BX842636_11	gene: "7C14.110"; product: "conserved hypothetical protein";	728.9	694.7	265.0	269.9	0		0
Pc12g16560	similarity to hypothetical protein YDR306c - Saccharomyces cerevisiae	1e-22	S61192	hypothetical protein YDR306c - yeast (Saccharomyces cerev	234.3	221.9	44.9	73.5	0		0
Pc12g16570	hypothetical protein	0	0	0	32.7	25.9	12.0	12.0	0		0

Pc13g00030	weak similarity to hypothetical protein An01g07930 - Aspergillus niger	0	0	0	158.3	95.1	69.5	61.6	0		0
Pc13g00280	hypothetical protein	0	0	0	118.3	82.3	55.6	56.5	0		0
Pc13g00640	strong similarity to hypothetical protein ncu00832.1 - Neurospora crassa	0	0	0	64.5	54.1	58.1	27.5	0		0
Pc13g00730	strong similarity to hypothetical protein contig5_part_ii.tfa_1400wg - Aspergillus fumigatus	0	0	0	116.0	167.5	77.4	35.3	6e-80	14.04 cell differentiation	
Pc13g00820	strong similarity to hypothetical protein contig_1_153_scaffold_12.tfa_240wg - Aspergillus nidulans	0	0	0	98.8	96.5	38.7	38.2	9e-39	99 UNCLASSIFIED PROTEINS	
Pc13g00980	weak similarity to hypothetical protein BAB55393.1 - Homo sapiens	1e-08	BX897677_20	gene: "B15B10.180"; product: "hypothetical protein"; Neuros	333.2	481.5	325.6	224.6	2e-38	11.05.05 virulence, disease factors	
Pc13g01470	similarity to hypothetical protein SPAC12G12.02 - Schizosaccharomyces pombe	7e-11	T37599	hypothetical protein SPAC12G12.02 - fission yeast (Schizosa	134.2	129.6	106.7	50.1	0		0
Pc13g01640	weak similarity to hypothetical protein SPAC24C9.05c - Schizosaccharomyces pombe	7e-63	T38346	hypothetical protein SPAC24C9.05c - fission yeast (Schizosa	536.8	554.8	302.9	246.2	2e-43	01.03 nucleotide metabolism	
Pc13g02070	strong similarity to hypothetical protein contig_1_26_scaffold_2.tfa_460cg - Aspergillus nidulans	0	0	0	479.0	171.0	136.3	124.8	8e-30	01.04 phosphate metabolism	
Pc13g02190	strong similarity to hypothetical UDP-galactose 4-epimerase - Mesorhizobium loti	2e-78	B97596	UDP-glucose-4-epimerase [imported] - Agrobacterium tumefa	74.8	44.9	35.2	42.4	0		0
Pc13g02380	strong similarity to hypothetical protein contig_1_68_scaffold_4.tfa_200cg - Aspergillus nidulans	3e-18	BX842624_9	gene: "B10D6.090"; product: "related to putative cytoplasmic	66.6	56.4	40.3	23.1	0		0
Pc13g03020	strong similarity to hypothetical protein An03g03340 - Aspergillus niger	0	0	0	96.9	88.2	46.2	65.5	0.0	10.01.99 other intracellular signal transduction activities	
Pc13g03040	hypothetical protein	0	0	0	82.6	83.1	33.9	34.3	0		0
Pc13g03430	strong similarity to hypothetical protein Kre33 - Saccharomyces cerevisiae	0.0	S55151	probable membrane protein YNL132w - yeast (Saccharomyce	173.0	153.4	97.7	58.9	1e-140	08.13 vacuolar transport	
Pc13g03450	strong similarity to hypothetical mixed-linked glucanase precursor related protein MLG1 - Neurospora crassa	1e-72	U81606_1	gene: "MLG1"; product: "mixed-linked glucanase precursor";	63.8	12.0	12.0	12.0	0		0
Pc13g03810	strong similarity to hypothetical protein contig31_part_i.tfa_890cg - Aspergillus fumigatus	2e-20	T40913	probable integral membrane protein - fission yeast (Schizosac	124.9	84.6	59.1	48.2	0		0
Pc13g03980	strong similarity to hypothetical protein An12g04010 - Aspergillus niger	3e-04	AF133696_1	gene: "bigA"; product: "putative surface-exposed virulence pro	419.6	390.5	262.6	181.8	0		0
Pc13g04190	strong similarity to hypothetical protein of the paxilline biosynthesis gene cluster paxU - Penicillium paxilli	1e-123	AF279808_7	gene: "paxU"; product: "PaxU"; Penicillium paxilli dimethylall	28.1	12.0	12.3	12.0	1e-99	06.04 protein targeting, sorting and translocation	
Pc13g04460	strong similarity to hypothetical protein contig_1_89_scaffold_6.tfa_690wg - Aspergillus nidulans	2e-07	BX842638_16	gene: "G17B7.160"; product: "putative protein"; Neurospora c	153.2	138.1	83.2	54.4	0		0
Pc13g04790	similarity to protein CG33196-PB - Drosophila melanogaster	2e-48	AE003576_35	product: "CG33196-PB"; Drosophila melanogaster chromoso	49.2	44.3	36.1	16.9	0		0
Pc13g04830	similarity to hypothetical protein An05g00600 - Aspergillus niger	0	0	0	23.8	24.6	12.1	12.0	3e-52	01.05 C-compound and carbohydrate metabolism	
Pc13g07350	strong similarity to hypothetical protein contig1492_0.tfa_6190cg - Aspergillus fumigatus	1e-104	AY281368_1	gene: "cip2"; product: "Cip2"; Hypocrea jecorina strain QM6a	18.5	47.5	43.6	14.3	0		0
Pc13g07600	strong similarity to hypothetical protein contig1488_2.tfa_850cg - Aspergillus fumigatus	2e-06	AY164486_1	gene: "Pkd1l3"; product: "polycystic kidney disease 1-like 3";	58.7	51.6	31.7	18.9	0		0
Pc13g08140	strong similarity to hypothetical protein contig1488_2.tfa_1050cg - Aspergillus fumigatus	4e-13	NCB9K17_10	gene: "B9K17.090"; product: "conserved hypothetical protein"	1283.0	545.1	806.6	561.1	0		0
Pc13g08150	similarity to hypothetical protein An04g03190 - Aspergillus niger	0	0	0	349.8	126.0	219.4	139.4	0		0
Pc13g08160	hypothetical protein	0	0	0	80.6	42.5	56.8	26.5	0		0
Pc13g09010	strong similarity to hypothetical protein An02g07410 - Aspergillus niger	0	0	0	280.7	249.9	146.5	99.5	0		0
Pc13g09060	strong similarity to hypothetical protein contig336.tfa_610wg - Aspergillus fumigatus	1e-04	AB083477_1	gene: "Pclo"; product: "Piccolo"; Mus musculus Pclo mRNA	103.1	92.0	50.1	50.7	0		0
Pc13g09280	strong similarity to hypothetical protein An02g06790 - Aspergillus niger	2e-12	CNS09S4S_42	DNA centromeric region sequence from BAC DP26B06, DP34	18.1	37.3	12.0	12.0	1e-94	14.04 cell differentiation	
Pc13g09400	strong similarity to hypothetical protein An02g06900 - Aspergillus niger	2e-14	CNS09S4S_56	DNA centromeric region sequence from BAC DP26B06, DP34	40.4	35.2	22.8	15.8	0		0
Pc13g09820	similarity to hypothetical protein F17H10.1 - Caenorhabditis elegans	1e-17	T21079	hypothetical protein F17H10.1 - Caenorhabditis elegans	786.3	456.5	214.1	142.9	0		0
Pc13g10170	weak similarity to hypothetical protein B8I24.160 - Neurospora crassa	8e-04	AF345640_1	gene: "Mybbp1a"; product: "myb-binding protein 1a"; Mus mu	60.7	50.5	31.9	18.7	0		0
Pc13g10220	strong similarity to hypothetical protein An15g06870 - Aspergillus niger	0	0	0	132.5	106.0	72.7	44.1	0		0
Pc13g10380	strong similarity to hypothetical protein An16g04440 - Aspergillus niger	0	0	0	67.2	54.5	30.1	32.8	0		0
Pc13g10610	strong similarity to hypothetical protein An16g03980 - Aspergillus niger	8e-45	BX908811_2	gene: "H4H7.020"; product: "putative protein"; Neurospora cr	245.4	239.9	261.0	116.8	0		0
Pc13g10720	hypothetical protein	0	0	0	171.8	173.7	115.2	68.7	0		0
Pc13g10840	strong similarity to hypothetical transcription factor IIIc-like protein CAE47909.1 - Aspergillus fumigatus	1e-117	BX649605_60	product: "possible transcription factor IIIc-like protein"; Asper	69.5	52.5	40.4	23.1	0		0
Pc13g10980	strong similarity to hypothetical protein An08g03680 - Aspergillus niger	4e-45	BX649605_48	product: "hypothetical protein, putative"; Aspergillus fumigatus	287.0	217.6	101.8	88.6	0		0
Pc13g11260	strong similarity to hypothetical protein contig_1_51_scaffold_3.tfa_100cg - Aspergillus nidulans	2e-05	AP002996_159	gene: "mll1065"; Mesorhizobium loti DNA, complete genome	28.8	12.0	12.0	12.0	0		0
Pc13g11360	strong similarity to hypothetical protein - Aspergillus fumigatus	6e-25	BX649606_23	product: "hypothetical protein"; Aspergillus fumigatus BAC pil	79.0	81.1	95.5	42.5	0		0
Pc13g11600	similarity to hypothetical protein An01g11780 - Aspergillus niger	5e-06	BX571859_231	Photorhabdus luminescens subsp. laumondii TTO1 complete	53.1	54.2	28.1	20.2	1e-140	98 CLASSIFICATION NOT YET CLEAR-CUT	
Pc13g11620	strong similarity to hypothetical protein - Aspergillus fumigatus	1e-114	BX649606_30	product: "hypothetical protein"; Aspergillus fumigatus BAC pil	93.5	41.8	64.5	63.1	0		0
Pc13g12370	strong similarity to hypothetical protein YLR063w - Saccharomyces cerevisiae	1e-107	BX649606_97	product: "hypothetical protein"; Aspergillus fumigatus BAC pil	56.0	55.5	44.1	21.9	0		0
Pc13g13090	hypothetical protein	0	0	0	118.1	133.6	84.3	57.6	0		0
Pc13g13230	strong similarity to hypothetical protein 99H12.80 - Neurospora crassa	1e-76	BX649605_117	product: "hypothetical protein, conserved"; Aspergillus fumiga	185.0	170.3	198.0	88.9	3e-31	01.04 phosphate metabolism	
Pc13g13310	hypothetical protein	0	0	0	116.1	96.3	94.6	12.0	3e-50	04.01.04 rRNA processing	
Pc13g13430	similarity to serine-repeat antigen 4 - Plasmodium vivax	2e-14	T30841	serine-repeat antigen 4 - Plasmodium vivax	55.3	45.0	29.0	12.0	0		0
Pc13g13570	strong similarity to hypothetical protein SPAC9B6.07 - Schizosaccharomyces pombe	3e-21	T40788	hypothetical protein SPAC9B6.07 - fission yeast (Schizosacc	79.3	89.8	84.7	41.5	4e-39	01.05.01.01.01 sugar, glucoside, polyol and carboxylate catabolism	
Pc13g14080	similarity to hypothetical protein An03g01740 - Aspergillus niger	2e-07	NCB19A17_10	gene: "B19A17.100"; product: "hypothetical protein"; Neuros	43.0	46.9	12.0	12.0	0		0
Pc13g14090	similarity to hypothetical suppressor of bem1 bud5 bem46p - Schizosaccharomyces pombe	1e-19	BC002138_1	gene: "6330583M11Rik"; product: "6330583M11Rik protein";	158.4	130.4	61.3	132.1	1e-60	20.25.01.03 hearing	
Pc13g14120	strong similarity to hypothetical protein An02g09000 - Aspergillus niger	0	0	0	441.6	389.8	325.4	155.1	0		0
Pc13g14140	similarity to hypothetical protein An02g09010 - Aspergillus niger	4e-20	AE003576_35	product: "CG33196-PB"; Drosophila melanogaster chromoso	413.4	166.8	178.1	58.1	0		0
Pc13g14200	strong similarity to hypothetical protein contig61.tfa_880cg - Aspergillus fumigatus	6e-45	T49586	related to nif-specific regulatory protein [imported] - Neurospo	74.5	81.4	58.9	38.0	1e-113	99 UNCLASSIFIED PROTEINS	
Pc13g14240	similarity to hypothetical protein An02g09070 - Aspergillus niger	0	0	0	216.2	264.3	186.8	92.2	0		0
Pc13g14470	strong similarity to hypothetical protein YOR311c - Saccharomyces cerevisiae	1e-91	NCB9B11_21	gene: "B9B11.210"; product: "conserved hypothetical protein"	288.0	271.4	132.2	134.3	0		0
Pc13g14490	weak similarity to hypothetical protein contig61.tfa_980cg - Aspergillus fumigatus	0	0	0	140.2	135.0	72.2	43.8	0		0
Pc13g15240	strong similarity to hypothetical protein contig61.tfa_1670cg - Aspergillus fumigatus	2e-12	NCG65A3_5	gene: "G65A3.060"; product: "hypothetical protein"; Neurospo	91.0	62.5	35.1	21.2	0		0
Pc13g15250	strong similarity to hypothetical transcriptional activator ptaA - Aspergillus nidulans	6e-37	AF320977_1	gene: "ptaA"; product: "PTAA"; Aspergillus nidulans PTAA (p	39.1	39.2	23.3	16.0	0.0	03.01.03 DNA synthesis and replication	
Pc13g15370	strong similarity to hypothetical protein contig61.tfa_1360wg - Aspergillus fumigatus	0	0	0	197.8	309.9	223.3	49.5	0		0
Pc13g15480	strong similarity to hypothetical DNA replication licensing factor nimQ - Aspergillus nidulans	0.0	AF014813_1	gene: "nimQ"; product: "DNA replication licensing factor"; En	276.8	174.0	134.3	104.8	0		0
Pc13g15640	weak similarity to hypothetical protein Rv0276 - Mycobacterium tuberculosis	4e-09	AE017240_191	product: "hypothetical protein"; Mycobacterium avium subsp.	182.7	47.8	86.0	48.5	2e-34	01.04.07 phosphate transport	
Pc13g15660	strong similarity to hypothetical protein contig61.tfa_1610cg - Aspergillus fumigatus	0	0	0	173.8	12.0	29.4	23.5	1e-156	99 UNCLASSIFIED PROTEINS	
Pc14g00160	similarity to hypothetical monocarboxylate permease Esbp6 - Saccharomyces cerevisiae	3e-20	AE003696_41	gene: "kar"; product: "CG12286-PA"; Drosophila melanogast	30.0	12.0	13.5	12.0	2e-27	04.05.01.04 transcriptional control	
Pc14g00170	strong similarity to hypothetical protein contig1490_3.tfa_630cg - Aspergillus fumigatus	2e-92	AX952974_1	unnamed ORF; Sequence 2 from Patent WO03097825.	35.2	12.0	12.0	12.0	5e-73	14.04 cell differentiation	
Pc14g00700	strong similarity to hypothetical protein An01g00090 - Aspergillus niger	4e-09	AY327407_1	product: "hypothetical protein"; Homo sapiens hypothetical p	175.6	189.9	123.2	94.4	3e-53	99 UNCLASSIFIED PROTEINS	
Pc14g00850	strong similarity to hypothetical protein CGI-35 - Homo sapiens	6e-61	CNSLT1I98_1	unnamed ORF; human full-length cDNA clone CS0DC020YI1	273.1	302.6	203.0	146.3	1e-100	63.03 nucleic acid binding	
Pc14g00890	strong similarity to hypothetical conserved protein SPAC31A2.02 - Schizosaccharomyces pombe	4e-38	NC18F11_16	gene: "18F11.160"; product: "conserved hypothetical protein";	119.8	119.1	96.2	47.9	0		0
Pc14g01220	strong similarity to hypothetical protein YOR3513c - Saccharomyces cerevisiae	8e-83	SC130KBXV_60	gene: "YOR3513c"; S.cerevisiae 130kb DNA fragment from c	430.6	485.8	330.5	199.7	3e-74	99 UNCLASSIFIED PROTEINS	
Pc14g01480	similarity to hypothetical protein An18g06430 - Aspergillus niger	7e-04	AE014753_3	product: "hypothetical protein"; Bifidobacterium longum NCC2	529.6	395.0	291.9	144.2	8e-35	06.07 protein modification	
Pc14g01490	weak similarity to hypothetical protein YKL051w - Saccharomyces cerevisiae	2e-58	NCB2F7_3	gene: "B2F7.030"; product: "conserved hypothetical protein";	149.8	54.5	67.0	32.3	4e-49	04.05.01.04 transcriptional control	
Pc14g01540	strong similarity to hypothetical conserved protein encoded by B2F7.170 - Neurospora crassa	1e-24	NCB2F7_15	gene: "B2F7.170"; product: "conserved hypothetical protein";	205.9	153.1	74.7	33.7	5e-83	99 UNCLASSIFIED PROTEINS	
Pc14g01730	strong similarity to hypothetical protein contig_1_98_scaffold_6.tfa_1210cg - Aspergillus nidulans	7e-04	BC055247_1	gene: "zgc:63801"; product: "similar to eukaryotic translation	730.6	790.8	472.1	370.6	0		0
Pc14g01850	strong similarity to hypothetical protein contig1492_0.tfa_440wg - Aspergillus fumigatus [putative sequencing error]	1e-36	AC116977_25	product: "similar to Mus musculus (Mouse). hypothetical prot	182.9	162.5	88.4	93.3	0		0
Pc14g01970	strong similarity to hypothetical protein contig1492_0.tfa_520wg - Aspergillus fumigatus	1e-32	T51915	hypothetical protein B23I11.270 [imported] - Neurospora crass	149.7	135.3	74.5	64.6	0		0
Pc14g02100	hypothetical protein	0	0	0	69.6	62.3	77.0	32.7	0		0
Pc14g02120	strong similarity to hypothetical protein An05g02110 - Aspergillus niger	0	0	0	21.8	24.4	12.0	12.0	0		0
Pc15g00460	weak similarity to hypothetical protein contig127.tfa_110cg - Aspergillus fumigatus	0	0	0	43.7	18.2	16.6	12.0	0		0
Pc15g00950	weak similarity to hypothetical protein SPCC645.13 - Schizosaccharomyces pombe	0	0	0	55.2	32.3	12.0	16.1	4e-53	01.03.16.01 RNA degradation	
Pc15g01220	strong similarity to hypothetical protein contig1487_1.tfa_1750wg - Aspergillus fumigatus	0	0	0	384.5	277.9	105.5	89.7	0		0
Pc15g01230	strong similarity to hypothetical protein az0aa013d09d1 - Kluyveromyces marxianus	8e-28	AF410318_1	product: "AT4g24770/F22K18_30"; Arabidopsis thaliana AT4	413.6	417.8	348.2	163.1	5e-83	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc15g01530	hypothetical protein	0	0	0	316.1	432.5	153.6	157.2	0		0
Pc16g00680	strong similarity to lipase - Penicillium allii	1e-151	AY303124_1	gene: "lipPA"; product: "lipase"; Penicillium allii lipase (lipPA)	95.1	16.6	36.1	12.0	0		0
Pc16g00970	similarity to hypothetical protein B14D6.5 - Neurospora crassa	3e-05	T49505	hypothetical protein B14D6.570 [imported] - Neurospora crass	61.3	48.9	29.2	15.6	1e-78	99 UNCLASSIFIED PROTEINS	
Pc16g01810	similarity to hypothetical protein contig46_part_i.tfa_70cg - Aspergillus fumigatus	0	0	0	48.0	38.2	23.4	21.3	6e-65	99 UNCLASSIFIED PROTEINS	
Pc16g01820	strong similarity to hypothetical protein An08g00280 - Aspergillus niger	1e-66	NCB24N11_10	gene: "B24N11.100"; product: "conserved hypothetical protein	153.3	175.8	118.4	85.7	1e-108	05.04 translation	
Pc16g02370	similarity to hypothetical protein SPBC16E9.02c - Schizosaccharomyces pombe	2e-15	T39577	hypothetical protein SPBC16E9.02c - fission yeast (Schizosa	367.3	328.4	187.4	137.0	2e-49	04 TRANSCRIPTION	
Pc16g02480	strong similarity to hypothetical branched-chain alpha-ketoacid dehydrogenase E1 beta subunit - Homo sapiens	2e-97	T48720	translation initiation factor 3 (47 kDa subunit) related protein [	444.9	461.8	244.0	190.8	0		0
Pc16g02560	strong similarity to hypothetical protein 1A9.260 - Neurospora crassa	3e-35	NC1A9_15	gene: "1A9.220"; product: "conserved hypothetical protein"; I	355.3	341.4	232.9	158.5	0		0
Pc16g02920	hypothetical protein	0	0	0	33.4	13.9	19.3	12.0	0		0
Pc16g03130	strong similarity to hypothetical protein 1190_scaffold_2.tfa_540wg - Fusarium graminearum	0	0	0	132.5	155.3	141.5	28.9	4e-92	14.04 cell differentiation	
Pc16g03220	strong similarity to hypothetical protein An09g03750 - Aspergillus niger	0	0	0	459.7	847.3	388.5	150.9	1e-115	08.16 extracellular transport, exocytosis and secretion	
Pc16g03970	strong similarity to hypothetical conserved protein SPCP1E11.11 - Schizosaccharomyces pombe	5e-81	T41690	conserved hypothetical protein SPCP1E11.11 - fission yeast	130.2	124.4	119.8	49.5	0		0
Pc16g04160	strong similarity to hypothetical protein YER006w - Saccharomyces cerevisiae	1e-105	S50464	hypothetical protein YER006w - yeast (Saccharomyces cerev	256.5	231.4	171.2	90.3	1e-101	40.03 cytoplasm	
Pc16g04360	similarity to hypothetical protein SPAC23H3.04 - Schizosaccharomyces pombe	2e-42	BX842682_15	gene: "B13C5.150"; product: "conserved hypothetical protein"	70.3	38.6	24.4	12.0	0		0
Pc16g05460	weak similarity to S-layer protein CipA - Clostridium thermocellum	1e-27	T18262	S-layer protein - Clostridium thermocellum	478.2	404.5	186.2	83.6	0		0
Pc16g06240	similarity to hypothetical protein contig50.tfa_270cg - Aspergillus fumigatus	0	0	0	128.2	83.6	41.7	22.1	8e-53	01.05 C-compound and carbohydrate metabolism	
Pc16g06280	hypothetical protein	8e-04	AF221108_1	gene: "larp"; product: "La related protein"; Drosophila melano	192.7	194.4	121.6	94.4	0		0
Pc16g06290	strong similarity to hypothetical protein contig46_part_i.tfa_740wg - Aspergillus fumigatus	4e-10	SPAC1527_3	gene: "SPAC1527.03"; S.pombe chromosome I cosmid c152	75.0	80.4	49.2	39.0	0		0
Pc16g06580	weak similarity to hypothetical protein SPAC15A10.09c - Schizosaccharomyces pombe	1e-63	NCB11H24_7	gene: "B11H24.070"; product: "conserved hypothetical protein	83.9	79.8	77.5	38.1	0.0	99 UNCLASSIFIED PROTEINS	
Pc16g06710	similarity to glutamyl endoprotease polypeptide like protein An12g06130 - Aspergillus niger	0	0	0	63.8	29.2	43.4	38.0	0		0
Pc16g07520	strong similarity to hypothetical protein YKR089c - Saccharomyces cerevisiae	1e-169	CNS07TIX_9	DNA centromeric region sequence from BAC DP15B03, DP38	169.1	136.5	73.1	59.8	0		0
Pc16g07730	strong similarity to hypothetical protein An04g03640 - Aspergillus niger	0	0	0	148.3	116.2	70.2	60.9	0		0
Pc16g07750	strong similarity to hypothetical protein contig1488_2.tfa_1420wg - Aspergillus fumigatus	8e-05	LME430204_1	gene: "dsrE"; product: "dextransucrase"; Leuconostoc meser	61.5	55.7	67.5	32.6	0		0
Pc16g07960	weak similarity to hypothetical protein spar_3045 - Saccharomyces paradoxus	2e-04	AB095187_1	gene: "RPB1"; product: "DNA-directed RNA polymerase II larg	34.8	27.3	19.3	12.0	0		0
Pc16g08010	hypothetical protein	0	0	0	38.7	35.8	18.9	12.0	1e-89	03.01.05.01 DNA repair	
Pc16g08810	strong similarity to hypothetical protein contig_1_7_scaffold_1.tfa_730wg - Aspergillus nidulans	1e-06	T31670	DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain -	1010.0	479.7	478.1	215.5	1e-62	13.07 cell adhesion	
Pc16g09000	similarity to hypothetical coiled-coil protein - Schizosaccharomyces pombe	6e-51	S49634	hypothetical protein YML093w - yeast (Saccharomyces cerev	76.6	73.8	64.2	24.7	6e-63	99 UNCLASSIFIED PROTEINS	
Pc16g09290	strong similarity to hypothetical zf-C3HC4 zinc finger protein - Schizosaccharomyces pombe	9e-93	BX842682_16	gene: "B13C5.160"; product: "conserved hypothetical protein"	414.7	371.4	190.7	160.7	2e-71	63.03 nucleic acid binding	
Pc16g09300	similarity to hypothetical protein YKL051w - Saccharomyces cerevisiae	6e-28	NCB2F7_3	gene: "B2F7.030"; product: "conserved hypothetical protein";	115.4	93.0	86.6	42.8	5e-60	06.04 protein targeting, sorting and translocation	
Pc16g09620	strong similarity to hypothetical protein pi029 - Schizosaccharomyces pombe	1e-167	BX842633_11	gene: "53H1.110"; product: "related to MRD1"; Neurospora c	174.3	150.1	124.8	55.5	9e-47	01.20 secondary metabolism	
Pc16g09840	strong similarity to hypothetical protein SPAC926.06c - Schizosaccharomyces pombe	2e-76	T39204	hypothetical protein SPAC926.06c - fission yeast (Schizosac	571.8	517.7	300.0	170.8	4e-50	01.20 secondary metabolism	
Pc16g09900	strong similarity to cDNA O-methyltransferase mt-I - Aspergillus parasiticus	7e-46	BX908810_7	gene: "G3C5.070"; product: "related to O-methyltransferase";	282.2	138.0	127.7	46.9	7e-26	03.03.01.01 mitotic cell cycle	
Pc16g09910	strong similarity to cDNA O-methyltransferase mt-I - Aspergillus parasiticus	9e-54	AF159789_1	gene: "omtB"; product: "O-methyltransferase B"; Aspergillus	322.1	175.9	155.0	133.3	0		0
Pc16g10600	strong similarity to hypothetical protein An12g04840 - Aspergillus niger	3e-04	AB053470_1	gene: "ELKS"; product: "ELKS delta"; Homo sapiens mRNA	134.0	121.4	77.4	42.8	0		0

Pc16g10730	similarity to hypothetical protein contig12.tfa_260wg - Aspergillus fumigatus	0	0	0	89.3	36.1	36.1	15.3	1e-47	03.03.01.01.11 mitosis	
Pc16g11580	hypothetical protein	0	0	0	137.4	74.5	31.8	29.8		0	0
Pc16g12330	similarity to hypothetical protein YNL124w - Saccharomyces cerevisiae	1e-101	BX649607_20	product: "hypothetical protein, conserved"; Aspergillus fumiga	29.9	24.1	12.0	12.0		0	0
Pc16g12480	similarity to hypothetical protein AAM35689.1 - Xanthomonas axonopodis	1e-147	BX649607_31	product: "hypothetical protein, conserved"; Aspergillus fumiga	36.9	64.7	42.7	24.9		0	0
Pc16g12590	strong similarity to hypothetical protein - Aspergillus fumigatus	4e-46	BX649607_38	product: "hypothetical protein"; Aspergillus fumigatus BAC pil	91.7	68.9	76.7	14.1	6e-87	40 SUBCELLULAR LOCALISATION	
Pc16g13040	strong similarity to hypothetical protein contig46_part_ii.tfa_780wg - Aspergillus fumigatus	1e-77	BX649607_81	product: "possible secreted cellulose-binding protein"; Asper	30.7	26.5	12.0	12.0		0	0
Pc16g13080	strong similarity to hypothetical protein F12L6.11 - Arabidopsis thaliana	0.0	BX649607_82	product: "possible cation efflux protein"; Aspergillus fumigatus	199.2	201.2	111.6	91.6		0	0
Pc16g13380	similarity to hypothetical protein mg05230.1 - Magnaporthe grisea	0	0	0	124.1	137.2	80.9	62.9	1e-115	01.04 phosphate metabolism	
Pc16g13550	weak similarity to hypothetical protein - Streptomyces avermitilis	3e-09	AP005045_235	product: "hypothetical protein"; Streptomyces avermitilis gen	126.7	118.3	82.7	54.3	2e-46	99 UNCLASSIFIED PROTEINS	
Pc16g13600	strong similarity to hypothetical protein kinase Kin3 - Saccharomyces cerevisiae	0.0	BX842682_3	gene: "B13C5.030"; product: "related to ser/thr protein kinase	177.0	135.5	96.1	64.3	2e-81	03 CELL CYCLE AND DNA PROCESSING	
Pc16g14160	similarity to hypothetical protein SMb20606 - Sinorhizobium meliloti	2e-16	BX572605_171	product: "conserved hypothetical protein"; Rhodopseudomona	197.9	287.7	162.9	101.2		0	0
Pc16g14620	strong similarity to hypothetical protein contig46_part_ii.tfa_1920wg - Aspergillus fumigatus	2e-97	NCB9B15_17	gene: "B9B15.200"; product: "related to 26S proteasome-ass	148.1	141.8	69.3	107.4		0	0
Pc16g15040	strong similarity to hypothetical protein contig_1_116_scaffold_8.tfa_60wg - Aspergillus nidulans	0	0	0	44.5	29.7	12.0	12.0		0	0
Pc16g15460	hypothetical protein	0	0	0	290.7	658.5	295.3	99.7	1e-136	04.05.01.04 transcriptional control	
Pc17g00090	weak similarity to hypothetical protein An09g01040 - Aspergillus niger [truncated ORF][putative pseudogene]	0	0	0	41.8	21.3	13.5	15.5		0	0
Pc17g00150	similarity to hypothetical transposase - Tolypocladium inflatum [truncated ORF][putative pseudogene]	3e-28	TIRESTLES_1	gene: "tnp"; product: "putative transposase"; T.inflatum transp	156.7	141.7	112.3	62.7		0	0
Pc17g00210	hypothetical protein	0	0	0	31.8	12.0	12.0	12.0		0	0
Pc17g00420	hypothetical protein	0	0	0	91.0	74.0	37.9	31.2		0	0
Pc17g00680	hypothetical protein	0	0	0	24.6	30.9	19.6	12.0		0	0
Pc17g00780	hypothetical protein	1e-04	T37193	enamelin matrix protein - mouse	1868.7	1820.6	1248.3	651.3		0	0
Pc17g01180	hypothetical protein	0	0	0	31.8	12.0	12.0	12.0		0	0
Pc17g01240	weak similarity to hypothetical protein contig36.tfa_140wg - Aspergillus fumigatus [truncated ORF][putative sequencing error]	0	0	0	70.1	73.4	41.0	36.5	2e-75	01.07.01 biosynthesis of vitamins, cofactors, and prosthetic groups	
Pc18g00880	strong similarity to hypothetical transcription regulator meaB - Aspergillus nidulans	1e-104	ANMEABG_1	gene: "meaB"; product: "MEAB protein"; Aspegillus nidulans	382.5	386.9	303.4	183.0	3e-36	01.01.04 regulation of amino acid metabolism	
Pc18g00980	strong similarity to hypothetical trunk lateral cell specific gene HrTLC1 - Halocynthia roretzi	0.0	NCB23G1_21	gene: "B23G1.210"; product: "conserved hypothetical protein"	594.3	428.8	524.4	235.1		0	0
Pc18g01480	strong similarity to putative transcriptional regulator CAF32162.1 - Aspergillus fumigatus	3e-25	BX649607_85	product: "transcriptional regulator, putative"; Aspergillus fumi	33.9	25.8	14.1	16.0	9e-46	03 CELL CYCLE AND DNA PROCESSING	
Pc18g01680	similarity to hypothetical protein An02g08040 - Aspergillus niger	0	0	0	36.6	29.6	12.0	12.0	0.0	01.05 C-compound and carbohydrate metabolism	
Pc18g02200	strong similarity to hypothetical protein contig_1_66_scaffold_4.tfa_140cg - Aspergillus nidulans	2e-06	AK081667_1	Mus musculus 16 days embryo head cDNA, RIKEN full-lengt	137.5	61.6	42.1	19.7		0	0
Pc18g02760	strong similarity to hypothetical aldehyde dehydrogenase CAB63554.1 - Schizosaccharomyces pombe	1e-164	T50272	probable aldehyde dehydrogenase [imported] - fission yeast (	482.1	313.1	141.7	179.1	2e-58	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc18g03070	similarity to hypothetical protein SPAC6F6.17 - Schizosaccharomyces pombe	4e-36	AY034033_1	gene: "tap1"; product: "Tap1"; Schizosaccharomyces pombe	160.6	145.2	64.7	58.5	3e-38	05.01 ribosome biogenesis	
Pc18g03270	strong similarity to sperm tail-specific protein like protein An18g05650 - Aspergillus niger	5e-05	S37907	hypothetical protein YKL082c - yeast (Saccharomyces cerevi	157.3	147.3	95.3	43.8		0	0
Pc18g03440	strong similarity to hypothetical protein contig1488_2.tfa_1500cg - Aspergillus fumigatus	2e-06	S14050	ribosomal protein YmL25, mitochondrial - yeast (Saccharomy	108.4	104.5	75.7	51.4	4e-62	03.03.01 mitotic cell cycle and cell cycle control	
Pc18g03770	weak similarity to hypothetical protein contig589.tfa_560cg - Aspergillus fumigatus	0	0	0	44.6	41.8	12.0	12.0		0	0
Pc18g03890	strong similarity to hypothetical protein An07g07810 - Aspergillus niger	7e-14	PFMAL13_585	gene: "MAL13P1.302"; product: "hypothetical protein"; Plasm	119.4	88.6	64.9	41.7	1e-45	01.05 C-compound and carbohydrate metabolism	
Pc18g03960	weak similarity to hypothetical protein HRIHFB2072 - Homo sapiens	0	0	0	127.2	106.9	54.1	45.8	8e-70	14.10.02.02.01 apoptotic mitochondrial changes	
Pc18g04150	strong similarity to hypothetical protein ncu08637.1 - Neurospora crassa	3e-10	CEAF3131_1	gene: "unc-89"; product: "Uncoordinated protein 89, isoform b	89.0	109.5	63.2	33.3		0	0
Pc18g04160	strong similarity to polypeptide sequence like protein An07g07480 - Aspergillus niger [putative sequencing error]	1e-46	T38840	hypothetical trp-asp repeats containing protein - fission yeast	293.7	205.3	133.2	87.7		0	0
Pc18g04450	strong similarity to hypothetical protein contig1492_0.tfa_580wg - Aspergillus fumigatus	3e-04	AK093494_1	unnamed ORF; Homo sapiens cDNA FLJ36175 fis, clone TE	1833.4	1058.9	843.8	625.7		0	0
Pc18g04750	strong similarity to hypothetical protein contig589.tfa_60wg - Aspergillus fumigatus	0	0	0	55.2	42.1	26.5	20.8	2e-44	63.17.09 heavy metal binding (Cu, Fe, Zn)	
Pc18g04810	strong similarity to hypothetical protein An07g07140 - Aspergillus niger	7e-04	AF350448_1	product: "envelope glycoprotein precursor"; Crimean-Congo h	196.0	149.3	68.0	50.0	2e-39	06.10 assembly of protein complexes	
Pc18g04840	strong similarity to Yippee like protein An07g07170 - Aspergillus niger	2e-25	BC050664_1	product: "hypothetical protein MGC10500"; Homo sapiens hy	272.3	262.5	152.2	108.5		0	0
Pc18g05260	similarity to Nbp2 - Saccharomyces cerevisiae	4e-10	S57986	NBP2 protein - yeast (Saccharomyces cerevisiae)	95.5	80.2	51.7	36.7		0	0
Pc18g05650	strong similarity to hypothetical protein An07g09260 - Aspergillus niger	0	0	0	104.8	60.5	22.8	24.1		0	0
Pc18g05810	strong similarity to hypothetical protein An07g09090 - Aspergillus niger	0	0	0	91.0	34.9	41.7	37.6		0	0
Pc18g05990	similarity to hypothetical protein SPAC26A3.14c - Schizosaccharomyces pombe	3e-04	T38402	hypothetical protein SPAC26A3.14c - fission yeast (Schizosa	38.6	33.5	12.0	14.6		0	0
Pc18g06400	similarity to hypothetical protein An07g08620 - Aspergillus niger	7e-06	AF155773_22	gene: "ORF21"; product: "ORF21 protein"; Gibberella monilifo	59.4	65.0	43.1	29.5		0	0
Pc18g06660	hypothetical protein	0	0	0	169.7	136.5	50.7	94.7		0	0
Pc19g00590	hypothetical protein	0	0	0	134.8	106.7	29.7	28.2	3e-92	14.04 cell differentiation	
Pc19g00680	hypothetical protein	0	0	0	66.8	12.0	12.0	12.0	4e-73	01 METABOLISM	
Pc19g00750	similarity to hypothetical protein - Oryza sativa	3e-21	AP002071_11	Oryza sativa (japonica cultivar-group) genomic DNA, chromos	29.6	18.7	12.0	12.0		0	0
Pc20g01160	strong similarity to hypothetical protein mg04979.1 - Magnaporthe grisea	4e-44	SCSMP3_1	gene: "SMP3"; product: "SMP3 protein"; S.cerevisiae SMP3	46.3	33.0	25.2	14.6		0	0
Pc20g01260	similarity to hypothetical protein AAK58053.1 - Ophiostoma novo-ulmi	2e-14	AF378550_1	product: "unknown"; Ophiostoma novo-ulmi clone 13 unknow	79.3	92.1	32.8	26.4		0	0
Pc20g01380	strong similarity to hypothetical protein An07g01650 - Aspergillus niger	0	0	0	37.4	38.0	20.2	12.1		0	0
Pc20g01490	strong similarity to hypothetical protein An07g02040 - Aspergillus niger	0	0	0	69.3	61.7	13.1	17.0		0	0
Pc20g01510	strong similarity to hypothetical protein An08g05278 - Aspergillus niger	0	0	0	126.3	69.1	49.5	31.0		0	0
Pc20g01570	similarity to hypothetical protein An07g02120 - Aspergillus niger	0	0	0	119.7	91.0	58.3	47.5	2e-63	06.01 protein folding and stabilization	
Pc20g01580	strong similarity to hypothetical protein CAD21228.1 - Neurospora crassa	0.0	AY522343_1	product: "HbrB"; Emericella nidulans HbrB gene, complete c	186.7	134.7	90.5	81.5	0.0	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc20g01600	similarity to hypothetical AAA-ATPase AAR34299.1 - Geobacter sulfurreducens	5e-17	AE017210_117	product: "ATPase, AAA family"; Geobacter sulfurreducens P	691.2	474.0	402.1	193.2		0	0
Pc20g01800	strong similarity to hypothetical protein contig42.tfa_690wg - Aspergillus fumigatus	1e-115	T52121	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal [validated] - Arab	438.6	118.1	125.4	230.9		0	0
Pc20g01950	strong similarity to hypothetical protein contig1492_0.tfa_3970wg - Aspergillus fumigatus	6e-05	SCARD1GN_8	gene: "ataP7"; product: "AtaP7 protein"; Saccharothrix mutab	93.1	72.8	59.5	34.2		0	0
Pc20g02060	strong similarity to hypothetical protein An02g13370 - Aspergillus niger	9e-72	BX842636_10	gene: "7C14.100"; product: "hypothetical protein"; Neurospor	107.6	101.8	60.8	41.8	2e-59	01.01.99 other amino acid metabolism activities	
Pc20g02150	strong similarity to hypothetical protein An02g13430 - Aspergillus niger	0	0	0	77.9	62.5	33.0	28.4	2e-55	03.01.03 DNA synthesis and replication	
Pc20g02780	strong similarity to hypothetical protein PA3829 - Pseudomonas aeruginosa	3e-60	B83167	hypothetical protein PA3829 [imported] - Pseudomonas aeru	31.1	12.0	12.0	12.0	7e-32	40 SUBCELLULAR LOCALISATION	
Pc20g02860	similarity to hypothetical myb-like DNA binding protein SPAC13G7.10 - Schizosaccharomyces pombe	3e-08	S67439	hypothetical protein SPAC13G7.10 - fission yeast (Schizosac	117.0	112.0	46.8	30.0		0	0
Pc20g03030	strong similarity to hypothetical protein contig1487_1.tfa_1020wg - Aspergillus fumigatus	5e-12	BX842641_13	gene: "B22I21.140"; product: "conserved hypothetical protein"	343.1	275.5	170.8	102.5	1e-155	98 CLASSIFICATION NOT YET CLEAR-CUT	
Pc20g03190	strong similarity to hypothetical protein An11g09750 - Aspergillus niger	0	0	0	102.0	104.3	66.7	14.2	3e-54	99 UNCLASSIFIED PROTEINS	
Pc20g03790	strong similarity to hypothetical protein SPBC1685.14c - Schizosaccharomyces pombe	0.0	SPBC1685_14	gene: "SPBC1685.14c"; S.pombe chromosome II cosmid c1	297.2	277.0	207.5	132.3		0	0
Pc20g04090	similarity to hypothetical protein YOR252w - Saccharomyces cerevisiae	1e-12	S67149	hypothetical protein YOR252w - yeast (Saccharomyces cere	178.0	145.6	103.3	68.6		0	0
Pc20g04190	weak similarity to hypothetical protein SPAC6B12.11 - Schizosaccharomyces pombe	0	0	0	96.4	87.7	63.4	43.4		0	0
Pc20g04290	hypothetical protein	0	0	0	34.4	48.7	19.4	17.6	4e-53	14.04 cell differentiation	
Pc20g04630	strong similarity to hypothetical protein contig_1_110_scaffold_8.tfa_760cg - Aspergillus nidulans	0	0	0	35.4	12.0	12.0	12.0		0	0
Pc20g04700	weak similarity to hypothetical protein F17H10.1 - Caenorhabditis elegans	7e-14	B97746	hypothetical protein RC0370 [imported] - Rickettsia conorii (s	31.7	12.0	12.0	12.0		0	0
Pc20g05020	weak similarity to hypothetical coiled-coil protein - Schizosaccharomyces pombe	4e-29	NCB7H23_23	gene: "B7H23.240"; product: "conserved hypothetical protein"	44.2	30.1	20.2	15.5	2e-30	05.01 ribosome biogenesis	
Pc20g05210	weak similarity to hypothetical protein ncu09167.1 - Neurospora crassa	0	0	0	48.5	22.8	25.3	12.0	2e-37	01.03.16.01 RNA degradation	
Pc20g05330	similarity to hypothetical mitochondrial ribosomal protein - Schizosaccharomyces pombe	1e-12	T41110	hypothetical protein SPCC1739.02c - fission yeast (Schizosa	277.7	287.5	174.8	133.1	1e-39	06.07 protein modification	
Pc20g05480	weak similarity to hypothetical forkhead nuclear signaling protein SPBC3H7.13 - Schizosaccharomyces pombe	7e-12	NCG65A3_6	gene: "G65A3.070"; product: "putative protein"; Neurospora c	819.7	662.3	337.1	256.7		0	0
Pc20g05610	strong similarity to hypothetical protein contig589.tfa_1510wg - Aspergillus fumigatus	3e-53	NC12F11_8	gene: "12F11.080"; product: "hypothetical protein"; Neurosp	68.9	75.4	33.5	32.7		0	0
Pc20g05970	similarity to hypothetical protein An02g12880 - Aspergillus niger	0	0	0	237.3	145.0	73.6	82.2		0	0
Pc20g05970	similarity to hypothetical protein An02g12880 - Aspergillus niger	0	0	0	237.3	145.0	73.6	82.2	1e-41	99 UNCLASSIFIED PROTEINS	
Pc20g06000	strong similarity to hypothetical protein An02g12840 - Aspergillus niger	0	0	0	58.7	47.5	22.8	29.0	3e-79	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc20g06220	similarity to hypothetical protein SPBC1734.10c - Schizosaccharomyces pombe	6e-08	T39657	hypothetical protein SPBC1734.10c - fission yeast (Schizosa	78.2	83.6	41.2	36.3		0	0
Pc20g06520	strong similarity to hypothetical protein ncu03285.1 - Neurospora crassa	1e-23	AC135207_3	gene: "OJ1261C08.3"; product: "SR-rich pre-mRNA splicing a	64.3	65.8	44.7	25.0	1e-49	03.03.01.01 mitotic cell cycle	
Pc20g07120	strong similarity to hypothetical protein An06g00470 - Aspergillus niger	0	0	0	345.4	165.6	94.4	146.4	2e-55	04.05.01.01 general transcription activities	
Pc20g07760	strong similarity to hypothetical protein An01g01020 - Aspergillus niger	1e-17	AE003616_22	product: "CG4502-PA"; "CG4502-PB"; Drosophila melanogas	77.8	21.3	37.8	13.8		0	0
Pc20g07870	strong similarity to hypothetical protein contig1487_1.tfa_550cg - Aspergillus fumigatus	2e-17	BT007762_1	product: "Homo sapiens TAF12 RNA polymerase II, TATA bo	187.0	152.1	112.0	60.7		0	0
Pc20g08120	strong similarity to hypothetical protein contig1487_1.tfa_350wg - Aspergillus fumigatus	0	0	0	251.0	232.4	108.2	72.1		0	0
Pc20g08670	hypothetical protein	0	0	0	53.8	51.9	27.9	12.7	2e-33	03 CELL CYCLE AND DNA PROCESSING	
Pc20g08990	similarity to hypothetical protein contig_1_145_scaffold_11.tfa_440wg - Aspergillus nidulans	2e-10	NC7F4_25	gene: "7F4.260"; product: "related to secretory pathway prote	520.2	288.0	181.5	194.3	8e-34	01.01.01 amino acid biosynthesis	
Pc20g09010	similarity to hypothetical protein YGR280c - Saccharomyces cerevisiae	9e-14	S64615	hypothetical protein YGR280c - yeast (Saccharomyces cere	119.0	115.6	103.2	47.2	7e-44	01.05 C-compound and carbohydrate metabolism	
Pc20g09160	strong similarity to hypothetical protein An13g00220 - Aspergillus niger	0	0	0	433.9	350.4	179.4	100.3		0	0
Pc20g09300	weak similarity to S-layer protein - Clostridium thermocellum	5e-09	AE017014_3	product: "Cell surface protein"; Bacillus cereus ATCC 14579	61.4	32.1	12.0	12.0		0	0
Pc20g09710	strong similarity to hypothetical protein An15g06870 - Aspergillus niger	0	0	0	166.6	111.5	48.2	51.1		0	0
Pc20g09720	similarity to hypothetical protein An01g07110 - Aspergillus niger [putative pseudogene]	0	0	0	58.9	46.5	24.5	17.4		0	0
Pc20g09920	hypothetical protein	0	0	0	915.2	982.3	707.1	329.0		0	0
Pc20g10010	weak similarity to hypothetical protein Rv1619 - Mycobacterium tuberculosis	3e-07	AP005050_1	gene: "lysS2"; product: "putative lysyl-tRNA synthetase"; St	47.6	21.2	20.0	12.0		0	0
Pc20g10260	strong similarity to hypothetical protein An16g07630 - Aspergillus niger	0	0	0	47.8	36.5	34.0	12.0		0	0
Pc20g10300	similarity to hypothetical protein contig_1_23_scaffold_2.tfa_100cg - Aspergillus nidulans	0	0	0	49.7	44.1	26.4	15.5	3e-69	11.05.01 resistance proteins	
Pc20g10540	strong similarity to 27 kDa antigen - Paracoccidioides brasiliensis	1e-64	PBU41503_1	product: "27 kDa antigen"; Paracoccidioides brasiliensis 27	73.0	28.8	30.7	12.0	3e-60	01.04 phosphate metabolism	
Pc20g10590	similarity to hypothetical beta-lactamase XF1621 - Xylella fastidiosa	4e-28	AE017271_166	product: "conserved hypothetical protein"; Bacillus cereus AT	75.8	37.5	48.8	29.0	1e-133	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc20g10780	weak similarity to hypothetical protein An04g07410 - Aspergillus niger	7e-07	AY461663_1	product: "testis-specific serine kinase 4"; Homo sapiens testi	74.8	67.2	37.7	22.1		0	0
Pc20g11330	weak similarity to hypothetical protein An12g05680 - Aspergillus niger	2e-09	C86212	hypothetical protein [imported] - Arabidopsis thaliana	44.0	22.0	12.0	12.0	1e-130	05 PROTEIN SYNTHESIS	
Pc20g11370	strong similarity to hypothetical protein An08g09690 - Aspergillus niger	0	0	0	64.0	40.2	23.8	23.3		0	0
Pc20g11540	strong similarity to hypothetical protein 99H12.140 - Neurospora crassa	0.0	NC99H12_14	gene: "99H12.140"; product: "putative protein"; Neurospora cr	221.2	233.4	147.9	106.2		0	0
Pc20g11600	strong similarity to hypothetical protein An15g00530 - Aspergillus niger	0	0	0	48.8	33.4	12.0	12.0		0	0
Pc20g11640	hypothetical protein	0	0	0	22.1	33.6	24.7	14.5		0	0
Pc20g12820	strong similarity to hypothetical protein 18_scaffold_1.tfa_360wg - Fusarium graminearum	0	0	0	76.7	31.5	29.8	12.0		0	0
Pc20g13050	strong similarity to hypothetical conserved protein B11N2.10 - Neurospora crassa	3e-34	NCB11N2_1	gene: "B11N2.010"; product: "conserved hypothetical protein"	31.5	32.9	14.0	16.1		0	0
Pc20g13100	strong similarity to hypothetical protein An15g01580 - Aspergillus niger	7e-07	AP005048_167	product: "hypothetical protein"; Streptomyces avermitilis gen	35.8	34.4	12.0	12.0	1e-134	06.04 protein targeting, sorting and translocation	
Pc20g13450	similarity to integral membrane protein PTH11 from patent WO9913094-A2 - Magnaporthe grisea	7e-11	AF329397_1	gene: "pth"; product: "integral membrane protein"; Blumeria	82.5	49.2	33.4	20.8	1e-157	01.04 phosphate metabolism	
Pc20g13750	strong similarity to hypothetical protein mg10547.1 - Magnaporthe grisea	2e-31	AE2149	hypothetical protein all2748 [imported] - Nostoc sp. (strain PC	306.1	82.7	131.0	41.1		0	0
Pc20g13820	strong similarity to hypothetical protein An02g03740 - Aspergillus niger	4e-07	AE003480_30	gene: "Ack"; product: "CG14992-PA"; Drosophila melanogas	164.2	115.0	63.1	48.2		0	0
Pc20g13860	strong similarity to hypothetical protein An02g03790 - Aspergillus niger	0	0	0	47.9	29.3	12.0	12.0		0	0
Pc20g14430	strong similarity to hypothetical protein SPCC4B3.08 - Schizosaccharomyces pombe	7e-30	T50440	hypothetical protein SPCC4B3.08 [imported] - fission yeast (	161.8	132.8	80.7	57.4	1e-34	01.05.04 regulation of C-compound and carbohydrate utilization	
Pc20g14460	strong similarity to hypothetical protein contig31_part_i.tfa_3340cg - Aspergillus fumigatus	1e-04	AE014799_1	product: "hypothetical protein"; Bifidobacterium longum NCC2	64.1	59.9	35.2	20.7		0	0
Pc20g14610	strong similarity to hypothetical protein An02g04350 - Aspergillus niger	7e-04	AE003670_1	gene: "Mio"; product: "CG18362-PC"; Drosophila melanogas	792.8	734.1	354.0	234.6	1e-68	14.10.02.02.01 apoptotic mitochondrial changes	

Pc20g14620	strong similarity to hypothetical protein An02g04360 - Aspergillus niger	3e-05	NCB14D6_25	gene: "B14D6.250"; product: "hypothetical protein"; Neurosp	161.0	210.0	44.4	48.0		0	0
Pc20g14660	strong similarity to hypothetical protein An02g04460 - Aspergillus niger	1e-124	NCB24N11_2	gene: "B24N11.020"; product: "hypothetical protein"; Neuros	91.1	77.9	38.2	30.8	1e-68	04 TRANSCRIPTION	
Pc20g14960	hypothetical protein	0	0	0	227.8	86.7	68.9	37.0	1e-158	99 UNCLASSIFIED PROTEINS	
Pc20g15000	strong similarity to hypothetical protein An02g04750 - Aspergillus niger	3e-04	S67612	hypothetical protein YDL076c - yeast (Saccharomyces cerevi	66.2	52.9	32.8	21.1		0	0
Pc20g15110	similarity to hypothetical protein YHR151c - Saccharomyces cerevisiae	5e-17	S46766	hypothetical protein YHR151c - yeast (Saccharomyces cerev	256.2	219.3	110.3	114.9		0	0
Pc20g15240	similarity to hypothetical protein CAD21260.1 - Neurospora crassa	3e-16	NC5E6_17	gene: "5E6.190"; product: "related to ARCA protein"; Neuros	105.2	139.9	63.8	61.2		0	0
Pc21g00410	hypothetical protein	0	0	0	75.9	30.2	13.2	17.1		0	0
Pc21g00810	strong similarity to hypothetical protein An07g04640 - Aspergillus niger	0	0	0	149.1	82.8	72.6	48.1	3e-68	03.01.03 DNA synthesis and replication	
Pc21g00830	strong similarity to hypothetical protein An03g02240 - Aspergillus niger [putative sequencing error]	0	0	0	36.7	29.6	19.9	12.9		0	0
Pc21g01180	similarity to hypothetical protein contig_1_144_scaffold_11.tfa_220cg - Aspergillus nidulans	7e-24	T40058	probable chromatin assembly factor subunit - fission yeast (S	239.0	161.8	89.2	89.1	1e-112	99 UNCLASSIFIED PROTEINS	
Pc21g01870	weak similarity to 47 kD subunit of DNA-directed RNA polymerase III Rpc53 - Saccharomyces cerevisiae	6e-05	T41150	probable DNA-directed RNA polymerase subunit - fission yea	114.0	105.6	76.9	47.1		0	0
Pc21g02000	strong similarity to hypothetical membrane protein YDL237w - Saccharomyces cerevisiae	7e-27	S67801	probable membrane protein YDL237w - yeast (Saccharomyce	49.5	67.3	26.1	23.2		0	0
Pc21g02030	strong similarity to hypothetical protein contig31_part_ii.tfa_2370cg - Aspergillus fumigatus	2e-23	NCB10N12_5	gene: "B10N12.050"; product: "putative protein"; Neurospora	48.9	38.8	41.6	20.8		0	0
Pc21g03110	strong similarity to hypothetical protein CAD21189.1 - Neurospora crassa	1e-180	NCB1K11_22	gene: "B1K11.220"; product: "hypothetical protein"; Neurosp	633.9	294.3	293.0	93.3	4e-28	02 ENERGY	
Pc21g03240	strong similarity to hypothetical protein contig_1_114_scaffold_8.tfa_40cg - Aspergillus nidulans	7e-11	NCB11C21_9	gene: "B11C21.090"; product: "hypothetical protein"; Neuros	127.0	127.4	91.1	43.8		0	0
Pc21g03360	strong similarity to hypothetical protein An14g04960 - Aspergillus niger	5e-27	T39803	hypothetical protein SPBC19C2.12 - fission yeast (Schizosac	395.6	444.7	220.4	187.9		0	0
Pc21g03680	weak similarity to hypothetical protein An18g00170 - Aspergillus niger	0	0	0	145.9	152.7	63.1	46.3		0	0
Pc21g04700	weak similarity to hypothetical protein An13g00570 - Aspergillus niger	0	0	0	85.9	92.0	83.1	36.1		0	0
Pc21g04810	similarity to hypothetical protein contig42.tfa_2390wg - Aspergillus fumigatus [truncated ORF]	0	0	0	69.1	131.8	26.4	48.6	4e-34	03.03.01.01.11 mitosis	
Pc21g04960	strong similarity to hypothetical protein An12g06000 - Aspergillus niger	0	0	0	128.9	12.8	28.8	46.6	2e-40	01.03.16.01 RNA degradation	
Pc21g05000	strong similarity to hypothetical protein An13g00320 - Aspergillus niger	2e-05	AB000516_1	product: "DSIF p160"; Homo sapiens mRNA for DSIF p160,	1186.4	528.7	614.9	254.2	2e-37	08.07 vesicular transport (Golgi network, etc.)	
Pc21g05350	strong similarity to hypothetical RNA-binding protein SPAC16E8.06c - Schizosaccharomyces pombe	5e-35	T37786	probable RNA-binding protein - fission yeast (Schizosaccharo	140.3	141.4	131.2	66.8	6e-42	06.07 protein modification	
Pc21g05410	similarity to hypothetical protein contig_1_22_scaffold_2.tfa_330wg - Aspergillus nidulans	3e-05	AF333235_9	gene: "orf15"; product: "Orf15"; Clostridium difficile conjugativ	66.1	67.7	34.0	24.5	4e-65	01.05.01 C-compound and carbohydrate utilization	
Pc21g05460	strong similarity to zinc metalloprotease like protein An16g08760 - Aspergillus niger	3e-22	T18262	S-layer protein - Clostridium thermocellum	64.6	32.0	26.2	20.2		0	0
Pc21g05780	strong similarity to hypothetical 6-hydroxy-D-nicotine oxidase related protein 13E11.250 - Neurospora crassa	1e-48	T48777	6-HYDROXY-D-NICOTINE OXIDASE related protein [imported	52.1	33.8	35.7	16.9		0	0
Pc21g05920	hypothetical protein	0	0	0	319.4	647.3	148.5	120.7		0	0
Pc21g05930	similarity to hypothetical protein An12g06840 - Aspergillus niger	0	0	0	52.3	37.6	20.2	12.0		0	0
Pc21g05980	strong similarity to hypothetical protein An01g02280 - Aspergillus niger	0	0	0	571.2	652.1	490.0	325.9		0	0
Pc21g06130	strong similarity to hypothetical protein An01g02510 - Aspergillus niger	0	0	0	364.7	290.0	240.1	142.8		0	0
Pc21g06260	similarity to hard surface induced protein 3 chip3 - Glomerella cingulata	3e-18	AF089807_1	gene: "chip3"; product: "hard surface induced protein 3"; Glo	90.3	24.9	25.7	53.9	1e-47	06.13 proteolytic degradation	
Pc21g06270	strong similarity to hypothetical protein contig1492_0.tfa_5930cg - Aspergillus fumigatus	0	0	0	45.6	12.0	12.0	15.9		0	0
Pc21g06290	strong similarity to hypothetical protein contig5_part_i.tfa_2590wg - Aspergillus fumigatus	3e-11	NC93G11_13	gene: "93G11.140"; product: "related to ser/arg-related nuclea	77.3	47.1	28.1	14.0	3e-35	03.01.05.03 DNA recombination	
Pc21g07160	strong similarity to hypothetical protein An18g02305 - Aspergillus niger	0	0	0	235.3	208.2	84.2	55.4		0	0
Pc21g07450	strong similarity to hypothetical protein contig5_part_i.tfa_1990cg - Aspergillus fumigatus	7e-38	NCB10N12_7	gene: "B10N12.070"; product: "related to rRNA processing pr	160.4	146.3	128.2	71.7	1e-149	99 UNCLASSIFIED PROTEINS	
Pc21g07770	hypothetical protein	0	0	0	62.4	37.0	17.7	12.0		0	0
Pc21g07830	strong similarity to hypothetical protein F28J12.200 - Arabidopsis thaliana	1e-164	AY254382_1	gene: "tmpA"; product: "TmpA"; Emericella nidulans TmpA (	226.0	145.0	61.4	137.8	1e-37	99 UNCLASSIFIED PROTEINS	
Pc21g07910	hypothetical protein	0	0	0	35.3	34.2	12.0	12.0		0	0
Pc21g07920	similarity to hypothetical protein F10B6.27 - Arabidopsis thaliana	4e-11	AC133339_8	gene: "OSJNBa0078D06.8"; product: "hypothetical protein";	232.8	130.8	108.9	76.0		0	0
Pc21g07980	strong similarity to hypothetical protein An04g06800 - Aspergillus niger	0	0	0	43.3	20.2	29.1	22.0		0	0
Pc21g08290	strong similarity to hypothetical protein contig49.tfa_1040wg - Aspergillus fumigatus	0	0	0	370.3	163.4	117.7	67.1		0	0
Pc21g08530	strong similarity to hypothetical protein contig_1_98_scaffold_6.tfa_760cg - Aspergillus nidulans	0	0	0	51.3	84.2	88.7	22.0	2e-44	01.05 C-compound and carbohydrate metabolism	
Pc21g08570	strong similarity to hypothetical protein An14g06360 - Aspergillus niger	0	0	0	132.6	131.7	119.7	47.2		0	0
Pc21g08620	weak similarity to hypothetical human microfibrillar-associated protein 1 homolog SPAC1782.03 - Schizosaccharomyces pombe	2e-31	NCB11H24_3	gene: "B11H24.030"; product: "related to microfibril-associate	44.0	42.2	18.1	15.9	2e-73	04.01.99 other rRNA-transcription activities	
Pc21g08860	strong similarity to acvA gene expression regulator Pc804 like protein An13g01050 - Aspergillus niger	0	0	0	87.3	83.9	62.4	40.1		0	0
Pc21g08900	strong similarity to hypothetical protein YOR294w - Saccharomyces cerevisiae	2e-32	S67198	hypothetical protein YOR294w - yeast (Saccharomyces cerev	251.6	221.6	153.1	100.1		0	0
Pc21g08970	strong similarity to hypothetical protein An13g00970 - Aspergillus niger	0	0	0	53.4	43.0	28.8	16.5		0	0
Pc21g09320	strong similarity to hypothetical protein An13g01320 - Aspergillus niger	1e-88	BX842630_12	gene: "B13D15.120"; product: "hypothetical protein"; Neuros	66.0	65.5	38.4	31.9	2e-60	01.01.01.11 biosynthesis of the cysteine-aromatic group	
Pc21g09760	hypothetical protein	0	0	0	126.4	12.0	25.3	12.0	1e-48	01.05.01 C-compound and carbohydrate utilization	
Pc21g10380	strong similarity to hypothetical protein SPAC19A8.06 - Schizosaccharomyces pombe	2e-65	T37955	hypothetical protein SPAC19A8.06 - fission yeast (Schizosac	36.7	30.7	15.2	23.3		0	0
Pc21g10600	strong similarity to hypothetical protein mg06600.1 - Magnaporthe grisea	2e-22	AE015689_5	gene: "SO2474"; product: "carbonic anhydrase family protein"	345.8	417.4	153.5	203.2	2e-54	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc21g10980	hypothetical protein	0	0	0	533.7	400.4	266.9	359.9		0	0
Pc21g11210	strong similarity to hypothetical protein contig1493_1.tfa_240cg - Aspergillus fumigatus	2e-08	CEAF3131_1	gene: "unc-89"; product: "Uncoordinated protein 89, isoform b	35.2	26.3	33.9	15.9	3e-43	04 TRANSCRIPTION	
Pc21g11740	strong similarity to hypothetical protein An12g00260 - Aspergillus niger	0	0	0	67.3	63.8	34.7	15.8		0	0
Pc21g11840	strong similarity to hypothetical protein SOM1 - Neurospora crassa	1e-38	AF265233_1	product: "SOM1 protein"; Neurospora crassa SOM1 protein	271.6	229.7	155.2	111.5		0	0
Pc21g11860	hypothetical protein	0	0	0	57.4	43.6	38.2	20.2		0	0
Pc21g11870	strong similarity to hypothetical protein An12g00400 - Aspergillus niger	0	0	0	23.1	22.3	26.1	12.0	2e-71	01.05 C-compound and carbohydrate metabolism	
Pc21g12050	weak similarity to hypothetical protein SPAC23G3.04 - Schizosaccharomyces pombe	5e-20	NCB8P8_19	gene: "B8P8.210"; product: "conserved hypothetical protein";	135.3	110.8	93.6	46.4		0	0
Pc21g12090	strong similarity to hypothetical protein contig49.tfa_370cg - Aspergillus fumigatus	2e-13	PFMAL6P1_235	gene: "MAL6P1.192"; product: "ATP-dependent DEAD box he	88.2	84.7	62.7	37.9		0	0
Pc21g12410	hypothetical protein	0	0	0	28.4	34.4	12.0	12.0	7e-44	01.04 phosphate metabolism	
Pc21g12730	hypothetical protein	0	0	0	45.1	27.1	30.3	14.3	6e-55	01.04 phosphate metabolism	
Pc21g12850	weak similarity to reticulocyte binding protein 2 homolog a - Plasmodium falciparum	3e-13	PFMAL13_350	gene: "PF13_0198"; product: "reticulocyte binding protein 2 h	86.5	57.8	60.0	21.1		0	0
Pc21g13360	similarity to phosphatidylinositol(3)-phosphate binding protein Pib1 - Saccharomyces cerevisiae	8e-09	S61199	hypothetical protein YDR313c - yeast (Saccharomyces cerev	116.3	98.5	58.0	39.6	1e-35	40.10 nucleus	
Pc21g13450	strong similarity to hypothetical protein contig_1_169_scaffold_15.tfa_700cg - Aspergillus nidulans	0	0	0	33.0	12.0	12.0	12.0		0	0
Pc21g13790	weak similarity to hypothetical protein dJ1042K10.5 - Homo sapiens	6e-16	AB037859_1	gene: "KIAA1438"; product: "KIAA1438 protein"; Homo sapien	1846.8	1405.1	952.1	586.2		0	0
Pc21g13880	strong similarity to hypothetical protein An12g01920 - Aspergillus niger	2e-31	CNS07TIX_29	DNA centromeric region sequence from BAC DP15B03, DP3	65.5	53.2	30.7	29.1	1e-154	40 SUBCELLULAR LOCALISATION	
Pc21g13910	strong similarity to hypothetical protein contig1493_1.tfa_1660cg - Aspergillus fumigatus	0	0	0	137.5	104.2	47.6	46.5	1e-42	05 PROTEIN SYNTHESIS	
Pc21g14400	weak similarity to hypothetical membrane protein YMR266w - Saccharomyces cerevisiae	1e-143	S54478	probable membrane protein YMR266w - yeast (Saccharomyc	419.4	298.1	129.8	105.4		0	0
Pc21g14530	weak similarity to hypothetical protein YBL051c - Saccharomyces cerevisiae	1e-78	NCB15B24_8	gene: "B15B24.070"; product: "conserved hypothetical protein	90.8	99.7	77.2	49.8		0	0
Pc21g14800	similarity to hypothetical protein contig_1_168_scaffold_14.tfa_210cg - Aspergillus nidulans	0	0	0	40.0	13.4	17.5	12.0		0	0
Pc21g14950	similarity to hypothetical protein F3E22.6 - Arabidopsis thaliana	1e-04	AC023912_6	gene: "F3E22.6"; Arabidopsis thaliana chromosome III BAC	653.8	275.3	406.8	179.4		0	0
Pc21g15070	hypothetical protein [putative pseudogene]	0	0	0	32.9	17.8	12.0	12.0		0	0
Pc21g15280	hypothetical protein	0	0	0	221.2	208.2	122.2	71.6	2e-65	01.06 lipid, fatty-acid and isoprenoid metabolism	
Pc21g15540	similarity to hypothetical protein CAD11786.1 - Neurospora crassa	2e-10	NC104H10_6	gene: "104H10.050"; product: "hypothetical protein"; Neurosp	147.8	110.8	85.6	47.7		0	0
Pc21g16470	strong similarity to hypothetical protein contig1490_3.tfa_1000wg - Aspergillus fumigatus	3e-10	AC084196_2	gene: "Y55D5A.3"; product: "Hypothetical protein Y55D5A.3"	29.8	16.8	26.4	12.0		0	0
Pc21g16510	similarity to hypothetical protein 1233_scaffold_3.tfa_1120cg - Fusarium graminearum	0	0	0	22.7	25.5	12.0	12.0	4e-38	04 TRANSCRIPTION	
Pc21g16750	similarity to hypothetical protein An13g01540 - Aspergillus niger	0	0	0	549.1	367.4	268.4	285.3		0	0
Pc21g16870	strong similarity to hypothetical protein smik_17056 - Saccharomyces mikatae	1e-27	HHBYD8	heat shock protein DDR48 - yeast (Saccharomyces cerevisia	724.8	1377.1	648.4	501.9		0	0
Pc21g17260	similarity to hypothetical protein An16g01460 - Aspergillus niger	0	0	0	80.8	64.9	38.6	28.7		0	0
Pc21g17270	weak similarity to hypothetical protein contig5_part_ii.tfa_850cg - Aspergillus fumigatus	0	0	0	121.7	106.9	65.9	47.3	1e-123	40.02 plasma membrane	
Pc21g17480	similarity to hypothetical protein MUA22.14 - Arabidopsis thaliana	1e-14	AB007650_12	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone	287.9	293.8	222.6	146.2	5e-85	08.16 extracellular transport, exocytosis and secretion	
Pc21g17570	weak similarity to hypothetical membrane protein YOR154w - Saccharomyces cerevisiae	2e-53	T40383	hypothetical protein SPBC3E7.09 - fission yeast (Schizosacc	159.5	150.5	74.5	68.5	2e-73	11.01 stress response	
Pc21g17600	strong similarity to hypothetical conserved protein B7A16.130 - Neurospora crassa	0.0	NCB7A16_12	gene: "B7A16.130"; product: "conserved hypothetical protein"	95.8	93.0	104.3	43.7	6e-39	13.07 cell adhesion	
Pc21g17610	strong similarity to hypothetical protein B7A16.140 - Neurospora crassa	2e-72	NCB7A16_13	gene: "B7A16.140"; product: "related to low-temperature viabi	143.3	139.2	129.2	51.9		0	0
Pc21g17920	strong similarity to hypothetical protein An17g00870 - Aspergillus niger	5e-29	NCB10H4_8	gene: "B10H4.080"; product: "hypothetical protein"; Neurosp	99.6	95.8	50.0	43.3	1e-98	01.05 C-compound and carbohydrate metabolism	
Pc21g17930	strong similarity to hypothetical protein contig1495_2.tfa_210cg - Aspergillus fumigatus	0	0	0	643.1	624.3	436.1	291.1	0.0	04.05.01 mRNA synthesis	
Pc21g18100	strong similarity to differentially expressed protein Sh3yl1 - Mus musculus	5e-28	BC061488_1	Mus musculus Sh3 domain YSC-like 1, mRNA (cDNA clone	52.0	72.9	38.7	26.8	6e-45	01.03.16.01 RNA degradation	
Pc21g18250	similarity to suppressor of S.cerevisiae sin4 mutation Rlr1 - Saccharomyces cerevisiae	1e-168	YA8E_SCHPO	HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I	67.5	68.2	36.5	21.0		0	0
Pc21g18310	similarity to hypothetical single-stranded TG1-3 binding protein tcg - Schizosaccharomyces pombe	7e-75	AF403297_1	product: "glycine-rich protein"; Coccidioides immitis glycine-	919.9	1046.0	565.0	338.0	1e-147	06.13 proteolytic degradation	
Pc21g18360	hypothetical protein	0	0	0	39.8	34.1	31.0	12.0		0	0
Pc21g19350	similarity to 2MDa_1 protein - Caenorhabditis elegans	2e-38	AY130758_1	gene: "isof"; product: "2MDa_1 protein"; Caenorhabditis elega	234.9	283.1	117.9	111.3	3e-41	01.05 C-compound and carbohydrate metabolism	
Pc21g19410	similarity to hypothetical protein contig31_part_ii.tfa_3240cg - Aspergillus fumigatus	0	0	0	99.5	55.0	44.1	35.1		0	0
Pc21g19540	strong similarity to hypothetical PHD-type zinc finger protein SPCC126.07c - Schizosaccharomyces pombe	3e-30	T40911	probable PHD-type zinc finger - fission yeast (Schizosacchar	78.1	49.9	45.0	23.3		0	0
Pc21g19680	hypothetical protein	0	0	0	42.7	30.6	22.5	12.8		0	0
Pc21g20150	similarity to hypothetical hard surface induced protein chip3 - Glomerella cingulata	2e-20	AF089807_1	gene: "chip3"; product: "hard surface induced protein 3"; Glo	707.8	647.9	370.0	247.9	2e-26	04 TRANSCRIPTION	
Pc21g20170	weak similarity to glycogen synthase - Sulfolobus acidocaldarius	1e-05	SAC294724_1	gene: "glgA"; product: "glycogen synthase"; Sulfolobus acido	265.6	335.8	252.6	144.5		0	0
Pc21g20230	strong similarity to hypothetical protein mg03902.1 - Magnaporthe grisea	1e-21	NCB11B23_1	gene: "B11B23.010"; product: "related to Elongin C transcript	339.6	298.4	158.7	149.7	2e-89	99 UNCLASSIFIED PROTEINS	
Pc21g20280	hypothetical protein	0	0	0	176.9	242.3	89.1	87.2		0	0
Pc21g20530	similarity to hypothetical protein DKFZp564A0772.1 - Homo sapiens	2e-21	T47153	hypothetical protein DKFZp564A0772.1 - human	61.1	62.4	24.9	21.3		0	0
Pc21g20850	strong similarity to hypothetical protein CAC28835.1 - Neurospora crassa	6e-36	NC17E5_9	gene: "17E5.090"; product: "conserved hypothetical protein";	177.3	165.1	113.1	44.9		0	0
Pc21g20980	weak similarity to hypothetical protein - Aspergillus fumigatus	3e-05	BX649605_120	product: "hypothetical protein"; Aspergillus fumigatus BAC pil	53.2	12.0	12.0	12.0		0	0
Pc21g21920	strong similarity to hypothetical protein CAD37162.1 - Aspergillus fumigatus	8e-83	AFA12H2_24	gene: "AfA12H2.24c"; product: "hypothetical protein"; Asper	419.0	339.8	364.7	178.5		0	0
Pc21g21970	strong similarity to hypothetical protein contig_1_100_scaffold_7.tfa_300wg - Aspergillus nidulans	5e-06	AE011670_2	gene: "XAC0432"; product: "conserved hypothetical protein";	342.8	627.0	285.8	232.8		0	0
Pc21g22020	weak similarity to hypothetical F-box domain protein - Schizosaccharomyces pombe	1e-06	T50319	hypothetical F-box domain protein [imported] - fission yeast (	289.7	269.6	169.6	125.9	1e-85	01.04 phosphate metabolism	
Pc21g22030	hypothetical protein	0	0	0	33.3	47.7	14.1	16.1		0	0
Pc21g22070	similarity to hypothetical protein CG16717 - Drosophila melanogaster	2e-78	NCB13O8_16	gene: "B13O8.170"; product: "conserved hypothetical protein"	81.5	60.5	34.3	24.9	2e-56	01.05 C-compound and carbohydrate metabolism	
Pc21g22100	strong similarity to hypothetical protein An04g09490 - Aspergillus niger	0	0	0	32.1	12.0	12.0	12.0	2e-26	98 CLASSIFICATION NOT YET CLEAR-CUT	
Pc21g23100	strong similarity to hypothetical membrane protein YOR206w - Saccharomyces cerevisiae	1e-123	SPAC1142_4	gene: "SPAC1142.04"; S.pombe chromosome I cosmid c114	88.0	75.0	61.9	34.5		0	0
Pc21g23120	strong similarity to hypothetical membrane protein YBR271w - Saccharomyces cerevisiae	4e-45	BX842633_14	gene: "53H1.140"; product: "conserved hypothetical protein";	56.9	84.8	35.0	38.4	2e-89	04 TRANSCRIPTION	
Pc21g23220	strong similarity to hypothetical protein An01g11000 - Aspergillus niger	0	0	0	31.5	39.2	16.0	17.5		0	0
Pc21g23370	strong similarity to hypothetical protein An01g10200 - Aspergillus niger	2e-07	E96686	probable PHD-finger protein F15E12.11 [imported] - Arabidops	62.8	50.8	45.5	24.8	2e-62	01.05.01 C-compound and carbohydrate utilization	
Pc21g23460	strong similarity to hypothetical protein 1289_scaffold_4.tfa_60cg - Fusarium graminearum	0	0	0	334.7	300.6	145.3	129.2	8e-42	01.04 phosphate metabolism	
Pc21g23600	strong similarity to hypothetical protein 119_scaffold_1.tfa_20cg - Fusarium graminearum	6e-63	NCB24P7_8	gene: "B24P7.150"; product: "related to nodulation protein no	60.1	65.9	40.8	27.9	1e-36	99 UNCLASSIFIED PROTEINS	
Pc21g23660	weak similarity to phosphatidylinositol(3)-phosphate binding protein Pib1 - Saccharomyces cerevisiae	6e-14	T40784	hypothetical zinc finger protein - fission yeast (Schizosacchar	302.5	257.6	145.1	102.3	2e-37	04.05.05 mRNA processing (splicing, 5'-, 3'-end processing)	
Pc22g00310	weak similarity to hypothetical protein T8B10.110 - Arabidopsis thaliana	0	0	0	268.2	257.9	81.8	71.7		0	0

Pc22g00530	similarity to hypothetical protein contig_1_93_scaffold_6.tfa_770cg - Aspergillus nidulans	9e-06	AF116907_26	product: "putative methylase"; Rhodococcus equi virulence p	1140.1	1351.6	509.0	292.6	2e-50	01.20 secondary metabolism	
Pc22g00780	strong similarity to hypothetical protein contig1492_0.tfa_5610wg - Aspergillus fumigatus	0	0	0	161.0	147.0	123.8	70.1	0		0
Pc22g01170	strong similarity to cDNA O-methyltransferase mt-I - Aspergillus parasiticus	2e-45	AB022905_1	gene: "mt-I"; product: "O-methyltransferase"; Aspergillus para	58.9	170.6	34.8	32.3	6e-73	06.04 protein targeting, sorting and translocation	
Pc22g01180	strong similarity to hypothetical protein contig_1_115_scaffold_8.tfa_70wg - Aspergillus nidulans	9e-07	NCB7H23_13	gene: "B7H23.130"; product: "related to L-fucose permease";	20.9	51.5	22.3	12.0	0		0
Pc22g01390	weak similarity to hypothetical protein An08g10130 - Aspergillus niger	4e-08	PFA929355_50	gene: "PFI0250c"; product: "hypothetical protein"; Plasmodiu	377.0	363.6	262.9	160.2	0		0
Pc22g02420	similarity to hypothetical protein contig1492_0.tfa_5260wg - Aspergillus fumigatus	0	0	0	209.6	200.2	134.6	60.9	2e-72	06.04 protein targeting, sorting and translocation	
Pc22g03910	hypothetical protein	0	0	0	121.6	110.6	98.4	52.8	0		0
Pc22g04330	strong similarity to hypothetical protein SPAC23G3.05c - Schizosaccharomyces pombe	4e-32	T50179	yeast bud pattern determination protein Rax1p homolog [impo	406.3	359.6	192.4	188.4	0		0
Pc22g04470	strong similarity to hypothetical protein SPAC32A11.02c - Schizosaccharomyces pombe	5e-75	T38648	hypothetical protein SPAC32A11.02c - fission yeast (Schizos	51.9	63.9	52.5	12.0	0		0
Pc22g04490	strong similarity to hypothetical protein contig1469.tfa_350wg - Aspergillus fumigatus	0	0	0	68.8	75.9	33.8	39.1	0		0
Pc22g04710	strong similarity to hypothetical protein contig12.tfa_2310wg - Aspergillus fumigatus	0	0	0	253.1	206.3	174.1	92.4	0		0
Pc22g04730	strong similarity to hypothetical intracellular protease amidase related enzyme of the ThiJ family CAC2826 - Clostridium acetobutylicu	1e-35	G97247	intracellular protease/amidase related enzyme (ThiJ family) [i	56.5	25.2	27.4	30.4	3e-81	01.01.99 other amino acid metabolism activities	
Pc22g05010	strong similarity to hypothetical protein An13g01780 - Aspergillus niger [putative pseudogene]	7e-05	AB025615_4	product: "AIG2 protein-like"; Arabidopsis thaliana genomic D	62.1	42.4	56.1	12.0	0		0
Pc22g05480	strong similarity to hypothetical oxidoreductase PA0147 - Pseudomonas aeruginosa	2e-34	C83628	probable oxidoreductase PA0147 [imported] - Pseudomonas	59.1	47.6	38.3	12.0	3e-65	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc22g05680	similarity to hypothetical protein contig_1_2_scaffold_1.tfa_150wg - Aspergillus nidulans [truncated ORF][putative pseudogene]	0	0	0	38.2	42.7	19.7	17.9	0		0
Pc22g05690	strong similarity to hypothetical protein contig12.tfa_1730cg - Aspergillus fumigatus	2e-10	CEAF3131_1	gene: "unc-89"; product: "Uncoordinated protein 89, isoform b	1061.9	1103.0	498.8	186.8	0		0
Pc22g05770	hypothetical protein	0	0	0	138.2	125.5	66.8	53.7	1e-108	99 UNCLASSIFIED PROTEINS	
Pc22g06900	similarity to hypothetical protein An04g05790 - Aspergillus niger	0	0	0	59.5	55.9	26.2	18.1	3e-60	03.01.09 DNA restriction or modification	
Pc22g07070	similarity to hypothetical protein B23I11.280 - Neurospora crassa	3e-24	T51916	hypothetical protein B23I11.280 [imported] - Neurospora cras	56.9	57.8	28.1	22.6	9e-72	03.03 cell cycle	
Pc22g07200	weak similarity to hypothetical protein YDR398w - Saccharomyces cerevisiae	2e-29	SPAC20H4_1	gene: "SPAC20H4.01"; "SPAC631.03"; S.pombe chromoson	133.4	105.7	118.4	58.7	1e-154	04 TRANSCRIPTION	
Pc22g08340	strong similarity to hypothetical protein SPBC29A3.06 - Schizosaccharomyces pombe	1e-133	BX842626_16	gene: "B18P24.170"; product: "conserved hypothetical protei	105.7	85.5	80.0	34.2	0.0	99 UNCLASSIFIED PROTEINS	
Pc22g08370	strong similarity to PHD-finger protein like protein An02g14310 - Aspergillus niger	4e-63	BT009941_1	gene: "CG11033"; product: "SD04170p"; Drosophila melanoga	143.9	135.5	69.5	67.8	0		0
Pc22g08500	strong similarity to hypothetical protein SPCC338.13 - Schizosaccharomyces pombe	2e-58	T41730	hypothetical protein SPCC338.13 - fission yeast (Schizosacc	55.1	51.1	31.2	25.0	0		0
Pc22g08660	hypothetical protein	0	0	0	26.9	18.8	12.0	12.0	0		0
Pc22g08830	hypothetical protein	0	0	0	61.8	52.7	29.8	31.4	0		0
Pc22g08850	hypothetical protein	0	0	0	372.6	483.5	204.8	162.4	0		0
Pc22g08930	strong similarity to hypothetical protein contig52.tfa_1040cg - Aspergillus fumigatus	0	0	0	49.5	21.8	21.6	12.0	0		0
Pc22g09060	similarity to hypothetical protein contig52.tfa_900cg - Aspergillus fumigatus [truncated ORF]	0	0	0	103.7	94.4	54.5	31.2	5e-86	99 UNCLASSIFIED PROTEINS	
Pc22g09330	hypothetical protein	0	0	0	138.5	120.7	143.0	60.7	0		0
Pc22g09950	similarity to hypothetical protein YDR489w - Saccharomyces cerevisiae	6e-34	BX842628_10	gene: "B23L4.100"; product: "conserved hypothetical protein"	34.9	29.7	12.0	12.0	0		0
Pc22g10100	hypothetical protein	0	0	0	85.8	84.7	58.2	39.7	1e-50	10.05 transmembrane signal transduction	
Pc22g10110	strong similarity to hypothetical protein An16g09170 - Aspergillus niger	0	0	0	170.9	150.2	95.6	74.3	0		0
Pc22g11730	similarity to hypothetical retroelement pol polyprotein - Arabidopsis thaliana	8e-21	F84811	probable retroelement pol polyprotein [imported] - Arabidopsis	27.2	17.7	12.0	12.0	0		0
Pc22g11800	hypothetical protein	0	0	0	68.4	71.4	39.0	18.9	0		0
Pc22g11930	similarity to hypothetical protein SPCC4B3.10c - Schizosaccharomyces pombe	1e-18	T43146	hypothetical protein - fission yeast (Schizosaccharomyces po	191.7	136.7	90.6	60.5	1e-131	99 UNCLASSIFIED PROTEINS	
Pc22g11950	strong similarity to hypothetical protein contig_1_39_scaffold_2.tfa_30wg - Aspergillus nidulans	0	0	0	220.8	89.0	103.0	58.2	0		0
Pc22g12080	strong similarity to hypothetical protein SPBC19C2.11c - Schizosaccharomyces pombe	4e-51	T39802	hypothetical protein SPBC19C2.11c - fission yeast (Schizosa	146.4	134.7	78.6	49.8	0		0
Pc22g12260	similarity to hypothetical protein contig28.tfa_440wg - Aspergillus fumigatus	0	0	0	1799.5	1866.3	1195.8	541.0	0		0
Pc22g12430	strong similarity to hypothetical protein contig_1_30_scaffold_2.tfa_190wg - Aspergillus nidulans	0	0	0	25.9	36.5	19.5	12.0	3e-29	03.03.01.01.11 mitosis	
Pc22g12710	weak similarity to hypothetical transcription factor Arg81 - Saccharomyces cerevisiae	3e-06	BX842620_46	gene: "B11E5.460"; product: "putative protein"; Neurospora c	91.5	88.7	38.7	36.1	0		0
Pc22g12740	similarity to hypothetical protein rfeF - Aspergillus nidulans	2e-53	AF467714_1	gene: "rfeF"; product: "RfeF"; Emericella nidulans RfeF (rfeF)	682.7	721.4	699.8	352.4	0		0
Pc22g13370	similarity to hypothetical protein SPAC4F10.13c - Schizosaccharomyces pombe	1e-15	T38817	hypothetical protein SPAC4F10.13c - fission yeast (Schizosa	117.6	108.9	88.1	42.5	1e-152	99 UNCLASSIFIED PROTEINS	
Pc22g13450	strong similarity to hypothetical Medusa medA - Aspergillus nidulans	1e-162	AF080599_1	gene: "medA"; product: "Medusa"; Emericella nidulans Medu	137.5	124.6	65.7	52.7	8e-34	99 UNCLASSIFIED PROTEINS	
Pc22g13880	strong similarity to hypothetical protein SPAC1B2.02c - Schizosaccharomyces pombe	6e-67	NC104H10_25	gene: "104H10.260"; product: "conserved hypothetical protein	65.3	61.0	48.6	29.2	0		0
Pc22g14060	strong similarity to hypothetical protein CAD21257.1 - Neurospora crassa	2e-26	NC5E6_14	gene: "5E6.160"; product: "conserved hypothetical protein"; N	167.4	152.2	80.5	84.5	0		0
Pc22g14380	strong similarity to hypothetical protein An07g03430 - Aspergillus niger	4e-23	NC100H1_16	gene: "100H1.220"; product: "conserved hypothetical protein"	223.4	207.1	97.7	92.3	8e-27	05 PROTEIN SYNTHESIS	
Pc22g14790	hypothetical protein	0	0	0	74.6	57.0	43.0	26.8	0		0
Pc22g14850	weak similarity to translocation protein Sec72 - Saccharomyces cerevisiae	9e-14	T38535	probable translocation protein - fission yeast (Schizosacchard	149.7	124.7	73.1	69.3	3e-85	25.05.15 myogenesis	
Pc22g15010	strong similarity to hypothetical protein contig5_part_ii.tfa_1970wg - Aspergillus fumigatus	0	0	0	371.3	349.6	126.5	83.8	0		0
Pc22g15570	strong similarity to hypothetical protein An03g03800 - Aspergillus niger	3e-07	AE003816_4	gene: "shot"; product: "CG18076-PG"; Drosophila melanogas	63.6	67.8	72.1	33.3	3e-52	99 UNCLASSIFIED PROTEINS	
Pc22g15670	strong similarity to hypothetical protein An03g03930 - Aspergillus niger	0	0	0	221.5	205.5	91.9	53.7	8e-55	11.05.05 virulence, disease factors	
Pc22g15820	strong similarity to hypothetical protein AAG38543.1 - Pneumocystis carinii	3e-21	AF309805_4	product: "Ydr124wp-like protein"; Pneumocystis carinii f. sp.	1101.0	897.6	328.5	431.9	0		0
Pc22g15890	strong similarity to hypothetical protein contig5_part_ii.tfa_1570wg - Aspergillus fumigatus	2e-20	AY007311_1	product: "cellulase CelA"; Clavibacter michiganensis subsp.	250.2	305.1	71.7	207.3	3e-89	01.05.01 C-compound and carbohydrate utilization	
Pc22g16040	strong similarity to hypothetical protein An03g04400 - Aspergillus niger	0	0	0	53.0	45.8	23.2	23.8	0		0
Pc22g16070	weak similarity to hypothetical membrane protein YIL151c - Saccharomyces cerevisiae	5e-05	S38174	probable purine nucleotide-binding protein YKR096w - yeast (	207.7	241.5	192.6	74.8	0		0
Pc22g16170	strong similarity to hypothetical protein ncu08538.1 - Neurospora crassa	0	0	0	61.4	44.0	17.3	17.7	0		0
Pc22g16710	strong similarity to hypothetical protein contig5_part_ii.tfa_1120wg - Aspergillus fumigatus	0	0	0	555.1	488.2	391.0	148.6	1e-100	01.06.01 lipid, fatty-acid and isoprenoid biosynthesis	
Pc22g16870	weak similarity to hypothetical protein An04g00550 - Aspergillus niger	0	0	0	129.8	116.2	103.3	55.6	0		0
Pc22g16960	strong similarity to hypothetical longevity-assurance protein 1 - Schizosaccharomyces pombe	3e-83	BX842631_30	gene: "B1O14.300"; product: "related to protein LAC1"; Neur	331.1	284.1	152.9	153.3	0		0
Pc22g17510	hypothetical protein	0	0	0	51.2	63.7	30.5	29.5	0		0
Pc22g18060	hypothetical protein	0	0	0	35.9	12.0	12.0	12.0	0		0
Pc22g18070	similarity to mucin like protein An04g01380 - Aspergillus niger	0	0	0	37.2	18.3	12.0	12.0	2e-25	04.05.01.04 transcriptional control	
Pc22g18370	strong similarity to hypothetical protein An04g01590 - Aspergillus niger	0	0	0	28.2	34.9	12.0	12.0	8e-67	03.03 cell cycle	
Pc22g18870	similarity to hypothetical zf-C3H4C zinc finger protein SPCC548.05c - Schizosaccharomyces pombe	2e-16	SPCC548_5	gene: "SPCC548.05c"; product: "zinc finger protein; zf-C3HC	91.3	77.6	47.4	34.2	0		0
Pc22g18960	similarity to hypothetical protein SPCC1795.08c - Schizosaccharomyces pombe	4e-21	T41135	hypothetical protein SPCC1795.08c - fission yeast (Schizosa	224.3	158.2	117.1	59.6	0		0
Pc22g19000	strong similarity to hypothetical protein contig1488_2.tfa_470cg - Aspergillus fumigatus	0	0	0	36.8	31.3	40.7	18.8	0		0
Pc22g19140	strong similarity to hypothetical protein An16g06890 - Aspergillus niger	0	0	0	404.0	507.4	200.0	113.6	0		0
Pc22g19150	strong similarity to hypothetical protein SPBC25B2.10 - Schizosaccharomyces pombe	4e-48	T39986	hypothetical protein SPBC25B2.10 - fission yeast (Schizosac	302.7	363.2	152.6	116.0	1e-114	03.01.05.01 DNA repair	
Pc22g19360	strong similarity to hypothetical protein CAD21410.1 - Neurospora crassa	4e-50	NC18F11_6	gene: "18F11.050"; product: "conserved hypothetical protein";	71.5	54.4	40.0	21.5	0		0
Pc22g19800	strong similarity to hypothetical protein contig31_part_i.tfa_3800cg - Aspergillus fumigatus	1e-150	BX842629_34	gene: "B20J13.340"; product: "hypothetical protein"; Neurosp	655.5	486.5	348.0	128.1	0		0
Pc22g19970	strong similarity to lovF gene expression regulator like protein An16g05120 - Aspergillus niger	0	0	0	247.4	197.1	162.1	89.0	0		0
Pc22g20160	weak similarity to hypothetical protein An12g10330 - Aspergillus niger	0	0	0	774.8	380.6	288.8	267.9	5e-60	10 CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM	
Pc22g20420	weak similarity to exo-alpha-sialidase - Trypanosoma cruzi	4e-04	AF467768_1	product: "glycoprotein precursor"; Crimean-Congo hemorrhagi	289.3	251.7	157.7	111.6	0		0
Pc22g20450	similarity to hypothetical protein YJL020c - Saccharomyces cerevisiae [putative sequencing error]	9e-15	S56791	hypothetical protein YJL020c - yeast (Saccharomyces cerevis	90.2	70.2	53.5	28.4	0		0
Pc22g20730	similarity to hypothetical protein CAD36993.1 - Neurospora crassa	8e-66	NC100H1_12	gene: "100H1.150"; product: "hypothetical protein"; Neurospo	80.5	68.0	31.4	51.9	5e-41	99 UNCLASSIFIED PROTEINS	
Pc22g20740	weak similarity to UDP-N-acetylglucosamine:alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV - Homo sapiens	8e-04	AB024911_1	gene: "hGnT-IV-H"; product: "UDP-N-acetylglucosamine:alpha	38.9	18.6	12.0	12.0	0		0
Pc22g20780	weak similarity to hypothetical protein F3E22.6 - Arabidopsis thaliana	3e-04	AC023912_6	gene: "F3E22.6"; Arabidopsis thaliana chromosome III BAC	158.5	107.5	50.3	28.9	6e-91	05 PROTEIN SYNTHESIS	
Pc22g20930	similarity to hypothetical protein An02g06010 - Aspergillus niger	0	0	0	48.4	53.5	20.8	12.0	0		0
Pc22g21110	similarity to hypothetical protein contig31_part_i.tfa_2410wg - Aspergillus fumigatus	1e-07	AY140094_1	product: "unknown protein"; Arabidopsis thaliana unknown pr	217.1	211.9	124.1	87.9	0		0
Pc22g21420	hypothetical protein	0	0	0	58.9	73.4	41.8	23.9	2e-90	99 UNCLASSIFIED PROTEINS	
Pc22g21740	hypothetical protein	0	0	0	36.2	33.4	15.9	12.0	0		0
Pc22g21800	similarity to hypothetical indole-diterpene gene cluster protein paxU - Penicillium paxilli	4e-18	NC64C2_2	gene: "64C2.020"; product: "conserved hypothetical protein";	56.5	72.8	37.0	26.7	0		0
Pc22g21870	similarity to hypothetical protein contig10.tfa_180wg - Aspergillus fumigatus	0	0	0	390.7	454.3	237.1	91.1	3e-54	01.05 C-compound and carbohydrate metabolism	
Pc22g22320	weak similarity to hypothetical protein related to VeA - Neurospora crassa	0	0	0	183.3	175.4	110.8	86.4	0		0
Pc22g22490	weak similarity to hypothetical protein contig1497_4.tfa_860cg - Aspergillus fumigatus	1e-05	AY164486_1	gene: "Pkd1l3"; product: "polycystic kidney disease 1-like 3";	60.1	52.0	36.6	22.8	6e-52	08.07 vesicular transport (Golgi network, etc.)	
Pc22g23090	hypothetical protein	0	0	0	427.0	252.9	269.2	119.3	0		0
Pc22g23650	strong similarity to hypothetical protein An12g08510 - Aspergillus niger	0	0	0	83.6	76.4	38.2	12.0	0		0
Pc22g24650	strong similarity to hypothetical protein An15g05550 - Aspergillus niger	0	0	0	116.7	111.6	70.7	21.0	0		0
Pc22g24660	similarity to hypothetical protein mg07603.1 - Magnaporthe grisea	1e-05	NCB11B22_6	gene: "B11B22.080"; product: "putative protein"; Neurospora	525.1	512.6	453.0	234.6	0		0
Pc22g25140	strong similarity to hypothetical protein An08g09690 - Aspergillus niger	0	0	0	33.4	12.0	14.1	12.0	6e-87	04.05.01.04 transcriptional control	
Pc22g25480	weak similarity to hypothetical protein contig_1_5_scaffold_1.tfa_1230cg - Aspergillus nidulans	0	0	0	713.7	605.6	310.0	211.8	0		0
Pc22g25580	strong similarity to hypothetical protein mg06328.1 - Magnaporthe grisea	2e-07	AE003589_26	gene: "EP2237"; product: "CG4427-PB"; Drosophila melanog	94.8	80.6	86.7	35.2	0		0
Pc22g26490	hypothetical protein	0	0	0	176.3	104.0	65.6	91.3	0		0
Pc23g00350	hypothetical protein BAC82546 - Penicillium chrysogenum	1e-110	AB091505_1	product: "hypothetical protein"; Penicillium chrysogenum mR	1038.5	260.9	316.1	734.9	0		0
Pc23g00430	hypothetical protein	0	0	0	36.9	35.9	23.1	27.7	0		0
Pc23g00560	similarity to hypothetical protein An01g08970 - Aspergillus niger	0	0	0	51.8	64.2	26.6	27.6	0		0
Pc23g00850	similarity to hypothetical protein contig1492_0.tfa_2320wg - Aspergillus fumigatus [truncated ORF]	0	0	0	181.5	142.9	85.5	81.9	5e-28	03.01.09.05 DNA conformation modification (e.g. chromatin)	
Pc23g00890	similarity to hypothetical protein SPAC1420.01c - Schizosaccharomyces pombe	3e-09	T37664	hypothetical protein SPAC1420.01c SPAC56E4.08c - fission	49.4	52.1	12.0	12.0	0		0
Pc23g00970	similarity to hypothetical protein An16g06250 - Aspergillus niger	8e-16	T31436	DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain -	39.1	44.7	12.0	12.0	0		0
Pc24g00260	strong similarity to hypothetical protein 1190_scaffold_2.tfa_540wg - Fusarium graminearum [truncated ORF][putative sequencing erro	0	0	0	40.5	23.7	12.0	12.0	0		0
Pc24g00350	hypothetical protein	0	0	0	29.3	12.0	18.0	12.0	0		0
Pc24g00360	hypothetical protein	0	0	0	37.6	12.0	12.0	12.0	0		0
Pc24g00370	strong similarity to hypothetical protein 1196_scaffold_3.tfa_500cg - Fusarium graminearum	0	0	0	1794.3	738.3	1046.2	198.4	0		0
Pc24g00400	strong similarity to hypothetical protein ncu08816.1 - Neurospora crassa	0	0	0	61.1	21.5	23.2	12.0	0		0
Pc24g00500	similarity to hypothetical protein An09g03310 - Aspergillus niger	0	0	0	132.2	126.2	62.5	36.8	1e-67	01.01.04 regulation of amino acid metabolism	
Pc24g00630	hypothetical protein	0	0	0	111.2	84.8	33.0	35.4	0		0
Pc24g00780	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	7e-40	NCX4G11_5	gene: "X4G11.050"; product: "hypothetical protein"; Neurosp	111.9	12.0	12.0	12.0	0		0
Pc24g00790	hypothetical protein	0	0	0	21.6	12.0	12.0	12.0	0		0
Pc24g00830	hypothetical protein	0	0	0	83.0	12.0	12.0	12.0	0		0
Pc24g00940	hypothetical protein	0	0	0	58.1	21.4	12.0	12.0	0		0
Pc24g01210	similarity to hypothetical protein contig1492_0.tfa_2370cg - Aspergillus fumigatus [putative pseudogene]	0	0	0	453.0	173.2	140.8	88.0	2e-26	01.01.04 regulation of amino acid metabolism	
Pc24g01440	hypothetical protein	0	0	0	126.2	12.0	12.0	12.0	0		0
Pc24g01630	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	7e-09	T37604	probable transcription activator - fission yeast (Schizosacchar	109.1	12.0	12.0	12.0	0		0
Pc24g01640	hypothetical protein BAC82546 - Penicillium chrysogenum	1e-99	AB091505_1	product: "hypothetical protein"; Penicillium chrysogenum mR	415.3	12.0	36.7	121.3	0		0

Pc24g01670	hypothetical protein	0	0	0	236.2	14.3	28.4	17.2	6e-30	01.05.01 C-compound and carbohydrate utilization
Pc24g01710	hypothetical protein	0	0	0	87.2	12.0	12.0	12.0	0	0
Pc24g01980	similarity to hypothetical protein mg07660.1 - Magnaporthe grisea [putative pseudogene]	4e-07	BC012625_1	product: "Similar to protein phosphatase 1, regulatory (inhibit	104.0	97.6	45.0	37.4	1e-136	04.05.01.04 transcriptional control
Pc24g02010	hypothetical protein	0	0	0	12.0	12.0	12.0	12.0	1e-125	10.01.01 unspecified signal transduction
Pc24g02380	similarity to hypothetical protein - Oryza sativa	8e-20	AP003221_23	gene: "P0003D09.25"; Oryza sativa (japonica cultivar-group)	72.9	38.5	57.3	22.0	0	0
Pc24g02510	strong similarity to gag-pol polyprotein - Oryza sativa [putative pseudogene]	7e-35	AC079889_11	gene: "OSJNBa0092M19.11"; product: "gag-pol polyprotein";	31.7	27.4	12.9	12.0	0	0
Pc24g02710	hypothetical protein	3e-04	T08613	hypothetical protein REA - Ehrlichia sp. (strain USG3)	598.1	368.7	256.5	143.7	0	0
Pc24g02730	strong similarity to hypothetical protein An08g11530 - Aspergillus niger	0	0	0	69.5	12.0	12.0	12.0	0	0
Pc24g02730	strong similarity to hypothetical protein An08g11530 - Aspergillus niger	0	0	0	69.5	12.0	12.0	12.0	#N/A	#N/A
Pc24g02760	weak similarity to hypothetical membrane protein YIL151c - Saccharomyces cerevisiae [putative pseudogene]	0	0	0	158.5	19.7	20.0	18.2	#N/A	#N/A

Supplementary Table 17. Transcription Factors involved in b-lactam biosynthesis. (a) Pfam trusted matches (domains scoring higher than the gathering threshold)

ORF code	Description of putative *P. chrysogenum* ORF	Regulation of b-lactam biosynthesis	Transcription Factor	Transcription Factor Domain (start-end) (a)	Binding sites upstream of the pcbAB, pcbC and penDE genes	Average transcript levels @			
						WIS - PAA	**WIS + PAA**	**DS - PAA**	**DS + PAA**
Pc20g13880	strong similarity to catabolite repressor creA - Aspergillus niger	**CARBON SOURCE**	**CreA**. Repressor involved in carbon catabolite repression	C2H2 (62-84), (90-114)	SYGGRG binding regions: pcbAB: 5; pcbC: 1; penDE: 7	243.5	195.3	159.9	111.5
Pc20g13890	similarity to hypothetical DNA-binding protein creA – Aspergillus oryzae			No domain identified		72.9	91.9	65.2	64.3
Pc22g17640	weak similarity to catabolite repressor creA - Aspergillus niger			No domain identified		45.4	52.8	73.2	36.7
Pc12g09670	strong similarity to hypothetical protein involved in carbon catabolite repression creC - Aspergillus nidulans		**CreC**. Repressor involved in carbon catabolite repression	WD40 domain, G-beta repeat (319-357), (361-399), (403-446)		145.2	172.0	125.9	136.3
Pc12g11600	GATA transcription factor nreB - Penicillium chrysogenum	**NITROGEN SOURCE**	**NreB.** Regulator of nitrogen metabolite repression	GATA zinc finger (17-51)	GATA binding regions: pcbAB: 3; pcbC: 2; penDE: 6	76.4	78.6	68.1	43.3
Pc22g24480	regulator of nitrogen metabolite repression nre - Penicillium chrysogenum [putative sequencing error]			Nitrogen regulatory protein AreA N terminus (1-73), GATA zinc finger (665-699)		182.5	149.6	144.4	113.1
Pc18g00420	transcription factor pacC - Penicillium chrysogenum	**pH**	**PacC**. Mediates regulation of genes in response to ambient pH	C2H2 (94-118), (124-146)	GCCARG binding regions: pcbAB: 3; pcbAB: 3; penDE: 3	211.5	171.5	219.2	151.2
Pc04g00010	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	**DEVELOPMENT**	**BrlA.** Required for activation of development	C2H2 (184-208), (214-239)	MRAGGGR binding regions: pcbAB: 1; pcbC: 1; penDE: 1	0.2	0.8	1.3	0.5
Pc06g00470	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans			C2H2 (321-345), (351-376)		299.2	306.6	69.6	22.2
Pc17g00170	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans			C2H2 (150-174), (180-204)		0.4	0.4	0.6	0.5
Pc22g26080	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans			C2H2 (202-226)		3.6	2.3	4.5	4.5
Pc22g26360	similarity to developmental regulatory protein brlA - Aspergillus nidulans [putative pseudogene]			No domain identified		0.5	1.8	3.4	1.6
Pc23g00400	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans			C2H2 (210-234), (240-264)		0.4	1.5	1.3	0.6
Pc24g00600	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans [putative sequencing error]			C2H2 (210-234), (240-264)		1.7	0.5	0.9	0.5
Pc24g00840	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans			C2H2 (238-262), (268-293)		0.4	1.3	0.8	0.3
Pc24g01490	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans			C2H2 (284-308)		1.5	3.0	1.2	3.4
Pc24g01720	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans			C2H2 (460-484), (490-515)		n.p.	n.p.	n.p.	n.p.
Pc24g02600	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans			C2H2 (210-234), (240-264)		12.4	10.6	12.4	8.1
Pc24g02650	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans [putative pseudogene]			C2H2 (29-53), (59-83)		5.7	5.4	9.3	19.7
Pc16g09610	strong similarity to protein abaA - Aspergillus nidulans		**AbaA**. Required for activation of development	TEA/ATTS (68-575)	CATTCY binding regions: pcbAB: 1	22.6	8.9	63.5	4.3
Pc12g01590	strong similarity to protein hapB - Aspergillus nidulans	**OTHERS**	**HAPB, HAPE, HAPC**. Heterotrimeric CCAAT-binding complex (PENR1-like)	CBF-B/NF-YA subunit B (228-285)	CCAAT binding regions: pcbAB: 4; pcbC: 2; penDE: 2	167.7	149.5	119.9	86.6
Pc12g04670	strong similarity to HAPE - Aspergillus oryzae			CBF/NF-Y and archaeal histone (86-150), Core histone H2A/H2B/ H3/H4 (80-153)		330.5	311.2	310.2	269.8
Pc14g01630	strong similarity to CCAAT-binding protein hapC - Aspergillus oryzae			CBF/NF-Y and archaeal histone (46-111)		339.7	388.1	289.1	316.3
Pc20g01690	transcription factor like protein RFX - Penicillium chrysogenum		**RFX**. Winged helix transcription factor, homologue to CPCR1	RFX DNA-binding domain (222-296)	X-box like binding regions (NNRCCNNRSYAAY): pcbAB: 1; pcbC: 1; penDE: 1	189.0	153.5	95.4	92.5
Pc16g14010	strong similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae		**LaeA**. Regulator of secondary metabolism	Methyltransferase domain (193-285)		365.6	361.9	373.8	395.3

@ Values given are the average of three independent experiments
n.p. No probeset present

Supplementary Table 18. PAA upregulated transporters

orf code	**Description of putative *P. chrysogenum* ORF**	**Best blast homolog to putative P. chrysogenum ORF**			**Average transcript levels @**			
		Species	**Gene code**	**e-value**	**WIS - PAA**	**WIS + PAA**	**DS - PAA**	**DS + PAA**
Pc13g10900	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	*Aspergillus fumigatus*	BX649605_57	1e-180	12	2661	33	2534
Pc16g02690	strong similarity to benomyl methotrexate resistance protein MDR1 - Candida albicans	*Aspergillus fumigatus*	BX649607_11	1e-78	12	281	12	910
Pc21g01300	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae	*Acremonium chrysogenum*	ACH487683_1	0.0	12	81	12	591
Pc12g13800	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	*Schizosaccharomyces pombe*	T41604	5e-80	12	483	12	471
Pc13g06330	similarity to hypothetical membrane protein YOL119c - Saccharomyces cerevisiae	*Neurospora crassa DNA*	NCB23B10_3	3e-51	12	160	26	355
Pc18g01290	strong similarity to dityrosine transporter Dtr1 - Saccharomyces cerevisiae	*Aspergillus terreus*	AF141925_12	3e-71	14	89	31	374
Pc12g13630	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	*Neurospora crassa*	BX842634_3	0.0	12	86	12	141
Pc13g10030	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	*Neurospora crassa*	NC64C2_19	1e-103	23	487	125	1344
Pc22g08750	strong similarity to mitomycin C translocase mct - Streptomyces lavendulae	*Neurospora crassa*	BX908808_43	1e-44	12	79	12	121
Pc21g14210	similarity to polyamine transport protein Tpo3 - Saccharomyces cerevisiae	*Schizosaccharomyces pombe*	T41018	2e-23	12	273	12	111
Pc16g09960	strong similarity to hypothetical protein contig_1_43_scaffold_2.tfa_610cg - Aspergillus nidulans	*Bdellovibrio bacteriovorus*	BX842647_291	6e-48	12	63	12	91
Pc21g19470	strong similarity to mitochondrial succinate-fumarate transporter Sfc1 - Saccharomyces cerevisiae	*Neurospora crassa*	BX897673_8	1e-125	25	344	48	361
Pc21g09220	strong similarity to fluconazole resistance transporter Flr1 - Saccharomyces cerevisiae	*Aspergillus fumigatus*	BX649607_11	4e-90	15	402	158	1119
Pc20g14390	strong similarity to mitochondrial phosphate transport protein G7 - Glycine max	*Saccharomyces cerevisiae*	S50556	1e-97	12	66	36	233
Pc20g06200	strong similarity to hypothetical membrane protein YIL166c - Saccharomyces cerevisiae	*Saccharomyces cerevisiae*	S50361	1e-118	12	26	96	526
Pc12g14890	strong similarity to fluconazole resistance protein FLU1 - Candida albicans	*Schizosaccharomyces pombe*	T41018	1e-123	12	67	18	95
Pc21g12990	strong similarity to polyamine transport protein Tpo1 - Saccharomyces cerevisiae	*Neurospora crassa*	BX908812_25	1e-149	12	93	40	202
Pc20g00130	strong similarity to myo-inositol transport protein Itr2 - Saccharomyces cerevisiae	*Neurospora crassa*	NCB17B1_7	1e-141	168	568	150	679
Pc21g05850	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	*Schizosaccharomyces pombe*	T41604	1e-84	22	101	127	554
Pc16g00500	strong similarity to hypothetical membrane protein YIL166c - Saccharomyces cerevisiae	*Neurospora crassa*	NC64C2_19	1e-43	33	71	178	717
Pc22g05400	strong similarity to hypothetical monocarboxylate permease Esbp6 - Saccharomyces cerevisiae	*Saccharomyces cerevisiae*	S38065	4e-76	23	89	67	267
Pc20g04510	similarity to multidrug resistance protein Hol1 - Saccharomyces cerevisiae	*Schizosaccharomyces pombe*	T39346	2e-39	12	44	12	42
Pc12g11990	strong similarity to fluconazole resistance transporter Flr1 - Saccharomyces cerevisiae	*Ustilago maydis*	UMPLOC_5	3e-79	54	172	63	214
Pc22g14600	strong similarity to ATP-binding cassette multidrug transport protein atrB - Aspergillus nidulans	*Botryotinia fuckeliana*	AB028872_1	0.0	35	399	176	567
Pc22g03710	strong similarity to hypothetical membrane protein YBR043c - Saccharomyces cerevisiae	*Neurospora crassa*	NCB8P8_18	1e-168	14	50	26	82
Pc22g20580	strong similarity to multidrug resistance protein Qdr1 - Saccharomyces cerevisiae	*Saccharomyces cerevisiae*	S49888	9e-67	12	141	53	163
Pc20g08470	strong similarity to protease Mch5 - Saccharomyces cerevisiae	*Neurospora crassa*	NCB23B10_3	8e-65	21	65	78	239
Pc16g00610	strong similarity to hypothetical membrane protein YMR088c - Saccharomyces cerevisiae	*Podospora anserina*	CNS07TIX_2	4e-91	55	122	220	657
Pc13g15950	strong similarity to choline permease Hnm1 - Saccharomyces cerevisiae	*Saccharomyces cerevisiae*	S11175	1e-59	12	62	12	34
Pc21g14260	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	*Schizosaccharomyces pombe*	SPBC1683_12	1e-120	44	88	407	1043
Pc06g01070	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae	*Neurospora crassa*	NCB19C19_12	1e-122	12	58	25	62
Pc18g05780	strong similarity to multidrug resistance protein fnx1p - Schizosaccharomyces pombe	*Schizosaccharomyces pombe*	T40380	9e-79	101	284	219	530
Pc21g12380	strong similarity to hypothetical neutral amino acid permease - Neurospora crassa	*Neurospora crassa*	S47892	2e-66	33	75	57	134
Pc21g05550	strong similarity to multidrug resistance protein fnx1p - Schizosaccharomyces pombe	*Neurospora crassa*	NCB13O8_14	5e-70	43	156	45	104
Pc16g12280	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae	*Aspergillus fumigatus*	BX649607_11	0.0	38	291	163	364
Pc18g03010	strong similarity to choline permease Hnm1 - Saccharomyces cerevisiae	*Saccharomyces cerevisiae*	S11175	1e-75	60	125	37	75

@ Values given are the average of three independent experiments

Supplementary Table 19. Upregulated Transporters in DS17690 vs Wisconsin and +PAA vs -PAA

orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels @			
		Species	**Gene code**	**e-value**	**WIS - PAA**	**WIS + PAA**	**DS - PAA**	**DS + PAA**
Pc16g02690	strong similarity to benomyl methotrexate resistance protein MDR1 - Candida albicans	*Aspergillus fumigatus*	BX649607_11	1.00E-78	12	281	12	910
Pc21g01300	strong similarity to membrane protein Tpo2 - Saccharomyces cerevisiae	*Acremonium chrysogenum*	ACH487683_1	0.0	12	81	12	591
Pc13g06330	similarity to hypothetical membrane protein YOL119c - Saccharomyces cerevisiae	*Neurospora crassa*	NCB23B10_3	3.00E-51	12	160	26	355
Pc18g01290	strong similarity to dityrosine transporter Dtr1 - Saccharomyces cerevisiae	*Aspergillus terreus*	AF141925_12	3.00E-71	14	89	31	374
Pc13g10030	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	*Neurospora crassa*	NC64C2_19	1.00E-103	23	487	125	1344
Pc21g09220	strong similarity to fluconazole resistance transporter Flr1 - Saccharomyces cerevisiae	*Aspergillus fumigatus*	BX649607_11	4.00E-90	15	402	158	1119
Pc20g14390	strong similarity to mitochondrial phosphate transport protein G7 - Glycine max	*Saccharomyces cerevisiae*	S50556	1.00E-97	12	66	36	233
Pc20g06200	strong similarity to hypothetical membrane protein YIL166c - Saccharomyces cerevisiae	*Saccharomyces cerevisiae*	S50361	1.00E-118	12	26	96	526
Pc21g12990	strong similarity to polyamine transport protein Tpo1 - Saccharomyces cerevisiae	*Neurospora crassa*	BX908812_25	1.00E-149	12	93	40	202
Pc21g05850	strong similarity to allantoate permease Dal5 - Saccharomyces cerevisiae	*Schizosaccharomyces pombe*	T41604	1.00E-84	22	101	127	554
Pc16g00500	strong similarity to hypothetical membrane protein YIL166c - Saccharomyces cerevisiae	*Neurospora crassa*	NC64C2_19	1.00E-43	33	71	178	717
Pc22g05400	strong similarity to hypothetical monocarboxylate permease Esbp6 - Saccharomyces cerevisiae	*Saccharomyces cerevisiae*	S38065	4.00E-76	23	89	67	267
Pc20g08470	strong similarity to protease Mch5 - Saccharomyces cerevisiae	*Neurospora crassa*	NCB23B10_3	8.00E-65	21	65	78	239
Pc16g00610	strong similarity to hypothetical membrane protein YMR088c - Saccharomyces cerevisiae	*Podospora anserina*	CNS07TIX_2	4.00E-91	55	122	220	657
Pc21g14260	strong similarity to high-affinity nicotinic acid permease Tna1 - Saccharomyces cerevisiae	*Schizosaccharomyces pombe*	SPBC1683_12	1.00E-120	44	88	407	1043

@ Values given are the average of three independent experiments

Supplementary Table 20. Regions with amplification or deletion in DS17690 vs. Wisconsin54-1255

The copy numbers and length are estimated. Only the genes with a putative functional annotation are listed per region. For most regions there are probe sets recognizing the both strands of large intergenic regions that confirm the copy number

Cluster #	Copy # estimate		Predicted ORFs spanned				
	Wis	DS17690	Start (ORF)	End (ORF)	Predicted # ORFs	Estimated length	**Remarks**
1	1	-	Pc09g00050	Pc09g00360	~30	~56kb	Pc0900010 is transposable element
	Pc09g00240 weak similarity to calcium-independent phospholipase A2 – H.sapiens Not expressed in DS17690						
2	2	1	Pc12g16490	Pc12g16580	~10	~24kb	Preceded by ORF “strong sim.to norsolorinic acid ketoreductase nor-1” End is border of contig
	Pc12g16490 strong similarity to cell polarity protein tea1p – S.pombe Pc12g16500 strong similarity to casein kinase-1 homolog hhp1p – S. pombe Pc12g16510 weak similarity to bZIP transcription factor Yap3 – S.cerevisiae Pc12g16520 strong similarity to phosducin homolog Plp2 – S.cerevisiae Pc12g16530 strong similarity to coatomer gamma subunit 2 copg2 - Homo sapiens Pc12g16540 strong similarity to cytosolic aspartate--tRNA ligase Dps1 – S. cerevisiae Pc12g16550 strong similarity to hypothetical phosphatidyl synthase – S. pombe Pc12g16560 similarity to hypothetical protein YDR306c – S.cerevisiae Pc12g16580 strong similarity to zinc-finger transcription factor Rdr1 – S.cerevisiae (all shared probe sets!) Expression ~2-fold higher in Wis than DS17690						
3	1	2	Pc13g04710	Pc13g04910	~21	~77kb	Adjacent to StuA developmental regulator
	Pc13g04720 weak similarity to vacuolar protein Vac7 – S. cerevisiae Pc13g04880 strong similarityto cytoplasmic ribosomal protein S. cerevisiae Pc13g04890 strong similarity to translational regulator HsGCN1 H. sapiens Pc13g04900 strong similarity to RNA helicase like protein A. niger Expression ~2-fold higher in DS17690 than Wis						
4	1	2	Pc16g15290	Pc16g15510	~24	~41kb	preceded by transposal element MARS Pc16g15280
	Pc16g15310 strong similarity to ORF1 of transposon Ant1 –A.niger Pc16g15440 weak similarity to ankyrin Ank2 - Homo sapiens Pc16g15470 strong similarity to P type ATPase ENA1 Pc16g15490 strong similarity to delta latroinsectotoxin like protein An08g12230 Expression for several of the ORFs is ~2-fold higher in DS17690 than Wis						
5	1	6	Pc21g21280	Pc21g21490	~22	~57kb	**Pen amplicon** Flanked by transposable elements, 21g21030,-40,-60,21g21240
	Pc21g21280 strong similarity to methyl sterol oxidase Erg25 - Saccharomyces cerevisiae Pc21g21370 acyl-coenzyme A:isopenicillin N acyltransferase (acyltransferase) AAT PenDE - Penicillium chrysogenum Pc21g21380 isopenicillin N synthase ips PcbC - Penicillium chrysogenum Pc21g21390 alpha-aminoadipyl-cysteinyl-valine synthetase pcbAB acvA - Penicillium chrysogenum [putative sequencing error] Expression of several ORFs is 2-12 fold higher in DS17690 than Wis						
6	1	-	Pc23g00800	Pc23g01020	~22		preceded by transposon Pc23g00700
	Pc23g00930 with similarity to transposase Not expressed in DS17690						

Supplementary Table 21. F Effect of gene silencing on b-lactam productivity

Category	Gene knock-out	Description	Pathway	Fold change Wisconsin54-1255 --> DS17690	Fold change without PAA --> with PAA	Relative b-lactam titer %	SD
control	none (DS17690)	-	-	-	-	100	± 0.09
control	Pc22g15510	strong similarity to ATP-dependent DNA helicase II subunit Ku70 - Mus musculus	NHEJ	0.9	1.1	99.8	± 0.09
1	Pc18g01330	strong similarity to saccharopine reductase LYS3 - Magnaporthe grisea	Lysine	2.2	1.6	no transformants*	-
1	Pc12g14370	strong similarity to lysine permease Lyp1 - Saccharomyces cerevisiae	Lysine	5.3	2.0	101.2	± 0.01
1	Pc16g10020	sulfate permease SutB - Penicillium chrysogenum	Cysteine	2.5	1.6	64.5	± 0.28
1	Pc22g16570	strong similarity to serine O-acetyltransferase cysA - Aspergillus nidulans	Cysteine	1.7	1.5	64.1	± 0.06
1	Pc22g23110	strong similarity to acetolactate synthase precursor ALS - Schizosaccharomyces pombe	Valine	8.4	1.0	no transformants*	-
2	Pc22g24780	strong similarity to 4-coumarate-CoA ligase 4CL - Arabidopsis thaliana	PAA activation	5.7	13.9	98.1	± 0.01
3	Pc20g02040	strong similarity to methicillin resistance gene HmrA - Staphylococcus aureus	Secretion	25.7	323.5	96.0	± 0.09
4	Pc21g04480	strong similarity to peroxisomal integral membrane protein Per8p - Pichia angusta	Peroxisome biogenesis	1.7	1.2	23.1	± 0.00
5	Pc12g13400	strong similarity to cephalosporin esterase - Rhodosporidium toruloides	b-lactam degradation	0.3	0.7	104.0	± 0.04
	Pc22g13680	strong similarity to hypothetical protein contig1495_1.tfa_1650cg - Aspergillus fumigatus	putative isopenicillinN-CoA epimerase	1.1	1.3	121.9	± 0.18
6	Pc16g01770	strong similarity to phenylacetate hydroxylase pahA - Penicillium chrysogenum	PAA degradation	1.3	46.1	95.3	± 0.00
7	Pc13g13200	strong similarity to dark repressor of conidiation velvet veA - Aspergillus nidulans	Regulation of sec metabolism	0.6	0.9	23.6	± 0.02

* = no transformants obtained; knock-out leads probably to an auxotroph, which is lethal on minimal acetamide selection plates

Supplementary Table 22. Orthologous genes from various fungal genome sequences to perform phylogenetic analysis and build sepcies tree

P. chrysogenum	P. marneffei	T. stipitatus	N. fischeri	A. clavatus	A. terreus	A. nidulans	A. oryzae	A. niger	G. zeae	A. fumigatus	Protein name
Pc22g25570	PMAA_051070	TSTA_021840	NFIA_021750	ACLA_031360	ATEG_02520	AN0272.3	AO090005000779	An01g05030	XP_380532.1	AFUA_1G02880	Phosphotransferase enzyme family domain protein
Pc13g03220	PMAA_053390	TSTA_019540	NFIA_021230	ACLA_031190	ATEG_02545	AN0259.3	AO090005000758	An01g04710	XP_389338.1	AFUA_1G03420	adenylate kinase Adk2, putative
Pc18g02590	PMAA_055450	TSTA_017480	NFIA_021070	ACLA_031030	ATEG_03104	AN4053.3	AO090009000419	An18g04110	XP_380924.1	AFUA_1G03590	importin 11, putative
Pc16g09250	PMAA_054260	TSTA_018720	NFIA_020210	ACLA_030130	ATEG_03746	AN0432.3	AO090003000873	An01g03570	XP_381102.1	AFUA_1G04540	NADH-cytochrome b5 reductase, putative
Pc21g07860	PMAA_024950	TSTA_033650	NFIA_019390	ACLA_029290	ATEG_03094	AN3895.3	AO090009000410	An18g04200	XP_383842.1	AFUA_1G05360	CAIB/BAIF family enzyme
Pc13g02760	PMAA_019960	TSTA_027970	NFIA_018480	ACLA_028290	ATEG_02990	AN4232.3	AO090001000427	An18g05140	XP_384203.1	AFUA_1G06230	ribosome biogenesis protein Ssf2, putative
Pc18g03350	PMAA_026300	TSTA_072610	NFIA_017990	ACLA_027870	ATEG_02957	AN5711.3	AO090001000465	An18g05750	XP_386525.1	AFUA_1G06690	RLI and DUF367 domain protein
Pc12g15080	PMAA_097790	TSTA_043320	NFIA_013440	ACLA_023490	ATEG_00405	AN1074.3	AO090001000337	An08g04390	XP_388527.1	AFUA_1G12070	glycine cleavage system H protein
Pc13g12860	PMAA_098210	TSTA_043060	NFIA_013260	ACLA_023210	ATEG_00423	AN1066.3	AO090001000304	An08g04880	XP_380839.1	AFUA_1G12250	mitochondrial hypoxia responsive domain protein
Pc13g11340	PMAA_068210	TSTA_088490	NFIA_012800	ACLA_022710	ATEG_00465	AN0999.3	AO090012000638	An08g05530	XP_382099.1	AFUA_1G12760	adenylyl cyclase-associated protein (cap)
Pc13g11860	PMAA_067400	TSTA_087550	NFIA_012140	ACLA_022060	ATEG_00539	AN0675.3	AO090012000545	An08g06440	XP_390392.1	AFUA_1G13370	aflatoxin B1-aldehyde reductase GliO-like, putative
Pc16g14390	PMAA_074230	TSTA_094780	NFIA_010480	ACLA_020420	ATEG_00856	AN0834.3	AO090005001238	An01g13070	XP_386820.1	AFUA_1G14940	protein translocation complex componenet (Npl1), putative
Pc21g22200	PMAA_066770	TSTA_086870	NFIA_008900	ACLA_019050	ATEG_05152	AN0956.3	AO090005001057	An01g10700	XP_387393.1	AFUA_1G16550	dihydrouridine synthase family protein, putative
Pc21g23610	PMAA_075880	TSTA_096320	NFIA_008390	ACLA_018520	ATEG_05095	AN0632.3	AO090005000976	An01g09860	XP_382709.1	AFUA_1G16990	mRNA splicing factor (Prp18), putative
Pc20g05910	PMAA_021980	TSTA_030260	NFIA_033510	ACLA_094520	ATEG_08153	AN7659.3	AO090701000397	An10g00360	XP_390263.1	AFUA_2G01210	ATP dependent RNA helicase (Dbp5), putative
Pc20g04400	PMAA_087690	TSTA_123080	NFIA_034500	ACLA_092690	ATEG_05703	AN4592.3	AO090011000488	An07g06770	XP_390021.1	AFUA_2G02130	fatty acid desaturase, putative
Pc18g04190	PMAA_055810	TSTA_016580	NFIA_035460	ACLA_091730	ATEG_09581	AN10563.3	AO090120000280	An07g07520	XP_384328.1	AFUA_2G03110	alkaline phosphatase Pho8
Pc18g04290	PMAA_055920	TSTA_016480	NFIA_035530	ACLA_091380	ATEG_09575	AN4510.3	AO090120000268	An07g07610	XP_380992.1	AFUA_2G03170	cyclic nucleotide-binding domain protein
Pc18g06270	PMAA_057540	TSTA_014440	NFIA_080890	ACLA_090430	ATEG_03666	AN5226.3	AO090005001538	An07g08810	XP_389550.1	AFUA_2G04080	GPR/FUN34 family protein
Pc13g04590	PMAA_070510	TSTA_090910	NFIA_083870	ACLA_080050	ATEG_09660	AN6176.3	AO090011000883	An05g00810	XP_380686.1	AFUA_2G08190	tubulin-specific chaperone Rbl2, putative
Pc13g04560	PMAA_070660	TSTA_090960	NFIA_083890	ACLA_080070	ATEG_09663	AN4180.3	AO090011000881	An05g00850	XP_380271.1	AFUA_2G08230	MFS transporter, putative
Pc13g04480	PMAA_070690	TSTA_091000	NFIA_083950	ACLA_080130	ATEG_09667	AN6170.3	AO090011000874	An05g00880	XP_390566.1	AFUA_2G08300	DnaJ domain protein, putative
Pc13g04040	PMAA_070950	TSTA_091380	NFIA_084220	ACLA_080430	ATEG_09696	AN6139.3	AO090011000843	An12g03960	XP_386818.1	AFUA_2G08600	1-acylglycerol-3-phosphate acyltransferase (AtaAp), putative
Pc13g03600	PMAA_071300	TSTA_091820	NFIA_084530	ACLA_080810	ATEG_09879	AN10472.3	AO090011000799	An12g04660	XP_387440.1	AFUA_2G08970	thiamine biosynthetic bifunctional enzyme, putative
Pc22g19950	PMAA_087090	TSTA_122460	NFIA_085350	ACLA_068990	ATEG_04429	AN6014.3	AO090011000642	An16g05150	XP_388719.1	AFUA_2G09910	fatty acid activator Faa4, putative
Pc22g20960	PMAA_047680	TSTA_037480	NFIA_085890	ACLA_069530	ATEG_01520	AN9470.3	AO090011000588	An02g06030	XP_384302.1	AFUA_2G10520	urate oxydase UaZ
Pc22g20850	PMAA_048100	TSTA_038000	NFIA_085960	ACLA_069600	ATEG_01513	AN5971.3	AO090011000578	An02g05880	XP_382117.1	AFUA_2G10600	NADH-ubiquinone oxidoreductase 299 kDa subunit, putative
Pc15g00450	PMAA_048570	TSTA_038630	NFIA_086590	ACLA_070280	ATEG_01445	AN5881.3	AO090026000518	An02g03290	XP_389764.1	AFUA_2G11320	conserved hypothetical protein
Pc15g00160	PMAA_048990	TSTA_038950	NFIA_086780	ACLA_070510	ATEG_01423	AN5861.3	AO090026000492	An02g03570	XP_385846.1	AFUA_2G11540	ketoreductase, putative
Pc20g13910	PMAA_092000	TSTA_049820	NFIA_087050	ACLA_070760	ATEG_01121	AN6200.3	AO090026000462	An02g03860	XP_381729.1	AFUA_2G11810	pre-rRNA processing protein Rrp12, putative
Pc20g14410	PMAA_092250	TSTA_049580	NFIA_087290	ACLA_070990	ATEG_01147	AN10806.3	AO090026000435	An02g04180	XP_386935.1	AFUA_2G12110	YagE family protein
Pc20g14430	PMAA_092270	TSTA_049560	NFIA_087310	ACLA_071010	ATEG_01149	AN6312.3	AO090026000433	An02g04200	XP_387432.1	AFUA_2G12130	conserved hypothetical protein
Pc12g07590	PMAA_092870	TSTA_048790	NFIA_088070	ACLA_071710	ATEG_01247	AN6265.3	AO090026000345	An02g01600	XP_384580.1	AFUA_2G12890	small nucleolar ribonucleoprotein complex subunit, putative
Pc12g07260	PMAA_076170	TSTA_096550	NFIA_088310	ACLA_071950	ATEG_01283	AN6244.3	AO090026000270	An02g01970	XP_391055.1	AFUA_2G13130	3' exoribonuclease family protein (Rrp42), putative
Pc12g13220	PMAA_022660	TSTA_031180	NFIA_089540	ACLA_073120	ATEG_01049	AN2406.3	AO090023000078	An03g03570	XP_388175.1	AFUA_2G14370	conserved hypothetical protein
Pc14g00060	PMAA_099060	TSTA_042050	NFIA_002920	ACLA_062780	ATEG_09071	AN3776.3	AO090103000095	An13g03680	XP_384132.1	AFUA_3G01840	MFS transporter, putative
Pc20g08410	PMAA_004660	TSTA_103160	NFIA_071470	ACLA_033730	ATEG_08962	AN3432.3	AO090020000042	An11g10890	XP_386235.1	AFUA_3G05740	aldose 1-epimerase, putative
Pc20g03160	PMAA_003380	TSTA_101100	NFIA_070650	ACLA_034560	ATEG_08758	AN4774.3	AO090020000339	An11g09700	XP_389624.1	AFUA_3G06600	siroheme synthase, putative
Pc20g02750	PMAA_002730	TSTA_100180	NFIA_070300	ACLA_034910	ATEG_08726	AN4802.3	AO090020000298	An02g13850	XP_389071.1	AFUA_3G06960	60S ribosomal protein L21, putative
Pc12g15750	PMAA_025630	TSTA_073360	NFIA_067520	ACLA_037580	ATEG_04499	AN5008.3	AO090005001272	An16g03410	XP_390969.1	AFUA_3G09780	conserved hypothetical protein
Pc12g15510	PMAA_025890	TSTA_073120	NFIA_067320	ACLA_037810	ATEG_04520	AN4990.3	AO090003000529	An16g03690	XP_387855.1	AFUA_3G09970	vacuolar iron transporter Ccc1, putative
Pc18g00590	PMAA_023810	TSTA_032240	NFIA_066580	ACLA_038600	ATEG_04600	AN4918.3	AO090003000616	An02g06370	XP_380999.1	AFUA_3G10710	conserved hypothetical protein
Pc18g01280	PMAA_021160	TSTA_029300	NFIA_065580	ACLA_039630	ATEG_04715	AN2877.3	AO090003000735	An02g07570	XP_382947.1	AFUA_3G11750	oxysterol binding protein (Osh5), putative
Pc13g09990	PMAA_015840	TSTA_023780	NFIA_064820	ACLA_040320	ATEG_04144	AN3095.3	AO090005000720	An02g08420	XP_390899.1	AFUA_3G12480	conidiophore development protein HymA
Pc13g14200	PMAA_019550	TSTA_027550	NFIA_064180	ACLA_040880	ATEG_04092	AN3178.3	AO090012000818	An02g09020	XP_381003.1	AFUA_3G13150	deacetylase complex subunit Sds3, putative
Pc20g00270	PMAA_028270	TSTA_070570	NFIA_110210	ACLA_045220	ATEG_06826	AN4303.3	AO090023001003	An04g00140	XP_384747.1	AFUA_4G05940	choline phosphate cytidylyltransferase Muq1, putative
Pc22g17740	PMAA_027920	TSTA_070900	NFIA_109510	ACLA_045950	ATEG_05558	AN4382.3	AO090023000914	An04g01100	XP_390498.1	AFUA_4G06710	ATP binding protein
Pc22g18450	PMAA_027040	TSTA_071920	NFIA_108970	ACLA_046570	ATEG_05486	AN4434.3	AO090023000850	An04g01650	XP_381829.1	AFUA_4G07250	37S ribosomal protein Rsm25
Pc13g08120	PMAA_058180	TSTA_013640	NFIA_107810	ACLA_047720	ATEG_05361	AN1721.3	AO090023000724	An04g03130	XP_380452.1	AFUA_4G08350	monosaccharide-P-dolichol utilization protein, putative
Pc18g03540	PMAA_056430	TSTA_015860	NFIA_107080	ACLA_048460	ATEG_05305	AN1639.3	AO090023000652	An04g04040	XP_381261.1	AFUA_4G09090	thioredoxin, putative
Pc22g12070	PMAA_097180	TSTA_043980	NFIA_106100	ACLA_049170	ATEG_00748	AN2056.3	AO090003001239	An04g07080	XP_386925.1	AFUA_4G09950	conserved hypothetical protein
Pc22g12080	PMAA_097090	TSTA_044080	NFIA_106090	ACLA_049180	ATEG_00747	AN2055.3	AO090003001238	An04g07090	XP_386912.1	AFUA_4G09960	conserved hypothetical protein
Pc22g05070	PMAA_041980	TSTA_076270	NFIA_104300	ACLA_050970	ATEG_03872	AN3629.3	AO090003001022	An01g07220	XP_388627.1	AFUA_4G11930	formamidopyrimidine-DNA glycosylase, putative
Pc22g05310	PMAA_042160	TSTA_076450	NFIA_104090	ACLA_051170	ATEG_03851	AN3649.3	AO090003000992	An01g07430	XP_381466.1	AFUA_4G12170	50S ribosomal protein L2
Pc21g14680	PMAA_081490	TSTA_115970	NFIA_040040	ACLA_003190	ATEG_09826	AN8049.3	AO090003001313	An02g11200	XP_387085.1	AFUA_5G02080	NADH-ubiquinone oxidoreductase subunit, putative
Pc21g18850	PMAA_080940	TSTA_115540	NFIA_039360	ACLA_002420	ATEG_09241	AN8119.3	AO090102000391	An02g09940	XP_387546.1	AFUA_5G02740	alpha-1,2-mannosyltransferase (Ktr4), putative
Pc21g18830	PMAA_080920	TSTA_115520	NFIA_039340	ACLA_002400	ATEG_09244	AN8117.3	AO090102000393	An02g09910	XP_387523.1	AFUA_5G02760	fatty acid elongase (Gns1), putative
Pc21g15910	PMAA_082230	TSTA_116920	NFIA_038640	ACLA_001700	ATEG_08067	AN8215.3	AO090102000557	An09g05860	XP_387303.1	AFUA_5G03480	methylenetetrahydrofolate reductase
Pc22g13980	PMAA_083530	TSTA_118420	NFIA_038120	ACLA_001180	ATEG_08011	AN8253.3	AO090102000602	An09g06180	XP_389213.1	AFUA_5G04000	proteasome maturation ans ribosome synthesis protein Nop10, putative
Pc12g05480	PMAA_095350	TSTA_045900	NFIA_037890	ACLA_000950	ATEG_07992	AN8273.3	AO090102000625	An09g06650	XP_380820.1	AFUA_5G04210	ubiquinol-cytochrome C reductase complex core protein 2, putative
Pc21g18000	PMAA_084770	TSTA_119810	NFIA_079930	ACLA_010590	ATEG_09344	AN2238.3	AO090701000219	An17g00770	XP_385309.1	AFUA_5G07340	DnaJ domain protein Psi, putative
Pc22g15750	PMAA_084090	TSTA_119180	NFIA_079330	ACLA_012550	ATEG_08330	AN7736.3	AO090701000709	An03g04080	XP_389021.1	AFUA_5G07960	C2H2 finger and ankyrin domain protein, putative
Pc21g10360	PMAA_073410	TSTA_093810	NFIA_076460	ACLA_013770	ATEG_07632	AN2751.3	AO090010000464	An14g03890	XP_389839.1	AFUA_5G10770	topisomerase II associated protein (Pat1), putative
Pc21g06050	PMAA_033130	TSTA_064500	NFIA_076130	ACLA_014180	ATEG_07684	AN0191.3	AO090026000732	An01g02210	XP_384450.1	AFUA_5G11130	PAXNEB protein superfamily

Pc21g06450	PMAA_030810	TSTA_067430	NFIA_075690	ACLA_014650	ATEG_02113	AN0138.3	AO090026000670	An18g03180	XP_391038.1	AFUA_5G11580	transcription factor TFIIH subunit Tfb4, putative
Pc21g06870	PMAA_031000	TSTA_067230	NFIA_075520	ACLA_014820	ATEG_02094	AN0121.3	AO090120000294	An18g02970	XP_389153.1	AFUA_5G11760	hydroxymethylbilane synthase, putative
Pc21g07110	PMAA_031210	TSTA_067000	NFIA_075300	ACLA_015010	ATEG_02076	AN0105.3	AO090120000318	An18g02370	XP_389830.1	AFUA_5G11985	eukaryotic translation initation factor eIF1a-like protein, putative
Pc21g07430	PMAA_072220	TSTA_092770	NFIA_074990	ACLA_015280	ATEG_02048	AN0075.3	AO090120000344	An18g02020	XP_387356.1	AFUA_5G12260	disulfide isomerase (TigA), putative
Pc21g04300	PMAA_071960	TSTA_092530	NFIA_074670	ACLA_015590	ATEG_02015	AN0056.3	AO090120000378	An14g06670	XP_382665.1	AFUA_5G12530	arrestin (or S-antigen), N-terminal domain protein
Pc21g03150	PMAA_036920	TSTA_055260	NFIA_073060	ACLA_016910	ATEG_06135	AN6920.3	AO090113000079	An14g05310	XP_391008.1	AFUA_5G13890	SNF7 family protein
Pc22g24340	PMAA_018790	TSTA_026810	NFIA_048320	ACLA_098430	ATEG_07240	AN8676.3	AO090120000095	An12g08730	XP_388872.1	AFUA_6G02110	SRF-type transcription factor (Umc1), putative
Pc22g23790	PMAA_018440	TSTA_026470	NFIA_048700	ACLA_098030	ATEG_07208	AN8704.3	AO090120000131	An12g07830	XP_388852.1	AFUA_6G02440	60S ribosomal protein L24a
Pc20g13010	PMAA_017950	TSTA_025990	NFIA_050480	ACLA_096610	ATEG_07054	AN6614.3	AO090701000148	An15g01510	XP_385325.1	AFUA_6G03950	phospholipid-translocating P-type ATPase, putative
Pc20g12570	PMAA_018110	TSTA_026150	NFIA_050630	ACLA_096430	ATEG_07037	AN6599.3	AO090701000133	An15g01330	XP_387080.1	AFUA_6G04090	DUF28 domain protein
Pc12g04760	PMAA_011510	TSTA_005630	NFIA_051780	ACLA_095330	ATEG_05654	AN6500.3	AO090701000014	An15g00080	XP_382679.1	AFUA_6G05200	60S ribosomal protein L28
Pc22g13280	PMAA_073030	TSTA_093480	NFIA_054060	ACLA_082260	ATEG_05813	AN3923.3	AO090001000497	An11g01610	XP_381370.1	AFUA_6G08420	ubiquitin-protein ligase E3 component (UBR1), putative
Pc12g11370	PMAA_029790	TSTA_068650	NFIA_054280	ACLA_083780	ATEG_06604	AN9512.3	AO090001000524	An11g05700	XP_387040.1	AFUA_6G08630	mitochondrial protein, putative
Pc21g20430	PMAA_035630	TSTA_056610	NFIA_056370	ACLA_084330	ATEG_02371	AN2441.3	AO090023000210	An11g00460	XP_384444.1	AFUA_6G10600	ubiquitin-like activating enzyme (UlaA), putative
Pc22g04060	PMAA_080130	TSTA_114700	NFIA_058290	ACLA_085580	ATEG_03285	AN3737.3	AO090009000186	An06g01480	XP_388025.1	AFUA_6G12330	WD domain protein
Pc22g02350	PMAA_077960	TSTA_112390	NFIA_059110	ACLA_086430	ATEG_03352	AN5493.3	AO090003000443	An08g10300	XP_390707.1	AFUA_6G13190	NupC family nucleoside cotransporter
Pc22g00860	PMAA_062870	TSTA_082450	NFIA_059530	ACLA_086870	ATEG_03406	AN5440.3	AO090103000329	An08g08720	XP_390782.1	AFUA_6G13570	cytochrome c peroxidase, putative
Pc21g12230	PMAA_010440	TSTA_006720	NFIA_114740	ACLA_065510	ATEG_01829	AN9108.3	AO090038000578	An12g00660	XP_389216.1	AFUA_7G02010	indoleamine 2,3-dioxygenase family protein
Pc21g11500	PMAA_011130	TSTA_006070	NFIA_115310	ACLA_064960	ATEG_01886	AN9057.3	AO090311000001	An09g03040	XP_380881.1	AFUA_7G02600	conserved hypothetical protein
Pc21g04880	PMAA_069380	TSTA_089580	NFIA_024940	ACLA_005680	ATEG_04279	AN4259.3	AO090026000816	An13g00430	XP_387298.1	AFUA_7G03980	PCI domain protein
Pc21g04340	PMAA_069250	TSTA_089450	NFIA_025290	ACLA_006020	ATEG_04313	AN5675.3	AO090005000117	An13g00870	XP_385911.1	AFUA_7G04320	UBX domain protein (Ubx5), putative
Pc21g08790	PMAA_088500	TSTA_123800	NFIA_025500	ACLA_006230	ATEG_04342	AN6817.3	AO090005000137	An13g01120	XP_391096.1	AFUA_7G04530	alcohol dehydrogenase, zinc-containing
Pc12g06170	PMAA_091190	TSTA_050820	NFIA_026670	ACLA_007150	ATEG_06387	AN6698.3	AO090005000411	An07g02690	XP_385155.1	AFUA_7G05460	conserved hypothetical protein
Pc16g01080	PMAA_060730	TSTA_010590	NFIA_096460	ACLA_042950	ATEG_10389	AN8881.3	AO090010000768	An03g06860	XP_381208.1	AFUA_8G02760	mitochondrial ornithine carrier protein AmcA/Ort1, putative
Pc21g11120	PMAA_060250	TSTA_011290	NFIA_096990	ACLA_057610	ATEG_00039	AN1442.3	AO090103000044	An16g08830	XP_381391.1	AFUA_8G04260	translocation protein (Sec66), putative
Pc20g09960	PMAA_059540	TSTA_012190	NFIA_097700	ACLA_058300	ATEG_00107	AN1491.3	AO090005000655	An16g07940	XP_382708.1	AFUA_8G04880	COP9 signalosome subunit 1 (CsnA), putative

Title

Molecular analysis of a microbial strain improvement paradigm:

Genome sequencing and analysis of *Penicillium chrysogenum* Wisconsin54-1255

SUPPLEMENTARY DATA

Genome assembly. Approximately 99% of the *P. chrysogenum* genome is represented by the 14 largest scaffolds (greater than 100 kb). Previous studies identified at least four chromosomes in *P. chrysogenum*[1]. Most fungi contain from 7 to 20 chromosomes[2,3], whereas many closely related *Aspergillus* species contain eight chromosomes[4-6]. Preliminary attempts to use PCR amplification of the sequence gaps to elucidate their sequence and to link individual contigs, identified that many of gaps consist of repetitive DNA hampering a solid understanding of these.

Genome sequence and analysis. We have identified a total of 145 nuclear genome encoded tRNA genes, corresponding to 19 amino acids (**Table 1**). The tRNA gene(s) for tryptophan is (are) missing and most likely in gaps in the sequence. The tRNA genes are scattered all over the genome, although sometimes small clusters of 2-3 tRNAs are observed. **Supplementary Tables 23 and 24** present the specificity and codon usage of the identified tRNA genes, which differs from the published usage[7] (**Supplementary Table 25**). Previously, mycovirus sequences were isolated from the type strain NRRL1951[8], although there was no evidence for a genomic integration. We have detected no mycovirus sequence in the genome sequence of Wiscons54-1255. As there were already a dozen mutagenesis treatments needed to obtain the Wiscon54-1255 strain from NRRL1951 the virus might very well be lost.

Fungal genome comparison. The most conserved functional categories between the different fungi are cell cycle and protein synthesis (**Supplementary Fig. 1**). Compared to all other fungal genomes about 65-94% of these *P. chrysogenum* proteins have an ortholog. *P. chrysogenum* proteins involved in cell rescue, transport and metabolism show a larger number of unique proteins. *P. chrysogenum* proteins that have not been assigned to any functional category due to lack of homologies or functionally described protein domains show the lowest number of orthologs in other fungal genomes.

Supplementary Fig. 2 summarizes the functional classification of *P. chrysogenum* specific ORFs and ORFs with orthologs. Proteins related to TCA cycle and respiration are highly conserved over all fungal genomes (**Supplementary Fig. 3**), including *P. chrysogenum*. In contrast, proteins related to biosynthesis of antibiotics, polyketides, metabolism of aliphatic hydrocarbon compounds, and catabolism of aromatic compounds have generally only few orthologs in other fungal genomes.

Drug and ABC transporters of *P. chrysogenum* show only few orthologs in other fungal genomes, whereas electron/hydrogen carrier proteins, lipid transporter and ion channels are more conserved (**Supplementary Fig. 4**).

Life cycle and sex genes. The comparison of the *P. chrysogenum* and *A. fumigatus* Af293 genomes confirmed the presence of over 40 previously identified euascomycete sex genes (data not shown). The divergence of these genes at the amino acid level is similar to average for these genomes (data not shown). The *P. chrysogenum* mating (MAT) locus contains the MAT1 (alpha-domain) gene, which determines the mating type, confirming the recently reported findings[9].

Horizontal Gene Transfer (HGT). The origin of the isopenicillinN gene *pcbC.*
HGT of *pcbC* from Gram-positive bacteria to fungi has been concluded from sequence similarities with the “evolutionary distance argument” and the “topological argument”. In the evolutionary distance argument[10] the similarity at the DNA- and protein level of 4 isopenicillinN synthase (IPNS) and the highly invariable proteins glyceraldehyde-3-phosphate dehydrogenase, triose phosphate isomerase, Hsp70 and Hsp83 was compared, concluding that HGT from a prokaryotic source to a eukaryotic precursor of *Penicillium*, *Aspergillus* and *Acremonium* took place about 370 Mio years ago. This estimate has been based on the respective DNA-sequences and a nucleotide substitution rate of 10^{-9} nucleotide exchanges per site and year[11]. A similar conclusion was obtained using 5S rRNA gene sequences as internal control[12,13]. However, when the related deacetoxycephalosporin C synthetase (DAOCS) and IPNS proteins were taken as orthologs (based on an average amino acid identity of 57%) it was concluded to be ordinary evolution with duplication of genes without HGT[14]. However, sequence based trees clearly support HGT for the IPNS-encoding genes from Gram-positives to fungi, followed by adaptation to the fungal background. The branching date between the fungal and prokaryotic IPNS-encoding sequences was estimated to be 852 ± 106 Mio

years based on a maximum likelihood approach[15]. Still, some questions remain open. To what fungal ancestor did gene transfer take place? Were there several independent transfers, e.g. to *Aspergillus/Penicillium* ancestors and *Acremonium/Kallichcroma* ancestors? Why are α-aminoadipoyl-L-cysteinyl-D-valine synthetase (ACVS) and IPNS of *Penicillium* more similar to *A. oryzae* than to *A. nidulans*? If vertical inheritance would be the case, the *pcbAB*- and *pcbC*-related genes should have been lost from all groups of present organisms except the small number of ß-lactam producers.

The origin of the ACV synthetase gene pcbAB. As *pcbAB* and *pcbC* are always linked, a common (bacterial) origin is likely. Neighbour Joining (NJ)-trees based on their amino acid structure are very similar (**Supplementary Fig. 5**). Sequence identities/similarities for different ACVS proteins compared to *P. chrysogenum* are:

	Pchr	Aory	Anid	Acep	Ktet	Nlac	Llys
Pchr	100	79/88	67/80	54/70	53/69	44/61	41/59
Aory		100	66/80	55/70	53/69	53/61	52/60
Anid			100	52/68	51/67	43/60	41/59
Acep				100	63/77	43/60	41/58
Ktet					100	42/59	49/58
Nlac						100	53/67
Llys							100

Pchr = *Penicillium chrysogenum*
Aory = *Aspergillus oryzae*
Anid = *Aspergillus nidulans*
Acep = *Acremonium cephalosporium*
Ktet = *Kallichroma tethys*
Nlac = *Nocardia lactamdurans*
Llys = *Lysobacter lactamgenus*

If non-identical domains are aligned (this means module 1, used for aminoadipate, against module 2, for cysteine, or 3, for valine), identities shrink to about 30%. Likewise all other Non-Ribosomal Peptide Synthetase (NRPS) systems regardless of bacterial or fungal origin, have identities below 31%, which seems to be a threshold due to conservation of functional motifs. Thus fungal and bacterial ACVS have at least 41% identity at the amino acid level (being the lowest value of the above comparison). For

IPNS, the identities are significantly higher, presumably due to a higher constraint on functionality:

	Pchr	Aory	Anid	Acep	Ktet	Nlac	Llys
Pchr	100	89/93	80/89	76/87	73/84	57/72	55/71
Aory		100	85/92	77/89	74/85	58/73	56/72
Anid			100	74/85	72/84	60/74	56/73
Acep				100	81/87	57/72	55/69
Ktet					100	57/72	55/71
Nlac						100	60/73
Llys							100

Pchr = *Penicillium chrysogenum*
Aory = *Aspergillus oryzae*
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Nlac = *Nocardia lactamdurans*
Llys = *Lysobacter lactamgenus*

Within certain domain regions of ACVS, similar high conservations can be detected. Closely IPNS-related oxoglutarate-Fe(II) oxygenases have again less than 31% identity (*Stigmatella aurantiaca*), which is very similar comparing ACVS to non-related NRPS.

Does the GC-content of these genes point to their bacterial origin? Although sometimes brought forward, there is no evidence for non-fungal GC-content:

Region	Length (bp)	GC content
Upstream	9271	49%
*penDE*_exon1	711	**56%**
*penDE*_intron1	59	37%
*penDE*_exon2	162	**53%**
*penDE*_intron2	68	51%
*penDE*_exon3	175	**54%**
*penDE*_intron3	64	44%
*penDE*_exon4	46	**47%**
Intergenic1	1489	51%
pcbC	1005	**57%**

Intergenic2	1015	53%
pcbAB	11371	**54%**
Downstream	14714	47%

For *P. chrysogenum* the overall GC content is 48.9%, 52.8% when only considering the exons, 45.3% for introns, and 44.4% for intergenic regions. Here, it is thus only slightly higher. The *penDE* gene, always considered to be the eukaryotic gene of this biosynthetic cluster, also has a somewhat higher GC-content. However, the GC content of *lys2*[16], considered a typical fungal gene of primary metabolism, is with 54% also above the average. The *pcbAB* gene from *A. nidulans* has a GC content of only 50%, compared to a 53.3% average of coding regions (overall genome is 50.3%). The *pcbAB* gene from *A. oryzae* has a GC content of 52 %, and the *penDE* 54%, while the overall genome value is 48.2%; the exons of an adjacent ankyrin-repeat gene have a GC content of 48% GC. So, there are no clear indications for an increased GC content of the penicillin biosynthetic genes of several fungi.

Why is the penDE gene linked to pcbAB and pcbC? pcbAB and *pcbC* have been found linked in all known pro- and eukaryotic systems studied so far and represents a fairly large syntenic region due to the size of the NRPS gene. Strikingly, although the genes are linked, their orientation differs in fungi from bacteria, as fungi have a bi-directional promoter region. The acyl transferase (*penDE*) is only linked in systems producing penicillins, which are restricted so far to the mitosporic Trichocomaceae within the class Eurotiomycetes, including strains of Aspergilli and Penicillia. The gene is not found in bacteria and ß-lactam producing ascomycetes of the class Sordariomycetes, with the known examples *Acremonium chrysogenum* and *Kallichroma tethys*. In Sordariomycetes an additional bacterial gene of ß-lactam clusters is found (*cefEF*), implying multiple gene transfer events[17]. Alternatively all genes could have been transferred in a single event and lost in Eurotiomycetes. IPN epimerase is another gene from the bacterial ß-lactam pathway with a possible homolog in the *P. chrysogenum* genome, Pc12g11540 (*cefD S. clavuligerus*, see **Supplementary Table 6**), which more likely represents a fungal aminotransferase not related to penicillin with some sequence homology to IPN epimerase. Since *penDE* contains 3 introns a eukaryotic origin has been suggested. Association with the ß-lactam cluster is thought to be an example of the selfish cluster hypothesis, providing the advantage of process stabilization[18]. At least in industrial selection programmes this biosynthetic cluster did permit the coordinated amplification of all 3 genes[19].

Blastp analysis of acyl-coenzyme A:Isopenicillin N acyltransferase (AT) recovers a set of early branching bacterial and fungal members, where close homologues represent a subset of the fungal branch, restricted to the ACVS-IPNS associated genes in *A. nidulans, A. oryzae, A. flavus* and *P. chrysogenum*. Functions of other fungal branches are unknown. Most enzymes, also bacterial ones, have the Gly-Cys cleavage site required for autocatalytic activation. A distance tree clearly supports *penDE* as a eukaryotic/fungal gene. The AT-branch could be considered as recruitment of a hydrolase/transferase to facilitate side chain exchange of IPN in the microbody compartment, which also requires IPN import. Both the *P. chrysogenum* and *A. oryzae* AT have C-terminal microbody targeting sequences (ARL and AKL, respectively), while the *A. nidulans* targeting sequence is less obvious (ANI).

Are there other genes of bacterial origin involved in secondary processes? Arsenate reductase ArsC. The *A. fumigatus* genome hosts 2 orthologous arsenite resistance clusters combining arsenate reductase, thought to be of actinobacterial origin, an arsenite efflux transporter and an arsenic methyltransferase, both fungal genes, and an arsenic resistance protein, presumably proteobacterial origin[20]. Only the reductase genes contain no introns. Historically, *Penicillium* has been connected with notorious arsenic fungi in 1892 (a rat exposed to the vapor of fungi grown on arsenic compounds was quickly killed – a sort of gaseous antibiotic), although it is not clear if the respective strain has been *Penicillium* or *Scopulariopsis*[21]. In *P. chrysogenum* an arsenite resistance cluster is located between two retrotransposon homologs (Pc06g02160 and Pc06g02260):

Gene-ID	Protein	Introns	Protein Length	Identities
Pc06g02170	ArsH	1	286	*A. terreus* 80%, *A fumigatus* 80%
Pc06g02180	?	0	236	low sim to fungal proteins (>31%)
Pc06g02190	ArsH-fragment	1	110	*A. clavatus* 32% (315 AA)
Pc06g02200	regulator?	1	328	>60% larger fungal proteins
Pc06g02210	ArsB	4	366	*A. fumigatus* 85%
Pc06g02220	ArsC	0	134	*A. fumigatus* 79%, bacterial 72%
Pc06g02230	transcription factor?	1	108	*A. fumigatus* 34%

Pc06g02240	transcription factor?	1	102	*A. fumigatus* 33%, large subunit carbamoyl-P-synthase 30%

Striking is the very high similarity of ArsC with bacterial reductases (72% identity). Phylogenetic trees reveal close branching of the bacterial and fungal enzymes. This could suggest a more recent transfer than the *pcbAB-pcbC* cluster. Closest homologs are found in *Rhodococcus*, *Brevibacterium*, *Frankia* and *Salinispora*. Recently a transposon containing a set of arsenate-resistance genes has been characterized from *Acidibacillus caldus*[22]. It is remarkable that *P. chrysogenum* and Aspergilli have the bacterial reductases, differing from the yeast reductase Acr2p, which was described as the only known eukaryotic enzyme, besides two types of bacterial reductases using either GSH (also Pc16g02220) or thioredoxin[23].

The resistance protein ArsH has also bacterial homologs, e.g. *Agrobacterium* (57% identity). Aligning the *Pseudomonas* ArsH (ZP_00898054, 233 AA) with the *P. chrysogenum* ArsH (286 AA), there is a core region of 61% identity, while *P. chrysogenum* has extra and deviating terminal regions. The 90 amino acid N-terminus is homologous to all the fungal ArsH proteins. Is this a split gene, partially bacterial, partially fungal, with respect to the one intron in some cases? Does gene adaptation include the gain of additional pieces, like *penDE* in the penicillin cluster, besides codon adjustment?

6- methylsalicylic acid (6-MSA) synthases. 6-MSA and the related orsellinic acid are the precursors for various active metabolites, including patulin (various fungi), chlorotricine (*Streptomyces antibioticus*), neocarzinostatin (*Streptomyces neocarzinostaticus*)[24-26]. While there are no bacterial homologs of the *P. chrysogenum* NRPS genes except *pcbAB*, the two 6-MSA synthase genes (Pc16g00370 and Pc22g08170) do have bacterial homologs. This may seem surprising, as the 6-MSA is considered as a typical fungal multienzyme. But all the sequencing projects revealed hundreds of PKS genes, with the top 20 having a similar size and domain organization and grouping into a fungal and a bacterial subcluster. However, the fungal 6-MSA synthases genes fall into the bacterial class of PKS genes[27].

Pc22g08170 (cluster 42 in **Supplementary table 4**) has 82% identity to the 6-MSA synthase from *P. griseofulvum*[28]. A very similar gene cluster is seen in *A. clavatus* with identities mostly in the 74-82% range. The initial steps in the conversion of 6-MSA to patulin involve a decarboxylation, two hydroxylation and oxidation steps. The *P. chrysogenum* amidohydrolase and the 2 P450 enzymes are presumably involved in this conversion. A gene encoding an isoepoxidon dehydrogenase[29] cannot be identified in the genome, suggesting that *P. chrysogenum* is not a patulin producer. Also, in non-producing strains of *Byssochlamys* this enzyme is absent[30]. Bacterial synthases have 42% identity, suggesting horizontal gene transfer. The amidohydrolase Pc22g08120 is another candidate with bacterial homologs (up to 39% identity).

Pc16g00370 shows only 46% identity to the *P. griseofulum* original identified 6-MSA synthase, but 85% identity to a second MSA-type gene of this strain[31]. Similarities with other fungal and bacterial homologs are comparable to Pc22g08170. The cluster structure suggests the synthesis of a prenylated and hydroxylated 6-MSA derivative (cluster 14 in **Supplementary table 4**).

NRPS enzymes. There are 10 Non-Ribosomal Peptide Synthetases (NRPS) in the *P. chrysogenum* genome (included in the table is one hybrid NRPS-PKS):

	Gene Id	**Length (AA)**	**Domain-architecture**	**Product**
ACV-synthetase	Pc21g21390	3790	ATCATCATEte	penicillin
Siderophores	Pc16g03850	1900	ATCTC	TAF
	Pc22g20400	2076	ATCTC	TAF
	Pc13g05250	5081	ATCATCTCATCTCT	ferrichrome
Dipeptides	Pc21g01710	2104	ATCAT	?
	Pc21g12630	2268	ATCATC	?
	Pc21g15480	2382	ATCATC	?
PKS-associated (equisetin-type)	Pc16g13930	3962	ks-at-mt-ATd	?
Tetrapeptides	Pc13g14330	5267	CATECATCATCATC	?
	Pc16g04690	6064	ATECAATCATECTCT	?
Hexapeptide	Pc21g10790	7287	ATCATCATECATCATCATC	?

A -adenylate domain, T- carrier domain, C-condensation domain, E- epimerization domain, te-thioesterase domain, ks-ketosynthase domain, at-acyltransferase domain, mt-methyltransferase domain, d-dehydrogenase domain (NAD-binding)

Ferrichrome synthetase The ferrichrome synthetase (Pc13g05250, part of cluster 7 in **Supplementary table 4**) represents a type IV synthetase as *in Neurospora crassa, Fusarium graminaerum, Gibberella zeae* and *Aureobasidium pullulans* forming ferricrocin[32]. In *P. chrysogenum* the second A-domain contributing Ser is missing the major motif SGTTGxPKG and is therefore considered as inactive, and just the first Gly-domain may be used to include small amino acids. These leads to a product shift from ferricrocin to ferrichrome due to domain inactivation, confirming the observation that *P. chrysogenum* forms ferrichrome[33]. The Gly code[34,35] of the first domain DVFELIMIHK is identical to the other type IV synthetases, and also to related enzymes from *S. pombe* and *C. heterostrophus*. The N(5)-acetyl-N(5)-hydroxy-L-ornithine (Aho) code of the third adenylate domain, DVLDIGGIGK, fits to a set of 3 related codes, with position 7 being variable (A, F, G). This particular code is found in the *C. heterostrophus* ferricrocin synthetase and suggests that the second A-domain has been inactivated by some recombination event, whereupon the system has been self-repaired by selection for siderophore production. Some fungi may have two types of ferrichrome-synthetases, ascomycetes (*Chaetomium globosum* and *G. zeae* have type II and IV) as well as basidiomycetes (*Ustilago maydis*, type I and II), but apparently most ascomycetes as *P. chrysogenum* have lost each one of the loci. The divergence of the most prominent types II and IV must have been quite ancient, since similarities are only about 32% identity at the amino acid level. Interestingly, most Aspergilli share the type II synthetase with basidiomycetes, while only *A. clavatus* shares the type IV with *P. chrysogenum* (**Supplementary Fig. 6**). Pc13g05250 is linked to two other known siderophore biosynthesis associated genes: Ornithine N5-oxygenase (Pc13g05260) and SidR DHHC-type Zn-finger protein (Pc13g05270). Ornithine-N5-monooxygenases (OMO) are frequently found next to ferrichrome type or triacetylfusarinineC (TAF)-type (see below) NRPS. At first sight type III/IV/V systems cluster with OMO, as well as type I, but not type II. Type II systems have mostly similar adjacent genes to OMO and Sid2.

Extracellular siderophores TAFs are extracellular siderophores found as cyclic or linear variants. The cyclic and open esters of fusigen, fusarinine B and C have been decribed for *P. chrysogenum*[36]. The presence of two related synthetases underlines the importance of iron acquisition. Pc16g03850 (1900 AA) (part of cluster 15 in **Supplementary table 4**): the code DVDHGGAVGK is identical to the *A. terreus*, *N. crassa, Coccidioides immitis* and *Magnaporthe grisea* triacetylfusarinine synthetases, as is the general structure. The synthetase is linked to a PKS-cluster and contains two transporters. Pc22g20400 (part of cluster 44 in **Supplementary table 4**), 2076 AA: The well-known A-domain code DVDGGGGIGK matches the TAF synthetases from *A. niger* (An03g03520), *A. nidulans* (2086 AA), *A. oryzae* (1932 AA), *A. fumigatus* (2047 and 2083 AA, largely identical), *Botryotinia fuckeliana* (2058 AA) and *Chaetomium globosum*

(1733 AA). The putative gene cluster contains an acetylase and a highly conserved transporter.

Dipeptide synthetases Pc21g01710 (part of cluster 28 in **Supplementary table 4**), similar to An04g06260 of *A. niger* (2196 AA) matching a 2323 AA sequence, with N- and C-terminal deviations and a 58 AA gap. Both specificity regions are similar to *A. fumigatus* enzymes with 2336 and 2210 AA, respectively. The smaller *A. fumigatus* NRPS (2210 AA) has identical codes SARGTVSQLK and DVYFTGGVLK. While the *A. fumigatus* NRPS have the ATCATC structure, no terminal C-domains are detected in the NRPS of *A. niger* and *Penicillium*. Both *A. fumigatus* and two related *A. terreus* NRPS (2610 AA, codes SARDTAAQVK, DAFMLCGILK and 2923 AA, codes SARGTVTQLK, DAQIIGVMVK with the structures CATCATC) has been classified by as "putative unknown siderophore synthetases", based on a phylogenetic grouping of a set of Aspergilli-NRPS[37]. Pc21g12630 (part of cluster 35 in **Supplementary table 4**), 2382 AA, represents a cyclodipeptide synthetase, the structure has no significant homologs. The codes DVRSVGAGIK and DIGLGAMVIK have no matches with known NRPS, the second A domain specificity region is related to Ala/Gly/Pro-substrates. Pc21g15480 (part of cluster 37 in **Supplementary table 4**), 2372 AA, represents a cyclodipeptide synthetase, the structure has no significant homologs. The first A-domain code DVRSVGAGIK is identical to Pc21g12630, while the second domain code DSLELVAVVK differs. The linked dimethylallyltransferase and methyltransferase suggest a dimethylallyl-modified methylated cyclodipeptide, or piperazinedione, or diketopiperazine. Roquefortine- and meleagrin-like compounds are candidates, but both are not methylated. Such peptides interfere with bacterial quorum sensing, and could suppress bacterial interactions**. Similarly, diketopiperazines were found to be capable of activating or antagonizing other LuxR-based quorum-sensing systems, such as the N-butanoylhomoserine lactone-dependent swarming motility of *Serratia liquefaciens*. Although the physiological role of these diketopiperazines has yet to be established, their activity suggests the existence of cross talk among bacterial signalling systems. Interestingly, Pc21g12630 is 40-fold overexpressed in the high-producing strain, as well as other members of this cluster. So, together with penicillin production this very well could be a concerted antibacterial response.

Tetrapeptide synthetase Pc13g14330 (part of cluster 10 in **Supplementary table 4**), 5267 AA, represents a cyclotetrapeptide synthetase, the first module epimerises its amino acid. The N-terminal condensation domain could indicate a precursor transfer, common in bacterial systems, if an associated system providing a carrier protein linked intermediate is available, or this region may just be considered as a remnant from domain deletion events. The codes DSICVVAAVK, DAVLVGAVIK, DVLIMITVVK, DVMFGQAVIK have no match and specificity region analysis provides no clear result, except for module 2 hinting at the Leu/Phe type. Orthologs with 52 and 47% identity are found in *A. terreus* (EAU30156) and *A. clavatus* (EAW15286). All 3 NRPS are linked with transporters, indicating export of the product. No other adjacent genes are shared. The adjacent Pc13g14340, an unknown protein of more than 2000 AA, may be associated with signalling, as it is related to ß-transducin regions and NACHT-protein sequences involved in secretion processes. Similar sized unknown proteins can be found in *A. terreus* and *A. clavatus* in different genomic regions. Likewise very often NRPS genes are found next to genes containing ankyrin repeats.

Pentapeptide/hexapeptide synthetases Pc16g04690 (part of cluster 16 in **Supplementary table 4**), 6064 AA, is an ortholog of *A. niger* An08g02310 (54% identity), which has been connected to malformin due to its epimerisation domains and its high similarity to a set of 5 module NRPS resembling the malformin NRPS. A malformin-like product has been reported for *P. roquefortii* [38]. Similar NRPS are also found in *A. fumigatus* (6229 AA), *A. oryzae* (5199 AA, with the second A-domain deleted), *A. nidulans* (even two with 5935 and 6077 AA) and *A. terreus* (5842 AA). More than 50% identity links this group to a set of 5-module NRPS of the structure ATEC-ATC-ATEC-ATC-ATEC-TCT. Pc21g10790 (part of cluster 33 in **Supplementary table 4**), 7287 AA, shows a 57% identity to a 6885 AA NRPS from *A. oryzae*. This NRPS has an identical structure ATCATCATECTCATCATC, except for loss of the fourth A-domain, suggesting an inactive domain in the *Penicillium* enzyme. The codes of modules 1-3 are identical in *Penicillium* and *A. oryzae*: DVLFAGGVAK, DASFIGVIYK, DVGFVGSIWK, the 5th module is slightly altered DVDEVSSVCK/DVEEASTVSK (Aory/Pchry, respectively), as is the 6th module in a single position DVACVSAVWK/DIACVSAVWK. All codes are unknown. Despite the inactive A-domain the product could be a cyclohexapeptide, as carrier and condensation domains are present, and *in trans* charging could occur, so that even two adjacent D-amino acids are possible. Alternatively, the product is a cyclopentapeptide with one D-amino acid. An identical product should be present in *A. oryzae*. Since a fatty acid synthase, hydroxylase and aminotransferase are linked, an aliphatic ß-amino acid may be involved. Pc16g13930 (part of cluster 20 in **Supplementary table 4**), 3962 AA, is a mixed type PKS-NRPS.

Similar structures are equisetin synthetase (*Fusarium heterosporum*, 3953 AA), a 4034 AA PKS from *Magnaporthe grisea*, an 3821 AA PKS from *Coccidioides immitis*, a 3946 AA PKS from *A. oryzae*, and a 3930 PKS from *A. nidulans*. The A-domain specificity is unknown, the code DIALYGAIAK has no match; the specificity region has a weak Arg connection.

PKS enzymes Known polyketide metabolites from *P. chrysogenum* are secalonic acids (octaketides), sorbicillins, sorrentanones (hexaketides), emodic acids (octaketides), chrysogenin (structure not fully elucidated), and the possible PKSIII derived xanthocillins[39]. Twenty-four putative PKS encoding genes can be extracted from the genome (**Supplementary table 3**). Pc21g16000 can be assigned by similarity to the *A. nidulans* wA and the *A. fumigatus* PksP to conidial yellow pigment biosynthesis (naphthopyrone), and could be the chrysogenin synthase. Pc22g08170 has almost 90% identity to the original 6-MSA sequence from *P. griseofulvum*, and is thus involved in formation of a patulin-like product. The only chalcone synthase type Pc22g09640 could be tentatively related to xanthocillins, also produced by *A. candidus, A. chevalieri, E. chevalieri*. None of the remaining 21 PKS can be clearly correlated with a product. Pc16g03800 is associated with one of the TAF clusters, and could be involved in synthesis of cis-5-hydroxy-3-methylpent-2-enoic acid, one constituent of fusarinine, the substrate of TAF synthetase.

Amplified chromosomal region with penicillin biosynthetic genes Industrial *Penicillium* strains have a 60-100 kb chromosomal region amplified several times[19,40]. Sequences and lengths reported[19] were used to extract the exact sequence from the genome. A region of well over 120 kb, covering all reported amplified fragments, is represented in **Supplementary Fig. 7**. Forty-two putative ORFs were identified in the amplified part (4 surrounding putative ORFs are also shown). Twenty-four of these reside in the 57 kb region recently reported in more detail[41,42], which is amplified in all industrial strains. This region contains the three genes encoding the key steps in penicillin biosynthesis (ACVS, IPNS and AT). From annotation alone none of the other ORFs can be directly related to penicillin biosynthesis (**Supplementary Table 5**), confirming the recent publications[41,42]. Some of these ORFs are expressed significantly higher (e.g. more than 2-fold) during penicillinG producing conditions, but this is mostly limited to the Wisconsin54-1255 strain (**Supplementary Table 6** and **Supplementary**

Fig. 8). While the high producing strain DS17690 has 5-7 copies of this region (M.A. van den Berg, unpublished results) it is obvious that the increased gene dosage is not balanced throughout the region. For example ORFs Pc21g21460 through Pc21g21490 show 4- to 8-fold higher mRNA levels, while Pc21g21290 and Pc21g21440 both come close to 30-fold increased levels. As the latter two encode hypothetical proteins this complex regulation effect needs further attention.

The other part of the region is also amplified in strains from the Panlabs lineage[19,43]. Here, several ORFs with membrane spanning regions are present, including a MFS type transporter, Pc21g21510, homologous to the cercosporin transporter of *Cercospora kikuchii*, which is involved in the secretion and resistance against this PKS-derived toxin[44]. However, as most of the genes in this region it does not show a high transcription level or an increased transcription during penicillin biosynthesis, the exact function remains unclear.

Transcription factors The transcription profiles of the 612 ORFs encoding the putative transcriptional factors showed that approximately half of these are not very actively transcribed (e.g. an average signal <50; **Supplementary Table 26**). Down-regulation under penicillin producing conditions was observed in ORFs putatively encoding important transcription factors such as *abaA*, involved in growth and development; *aflR* (only down-regulated in the DS17690 strain), a transcription factor required for the expression of the aflatoxin pathway genes which negatively regulates the expression of LaeA (a transcription factor directly involved in regulation of secondary metabolism in *Aspergillus* spp.); *amdX* (only down-regulated in the DS17690 strain), a transcription factor regulating the acetamidase-encoding *amdS* gene and *brlA*, involved in growth and development. Up regulated ORFs during penicillin production are *alcR* (only up regulated in the DS17690 strain), a positive regulatory protein for the ethanol regulon, alcA and aldA; *amdA* (only up regulated in the Wis54-1255 strain) controlling the expression of the acetamidase-encoding *amdS* and *aciA* genes, which allows the utilization of certain amides as carbon and/or nitrogen sources; *arg81*, which mediates the repression of specific arginine biosynthetic genes (ARG) and also functions as an inducer of the arginine catabolic genes (CAR) in response to exogenous arginine; *aro80*, a transcription activator required for the expression of genes involved in the catabolism of aromatic amino acids; a pathway-specific regulatory protein of nitrate assimilation (only up regulated in the DS17690 strain) and SPBC530.05, a transcriptional regulator similar to the *A. nidulans facB* DNA binding protein, which is required for growth on acetate. The strongest responses were observed for uncharacterized factors like Pc22g16820 (e.g. weak similarity to hypothetical transcription regulator SPBC530.05 – *S. pombe*) with a 10-fold signal increase from 155 to 1502 and Pc21g23810 (e.g. strong similarity to hypothetical transcriptional regulator CAF32162.1 – *A. fumigatus*) with a 50-fold signal increase from 13 to 648.

Among the transcription factors reported to control penicillin biosynthesis (like *pacC*, *creA*, *cpcR1*, *laeA*) none were found to be significantly changed in the data analysed. For most of these the *P. chrysogenum* homologues can be readily identified (**Supplementary table 17**). For *creA*, exerting glucose repression, three homologous ORFs can be identified, but Pc20g13880 seems to be the best candidate, which shows a negative mRNA level with increasing penicillin productivity. Although, in all *A. nidulans creA* mutants tested, glucose still represses the *ipn*A (=*pcb*C) gene expression[45,46], recent studies in *P. chrysogenum* with antisense *creA* RNA and directed mutation of the CreA binding sites indicate that CreA has an important role in glucose regulation of penicillin biosynthesis (C. Cepeda, F. Fierro and J.F. Martín, unpublished results; L. Cova and M.A. van den Berg, unpublished results). Comparing the transcriptional map of the (extended) amplified region containing the penicillin cluster (**Supplementary Fig. 8**) with the extracted binding sites for transcription factors (**Supplementary Fig. 9**) does not give any further clues for the specific regulation or roles of the co-amplified genes.

Biosynthesis of secondary metabolism is quite often highly regulated. In several examples it was shown that pathway specific transcription factor genes can be physically associated with the biosynthetic genes[47].

C2H2/Zn(II)2Cys6 transcription factor genes (CMR1-type). Seven putative CMR1-type transcription factors were identified in the genome (**Supplementary table 26**). Each ORF contains two C2H2 DNA-binding domains and one Zn(II)2Cys6 DNA-binding domain. The Zn(II)2Cys6 motif is present at the N-terminal region of CMR1 and the two C2H2 zinc fingers are present N-terminal to the Zn(II)2Cys6 DNA-binding motif corroborating earlier reports[48].

	C2H2 (Positions)	Zn(II)2Cys6 (Positions)
Pc6g01890	(23-47), (53-76)	(87-124)
Pc12g09540	(17-39), (45-67)	(88-125)
Pc16g05230	(14-36), (42-64)	(78-115)

Pc20g05960	(18-40), (46-68)	(80-117)
Pc21g07180	(37-56), (65-87)	(107-144)
Pc21g07310	(4-28), (34-57)	(69-106)
Pc22g15230	(2-24), (30-52)	(71-109)

Regulators of the P. chrysogenum putative secondary metabolite clusters. From the 47 clusters containing PKS and NRPS only ten contain regulatory genes associated to them. However, all of them remain to been studied at the functional level in *Penicillium chrysogenum*.

Hybrid cluster 11 (Supplementary table 4)

In the hybrid cluster 11 there is one ORF (Pc14g00020) encoding a protein with weak similarity to hypothetical transcription regulator protein from *S. Pombe.*

PKS-NRPS cluster 15 (Supplementary table 4)

In the PKS-NRPS cluster 15 there is one ORF (Pc16g03740) encoding a protein with weak similarity to siderophore biosynthesis repressor sREA from *A. nidulans*.

PKS cluster 17 (Supplementary table 4)

In the PKS cluster 17 there is one ORF (Pc16g04880) encoding a protein wiith weak similarity to hypothetical transcription activator SPAC139.03 from *S. pombe.*

NRPS-like cluster 21 (Supplementary table 4)

In the NRPS-like cluster 21 there is one ORF (Pc18g00330) encoding a protein with strong similarity to hypothetical phd finger transcription regulator from *S. pombe*, one ORF (Pc18g00400) encoding a protein with similarity to hypothetical transcription regulator SPBC530.05 from *S. pombe* and the ORF Pc18g00420, encoding the transcription factor pacC.

PKS cluster 27 (Supplementary table 4)

In the PKS cluster 27 there is one ORF (Pc21g00920) encoding a protein with similarity to transcription activator of lysine pathway Lys14 from *S. cerevisiae.*

PKS cluster 29 (Supplementary table 4)

In the PKS cluster 29 there is one ORF (Pc21g03950) encoding a protein with similarity to hypothetical transcription regulator SPBC530.05 from *S. pombe.*

PKS cluster 31 (Supplementary table 4)

In the PKS cluster 31 there is one ORF (Pc21g04750) encoding a protein with similarity to aflatoxin biosynthesis regulatory protein aflR from *A. parasiticus.*

PKS cluster 32 (Supplementary table 4)

In the PKS cluster 32 there is one OFR (Pc21g05050) encoding a protein with weak similarity to positive regulator qa-1F from *N. crassa* and one ORF (Pc21g05090) encoding a protein with weak similarity to positive regulator of purine utilisation uaY from *A. nidulans.*

PKS cluster 34 (Supplementary table 4)

In the PKS cluster 34 there is one ORF (Pc21g12340) encoding a protein with similarity to hypothetical transcription regulator SPAC139.03 from *S. pombe* and one ORF (Pc21g12360) encoding a protein with strong similarity to hypothetical transcriptional regulator CAF32162.1 from *A. fumigatus*

PKS cluster 42 (6-MSA synthases cluster, Supplementary table 4):

6- methylsalicylic acid (6-MSA) synthases. 6-MSA and the related orsellinic acid are the precursors for various active metabolites, including patulin (various fungi), chlorotricine (*Streptomyces antibioticus*), neocarzinostatin (*S. neocarzinostaticus*).

In the cluster there is one ORF (Pc22g08140) encoding a protein with weak similarity to hypothetical transcription regulator SPBC530.05 from *S. pombe.*

Transporters related to secondary metabolite genes Based on common regulation patterns observed via the MicroArray studies, clusters around several NRPS genes can be identified. Pc21g12630 is predicted to be a cyclodipeptide synthetase, but in the vicinity there are no transporter genes. NRPS Pc21g15480 is an NRPS that is down regulated under penicillinG producing conditions. The neighboring gene, Pc21g15420, shows strong similarity to the cercosporin transporter CFP of *Cercospora kikuchii*. This gene is regulated in concert with the NRPS and thus might be involved in secretion of the peptide. Pc21g21390 (*pcbAB*; ACV synthetase) is part of the penicillin cluster of three genes (*pcbAB*, *pcbC*, and *penDE*). In contrast to the penicillin cluster in *A. chrysogenum*, the minimal penicillin cluster (e.g. the core 17 kb region covering the three biosynthetic genes) in *P. chrysogenum* does not contain any transporter gene in its proximity. Three transporter genes localize downstream: e.g., Pc21g21510 which is not expressed and shows strong similarity to cercosporin transporter CFP of *C. kikuchii*, Pc21g21530, also not expressed and with strong similarity to allantoate permease Dal5 of *S. cerevisiae*; and Pc21g21590, homologous to the glucose transporter Rco-3 of *N. crassa,* which is expressed at low levels but appears to be down regulated under penicillinG producing conditions (see also **Supplementary table 5)**. The latter protein is homologous to the glucose transporter Rco-3 of *N. crassa*.

Two physically close transporter genes are slightly co-upregulated under penicillin producing conditions: Pc22g20390 with a strong similarity to multidrug resistance (MDR) protein AtrD of *A. nidulans* and Pc22g20360 with a strong similarity to siderophore-iron transporter for enterobactin Enb1 of *S. cerevisiae*. In the DS17690 strain Pc22g20390 is up-regulated 3-fold. Recent data shows that it localizes to the plasma membrane as verified by a GFP fusion protein (A. Kovalchuk, unpublished results), and thus seems an interesting candidate for secretion system for penicillin. It should however be stressed that penicillin secretion might be the result of the activity of multitude of MDR-like transporters as the genomic analysis suggests a high level of redundancy in the distribution of such transporters. Most of the common up-regulated genes seem to respond to the high concentration of phenylacetic acid (PAA) used in the fermentation broth. PAA enters the cell mostly by means of passive diffusion, but it is also metabolised[49] and the conversion products might be secreted. Up to 143 transporter genes are significantly up-regulated in the DS17690 strain versus the Wisconsin54-1255 strain when grown in the presence of PAA. Of this group of transporters, 15 transporter genes seems to be expressed at a higher level in the DS17690 versus Wisconsin54-1255 strain fermentations in the absence of PAA (**Supplementary Fig. 10**). Except for Pc20g14390 that shows homology to mitochondrial phosphate transporters, all other of these 15 up-regulated transporter genes belong to the major facilitator superfamily (MFS) type. These transporters could be involved in PAA uptake and secretion, precursor uptake and secretion into and out of the microbody and penicillin secretion, or reflect some stress response to the fermentation conditions.

Five (Pc13g10900, Pc16g02690, Pc12g13800, Pc13g06330 and Pc13g10030) of the 36 genes up-regulated under penicillin producing conditions are at least up-regulated 10-fold (**Supplementary table 18**). These likely respond to the added PAA. Pc13g10900 (220- and 77-fold up in the Wisconsin54-1255 and DS17690, respectively) and Pc13g10300 (21- and 11-fold up in the Wisconsin54-1255 and DS17690, respectively) show a strong similarity to high-affinity nicotinic acid permease Tna1 of *S. cerevisiae*. Nicotinic acid and PAA are both small molecules with aromatic rings, suggesting that these two transporters are likely candidates for PAA uptake systems.

Microbodies *Development* All genes encoding proteins essential for microbody formation[50] (designated peroxins) can be identified in the *P. chrysogenum* genome suggesting that these organelles are formed via conserved machineries. Additionally, all components essential for microbody fission (e.g. Vps1, Dnm1, Fis1[51,52]) are present, indicating that organelle fission as a mode for microbody multiplication may normally occur.

Stability. Yeast microbody-borne proteins as well as the microbodies themselves have a limited life span and are subject to gradual continuous degradation. In this process both microbody-borne hydrolases (e.g. Lon protease)[53] and selective autophagy machineries (pexophagy[54]) play a distinct role. Such degrading AuTophaGy (*ATG*) genes are conserved in the *P. chrysogenum* genome[55] and shown to play a role in selective microbody turnover (W.H.Meijer *et al*., unpublished data). . A Lon protease with a putative PTS1 is also present in *P. chrysogenum* (Pc21g06860, see **Supplementary table 7**).

Penicillin biosynthesis. Two proteins involved in penicillin biosynthesis have PTS1 signals namely AT (ARL)[56] and phenylacetyl-CoA ligase (PCL;KI)[57]. Blast analyses demonstrate that AT is only conserved in the few filamentous fungi that synthesize penicillin (*P. chrysogenum*, *A. oryzae*, *A. nidulans* and *A. flavus*). In contrast to AT, the PCL protein is conserved in all filamentous fungi. Furthermore, the *P. chrysogenum* genome encodes multiple other CoA ligases/synthetases with similarity to PCL, many of which contain a putative PTS (see **Supplementary table 7**).

PTS-signals. Of the 197 identified proteins with a putative PTS1 the most frequently observed signals are: SKL (41), AKL (41), ARL (25), SRL (16) and SKI (16), comprising 71 % of all the signals. Furthermore, a leucine residue at the carboxy terminal position appears to be preferred (in 68 % of the cases). Nevertheless, many of the identified proteins represent either hypothetical ORFs or proteins of yet unknown function. Our analysis identified only few proteins (18) with a putative PTS2, a phenomenon that is also observed in other species. This includes three separate 3-ketoacyl CoA thiolases, a typical PTS2 protein in almost all species. However, information on PTS2 sequences in filamentous fungi is scarce, implying that the ultimate PTS2 consensus may vary from that used in other species.Remarkably, in some cases genes encoding proteins with a PTS show clustering (see **Supplementary table 7**), suggesting that they have a function in the same metabolic pathway. This applies to Pc13g03340/Pc13g03350; Pc13g14410/Pc13g14420; Pc14g01040/Pc14g01070/Pc14g01090; Pc15g00410/Pc15g00420; Pc16g07060/Pc16g07070; Pc16g10060/Pc16g10070; Pc20g03610/Pc20g03630; Pc20g15650/Pc15660; Pc21g05470/Pc21g05490; Pc21g09440/Pc21g09460/Pc21g09470/Pc21g09480; Pc21g21120/Pc21g21140 and Pc22g20370/Pc22g20380. In many cases, the clustered genes show no or only weak transcription under the conditions tested. Remarkably, the Pc13g14410/Pc13g14420 genes are situated rather close to Pc13g14330, a putative cyclotetrapeptide synthetase. Additionally, the Pc22g20370/Pc22g20380 genes are located close to Pc22g20400, a putative TAF synthetase. Thus, like penicillin production, these biosynthetic routes might require microbody metabolism.

***GeneChip*® analysis of genomic DNA** *Validation of the GeneChip®*. Fragmented DNA of *P. chrysogenum* Wisconsin54-1255 was hybridized to the DSM_PENa520255F Affymetrix GeneChip® to verify the quality of the probe set design. Nearly all (99.4%) of the probe sets designed to measure *P. chrysogenum* ORFs report a signal and are classified as ‘present’ by the GCOS software (**Supplementary Table 27**). Likewise, 99% of the probe sets designed to measure intergenic regions report a ‘present’ call, as they should when hybridizing genomic DNA. After scaling to the arithmetic mean signal of 100, most of the observed signal intensities are distributed between 50 and 200 (**Supplementary Fig. 11**) due to differences in hybridization efficiency. Most ORFs are present in only one copy on the genome. Signals that are considerably higher than 200 may suggest sequences present in the genome in multiple copies, although other techniques should be applied to establish gene copy numbers.

There are 12943 unique (so, excluding shared probe sets) annotated ORF probe sets, of which only 50 (0.4%) were called absent in this experiment. 77% of the 259 annotated ORF probe sets with a signal >200 is (partially) shared by different sequences (_s or _x suffix). Of the 651 annotated ORF probe sets that report a signal <50, 94% is a shared probe set. Most of the unique probe sets with higher signals report for tRNAs, rRNAs and some other genetic elements expected in multiple copies in the genome. 17% of these 651 probe sets is annotated as a (putative) transposon, (retro)transposable element or transposase (see **Supplementary Fig. 12** for an genome distribution overview). The 651 comprise of only a few unique probe sets for predicted ORFs, mostly hypothetical proteins, but also a putative glutamate decarboxylase GAD1 (Pc22g00970), apocytochrome b (Pc22g10800) and ribonuclease H 3-5 exonuclease like protein (Pc09g00030).

Strain comparison at genomic DNA level. In addition to the GeneChip® validation, a comparative analysis of the genomic DNA of the high-producing DS17690 with Wisconsin54-1255 was performed in triplicate. Although the GeneChip® was primarily designed for expression analysis, genomic DNA copy number changes can be detected, as long as the duplications or deletions is covered by an entire probe set, i.e. the larger part of an ORF. In practice, we restricted the analysis to detection of altered regions spanning at least several ORFs to improve the confidence in the interpretation of the measurements.

The signal intensities of the triplicate GeneChips® were averaged per strain and a fold change was calculated. Only regions with more than two adjacent probe sets reporting a >2-fold difference were considered in this analysis. The fold change was plotted against the genome order of the probe sets (**Supplementary fig. 13**). In total, 6 obvious and considerably large regions with different copy numbers between both strains were found, and listed in **Supplementary table 20**. Interestingly, most of the regions are flanked by one or more transposable elements, which may be indicative for the mechanisms of DNA duplication and deletion. Two gene clusters (# 1 and 6) are completely deleted from the genome of DS17690, covering in total over 50 hypothetical genes. The data indicates that the cluster with the penicillin biosynthetic genes is most likely 6- or 7-fold amplified; a more precise determination could not be made due to (technical) variation in the measurements reported by the different probe sets in the region.

Knock-out mutants The expression of all genes in DS17690 was compared to that in the Wisconsin54-1255 strain under producing conditions (+PAA). Significant changes were selected by SAM analysis with a threshold fold change larger than 2, and FDR<1%, thus identifying 1605 genes. An additional, more stringent criterium was imposed to keep only genes where the highest average signal (in either Wisconsin54-1255 or DS17690) was larger than 200. In this way, 578 genes can be selected as and these were functionally categorized according to 8 categories (**Fig. 7**).

To be able to determine the actual validity of a transcriptome-based identification of gene-products involved in β-lactam productivity, 12 genes were selected for knock-out analysis. In order to facilitate an efficient gene targeting in DS17690, a derivative with Pc22g15510, the homolog of *Saccharomyces cerevisiae* KU70, deleted[58] was used as recipient strain for the knock-out studies. Two of the 12 attempts were unsuccessful; i.e. no transformants were obtained for Pc18g01330 and Pc22g23110, respectively part of the lysine and valine pathways (**Supplementary table 21**). It is very likely that both led to auxotrophic mutants for whom growth is not supported on the minimal acetamide selection medium used. Four mutants show a significant reduction in β-lactam productivity: two genes involved in cysteine biosynthesis (Pc16g10020 and Pc22g16570), a peroxisome biogenesis factor (Pc21g04480) and the *veA* homolog (Pc13g13200). The first 3 results are in line with their (slight) increase in mRNA levels from Wisconsin54-1255 to DS17690 and under penicillinG producing conditions (+PAA). Moreover, the disturbance of peroxisome biogenesis clearly illustrates again the importance of peroxisomes in penicillin production. The *veA* mRNA is reduced with increased β-lactam productivity (**Supplementary table 21**). In *Aspergillus nidulans* VeAp was reported to repress some of the penicillin biosynthesis genes[59,60], so it may seem logic to find decreased mRNA levels in the DS17690 strain. Still, like in *A. nidulans*, a knock-out of the gene resulted in a severe decrease in β-lactam productivity (23.6%). As VeAp controls many more target genes, a complete silencing of the gene might very well negatively influence other factors involved in penicillin production.

One silenced gene, Pc22g13680 the putative isopenicillinN-CoA epimerase, shows an increase in β-lactam productivity, while it showed no significant change in mRNA level.. The knock-outs of the other 5 genes had no significant effect on the β-lactam productivity, suggesting that their gene products have no direct role in β-lactam biosynthesis, although their (strong) increased mRNA levels suggested otherwise. Thus, while for some genes a clear link to β-lactam biosynthesis could be demonstrated, these results also illustrate the limitations of a solely transcriptome-based identification of targets for metabolic engineering and therefore a thorough follow-up in the form of functional analysis is needed.

SUPPLEMENTARY METHODS

Genome annotation and analysis The combined automatic and manual approach started with the analysis of all contigs larger than 5kb genes. Four different ORF predicting algorithms were applied: FGENESH[61], GeneMark[62], GENSCAN[63] and GeneWise[64]. FGENESH, GeneMark and GENSCAN were all three run on the entire genomic sequence to provide an initial set of predicted ORFs. Preference was given to FGENESH genes. For regions without any FGENESH prediction GeneMark or GENSCAN models were extracted with preference for the GeneMark models. In addition the genomic sequence was also searched against the following three protein databases using blastx[65]: a). *A. niger* proteins (Aniger)[66], b). Fungal proteins, compiled from all public available fungal sequences (Fungi), c). Non redundant protein database, compiled from all other publicly available protein sequences (PROT_NR). For all initially predicted ORFs a blastp[65] analysis against the protein databases was performed. Based on the blastp results for each gene GeneWise was run against the best blast matches. The genemodels of the initially predicted ORFs were manually adjusted in case that the blastp and GeneWise alignment indicated a suboptimal gene model.

For regions without any gene prediction with one of the three algorithms but with a significant blastx match, ORFs were manually extracted by usage of the respective GeneWise alignment. Incomplete GeneWise protein alignments were extended to the first exon upstream to the nearest start codon, and the last exon downstream to the first stop codon. For contigs smaller 5 kb only a six-frame translation was performed in order to extract all encoded exons. Transfer RNAs were identified using the tRNAScan-SE program[67]. Ribosomal RNAs were identified by blastn[66] against a database of all public available rRNA sequences.

For all ORFs resulting from the above described approach an exhaustive automatic bioinformatic analysis in respect to function and structure of the respective protein was performed using the PEDANT-Pro™ software[68]. Annotation of description, functional categories according to the Functional Catalog (FunCat) classification system[69], and EC numbers have been performed for each *P. chrysogenum* ORF with a multi-step semiautomatic approach:

(1) For all known *P. chrysogenum* ORFs description, functional categories and EC numbers have been manually annotated.

(2) *P. chrysogenum* ORFs having blastp matches against manually annotated *A. niger* ORFs[66] were assigned the respective *A. niger* annotations, if

  a. the *A. niger* ORF was a known protein
  b. the protein from which the *A. niger* ORF annotations where deduced from occurred also in the blast results of the *P. chrysogenum* ORF.

(3) For *P. chrysogenum* ORFs having a blastp match (e-val >= 9e-04) against either *A. niger*, Fungi, or PROT_NR database entries, annotations were assigned as follows according to the best blast match:

  a. Best match is *A. niger* ORF with putative function: Description and FunCat transferred, e.g. "similarity to adenosine deaminase like protein An16g02890 - *Aspergillus niger*"
  b. Best match is *A. niger* hypothetical protein: Description transferred, e.g. "strong similarity to hypothetical protein An11g00330 - *Aspergillus niger*"
  c. Best match is fungal protein: Description transferred, e.g. "similarity to hypothetical protein 11 10_scaffold_1.tfa_290cg - *Fusarium graminearum*"
  d. Best match against PROT_NR: Description transferred, e.g. "strong similarity to hypothetical enoyl-CoA hydratase - *Rhodopseudomonas palustris*"

(4) All other *P. chrysogenum* ORFs having no blastp match and a protein length <=79 aa, or >=80 aa, were assigned as ‘questionable ORF’ or ‘hypothetical protein’, respectively.

To compare *P. chrysogenum* with other fungi, pairwise lists of orthologs were obtained using bidirectional Blastp searching of the *P. chrysogenum* predicted ORFs with ORFs of each of *Saccharomyces cerevisiae*, *Neurospora crassa*, *Magnaportha grisea*, *Histoplasma capsulatum, Coccidioides immitis, Podospora anserina,* *Phanerochaete chrysosporium, Gibberella zeae, Trichoderma reesei, Aspergillus nidulans*, *Aspergillus fumigatus*, *Aspergillus oryzae*, *Aspergillus terreus Aspergillus flavus*, *Aspergillus clavatus* and *Aspergillus niger*. Bidirectional best hits with a blastp E-value of less than 1E-10 in both directions were considered as orthologous gene pairs.

Methods for Secondary metabolites, NJ-trees of ACVS, IPNS and siderophore synthetases Multiple alignments to identify the putative members of gene clusters were done by ClustalW (1.81). The parameters used were: gap open penalty 10, gap extension penalty 0.05, no weight transition, hydrophilic gaps permitted, weight matrix BLOSUM.

***In silico* analysis of peroxisomal targeting signals** *P. chrysogenum* proteins with putative microbody targeting signals (PTS1 or PTS2) were identified using the Genome 2D program[70]. For identification of putative PTS1 proteins, the sequence [SCA]-[KRH]-[LMI]-COOH was used as query, consisting of the well established consensus sequence for human PTS1 proteins[71] to which isoleucine was added at the C-terminal position based on the finding that *P. chrysogenum* PCL utilizes an SKI as PTS1[72]. For identification of PTS2 sequences the first 50 amino acids of each protein in the *P. chrysogenum* protein database was searched using as query: -[RK]-[LVIQ]-X-X-[LVIHQ]-[LSGAK]-X-[HQ]-[LAF]-[73].

Strains Independent triplicate chemostat cultivations of the *P. chrysogenum* strains Wisconsin54-1255[74] and the high producing penicillinG strain DS17690[75] were performed and monitored in the presence and absence of phenylacetic acid exactly as described before[76]. DS17690 is derived from the strain improvement program of DSM after several classical mutagenesis rounds and is an offspring of the sequenced Wisconsin54-1255 strain.

Generation of knock-out mutants and ß-lactam analysis The genes selected for further analysis were knocked-out in a derivative of DS17690 wherein the non-homologous end-joining pathway was deleted (by virtue of deleting the *KU70* homolog, encoded by Pc22g15510) to increase the efficiency of homologous recombination[58,78,79]. The transcription of the selected genes was completely blocked by insertion of the *amdS* selectionmarker between the promoter and ORF of each gene. As flanking regions to direct the targeted double homologous recombination event, 1500 basepairs of the promoter and 1500-2500 basepairs of the ORF were used (the latter depending on the length of the individual ORFs). Protoplast transformation and transformant selection was performed as described previously[79]. Acetamide-consuming transformants were obtained, verified by PCR (data not shown) and sporulated. Spores were used to inoculate shake flasks with synthetic media supporting ß-lactam production[79]. To verify the validity of the findings two different side chain precursors were added to the media, phenyl acetic acid (PAA) and adipate (Ad), at 0.3 and 0.5 g/l respectively. Cultivation was for 168 hours at 25 C and 280 rpm. As controls both parent strains, DS17690 and the ΔPc22g15510 derivative, were used.

Analysis of ß-lactams produced was done by quantitative ^{1}H NMR at 600 MHz on a Bruker Avance 600 spectrometer. To a known quantity of filtrate, a known quantity of internal standard (maleic acid), dissolved in phosphate buffer was added prior to lyophilisation. The residue was dissolved in D_2O and measured at 300 K. The delay between scans (30 s) was more than 5 times T1 of all compounds, so the ratio between the integrals of the compounds of interest and the integral of the internal standard is an exact measure for the quantity of the ß-lactams.

Media The mineral medium was set at pH 5.5 with KOH pellets and contained per liter of demineralised water 7.5 g glucose, 3.5 g $(NH4)_2SO_4$, 0.8 g KH_2PO_4, 0.5 g $MgSO_4$•$7H_2O$, 10 mL of a trace element solution. The trace element solution contained 15 g•L-1 Na_2EDTA•$2H_2O$, 0.5 g•L-1 Cu_2SO_4•$5H_2O$, 2 g•L-1 $ZnSO_4$•$7H_2O$, 2 g•L-1 $MnSO_4$•H_2O, 4 g•L-1 $FeSO_4$•$7H_2O$, and 0.5 g•L-1 $CaCl_2$•$2H_2O$ and was set at pH 6.0 by adding NaOH pellets. Production of penicillinG was induced by adding 0.58 g•L-1 phenylacetic acid (PAA) to the medium. The appropriate amount of PAA was dissolved in demineralised water. After the pH was set to 5.5 with KOH pellets, the PAA solution was autoclaved for 40 min at 121 °C. All other components were dissolved in demineralised water and added to the PAA solution in the medium vessel via filter sterilization with a sterile 0.2 µm capsule filter (Supor®DCF™; Pall Corporation, East Hills, USA). Glucose was heat-sterilized separately (110 °C) and added to the medium in a concentration of 7.5 g•L^{-1}. After filter sterilization and during the chemostat experiments the medium vessel was mixed continuously by a magnetic stirrer.

Chemostat cultivation Aerobic glucose-limited chemostat cultivation was performed at 25 °C in 3 - L turbine stirred bioreactors (Applikon, Schiedam, The Netherlands) with a working volume of 1.8 L. The pH was maintained at 6.5 via automated addition of 2 M NaOH (ADI 1030 biocontroller, Applikon, Schiedam, The Netherlands). The fermenter was sparged with air at a flow rate of 0.9 L•min^{-1} using a Brooks mass-flow controller (Brooks Instruments, Hatfield, USA) and stirred at 750 rpm. The dissolved-oxygen concentration was continuously monitored with an oxygen electrode (Applisens, Schiedam, The Netherlands). Continuous cultivation was initiated after 50-60 hours of batch cultivation. The feed medium was supplied continuously by a peristaltic pump (Masterflex, Cole Parmer, USA) and the dilution rate was set at 0.03 h^{-1} for all chemostat experiments in both the presence and absence of the penicillinG side-chain precursor phenylacetic acid (PAA). Effluent was removed discontinuously by means of a special overflow device, which has been described previously[79]. The time interval between effluent removals was fixed in such a way that each time approximately 1 % of the culture volume was removed. To prevent excessive foaming, silicone antifoam (10 % vol/vol, BDH) was discontinuously added at timed intervals.

	Y_{sx}[a] ($g \cdot g^{-1}$)	**q_{pen}[b] ($\mu mol \cdot g^{-1} \cdot h^{-1}$)**	**q_{PAA} ($\mu mol \cdot g^{-1} \cdot h^{-1}$)**	**q_{CO2} ($mmol \cdot g^{-1} \cdot h^{-1}$)**	**q_{O2} ($mmol \cdot g^{-1} \cdot h^{-1}$)**
DS17690 - PAA	0.37 ± 0.01	0.00 ± 0.00	0.00 ± 0.00	1.15 ± 0.08	1.19 ± 0.11
DS17690+ PAA	0.35 ± 0.01	19.81 ± 1.47	24.04 ± 2.38	1.42 ± 0.11	1.42 ± 0.17
Wis 54-1255 - PAA	0.35 ± 0.01	0.00 ± 0.00	0.00 ± 0.00	1.45 ± 0.05	1.44 ± 0.03
Wis 54-1255 + PAA	0.35 ± 0.02	2.21 ± 0.72	35.63 ± 3.72	1.67 ± 0.13	1.73 ± 0.13

[a] biomass yield on glucose (g of biomass per g of glucose consumed)

[b] biomass -specific penicillinG production rate. In addition to penicillinG, intermediates and byproducts are formed, which accounts for ~6% of the consumed phenylacetic acid.

Determination of culture dry weight Culture samples (10 mL) were filtered over preweighed glass fiber filters (Type A/E, Pall Life Sciences, East Hills, USA). The filters were washed with demineralized water and dried for 20 minutes at 600 W in a microwave oven and were subsequently weighed.

Substrate and metabolite analysis Glucose concentrations in the medium were determined by HPLC analysis using an Aminex HPX-87H column (Biorad, Hercules, USA) at 60 °C with 5 mM H_2SO_4 as the mobile phase. Phenylacetic acid and penicillinG concentrations were determined by isocratic HPLC analysis using a Platinum EPS C18 column (Alltech, Deerfield, USA) at 30 °C. The mobile phase consisted of 5 M acetonitrile with 5 mM KH_2PO_4 and 6 mM H_3PO_4.

Gas analysis The exhaust gas of chemostat cultures was first passed through a condenser kept at 4 °C. The fraction of the gas that was send to the off-gas analyzer was subsequently dried with a Perma Pure dryer (type MD-110-48P-4, Perma Pure, Toms River USA). Oxygen and carbon dioxide concentrations were determined with a NGA 2000 analyzer (Rosemount Analytical, Orville, USA). Off-gas flow rates were determined from an average of 10 measurements using a SAGA digital flow meter (Ion Science, Cambridge, UK). Specific rates of carbon dioxide and oxygen consumption were calculated as described previously[80].

GeneChip design Based on the genome sequence of Wisconsin54-1255, a proprietary GeneChip®, DSM_PENa520255F, was designed for DSM according to the Custom GeneChip® program by Affymetrix (Affymetrix, Inc., Santa Clara, CA). The chips of the 49-7875 format contain 11μm features. There are 11 pairs of 25-oligonucelotides in each probe set representing each of the approximately 13.670 annotated ORFs and supplemented with genetic elements and a selection of large intergenic sequences of *P. chrysogenum*. The probe sequences were designed based on the region in the (predicted) coding sequence stretching from 650 to 4 nt, from the 3' end. Typical Affymetrix control probe sets were included (*B. subtilis, E. coli, Bacteriophage P1 and A. thalinana* spike controls). For several known *P. chrysogenum* genes, separate 3' end, middle and 5' end probe sets were designed that allow to monitor the efficiency of the *in vitro* transcription reaction. In addition, 1551 probe sets were included to search for the presence of yet unpredicted ORFs within large sequences (>2500nt) between two predicted ORFs or genetic elements. For this, the 'intergenic' regions were split up in 800 nt fragments (skipping 300nt from each end) and probe sets were designed for both strands (coding and reverse complement) for the sequences stretching from 300-1100 (gn3, 494 sets); 1900-2700 (gn5, 177 sets); 3500-4300 (gn7, 44 sets); 5100-5900(gn9, 5 sets); 6700-7500 (gn11, 5 sets); 8300-9200 (gn13, 2 sets) and 10000-10800 (gn15, 2 sets) until the 300nt from the 5'end of the region. Intergenic regions on the border of two contigs were represented by two probe sets marked with A and B (e.g. gn3A, gn3B and gn5A, gn5B).

Genomic DNA isolation, labeling and hybridization Protoplasts of Wisonsin54-1255 were prepared as described[81]. The pellets were resuspended in 10 ml TES/SDS to lyse the cells; followed by phenol extraction and DNA precipitation[82]. RNAse was degraded for 2 hours at 37 C with 0.1 mg/ml DNAse-free RNAse (Qiagen). Samples were again extracted with phenol and DNA was precipitated. Genomic DNA was sheared using a HydroShear® (GenomicSolutions®) in 200 µl total volume for 20 cycles. Finally, the genomic DNA was shortened to an average length of 25-100 bp using DNAseI (Sigma) and precipitated. Quality control was performed using the Bioanalyzer (Agilent). Genomic DNA labeling and hybridization were performed at the MicroArray Division, University of Amsterdam. 15 µg purified, fragmented DNA in 36 µl 10 mM Tris pH7.5 was used for the labeling reaction. The GeneChip® DNA Labeling Reagent (Affymetrix, P/N 900542) was used to label the 3' termini of the DNA fragments, according to the Affymetrix GeneChip® Expression Analysis Technical Manual, Section 3.1.12. Hybridisation, washing, staining and scanning were performed according to Affymetrix protocol Section 2 (eukaryotic target hybridization protocol, for 49 format). Reproducibility was determined using two standard genes and is the average ± standard deviation of independent cultures (n indicated in table):

	Avg CV[a]	**PcACTA[b]**	**PcGDH2[c]**	**n**
DS17690 - PAA	0.21	4190 ± 170	1240 ± 120	3
DS17690+ PAA	0.18	3560 ± 360	1140 ± 270	4
Wis 54-1255 - PAA	0.10	2950 ± 290	1030 ± 110	3
Wis 54-1255 + PAA	0.13	3090 ± 190	850 ± 220	3

[a] represents the average coefficient of variation (standard deviation divided by the mean) for all genes except the genes with the mean below 12

[b] encoding actin; average signal and standard deviation

[c] encoding glutamate dehydrogenase; average signal and standard deviation

Sampling and RNA extraction procedures 60 mL of culture broth was sampled and rapidly filtered over a glass fiber filter (Type A/E, Pall Life Sciences, East Hills, USA). The filter with mycelium was wrapped in aluminum foil, quenched in liquid nitrogen and subsequently stored at -80 °C until further use. For total RNA extraction half of the pellet was ground by mortar and pestle under constant cooling with liquid nitrogen. The powder was taken up in 5 mL of Trizol reagent (Invitrogen) and 1 mL chloroform (Sigma) and mixed well. The two phases were separated by centrifugation (4600 g, 15 minutes). Total RNA was further purified by extraction with acid-phenol/chloroform/isoamyl alcohol (5:1, pH 4.8, Ambion), followed by a chloroform extraction. Each time the phases were separated by centrifugation (4600 g, 15 minutes). Total RNA was precipitated for 30 minutes at -20°C in 96% ethanol and 0.3 M sodium acetate. After centrifugation at 23000 g for 15 minutes the RNA was dissolved in RNAse free H_2O.

Probe preparation and Target hybridization Double stranded cDNA synthesis was carried out using 10 µg of total RNA and the components of the One Cycle cDNA Synthesis Kit (Affymetrix, Santa Clara, USA). The double-stranded cDNA was purified with the GeneChip® Sample Cleanup Module (Affymetrix/Qiagen) followed by in vitro transcription and labeling using the GeneChip® IVT labeling Kit (Affymetrix). Finally, labeled cRNA was purified (GeneChip® Sample Cleanup Module, Affymetrix/Qiagen) prior to fragmentation. 15 µg of fragmented, biotinylated cRNA was hybridized to the *P. chrysogenum* MicroArrays at 45 °C for 16 h as described in the Affymetrix users' manual. Washing and staining of arrays were performed using the GeneChip® Fluidics Station 400 and scanning with the Affymetrix GeneArray Scanner 3000.

Data analysis Acquisition and quantification of array images were performed using Affymetrix GeneChip® Operating Software (GCOS version 1.2). Before comparison, all arrays were globally scaled to a target value of 100 using the average signal from all gene features. To the 15,531 transcript features on the arrays, a filter was applied to extract 13,925 open reading frames. To represent the variation in triplicate measurements, the coefficient of variation (S.D. divided by the mean) was calculated. When the genes were ranked according to increasing average intensity, the average coefficient of variation showed a sharp increase for the genes with the lowest expression. Therefore, all genes in which the average expression in all conditions was below 12 were removed from the dataset. Subsequently, all remaining values below 12 were set to a value of 12. To assess differential expression, the Significance Analysis of Microarrays (SAM version 1.21) add-in to Microsoft^{TM} Excel was used for comparisons of replicate array experiments. The fold-change threshold and the false discovery rate values were set at 2 and 1% respectively. The data (.CEL files) were loaded into Genedata Expressionist (Genedata, Basel, Switzerland) and the genes with significantly changed expression in one of the comparisons were arranged in clusters by the *K*-means clustering tool.

Enrichment of MIPS categories was assessed for the differentially expressed genes by Fisher's Exact test employing hypergeometric distribution with a p-value cut-off of 10^{-4} (after Bonferroni correction). The probability was calculated as follows: the p-value of observing z genes, belonging to the same functional category is: $P = \sum_{x=z}^{\max(N,M)} \frac{\binom{N}{x}.\binom{G-N}{M-x}}{\binom{G}{M}}$, where N is the total number of genes in a category, M is the total number of differentially expressed genes in the cluster and G is the total number of *P. chrysogenum* genes.

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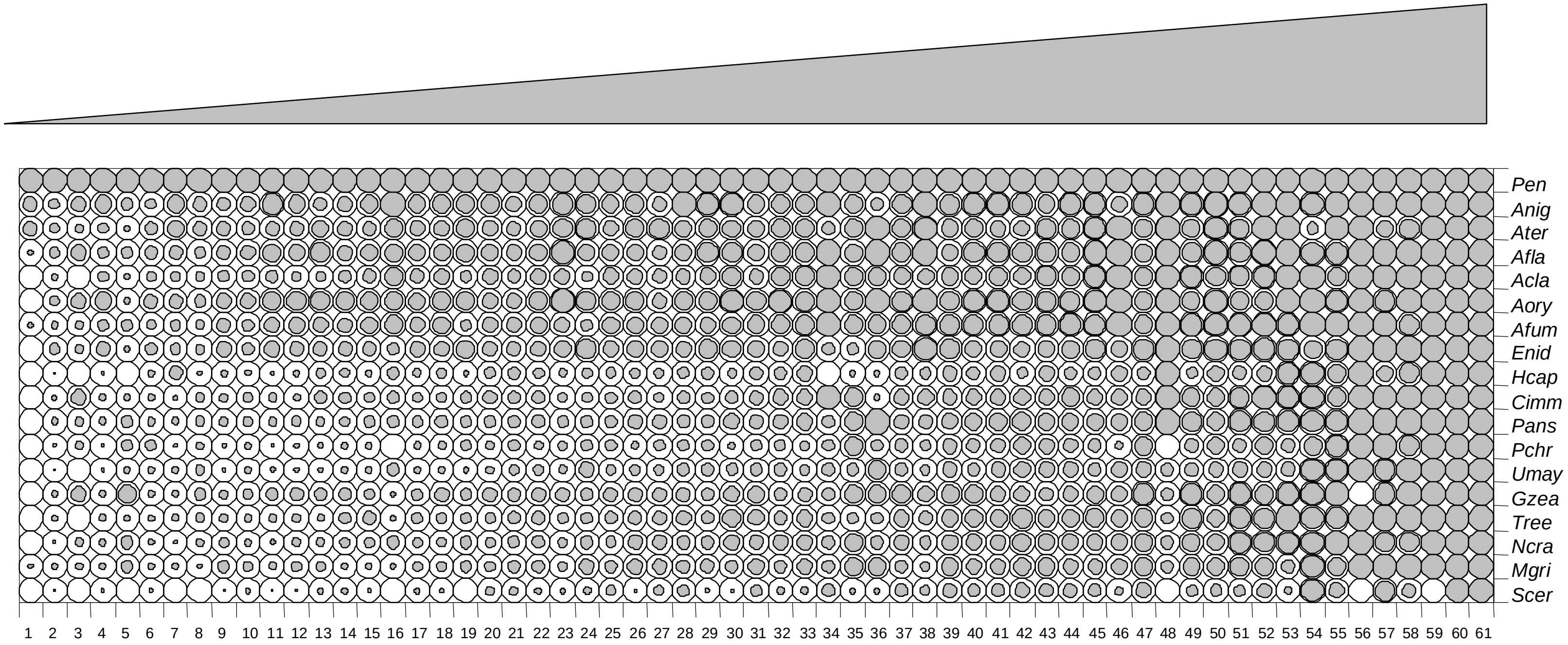
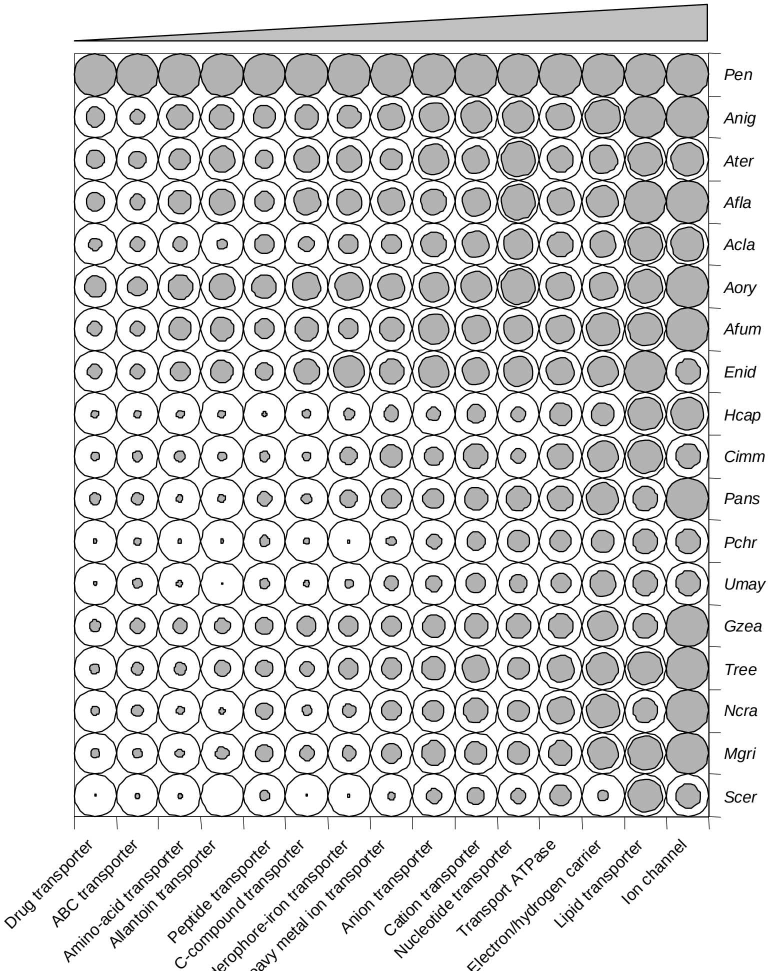
Supplementary Figure 3. Ortholog comparison of functional classes related to transporters in different fungal genomes. Pen: *Penicillium chrysogenum*, Anig: *Aspergillus niger*, Ater*: Aspergillus terreus*, Afla: *Aspergillus flavus*, Acla: *Aspergillus clavatus*, Aory: *Aspergillus oryzae*, Afum: *Aspergillus fumigatus*, Enid: *Emericella nidulans*, Hcap: *Histoplasma capsulatum*, Cimm: *Coccidioides immitis*, Pans: *Podospora anserina*, Pchr: *Phanerochaete chrysosporium*, Umay: *Ustilago maydis*, Gzea: *Gibberella zeae*, Tree: *Trichoderma reesei*, Ncra: *Neurospora crassa*, Mgri: *Magnaporthe grisea*, Scer *Saccharomyces cerevisiae*.

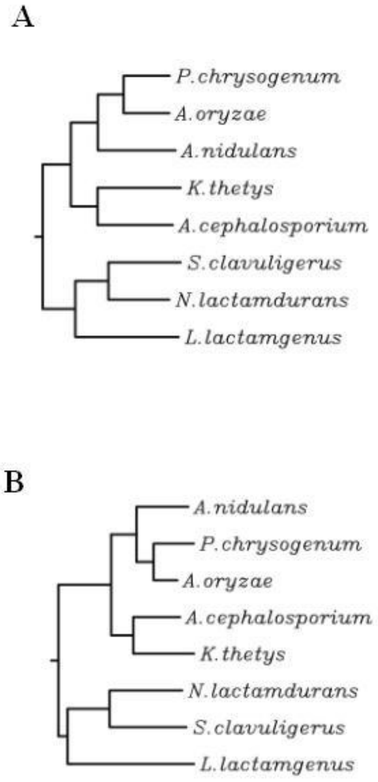
The size of the filled circles is proportional to the number of ortholog genes in each category. Categories have been sorted in respect to the number of ortholog genes over all indicated genomes increasing from left to right.



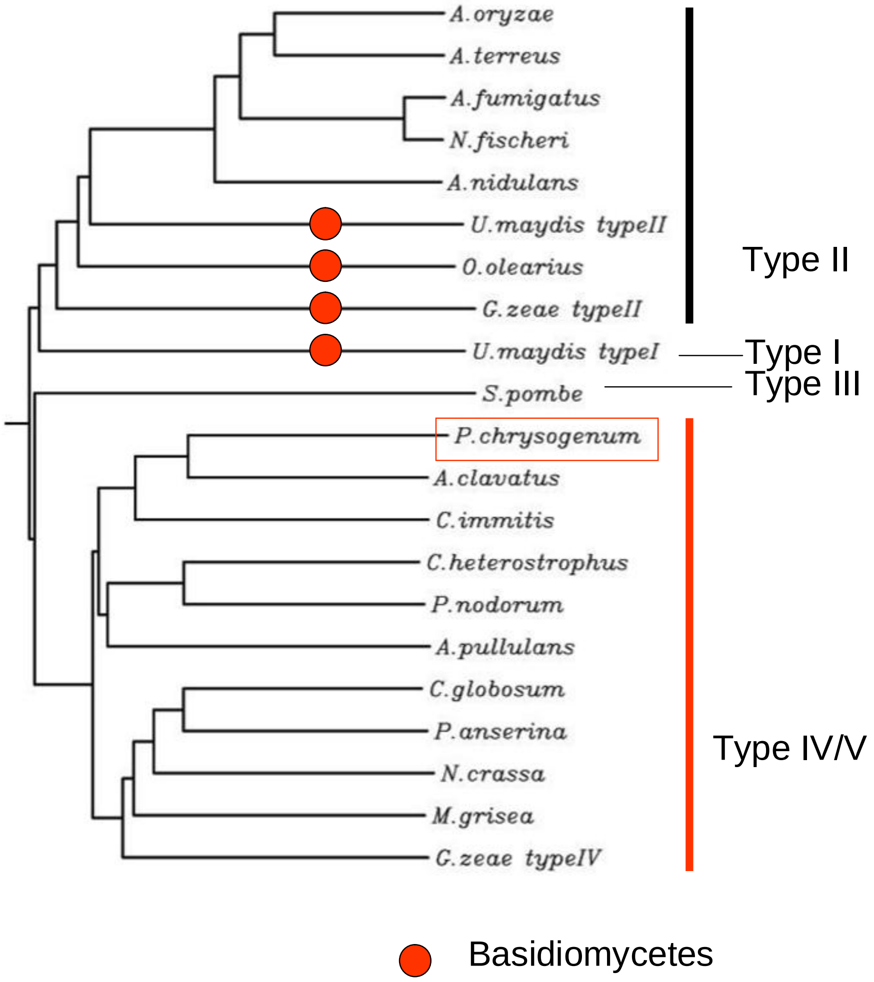
Supplementary Figure 4. Functional classification of *P. chrysogenum* specific ORFs (A), ORFs with fungal orthologs (B) and ORFs of the four non-syntenic assemblies (C). FunCat classes indicated are, 01 Metabolism, 02 Energy, 03 Cell cycle and DNA processing, 04 Transcription, 05 Protein synthesis, 06 Protein fate (folding, modification, destination), 67 Transport facilitation, 08 Cellular transport and transport mechanisms, 10 Cellular communication/Signal transduction mechanism, 11 Cell rescue, defense and virulence, 13 Regulation of/interaction with cellular environment, 40 Subcellular localization, 29 Transposable elements, 99 Unclassified proteins.



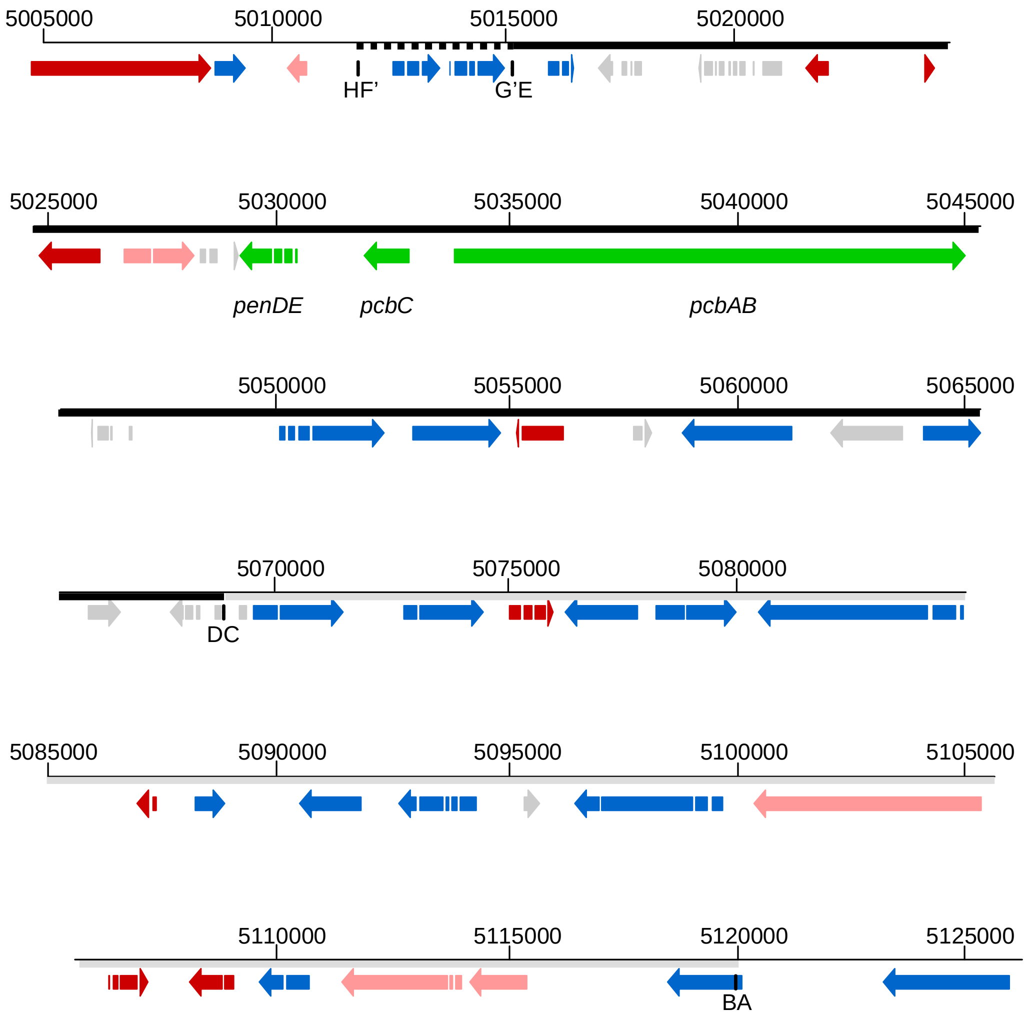
Supplementary Figure 5. NJ-tree obtained from standard ClustalW alignment of ACVS (A) and IPNS (B).



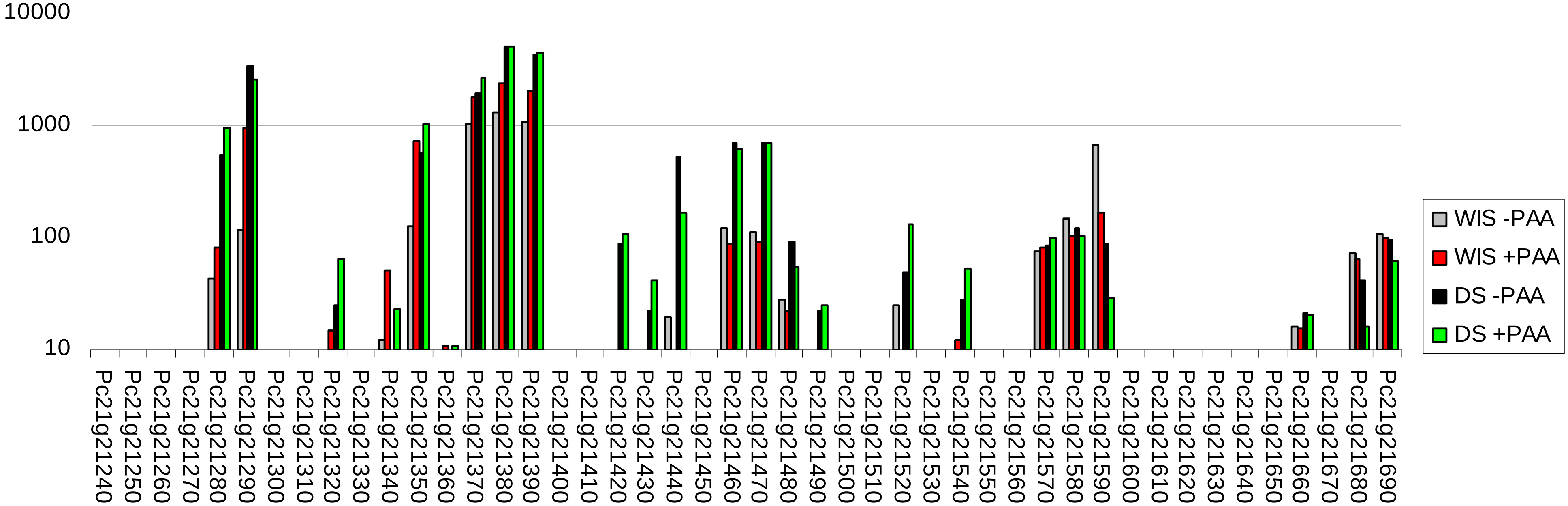
Supplementary Figure 6. NJ-tree of the known ferrichrome-type NRPS. There is an early divergence of type I/II and type III/IV/V-synthetases. Possibly two types were originally present, as still in *G. zeae* and *U. maydis*. The Ornithine N5-monooxygenase-gene is not clustered with type II although required for synthesis. Species are: *Aspergillus fumigatus, Aspergillus nidulans, Aspergillus oryzae, Aspergillus terreus, Aureobasidum pullulans, Chaetomium globosum, Cochliobolus heterostrophus, Gibberella zeae, Magnaporthe grisea, Neosartorya fischeri, Neurospora crassa, Omphalotus olearius, Podospora anserina*



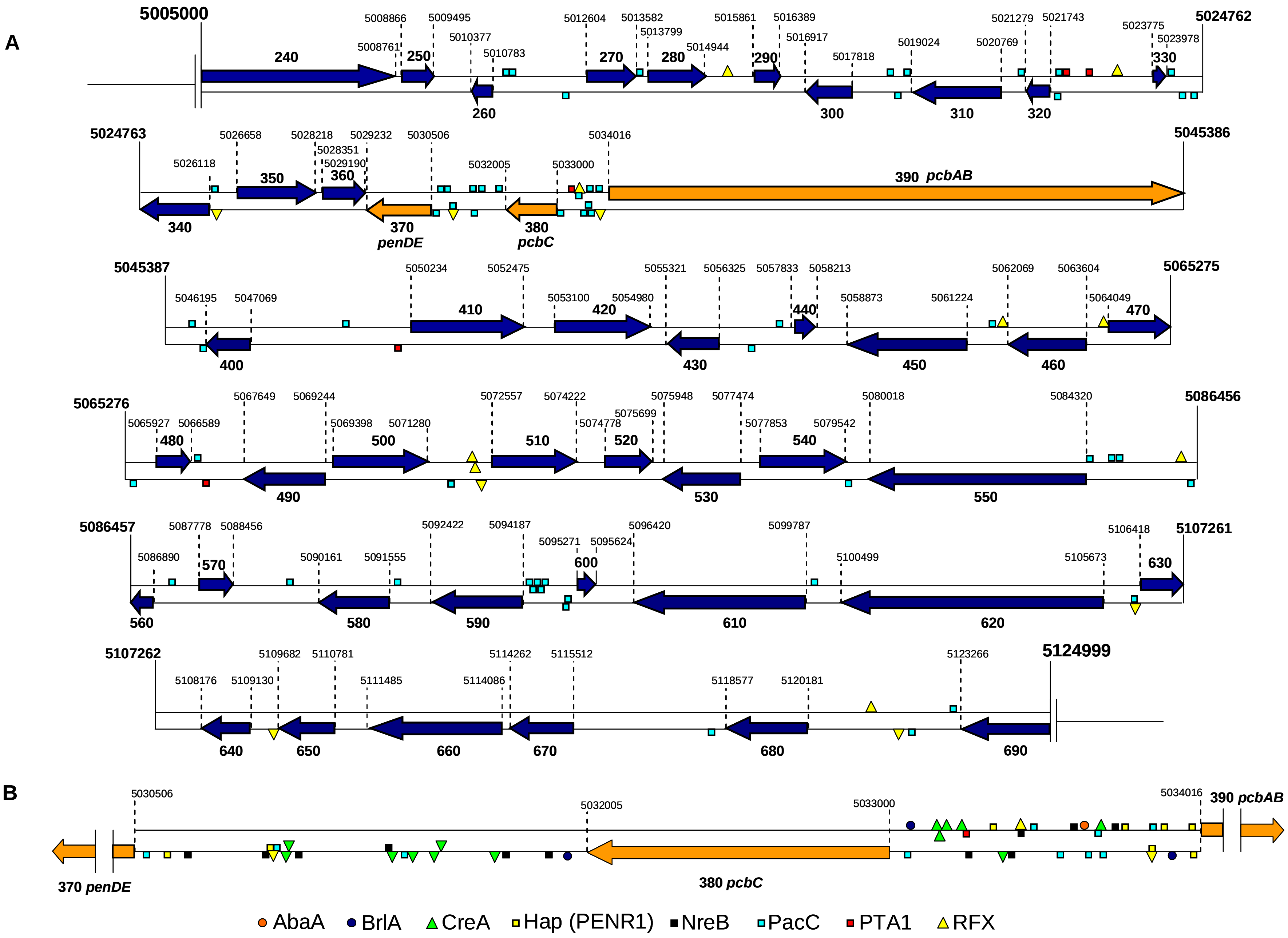
Supplementary Figure 7. Amplified chromosomal region in industrial *Penicillium* strains. Detailed overview of the region 5005000 to 5126000 from contig21 (part of chromosome I). HF', G'E, DC and AB indicate the hexamer sequences as reported[17]. Thick lines indicate the amplified regions: the 'flipped' region in the Wisconsin54-1255 lineage (dashed), the common part to all industrial strains (black), the part specific to the Panlabs lineage (grey). Colored arrows indicate the significance of the blastp results: hypothetical (grey), weak similarity (pink), similar (red), strong similarity (blue), known protein (green).



Supplementary Figure 8. Transcription profile of the amplified region in industrial *Penicillium* strains. The mean values of three individual experiments are shown (for details see **Supplementary methods**). Legend: Wisconsin54-1255 (Wis), DS17690 (DS), -PAA (no phenylacetic acid added, non-producing conditions), +PAA (phenylacetic acid added, penicillinG producing conditions).



Supplementary Figure 9. DNA binding sites of different transcription factors involved in penicillin biosynthesis. A). A schematic representation of the 120-kbp sequence which contains the amplified region of *P. chrysogenum* (see **Supplementary Fig. 8**). ORFs are indicated as blue arrows, except those corresponding to the three penicillin biosynthetic genes, which are represented as orange arrows. ORFs in both strands have been numbered according to the last three numbers of the ORF code (Pc21g21xxx) and their positions on contig 21 are also indicated. The DNA binding sites present in both strands of the intergenic regions are represented for the transcription factors PacC, RFX (CpcR1-like factor) and PTA1 as blue boxes, yellow triangles and red boxes, respectively. B). Detailed schematic representation of the region including the three penicillin biosynthetic genes. Positions of the *pcbAB*, *pcbC* and *penDE* genes on contig 21 are indicated. The DNA binding regions located on the coding strand of the intergenic regions are represented as follows: AbaA (orange circle), BrlA (blue circle), CreA (green triangle), Hap (PENR1) (yellow box), NreB (black box), PacC (blue box), PTA1 (red box) and RFX (CpcR1-like factor) (yellow triangle).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5009495
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5010783
5008761
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5012604
5013582
5013799
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5016917
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5023775
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5024762
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5026118
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5028218
5028351
5029190
5029232
5030506
5032005
5033000
5034016
5045386
340
350
360
370 penDE
380 pcbC
390 pcbAB
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5046195
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5052475
5053100
5054980
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5056325
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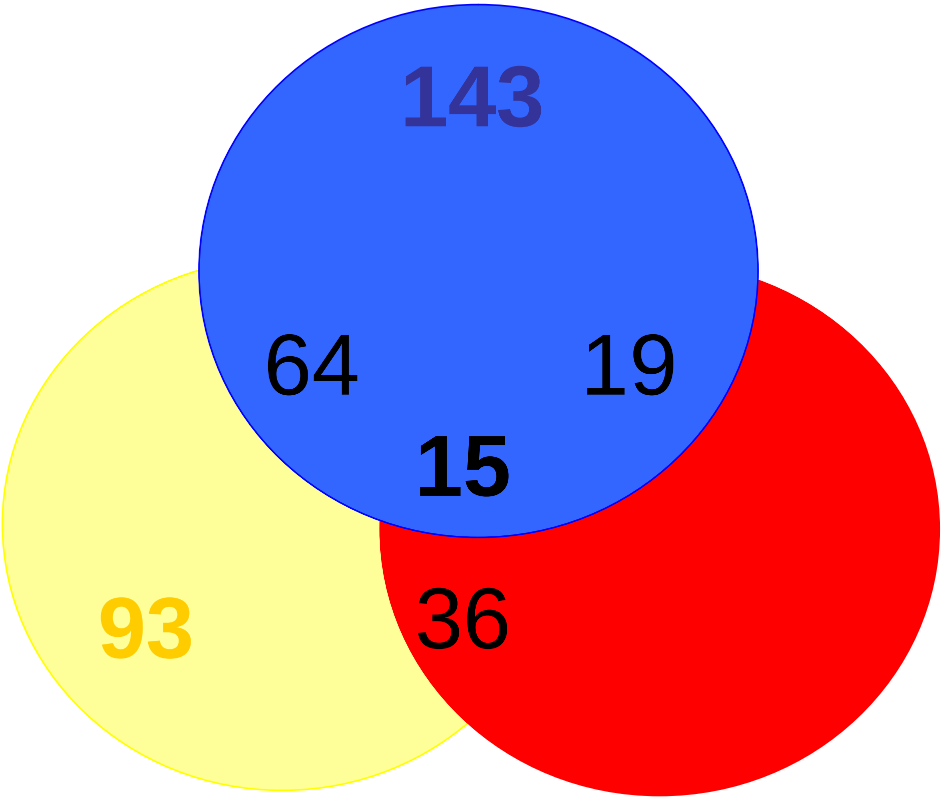
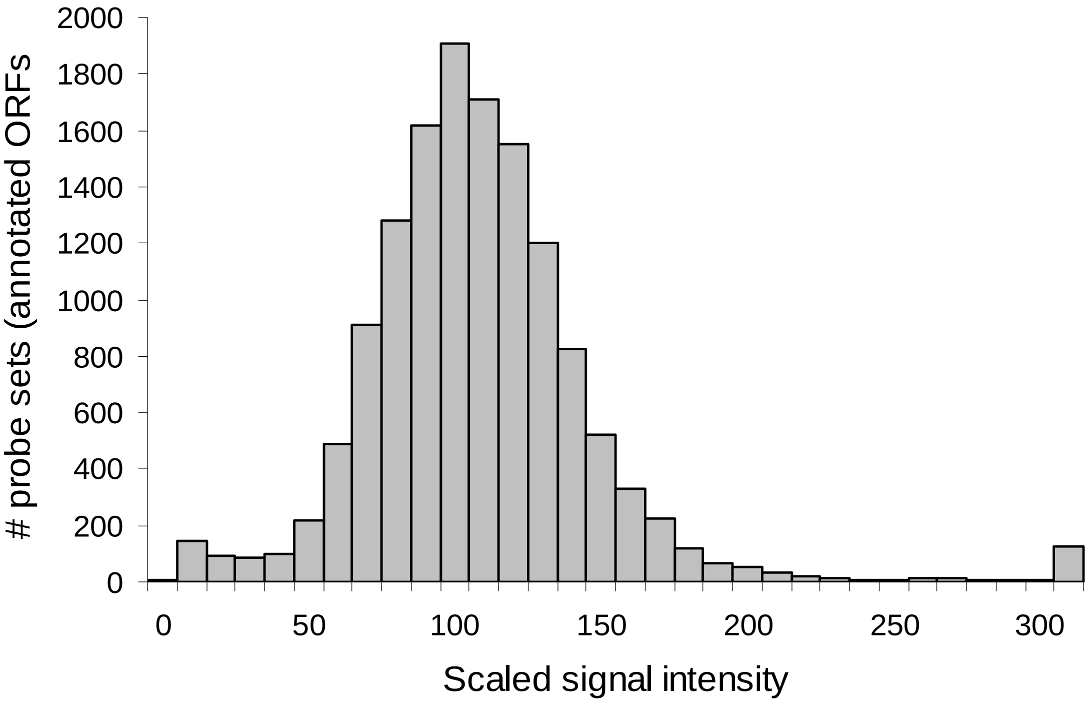
B
5030506
5032005
5033000
5034016
390 pcbAB
370 penDE
380 pcbC
● AbaA
● BrlA
▲ CreA
□ Hap (PENR1)
■ NreB
□ PacC
■ PTA1
△ RFX

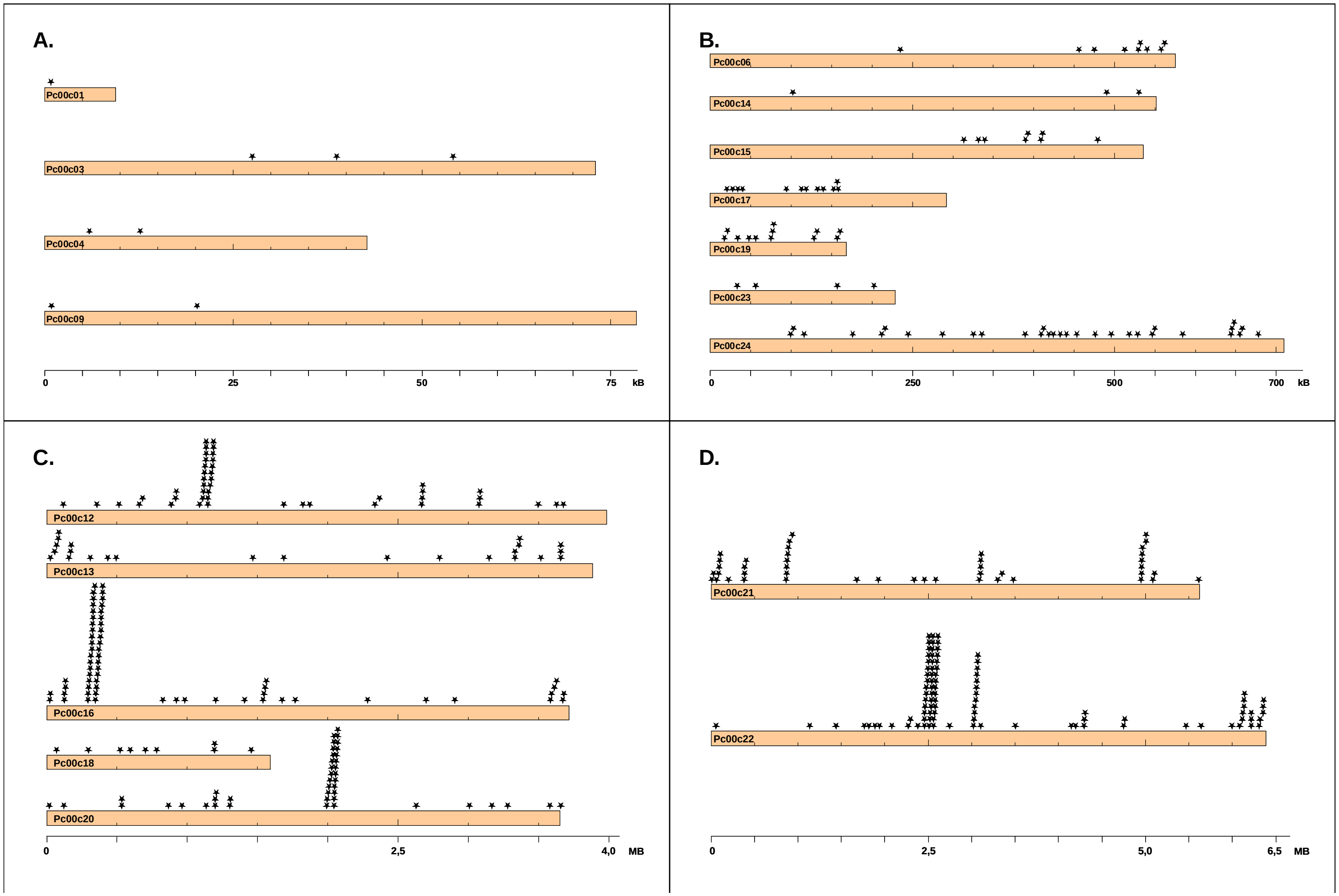
Supplementary Figure 10. Up-regulated transporter genes. Blue circle represents number of transporter genes up-regulated in the DS17690 strain with PAA versus Wisconsin54-1255 strain with PAA. Red circle represents number of genes up-regulated in the Wisconsin54-1255 strain with PAA versus Wisconsin54-1255 strain without PAA. Yellow circle represents number of genes up-regulated in the DS17690 strain with PAA versus DS17690 strain without PAA.



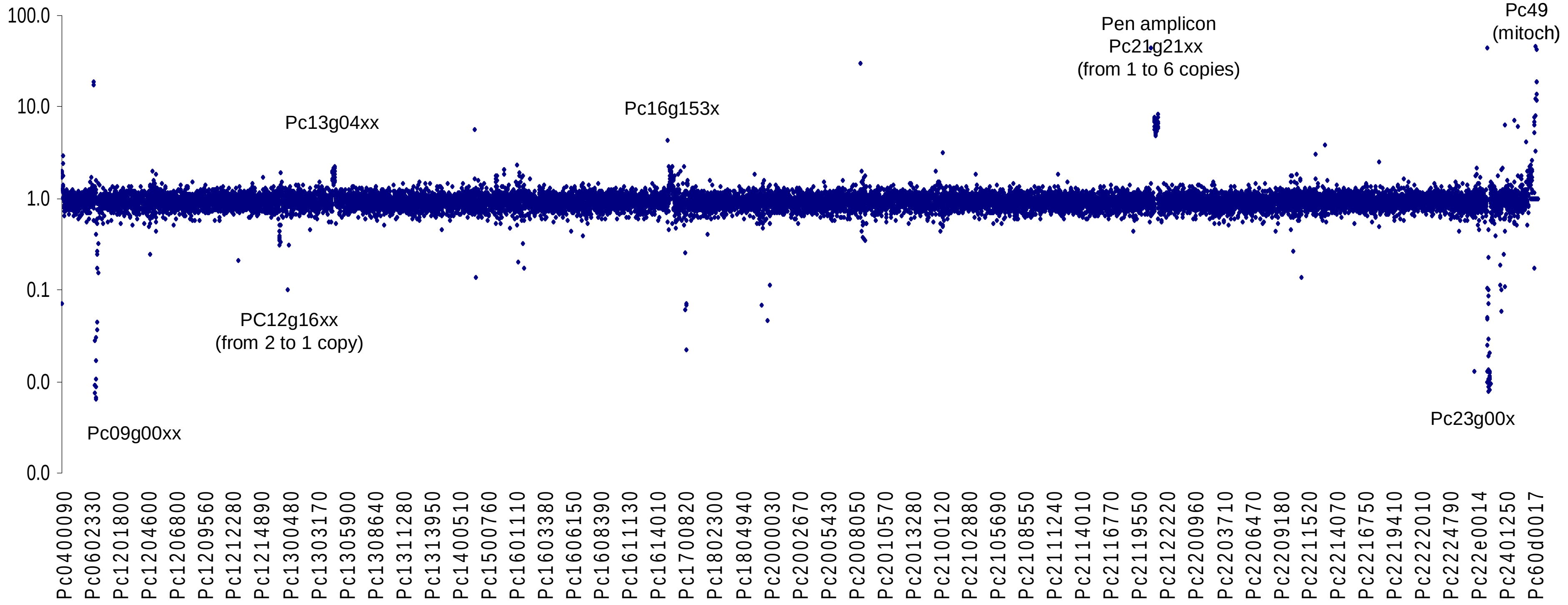
Supplementary Figure 11. Distribution of genomic DNA hybridization signal for annotated ORFs probe sets.



Supplementary Figure 12. Genome-wide comparison of genomic DNA copy number of the predicted ORFs in the production strain DS17690 vs. the reference Wisconsin54-1255. The ratios of the average intensities (n =3) were plotted on logarithmic scale. The indicated regions are detailed in **Supplementary table 20**.



Supplementary Figure 13. Schematic representation of genome distribution of transposon and transposon-like elements. A. 5kB - 100kB contigs with transposon-related sequences; **B.** 100kB - 1MB contigs with transposon-related sequences; **C.** 1MB - 5MB contigs with transposon-related sequences; **D.** >5MB contigs with transposon-related sequences. Detailed analysis of the individual elements is reported elsewhere[83].



Supplementary Table 23. Anticodon usage of *P. chrysogenum* tRNA genes

145 nuclear genome encoded tRNAs were identified. The number behind the amino acid indicates the number of tRNAs identified. No tRNA genes for Trp were identified. Three additional tRNA genes have been identified for which the specificity is unknown.

	.U.	.C.	.A.	.G.	
U..	Phe -	Ser 7	Tyr 1	Cys -	..U
	Phe 5	Ser -	Tyr 5	Cys 3	..C
	Leu -	Ser 1	Stop	Stop/1[1]	..A
	Leu -	Ser 2	Stop	Trp -	..G
C..	Leu 6	Pro -	His 1	Arg 10	..U
	Leu -	Pro -	His 6	Arg -	..C
	Leu -	Pro -	Gln 3	Arg 2	..A
	Leu 3	Pro 1	Gln 5	Arg 2	..G
A..	Ile 3	Thr 7	Asn -	Ser -	..U
	Ile -	Thr -	Asn 6	Ser 4	..C
	Ile 1	Thr 3	Lys 1	Arg -	..A
	Met 6	Thr 2	Lys 6	Arg 2	..G
G..	Val 8	Ala 4	Asp -	Gly -	..U
	Val -	Ala -	Asp 7	Gly 3	..C
	Val -	Ala 2	Glu 3	Gly 3	..A
	Val 3	Ala 1	Glu 4	Gly 1	..G

[1] Sec: selenocysteine

Supplementary Table 24. *P. chrysogenum* codon usage

Numbers (%) based on all identified *P. chrysogenum* ORFs.

	.T.	.C.	.A.	.G.	
T..	Phe 35	Ser 19	Tyr 44	Cys 43	..T
	Phe 65	Ser 21	Tyr 56	Cys 57	..C
	Leu 6	Ser 15	Stop 28	Stop 37	..A
	Leu 18	Ser 16	Stop 35	Trp 100	..G
C..	Leu 19	Pro 26	His 47	Arg 18	..T
	Leu 24	Pro 27	His 43	Arg 26	..C
	Leu 11	Pro 25	Gln 44	Arg 18	..A
	Leu 22	Pro 21	Gln 56	Arg 16	..G
A..	Ile 36	Thr 25	Asn 44	Ser 12	..T
	Ile 49	Thr 34	Asn 56	Ser 18	..C
	Ile 14	Thr 24	Lys 36	Arg 12	..A
	Met 100	Thr 18	Lys 64	Arg 10	..G
G..	Val 27	Ala 28	Asp 52	Gly 27	..T
	Val 36	Ala 32	Asp 48	Gly 33	..C
	Val 11	Ala 22	Glu 43	Gly 24	..A
	Val 27	Ala 18	Glu 57	Gly 16	..G

Supplementary Table 25. Differences in *P. chrysogenum* codon usage of this study to published data

Numbers refer to the codon frequency per thousand codons. The published data are based on 97 CDS (54,967 codons). This study is based on 13,663 CDS (6,077,249 codons).

Triplet	published	this study	Diff	Triplet	published	this study	Diff	Triplet	published	this study	Diff	Triplet	published	this study	Diff
UUU	10,7	13,1	-2,4	UCU	13,5	15,7	-2,2	UAU	11,8	12,5	-0,7	UGU	4,9	6	-1,1
UUC	29,1	24,4	4,7	UCC	22,4	17,6	4,8	UAC	21,7	16	5,7	UGC	7,6	7,9	-0,3
UUA	3	5,6	-2,6	UCA	8,7	12,6	-3,9	UAA	0,7	1,1	-0,4	UGA	0,6	1,5	-0,9
UUG	14,4	16,3	-1,9	UCG	11,7	13,4	-1,7	UAG	0,5	1,4	-0,9	UGG	14,1	15	-0,9
CUU	14,3	17,2	-2,9	CCU	14	16	-2	CAU	9,3	11,8	-2,5	CGU	11,9	11,1	0,8
CUC	25,4	21,7	3,7	CCC	18,1	16,7	1,4	CAC	15	13,1	1,9	CGC	17,2	16,5	0,7
CUA	6,3	9,9	-3,6	CCA	10,6	15,3	-4,7	CAA	12,1	17,4	-5,3	CGA	6,8	11,1	-4,3
CUG	23,7	19,6	4,1	CCG	10,7	12,8	-2,1	CAG	23,9	22,3	1,6	CGG	7,5	16,5	-9
AUU	20	18,6	1,4	ACU	15,5	15	0,5	AAU	14,2	16,1	-1,9	AGU	7,5	10,1	-2,6
AUC	29,9	25,3	4,6	ACC	24,5	19,9	4,6	AAC	26,9	20,8	6,1	AGC	15,6	14,9	0,7
AUA	3,7	7,3	-3,6	ACA	10,5	14	-3,5	AAA	11,1	16,5	-5,4	AGA	4,3	7,7	-3,4
AUG	20,5	21,9	-1,4	ACG	9,8	10,4	-0,6	AAG	35,7	29,5	6,2	AGG	3,6	6,2	-2,6
GUU	17,7	16,3	1,4	GCU	24,7	22,5	2,2	GAU	25,3	28,5	-3,2	GGU	25,2	18,3	6,9
GUC	26,8	21,5	5,3	GCC	35,6	25,9	9,7	GAC	31	26,5	4,5	GGC	26,1	22	4,1
GUA	4,5	6,5	-2	GCA	14,7	18,2	-3,5	GAA	18,7	25,7	-7	GGA	16,4	15,7	0,7
GUG	19,2	16,2	3	GCG	13,3	14,9	-1,6	GAG	38	33,8	4,2	GGG	7,3	10,8	-3,5

Supplementary Table 26. Transcription Factors identified in the *P. chrysogenum* genome. [a]Pfam trusted matches (Domains scoring higher than the gathering threshold)

General Transcription Factors involved in transcription initiation and elongation by RNA polymerases I, II and III

Transcription Factor	orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels @				Transcription factor Domain[a]
			Species	**Gene code**	**e-value**	**WIS - PAA**	**WIS + PAA**	**DS - PAA**	**DS + PAA**	
BDF1	Pc22g07210	strong similarity to transcription factor Bdf1 - Saccharomyces cerevisiae	bromodomain protein BDF1 - yeast (Saccharomyces cerevisiae)	S55955	1e-69	373.8	342.2	261.2	215.6	Bromodoamain. It associates with Saccharomyces cerevisiae TFIID and
RRN3	Pc22g21540	strong similarity to RNA polymerase I transcription factor RRN3 - Homo sapiens	gene: "B8J22.220"; product: "related to RNA Polymerase I	BX842627_22	3e-86	256.9	215.8	157.3	91.9	RNA polymerase I specific transcription initiation factor RRN3
RRN6	Pc16g01890	weak similarity to transcription initiation factor Rrn6 - Saccharomyces cerevisiae	gene: "B24N11.080"; product: "hypothetical protein"; Neurospora	NCB24N11_8	4e-11	51.4	40.7	29.9	17.5	No domain identified
SPBC336.07	Pc21g01450	similarity to hypothetical transcription factor subunit SPBC336.07 - Schizosaccharomyces pombe	gene: "B10N12.040"; product: "hypothetical protein"; Neurospora	NCB10N12_4	7e-29	84.7	54.1	70.5	60.5	B-block binding subunit of TFIIIC
TFIIA	Pc16g13800	strong similarity to large subunit of transcription initation factor TFIIA like protein An01g12770 - Aspergillus niger	probable transcription initiation factor IIA large subunit - fission yeast	T40052	5e-25	74.8	48.8	41.7	21.1	Transcription factor IIA, alpha/beta subunit
	Pc21g02570	strong similarity to small subunit of transcription factor TFIIA Toa2 - Saccharomyces cerevisiae	probable transcription factor iia small subunit - fission yeast	T41393	3e-32	416.2	387.1	256.8	320.1	Transcription initiation factor IIA, gamma subunit, helical domain, Transcription
TFIIB	Pc18g01520	strong similarity to transcription initiation factor TFIIB - Kluyveromyces lactis	probable transcription initiation factor TFIIB subunit - fission yeast	T37796	1e-90	813.3	986.2	728.7	679.8	TFIIB zinc ribbon, Transcription factor TFIIB repeat
TFIIIB	Pc18g01030	strong similarity to TFIIIB related factor hBRF - Homo sapiens	gene: "SPBC13E7.10c"; "SPBC30D10.20"; "brf1"; S.pombe	SPBC13E7_10	5e-84	26.6	29.8	20.2	16.0	TFIIB zinc ribbon, Transcription factor TFIIB repeat, Brf1-like TBP-binding
	Pc20g12070	strong similarity to transcription initiation factor IIIB chain like protein An15g00960 - Aspergillus niger	probable transcription factor tfiiib component - fission yeast	T41239	2e-20	93.9	89.1	76.9	61.3	Myb-like DNA-binding domain
TFIIIC	Pc13g10240	strong similarity to RNA polymerase III transcription initiation factor TFIIIC subunit like protein An16g04310 - Aspergillus niger	probable transcription factor - fission yeast (Schizosaccharomyces	T39931	3e-27	42.8	34.8	41.2	32.9	No domain identified
	Pc13g10840	strong similarity to hypothetical transcription factor IIIc-like protein CAE47909.1 - Aspergillus fumigatus	product: "possible transcription factor IIIc-like protein"; Aspergillus	BX649605_60	1e-117	69.5	52.5	40.4	23.1	No domain identified
	Pc16g09970	strong similarity to assembling subunit of transcription factor IIIC Tfc4 - Saccharomyces cerevisiae	probable transcription factor subunit, TPR domai ns - fission yeast	T41104	1e-76	126.1	111.3	90.8	104.2	TPR 1 tetratricopeptide repeat
	Pc21g15530	similarity to transcription factor IIIC 95K chain Tfc1 - Saccharomyces cerevisiae	gene: "B18D24.130"; product: "conserved hypothetical protein";	NCB18D24_11	3e-65	26.6	22.0	13.3	12.3	No domain identified
TFIID (TBP and TBP Associated Factors; TAFs)	Pc12g01100	similarity to component of the TBP-associated protein complex Taf47 - Saccharomyces cerevisiae	gene: "SPAC823.06"; S.pombe chromosome I cosmid c823.	SPAC823_6	2e-10	126.0	111.1	93.1	71.5	Bromodomain associated domain
	Pc12g01110	strong similarity to subunit of transcription initiation factor TFIID ptr6p - Schizosaccharomyces pombe	transcription initiation factor tfiid 55 kd subunit - fission yeast	T43401	9e-38	154.4	137.8	107.4	86.2	TAFII55 protein conserved region
	Pc12g11400	strong similarity to subunit of transcription initiation factor TFIID like protein An11g05530 - Aspergillus niger	probable transcription initiation factor tfiid subunit - fission yeast	S62469	1e-149	333.3	272.3	173.8	107.4	No domain identified
	Pc13g10670	strong similarity to subunit of transcription initiation factor TFIID TATA-box binding protein TBP - Aspergillus nidulans	TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR)	TF2D_EMENI	1e-121	1588.0	1751.4	1377.6	1077.5	TATA binding protein
	Pc16g02510	similarity to subunit of transcription initation factor TFIID Taf19 - Saccharomyces cerevisiae	gene: "B8J24.120"; product: "related to TFIID subunit TAF19";	NCB8J24_10	4e-20	91.4	73.1	60.7	45.5	Transcription initiation factor IID, 18kD subunit
	Pc16g14080	strong similarity to subunit of transcription initiation factor TFIID Taf17 - Saccharomyces cerevisiae	hypothetical protein YMR236w - yeast (Saccharomyces cerevisiae)	S57603	3e-24	74.2	79.8	64.1	74.3	Transcription initiation factor IID, 31kD subunit
	Pc20g10490	strong similarity to subunit of transcription initiation factor TFIID Tsm1 - Saccharomyces cerevisiae	gene: "B2I10.020"; product: "related to TSM1-component of TFIID	BX842623_1	0.0	211.5	186.3	163.8	153.9	No domain identified
	Pc21g01240	strong similarity to subunit of transcription initiation factor TFIID p80 - Xenopus laevis	transcription initiation factor tfiid 60 kd subu nit - fission yeast	T41108	1e-112	137.6	136.9	114.3	154.8	TATA box binding protein associated factor, Protein of unknown function
	Pc21g01260	strong similarity to subunit of transcription initiation factor TFIID like protein An09g06040 - Aspergillus niger	gene: "104H10.090"; product: "related to transcription initiation factor	NC104H10_10	5e-18	29.6	26.8	27.4	21.2	hTAFII28-like protein conserved region
	Pc21g06340	similarity to subunit of transcription initiation factor TFIID TAFII30 - Homo sapiens	gene: "B11O9.060"; product: "related to transcription factor TAF25";	NCB11O9_6	7e-35	214.5	200.1	134.9	113.4	Transcription initiation factor TFIID 23-30kDa subunit
	Pc22g12900	strong similarity to transcription initiation factor TFIID 100 kD subunit like protein An08g12200 - Aspergillus niger [truncated ORF][putative				0.8	1.1	0.3	0.9	No domain identified
	Pc22g25300	strong similarity to subunit of transcription initiation factor TFIID taf72p - Schizosaccharomyces pombe	gene: "9G6.220"; product: "related to TRANSCRIPTION INITIATION	NC9G6_20	1e-175	193.3	184.3	140.1	110.7	LisH, WD40 associated region in TFIID subunit (90 kDa), WD 40 domain, G-
TFIIE	Pc13g04320	strong similarity to alpha subunit of transcription initiation factor TFIIE Tfa1 - Saccharomyces cerevisiae	gene: "12F11.030"; product: "related to transcription initiation factor IIE	NC12F11_3	2e-47	57.0	61.1	77.3	53.2	TFIIE alpha subunit
	Pc22g02300	strong similarity to beta subunit of transcription initiation factor TFIIE Tfa2 - Saccharomyces cerevisiae	transcription initiation factor IIE beta subunit (TFIIE-BETA) - fission	T41052	3e-44	131.9	138.6	118.5	123.1	No domain identified
TFIIF	Pc12g03030	strong similarity to beta subunit of transcription initiation factor TFIIF Tfg2 - Saccharomyces cerevisiae	transcription initiation factor iif, beta subunit - fission yeast	T40615	3e-37	66.2	70.7	58.8	60.2	Transcription initiation factor IIF, beta subunit
	Pc14g00760	weak similarity to alpha subunit of transcription initiation factor TFIIF Tfg1 - Saccharomyces cerevisiae	gene: "29E8.530"; product: "related to transcription initiation factor	BX908809_53	6e-48	63.3	64.2	65.0	54.6	No domain identified
	Pc21g07350	strong similarity to small subunit of transcription initiation factor TFIIF Tfg3 - Saccharomyces cerevisiae	gene: "B13B7.010"; product: "related to transcription initiation factor IIF	BX908807_1	2e-56	359.7	396.5	270.1	260.3	YEATS family
TFIIH	Pc12g16480	weak similarity to subunit of transcription initation factor TFIIH DNA repair helicase rad15p - Schizosaccharomyces pombe				3.1	3.5	2.6	1.9	No domain identified
	Pc13g06540	strong similarity to subunit of transcription initiation factor TFIIH Tfb2 - Saccharomyces cerevisiae	hypothetical protein SPBC13G1.13 - fission yeast	T39414	2e-93	101.6	98.2	107.4	107.3	Transcription factor Tfb2
	Pc16g07740	strong similarity to subunit of transcription initiation factor TFIIH Tfb3 - Saccharomyces cerevisiae	hypothetical protein YDR460w - yeast (Saccharomyces cerevisiae)	S69628	1e-51	109.5	96.6	87.4	91.4	CDK-activating kinase assembly factor MAT1 , C3HC4 type (RING finger)
	Pc16g12370	strong similarity to subunit of transcription initation factor TFIIH DNA repair helicase rad15p - Schizosaccharomyces pombe	probable excision repair protein rhp3 [imported] - Neurospora crassa	T49560	0.0	72.0	73.9	58.6	59.2	DEAD_2 , Protein of unknown function (DUF1227) representing a conserved
	Pc20g09050	strong similarity to subunit of transcription initiation factor TFIIH protein kinase Kin28 - Saccharomyces cerevisiae	gene: "B2F7.040"; product: "probable cyclin-dependent ser/thr protein	NCB2F7_4	1e-126	177.8	156.8	170.0	122.4	Protein kinase domain, Protein tyrosine kinase
	Pc21g06450	strong similarity to subunit of transcription initiation factor TFIIH BTFII - Homo sapiens	probable transcription factor - fission yeast (Schizosaccharomyces	T40173	1e-66	34.3	36.4	30.6	29.3	Transcription factor Tfb4
	Pc21g16090	strong similarity to subunit of transcription initation factor TFIIH DNA helicase Rad25 - Saccharomyces cerevisiae	gene: "RAD25"; product: "DNA helicase"; Saccharomyces cerevisiae	SCRAD25A_1	0.0	287.6	399.8	245.7	277.4	Type III restriction enzyme, res subunit , DEAD/DEAH box helicase, Helicase
	Pc22g04800	strong similarity to subunit of transcription initiation factor TFIIH Tfb1 - Saccharomyces cerevisiae	RNA polymerase II transcription factor related protein [imported] -	T49685	1e-112	116.5	110.4	107.6	95.5	TFIIH p62 subunit, N-terminal domain, BSD domain
	Pc22g11160	strong similarity to subunit of transcription initiation factor TFIIH Ssl1 - Saccharomyces cerevisiae	transcription factor TFIIH chain p47 - fission yeast	T43534	1e-135	114.0	115.8	94.2	135.7	Ssl1-like protein (40kDa subunits of the Transcription factor II H complex),
	Pc22g25000	weak similarity to subunit of transcription initiation factor TFIIH protein kinase Kin28 - Saccharomyces cerevisiae [putative pseudogene]				1.4	1.5	0.5	2.9	No domain identified
Transcription elongation factor	Pc12g08440	weak similarity to transcription factor CA150 - Homo sapiens	hypothetical WW domain protein SPAC13C5.02 - fission yeast	S58094	4e-23	55.9	60.5	53.5	51.4	WW domain, FF domain. Transcription elongation regulator 1. Coactivator of
	Pc13g04600	strong similarity to transcription elongation factor like protein An05g00780 - Aspergillus niger	hypothetical protein SPBC29A3.08 - fission yeast	T40079	7e-06	58.2	54.2	27.7	23.6	No domain identified
	Pc15g01750	strong similarity to transcription elongation factor TFIIS encoded by tfs1p - Schizosaccharomyces pombe	gene: "B5K2.220"; product: "related to transcription elongation factor	BX842632_22	5e-49	161.7	138.1	124.3	105.0	Transcription elongation factor S-II protein N terminal, Transcription factor S-II
	Pc16g07580	strong similarity to transcription elongation protein Spt5 - Saccharomyces cerevisiae	acidic nuclear protein SPT5 - yeast (Saccharomyces cerevisiae)	A40253	1e-103	233.3	235.4	191.4	122.7	No domain identified
	Pc20g05030	similarity to transcription elongation factor Rtf1 - Saccharomyces cerevisiae	gene: "G17A4.140"; product: "related to Pol II transcription elongation	BX908812_14	6e-71	220.6	199.9	156.7	134.1	Plus-3 domain
	Pc20g08080	strong similarity to transcription elongation protein Spt6 - Saccharomyces cerevisiae	gene: "B13H18.030"; product: "related to transcriptional regulator	NCB13H18_3	0.0	117.9	106.3	107.8	116.8	SH2 domain
	Pc21g11560	weak similarity to transcription elongation protein Spt5 - Saccharomyces cerevisiae	gene: "glh-2"; product: "RNA helicase GLH-2"; Caenorhabditis elegans	CE60194_1	7e-05	37.8	33.9	37.4	35.4	No domain identified
	Pc21g17890	similarity to protein Spt4 - Saccharomyces cerevisiae	TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1.	SPT4_HUMAN	2e-26	302.5	355.0	258.3	268.7	Transcription elongation protein Spt4

Specific Transcription Factors

Transcription Factor	orf code	Description of putative *P. chrysogenum* ORF	Best blast homolog to putative *P. chrysogenum* ORF			Average transcript levels				Transcription factor Domain[a]
			Species	**Gene code**	**e-value**	**WIS -PAA**	**WIS +PAA**	**DS -PAA**	**DS +PAA**	
ABAa	Pc16g09610	strong similarity to protein abaA - Aspergillus nidulans	abaA protein - Emericella nidulans	A32434	0.0	22.6	8.9	63.5	4.3	TEA/ATTS
ACE1	Pc20g06400	strong similarity to Cys2-His2 zinc finger transcription factor ACEI - Hypocrea jecorina	product: "zinc finger transcription factor ACE I"; Talaromyces	AY072919_1	1e-165	838.7	772.8	611.2	373.9	C2H2
ACR-2	Pc03g00220	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa [putative sequencing error]	gene: "B11E5.460"; product: "putative protein"; Neurospora crassa	BX842620_46	2e-04	2.5	3.7	6.1	3.8	Zn(II)2Cys6
	Pc06g01550	similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	gene: "B11E5.460"; product: "putative protein"; Neurospora crassa	BX842620_46	5e-10	64.8	67.4	57.4	51.1	Zn(II)2Cys6
	Pc12g08760	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	gene: "17E5.150"; product: "conserved hypothetical protein";	NC17E5_14	3e-18	5.4	7.3	7.5	5.4	No domain identified
	Pc13g08450	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	gene: "B11E5.460"; product: "putative protein"; Neurospora crassa	BX842620_46	7e-12	86.4	89.2	98.8	99.1	Zn(II)2Cys6
	Pc16g12430	similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	acr-2 protein - Neurospora crassa	S72537	3e-18	67.1	79.8	63.0	87.6	Zn(II)2Cys6
	Pc17g00670	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa				4.3	4.9	4.1	3.4	Zn(II)2Cys6
	Pc18g00950	similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	gene: "acr-2"; Neurospora crassa acr-2 DNA, complete cds.	NCD893_3	3e-24	104.9	109.0	113.5	96.5	Zn(II)2Cys6
	Pc20g06350	similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	acr-2 protein - Neurospora crassa	S72537	9e-12	60.4	48.6	51.7	68.7	Zn(II)2Cys6
	Pc20g11000	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa [putative sequencing error]				124.9	107.3	55.9	53.0	Zn(II)2Cys6
	Pc20g11950	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	gene: "B7F21.070"; product: "hypothetical protein"; Neurospora crassa	NCB7F21_6	3e-04	9.1	7.1	13.0	16.5	No domain identified
	Pc21g04570	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	zinc finger protein 1 homolog [imported] - Neurospora crassa	T49729	9e-09	81.0	69.7	53.4	54.9	Zn(II)2Cys6
	Pc21g08180	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	gene: "B11E5.460"; product: "putative protein"; Neurospora crassa	BX842620_46	2e-21	244.6	260.2	203.5	193.2	Zn(II)2Cys6
	Pc21g09390	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa				31.0	22.3	66.2	78.3	No domain identified
	Pc22g23130	weak similarity to transcription factor involved in acriflavine resistance acr-2 - Neurospora crassa	gene: "B7F21.070"; product: "hypothetical protein"; Neurospora crassa	NCB7F21_6	1e-12	15.6	16.1	22.5	29.4	Zn(II)2Cys6
ADA	Pc13g06500	similarity to adaptive response regulatory protein Ada - Escherichia coli	O6-methylguanine-DNA methyltransferase [imported] - Escherichia	F91016	5e-19	12.5	11.6	29.7	44.5	Ada Zn finger, Bacterial regulatory helix-turn-helix proteins (AraC family)
	Pc21g17410	strong similarity to adaptive response regulatory protein Ada - Escherichia coli	gene: "ada"; product: "ada regulatory protein"; Brucella suis 1330	AE014348_9	2e-27	27.7	28.1	29.3	44.5	Ada Zn finger, Bacterial regulatory helix-turn-helix proteins (AraC family)
ADA2, ADA3	Pc16g09180	strong similarity to ADA and SAGA histone acetyltransferase subunint Ada3 - Saccharomyces cerevisiae	gene: "ADA3"; product: "alteration/deficiency in activation 3 protein";	SCADA3A_1	8e-32	31.6	18.0	9.7	10.1	No domain identified
	Pc22g20820	strong similarity to transcription adaptor Ada2 - Saccharomyces cerevisiae	gene: "G21B4.020"; product: "related to transcription adaptor ADA2";	BX908808_2	1e-167	254.0	265.0	119.6	104.7	ZZ zinc finger Myb DNA bindin domain, SWIRM domain
ADR1	Pc22g05790	strong similarity to transcription activator Adr1 - Saccharomyces cerevisiae	gene: "SPBC1711.08"; S.pombe chromosome II cosmid c1711.	SPBC1711_8	1e-70	864.8	1161.1	857.8	1036.5	Aha1N (Activator of Hsp90 ATPase, N-terminal) , AHSA1 (Activator of Hsp90
AFLR	Pc13g10310	similarity to sterigmatocystin synthesis transcription regulator aflR - Aspergillus nidulans	gene: "gsp"; product: "unknown"; Glarea lozoyensis polyketide	AF549411_2	1e-06	645.5	638.9	660.1	91.2	Zn(II)2Cys6
	Pc16g02310	weak similarity to aflatoxin biosynthesis regulatory protein aflR - Aspergillus parasiticus	transcription regulator, binuclear cluster zinc-finger protein - fission	T39677	4e-05	144.2	130.1	125.5	95.4	Zn(II)2Cys6
	Pc16g02830	similarity to aflatoxin biosynthesis regulatory protein aflR - Aspergillus parasiticus	gene: "aflR"; product: "AFLR"; Aspergillus flavus isolate BN040 AFLR	AF441440_1	2e-04	10.6	8.4	11.1	9.8	Zn(II)2Cys6
	Pc16g09740	similarity to aflatoxin biosynthesis regulator aflR - Aspergillus flavus	gene: "aflR"; product: "AFLR"; Aspergillus nomius isolate A25O AFLR	AF441426_1	8e-09	145.2	142.3	209.7	146.3	Zn(II)2Cys6
	Pc20g15060	similarity to aflatoxin biosynthesis regulator aflR - Aspergillus flavus	gene: "aflR"; product: "AFLR"; Aspergillus nomius isolate BN013P	AF441421_1	6e-05	32.3	26.4	47.1	70.4	C2H2, Zn(II)2Cys6
	Pc21g04750	similarity to aflatoxin biosynthesis regulatory protein aflR - Aspergillus parasiticus	gene: "AfA12H2.19c"; product: "hypothetical protein"; Aspergillus	AFA12H2_19	9e-68	68.6	49.0	50.7	39.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g07530	similarity to sterigmatocystin synthesis transcription regulator aflR - Aspergillus nidulans	sterigmatocystin synthesis transcription regulator aflR - Emericella	S69999	4e-04	73.2	73.8	87.6	95.3	Zn(II)2Cys6
ALCR	Pc21g22800	strong similarity to transcription regulator alcR - Aspergillus nidulans	REGULATORY PROTEIN ALCR.	ALCR_EMENI	0.0	108.0	112.8	142.8	295.0	Zn(II)2Cys6
AMDA	Pc06g01210	similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	gene: "MIG1"; product: "MIG repressor"; Candida utilis MIG1 gene for	CUT277830_1	4e-07	1.9	2.6	2.1	1.0	C2H2
	Pc12g12000	similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	DNA-binding protein amdA - Emericella nidulans	S61908	6e-11	35.5	74.4	40.1	53.7	C2H2
	Pc16g09130	similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	product: "Ste12-like transcription factor"; Neurospora crassa Ste12-like	AY027529_1	5e-11	27.4	30.2	50.2	77.7	C2H2
	Pc16g11660	weak similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	DNA-binding protein amdA - Emericella nidulans	S61908	5e-95	4.3	2.5	6.2	12.2	C2H2
	Pc20g06540	weak similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	Aspergillus fumigatus regA gene for transcription factor RegA,	AJ582911_1	8e-64	42.1	45.2	64.6	121.8	Zn(II)2Cys6
	Pc21g01800	weak similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	DNA-binding protein amdA - Emericella nidulans	S61908	4e-28	539.9	452.3	270.1	256.9	C2H2
	Pc21g17100	strong similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	DNA-binding protein amdA - Emericella nidulans	S61908	1e-123	160.1	94.7	69.3	73.1	C2H2
	Pc21g17490	strong similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	DNA-binding protein amdA - Emericella nidulans	S61908	0.0	45.6	40.9	59.1	83.9	C2H2
	Pc21g21660	weak similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	DNA-binding protein amdA - Emericella nidulans	S61908	7e-89	16.4	15.8	21.2	20.3	C2H2
	Pc21g22480	similarity to zinc-finger transcription factor amdA - Aspergillus nidulans	DNA-binding protein amdA - Emericella nidulans	S61908	2e-14	53.5	48.9	54.0	54.6	C2H2
	Pc22g02870	weak similarity to zinc-finger transcription factor amdA - Aspergillus nidulans				3.2	2.5	3.1	4.8	No domain identified
AMDR	Pc16g08250	strong similarity to transcription regulator amdR - Aspergillus nidulans	gene: "amdR"; product: "regulatory protein"; Aspergillus oryzae	AOAMDR_1	0.0	214.9	209.5	214.1	206.1	Zn(II)2Cys6, Fungal specific transcription factor domain
AMDX	Pc12g15680	similarity to DNA binding regulatory protein amdX - Aspergillus nidulans	gene: "RGM1"; product: "proline-rich zinc finger protein"; S.cerevisiae	SCRGM1_1	1e-11	137.0	104.1	83.7	40.0	C2H2
	Pc20g04780	similarity to DNA binding regulatory protein amdX - Aspergillus nidulans	DNA binding regulatory protein - Emericella nidulans	T18303	6e-04	96.7	171.7	171.2	134.0	C2H2
	Pc21g19860	strong similarity to DNA binding regulatory protein amdX - Aspergillus nidulans	DNA binding regulatory protein - Emericella nidulans	T18303	0.0	195.7	248.2	179.7	215.6	C2H2
	Pc12g04420	similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	gene: "104H10.220"; product: "related to transcription activator amyR";	NC104H10_21	6e-23	176.1	155.2	137.9	156.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g08700	weak similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	gene: "facB"; product: "FacB"; Aspergillus niger putative DNA binding	ANU56099_1	3e-07	69.5	63.7	138.1	148.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g10640	similarity to transcription regulator of maltose utilization amyR - Aspergillus nidulans	gene: "sugR"; product: "sugar regulator"; Aspergillus parasiticus NADH	AF168613_4	3e-28	6.4	16.6	10.1	12.7	Zn(II)2Cys6

AMYR	Pc13g12950	weak similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	gene: "CAT8"; product: "Cat8"; Candida albicans Ntg1 (NTG1) gene,	AF222908_3	4e-08	11.0	11.0	25.4	12.9	Zn(II)2Cys6
	Pc16g08580	weak similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	gene: "18F11.070"; product: "hypothetical protein"; Neurospora crassa	NC18F11_8	4e-04	17.7	13.8	17.7	21.1	Zn(II)2Cys6
	Pc20g12660	strong similarity to transcription regulator of maltose utilization amyR - Aspergillus nidulans	gene: "104H10.220"; product: "related to transcription activator amyR";	NC104H10_21	5e-63	5.2	9.4	6.0	6.8	Zn(II)2Cys6
	Pc21g22520	weak similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	transcription regulator SPBC16G5.17 - fission yeast	T39609	2e-04	22.6	18.4	24.9	26.2	Zn(II)2Cys6
	Pc22g07890	similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	gene: "104H10.220"; product: "related to transcription activator amyR";	NC104H10_21	2e-22	49.4	49.0	48.0	51.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g12360	strong similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	gene: "amyR"; product: "unknown"; Aspergillus niger (amyR) gene,	AF155808_1	0.0	121.5	83.0	353.7	458.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g17270	weak similarity to transcription regulator of maltose utilization amyR - Aspergillus oryzae	gene: "B11A5.030"; product: "conserved hypothetical protein";	NCB11A5_2	1e-137	34.8	32.5	31.3	44.2	Zn(II)2Cys6, Fungal specific transcription factor domain
An01g04370	Pc16g10300	strong similarity to transcription factor like protein An01g04370 - Aspergillus niger	zinc-finger protein - fission yeast (Schizosaccharomyces pombe)	T37676	6e-42	58.6	106.5	49.7	39.2	C2H2
An01g06240	Pc22g22250	strong similarity to SWI SNF complex subunit like protein An01g06240 - Aspergillus niger	hypothetical protein SPCC285.17 - fission yeast	T41263	2e-17	122.2	123.3	84.7	74.4	DEK C terminal domain, SWIB/MDM2 domain
An01g07600	Pc22g05440	strong similarity to pax transcription activation domain interacting protein like protein An01g07600 - Aspergillus niger	gene: "B23L21.340"; product: "conserved hypothetical protein";	NCB23L21_20	0.0	145.0	119.1	112.6	102.0	BRCA1 C Terminus (BRCT) domain
An02g02190	Pc12g11550	strong similarity to human regulatory molecule HRM-7 like protein An02g02190 - Aspergillus niger	product: "putative mitochondrial fission protein Tbfis1p"; Tuber borchii	AY273171_1	2e-52	266.9	275.6	226.2	275.6	No domain identified
An02g05220	Pc12g12410	strong similarity to transcription regulator like protein An02g05220 - Aspergillus niger	product: "RING zinc finger protein SMRZ"; Homo sapiens striated	AF361946_1	3e-08	112.1	107.7	99.8	85.3	C3HC4 type (RING finger), Zinc finger ZZ type, SH3 (Src homology 3) domain
An02g06940	Pc13g09440	strong similarity to transcription factor like protein An02g06940 - Aspergillus niger	gene: "Tcfcp2l3"; product: "Tcfcp2l3 protein"; Mus musculus	BC055035_1	7e-15	112.1	101.6	251.6	238.0	CP2 transcription factor
	Pc16g03530	strong similarity to transcription factor like protein An02g06940 - Aspergillus niger [putative pseudogene]				5.3	7.5	7.1	3.9	No domain identified
	Pc23g00420	strong similarity to transcription factor like protein An02g06940 - Aspergillus niger	product: "p61 MGR"; Mus musculus p61 MGR mRNA, complete cds.	AF411211_1	1e-12	2.4	1.6	7.3	3.5	CP2 transcription factor
	Pc24g02200	similarity to transcription factor like protein An02g06940 - Aspergillus niger				0.8	1.6	3.4	2.3	No domain identified
An02g07140	Pc13g09650	strong similarity to transcription regulator like protein An02g07140 - Aspergillus niger	hypothetical protein SPBC30B4.04c - fission yeast	T40170	1e-39	328.0	295.2	259.0	225.5	ARID/BRIGHT DNA binding domain
An02g13870	Pc22g09070	strong similarity to transcription silencing protein like protein An02g13870 - Aspergillus niger [truncated ORF]	probable histone acetyl transferase - fission yeast	T39004	1e-131	108.3	89.6	100.0	86.0	MOZ/SAS family
An02g14310	Pc22g08370	strong similarity to PHD-finger protein like protein An02g14310 - Aspergillus niger	gene: "CG11033"; product: "SD04170p"; Drosophila melanogaster	BT009941_1	4e-63	143.9	135.5	69.5	67.8	PHD-finger, JmjC domain
An05g00720	Pc23g00340	strong similarity to acetate regulatory DNA binding protein like protein An05g00720 - Aspergillus niger [truncated ORF][putative pseudogene]				5.0	3.3	1.1	1.0	No domain identified
An08g02780	Pc16g04450	strong similarity to transcription factor like protein An08g02780 - Aspergillus niger	gene: "B7F18.040"; product: "related to transcription factor TMF";	NCB7F18_3	2e-81	90.5	77.6	69.7	63.0	No domain identified
An09g04970	Pc13g13510	strong similarity to transcription cofactor like protein An09g04970 - Aspergillus niger	Gloeobacter violaceus PCC 7421 DNA, complete genome, section	AP006574_135	3e-38	30.8	48.2	64.1	55.2	Pirin domain
An09g05800	Pc21g15950	strong similarity to transcription regulator like protein An09g05800 - Aspergillus niger	gene: "3H10.130"; product: "related to regulator protein rum1";	NC3H10_12	0.0	171.6	136.4	127.4	97.6	JmjN domain, ARID/BRIGHT DNA binding domain, PHD-finger, JmjC domain,
An11g04480	Pc12g10970	strong similarity to non-specific RNA polymerase II transcription factor like protein An11g04480 - Aspergillus niger	gene: "G17A4.100"; product: "hypothetical protein"; Neurospora crassa	BX908812_10	1e-83	120.2	95.5	60.8	61.6	No domain identified
An12g00210	Pc21g11700	strong similarity to transcription activator like protein An12g00210 - Aspergillus niger	probable snf2 family helicase - fission yeast (Schizosaccharomyces	T37528	0.0	100.0	82.3	67.0	59.2	Res III (Type III restriction enzyme, res subunit), SNF2 family N-terminal
An12g08240	Pc22g24070	strong similarity to human transcriptional regulatory protein like protein An12g08240 - Aspergillus niger	gene: "smcA"; product: "structural maintenance of chromosome	AY081008_1	0.0	31.2	38.7	25.1	35.7	RecF/RecN/SMC (structural maintenance of chromosomes) N terminal
An12g10110	Pc22g10440	similarity to transcription factor like protein An12g10110 - Aspergillus niger [truncated ORF][putative pseudogene]				0.3	0.6	2.5	0.5	No domain identified
An13g00370	Pc21g04980	strong similarity to calcineurin responsive zinc-finger transcription factor like protein An13g00370 - Aspergillus niger	gene: "B16B8.160"; product: "related to zinc finger protein crol	BX842634_16	3e-41	85.5	44.4	51.2	22.2	C2H2
An13g01050	Pc21g08860	strong similarity to acvA gene expression regulator Pc804 like protein An13g01050 - Aspergillus niger				87.3	83.9	62.4	40.1	No domain identified
An14g00030	Pc13g05610	strong similarity to general activator of pre-mRNA splicing like protein An14g00030 - Aspergillus niger	probable splice factor - fission yeast (Schizosaccharomyces pombe)	T39995	2e-05	162.5	143.4	131.6	109.8	RNA recognition motif (RRM 1 motif)
An14g03210	Pc13g09920	strong similarity to transcriptional regulator like protein An14g03210 - Aspergillus niger	gene: "dJ423B22.2"; product: "dJ423B22.2 (novel protein similar to	HS423B22_2	2e-28	33.1	41.4	30.6	35.2	FHA (Forkhead-associated) domain
An14g04070	Pc21g10170	strong similarity to CCAAT binding transcription factor subunit like protein An14g04070 - Aspergillus niger	product: "hypothetical protein"; Dictyostelium discoideum chromosome	AC117076_21	4e-11	101.2	96.3	68.7	57.1	Histone-like transcription factor (CBF/NF-Y)
An14g04590	Pc21g07940	strong similarity to transcription factor like protein An14g04590 - Aspergillus niger	unnamed ORF; Sequence 22 from Patent WO02059324.	AX513585_1	1e-79	171.8	142.0	85.8	66.3	IPK (Inositol polyphosphate kinase) domain
An16g01640	Pc20g10250	strong similarity to transcription factor like protein An16g01640 - Aspergillus niger				14.7	10.0	9.5	6.7	No domain identified
An16g05120	Pc22g19970	strong similarity to lovF gene expression regulator like protein An16g05120 - Aspergillus niger				247.4	197.1	162.1	89.0	No domain identified
An16g08800	Pc21g11090	strong similarity to zinc-finger transcription factor like protein An16g08800 - Aspergillus niger	gene: "B13H18.230"; product: "hypothetical protein"; Neurospora	NCB13H18_21	2e-21	231.6	258.0	230.6	115.2	C2H2
An18g01300	Pc23g00520	similarity to transcription regulator like protein An18g01300 - Aspergillus niger [truncated ORF]				2.0	2.3	2.4	3.8	No domain identified
AP1p	Pc12g01640	similarity to transcription factor ap1p - Schizosaccharomyces pombe	related to AP-1-like transcription factor [imported] - Neurospora crassa	T49700	3e-05	206.0	177.2	137.0	98.9	No domain identified
	Pc17g00460	similarity to transcription factor ap1p - Schizosaccharomyces pombe [truncated ORF][putative pseudogene]	related to AP-1-like transcription factor [imported] - Neurospora crassa	T49700	2e-18	3.4	6.2	8.6	9.8	bZIP-like leucine zipper (bZIP 1, bZIP 2)
	Pc20g15280	similarity to transcription factor ap1p - Schizosaccharomyces pombe	gene: "B23L21.130"; product: "related to AP-1-like transcription factor";	NCB23L21_7	4e-54	401.7	454.2	357.8	395.6	bZIP-like leucine zipper (bZIP 1), PAP1 domain
	Pc22g27000	similarity to transcription factor ap1p - Schizosaccharomyces pombe [truncated ORF][putative pseudogene]	related to AP-1-like transcription factor [imported] - Neurospora crassa	T49700	6e-15	1.6	2.3	3.3	1.7	bZIP-like leucine zipper (bZIP 1, bZIP 2)
ARCA	Pc12g06020	similarity to transcription regulator of arginine catabolism arcA - Aspergillus nidulans	gene: "ARCA"; product: "ARCA protein"; Emericella nidulans ARCA	ENI294750_1	2e-04	233.7	218.8	209.4	212.8	No domain identified
ARG81	Pc06g00570	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	gene: "pro1"; product: "PRO1 protein"; Sordaria brevicollis pro1 gene	SBR238536_1	1e-06	32.1	42.4	49.1	73.1	Zn(II)2Cys6
	Pc12g12960	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae				31.2	59.0	46.5	114.3	No domain identified
	Pc12g13730	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae	regulatory protein ARGR2 - yeast (Saccharomyces cerevisiae)	S49627	2e-04	3.0	2.2	1.1	3.2	No domain identified
	Pc13g03330	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	S. cerevisiae ARGR II regulatory gene	SCARGRII_1	4e-09	15.9	43.2	132.4	148.8	Zn(II)2Cys6
	Pc13g07260	similarity to regulator protein Arg81 - Saccharomyces cerevisiae	regulatory protein ARGR2 - yeast (Saccharomyces cerevisiae)	S49627	1e-04	45.2	49.1	60.3	46.6	Zn(II)2Cys6
	Pc16g04470	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	gene: "pro1"; product: "PRO1 protein"; Sordaria macrospora pro1	SAJ10151_1	8e-06	148.1	133.2	118.7	124.4	Zn(II)2Cys6
	Pc16g07620	similarity to hypothetical transcription factor Arg81 - Saccharomyces cerevisiae	gene: "B11E5.460"; product: "putative protein"; Neurospora crassa	BX842620_46	8e-10	20.8	16.4	12.8	22.8	Zn(II)2Cys6
	Pc16g10640	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae	regulatory protein ARGR2 - yeast (Saccharomyces cerevisiae)	S49627	8e-08	25.2	64.0	54.8	131.0	Zn(II)2Cys6
	Pc20g04200	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	regulatory protein ARGR2 - yeast (Saccharomyces cerevisiae)	S49627	9e-05	43.1	44.8	60.6	85.0	Zn(II)2Cys6
	Pc20g06630	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	regulatory protein ARGR2 - yeast (Saccharomyces cerevisiae)	S49627	1e-13	12.5	18.7	31.4	55.3	Zn(II)2Cys6
	Pc20g09530	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae	gene: "17E5.150"; product: "conserved hypothetical protein";	NC17E5_14	8e-09	26.2	16.0	21.9	22.6	Zn(II)2Cys6
	Pc20g14370	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	gene: "B3E4.120"; product: "related to negative acting factor";	NCB3E4_9	8e-23	91.1	90.7	75.4	72.1	Zn(II)2Cys6
	Pc21g06560	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	S. cerevisiae ARGR II regulatory gene	SCARGRII_1	4e-08	25.2	45.4	41.0	71.9	Zn(II)2Cys6
	Pc22g00630	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	2e-04	78.2	79.5	87.8	104.7	Zn(II)2Cys6
	Pc22g10470	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae [truncated ORF][putative pseudogene]				0.3	3.5	0.9	2.3	No domain identified
	Pc22g12710	weak similarity to hypothetical transcription factor Arg81 - Saccharomyces cerevisiae	gene: "B11E5.460"; product: "putative protein"; Neurospora crassa	BX842620_46	3e-06	91.5	88.7	38.7	36.1	Zn(II)2Cys6
	Pc22g17210	similarity to hypothetical transcription factor Arg81 - Saccharomyces cerevisiae	regulatory protein ARGR2 - yeast (Saccharomyces cerevisiae)	S49627	2e-10	5.0	5.9	5.1	6.1	Zn(II)2Cys6
	Pc22g19280	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae	S. cerevisiae ARGR II regulatory gene	SCARGRII_1	3e-08	8.5	8.2	12.1	17.3	Zn(II)2Cys6
	Pc22g19540	weak similarity to transcription factor Arg81 - Saccharomyces cerevisiae	gene: "B3E4.120"; product: "related to negative acting factor";	NCB3E4_9	3e-10	193.2	157.1	113.0	88.6	Zn(II)2Cys6
	Pc22g23360	similarity to transcription factor Arg81 - Saccharomyces cerevisiae	gene: "B7F21.070"; product: "hypothetical protein"; Neurospora crassa	NCB7F21_6	7e-07	25.4	35.7	36.9	45.5	Zn(II)2Cys6
ARG82	Pc21g06320	strong similarity to regulator protein of the arginin metabolism Arg82 - Saccharomyces cerevisiae	regulatory protein ARG82 - yeast (Saccharomyces cerevisiae)	RGBYR3	6e-31	63.3	66.6	66.0	83.1	Inositol polyphosphate kinase (IPK) domain
ARO80	Pc12g09010	weak similarity to transcription factor Aro80 - Saccharomyces cerevisiae	hypothetical protein YDR421w - yeast (Saccharomyces cerevisiae)	S69704	3e-27	24.0	83.2	49.3	128.8	Zn(II)2Cys6
	Pc16g10200	weak similarity to transcription factor Aro80 - Saccharomyces cerevisiae [putative sequencing error]				1.2	2.5	1.0	5.4	Zn(II)2Cys6
	Pc16g12950	weak similarity to hypothetical transcription factor Aro80 - Saccharomyces cerevisiae	gene: "nirA"; product: "nitrogen assimilation transcription regulator,	BX649607_74	0.0	21.9	15.5	17.5	28.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g09600	similarity to transcription factor Aro80 - Saccharomyces cerevisiae	hypothetical protein YDR421w - yeast (Saccharomyces cerevisiae)	S69704	3e-23	14.5	10.2	39.4	33.0	Zn(II)2Cys6
	Pc21g03530	weak similarity to transcription factor Aro80 - Saccharomyces cerevisiae	gene: "nirA"; product: "nitrogen assimilation transcription regulator,	BX649607_74	1e-13	73.9	71.8	75.9	83.8	Zn(II)2Cys6
	Pc21g19740	similarity to transcription factor Aro80 - Saccharomyces cerevisiae [putative sequencing error]	hypothetical protein YDR421w - yeast (Saccharomyces cerevisiae)	S69704	1e-20	18.6	23.2	19.9	25.4	Zn(II)2Cys6
	Pc22g16210	similarity to hypothetical transcription factor Aro80 - Saccharomyces cerevisiae	gene: "nirA"; product: "nitrogen assimilation transcription regulator,	BX649607_74	9e-85	8.6	9.7	20.6	36.8	Zn(II)2Cys6, Fungal specific transcription factor domain
ARP9	Pc16g11940	similarity to chromatin remodeling Snf Swi complex subunit Arp9 - Saccharomyces cerevisiae	actin-like protein - fission yeast (Schizosaccharomyces pombe)	T37488	4e-34	203.6	197.8	179.9	181.7	Actin domain
ATF21p	Pc13g07770	similarity to transcription factor atf21p - Schizosaccharomyces pombe	gene: "cptf1"; product: "putative bZip transcription factor"; Claviceps	CPU428492_1	8e-07	13.7	8.4	16.6	13.1	bZIP-like leucine zipper (bZIP 2)
	Pc13g09580	similarity to transcription factor atf21p - Schizosaccharomyces pombe	gene: "atfA"; product: "AtfA"; Emericella nidulans AtfA (atfA) gene,	AY166595_1	1e-121	255.7	228.2	221.0	233.2	bZIP-like leucine zipper (bZIP 1, bZIP 2)
	Pc19g00240	similarity to transcription factor atf21p - Schizosaccharomyces pombe	ATF/CREB-family transcription factor atf21 - fission yeast	T40132	4e-06	6.4	5.1	3.3	2.1	bZIP-like leucine zipper (bZIP 2)
	Pc21g08330	similarity to transcription factor atf21p - Schizosaccharomyces pombe	ATF/CREB-family transcription factor atf21 - fission yeast	T40132	4e-13	77.7	97.5	135.0	211.8	bZIP-like leucine zipper (bZIP 1, bZIP 2)
	Pc22g26790	similarity to transcription factor atf21p - Schizosaccharomyces pombe	ATF/CREB-family transcription factor atf21 - fission yeast	T40132	2e-06	2.0	2.5	1.7	1.9	bZIP-like leucine zipper (bZIP 1, bZIP 2)
	Pc22g26820	similarity to transcription factor atf21p - Schizosaccharomyces pombe	gene: "cptf1"; product: "putative bZip transcription factor"; Claviceps	CPU428492_1	2e-06	6.6	3.5	4.2	3.2	bZIP-like leucine zipper (bZIP 1, bZIP 2)
BAB47239.1	Pc22g13920	strong similarity to hypothetical transcription factor BAB47239.1 - Aspergillus oryzae	product: "putative transcriptional activator"; Aspergillus nidulans gene	AB052971_1	1e-131	37.4	44.7	24.5	20.3	bZIP-like leucine zipper bZIP 1
BIKLF	Pc22g03750	weak similarity to Kruppel-like transcription factor biklf - Danio rerio	hypothetical protein 13E11.260 [imported] - Neurospora crassa	T48778	6e-12	9.1	2.0	16.9	12.6	C2H2
BIMD	Pc21g19250	strong similarity to hypothetical mitosis regulatory protein bimD - Aspergillus nidulans	bimD protein - Emericella nidulans	S52957	0.0	104.9	80.3	61.2	42.5	HEAT repeat domain
BRLA	Pc04g00010	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	regulatory protein brlA - Emericella nidulans	A28913	4e-37	0.2	0.8	1.3	0.5	C2H2
	Pc06g00470	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	gene: "brlA"; product: "BRLA"; Aspergillus parasiticus BRLA (brlA)	AF533070_1	1e-134	299.2	306.6	69.6	22.2	C2H2
	Pc17g00170	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	gene: "brlA"; product: "putative C2H2 transcription factor BrlA";	AY078193_1	1e-25	0.4	0.4	0.6	0.5	C2H2
	Pc22g26080	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	gene: "brlA"; product: "BRLA"; Aspergillus oryzae DNA for BRLA,	AOD010_1	1e-26	3.6	2.3	4.5	4.5	C2H2
	Pc22g26360	similarity to developmental regulatory protein brlA - Aspergillus nidulans [putative pseudogene]	gene: "brlA"; product: "BRLA"; Aspergillus oryzae DNA for BRLA,	AOD010_1	2e-14	0.5	1.8	3.4	1.6	No domain identified
	Pc23g00400	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	gene: "brlA"; product: "BRLA"; Aspergillus oryzae DNA for BRLA,	AOD010_1	2e-26	0.4	1.5	1.3	0.6	C2H2
	Pc24g00600	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans [putative sequencing error]	gene: "brlA"; product: "BRLA"; Aspergillus oryzae DNA for BRLA,	AOD010_1	1e-25	1.7	0.5	0.9	0.5	C2H2
	Pc24g00840	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	regulatory protein brlA - Emericella nidulans	A28913	5e-33	0.4	1.3	0.8	0.3	C2H2
	Pc24g01490	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	regulatory protein brlA - Emericella nidulans	A28913	2e-31	1.5	3.0	1.2	3.4	C2H2
	Pc24g01720	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	gene: "brlA"; product: "putative C2H2 transcription factor BrlA";	AY078193_1	7e-36	-	-	-	-	C2H2
	Pc24g02600	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans	gene: "brlA"; product: "BRLA"; Aspergillus oryzae DNA for BRLA,	AOD010_1	3e-25	12.4	10.6	12.4	8.1	C2H2
	Pc24g02650	strong similarity to developmental regulatory protein brlA - Aspergillus nidulans [putative pseudogene]	gene: "brlA"; product: "BRLA"; Aspergillus oryzae DNA for BRLA,	AOD010_1	2e-27	5.7	5.4	9.3	19.7	C2H2
BTD	Pc20g11080	weak similarity to hypothetical transcription factor btd - Schizosaccharomyces pombe	gene: "80A10.010"; product: "related to transcriptional activator CMR1";	NC80A10_1	9e-13	12.1	14.3	19.7	31.6	C2H2, Zn(II)2Cys6
	Pc21g17730	similarity to hypothetical transcription factor btd - Schizosaccharomyces pombe	probable transcription factor btd - fission yeast (Schizosaccharomyces	T37526	8e-07	44.4	74.5	53.9	81.1	C2H2
BTF3p	Pc22g23300	strong similarity to transcription factor btf3p - Schizosaccharomyces pombe	gene: "5C2.050"; product: "probable transcription factor BTF3a";	BX842637_5	3e-52	950.1	1002.7	1166.3	1053.1	NAC domain
CAA19035.1	Pc16g11120	similarity to zinc-finger transcription factor CAA19035.1 - Schizosaccharomyces pombe	gene: "ZFR1"; product: "Zfr1"; Gibberella moniliformis Zfr1 (ZFR1)	AY493199_1	1e-05	15.8	11.6	10.5	10.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g12390	weak similarity to zinc-finger transcription factor CAA19035.1 - Schizosaccharomyces pombe				1.5	0.9	1.8	1.1	Zn(II)2Cys6, Fungal specific transcription factor domain
CAA91958.1	Pc12g08390	weak similarity to hypothetical transcription regulator protein CAA91958.1 - Schizosaccharomyces pombe	probable transcription activator protein [imported] - fission yeast	T50198	9e-14	57.9	61.3	80.9	100.6	Fungal specific transcription factor domain
	Pc13g02290	similarity to hypothetical transcription regulator protein CAA91958.1 - Schizosaccharomyces pombe	probable transcription regulatory protein - fission yeast	S62583	2e-20	2.9	3.2	6.4	10.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc18g02690	weak similarity to hypothetical transcription regulator protein CAA91958.1 - Schizosaccharomyces pombe	finger protein YJL206c - yeast (Saccharomyces cerevisiae)	S46625	2e-11	52.2	43.1	27.7	49.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g06460	weak similarity to hypothetical transcription regulator protein CAA91958.1 - Schizosaccharomyces pombe [putative pseudogene]				22.1	24.9	25.8	43.4	Fungal specific transcription factor domain
CAB59617.1	Pc16g10860	similarity to hypothetical transcription activator CAB59617.1 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	2e-87	70.8	84.1	76.0	75.5	Zn(II)2Cys6, Fungal specific transcription factor domain
CAD37059.1	Pc13g12350	similarity to hypothetical transcription factor CAD37059.1 - Neurospora crassa	product: "possible zinc finger protein"; Aspergillus fumigatus BAC pilot	BX649606_48	1e-79	179.3	166.2	124.4	104.2	C2H2
	Pc13g15550	weak similarity to hypothetical transcription factor CAD37059.1 - Neurospora crassa	product: "possible zinc finger protein"; Aspergillus fumigatus BAC pilot	BX649606_48	8e-09	164.3	108.2	40.6	17.6	No domain identified
	Pc12g03590	weak similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus	gene: "B14A6.150"; product: "hypothetical protein"; Neurospora crassa	NCB14A6_15	4e-04	60.4	27.9	40.6	21.2	No domain identified
	Pc13g11990	strong similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus	product: "possible transcription factor"; Aspergillus fumigatus BAC pilot	BX649606_79	1e-152	14.7	10.1	14.6	13.8	No domain identified
	Pc16g06640	similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus	product: "possible transcription factor"; Aspergillus fumigatus BAC pilot	BX649606_79	2e-13	19.8	32.2	25.7	26.5	No domain identified
	Pc16g13480	similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus	product: "possible transcription factor"; Aspergillus fumigatus BAC pilot	BX649606_79	6e-07	8.2	3.0	2.2	2.9	No domain identified

CAF32051.1	Pc17g00180	similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus [truncated ORF][putative pseudogene]	product: "possible transcription factor"; Aspergillus fumigatus BAC pilot	BX649606_79	3e-13	0.5	1.8	2.0	3.0	No domain identified
	Pc20g01830	weak similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus				39.5	43.3	52.6	44.9	No domain identified
	Pc20g10230	weak similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus				15.7	13.3	11.7	2.5	No domain identified
	Pc22g26370	similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus [putative pseudogene]	product: "possible transcription factor"; Aspergillus fumigatus BAC pilot	BX649606_79	1e-10	1.7	0.9	1.3	1.1	No domain identified
	Pc24g00590	similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus [putative sequencing error]	product: "possible transcription factor"; Aspergillus fumigatus BAC pilot	BX649606_79	7e-12	0.3	0.8	0.4	1.5	No domain identified
	Pc24g02610	similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus [putative pseudogene]	product: "possible transcription factor"; Aspergillus fumigatus BAC pilot	BX649606_79	6e-16	1.4	1.5	0.8	2.9	No domain identified
	Pc24g03030	similarity to putative transcription factor CAF32051.1 - Aspergillus fumigatus [putative pseudogene]	product: "possible transcription factor"; Aspergillus fumigatus BAC pilot	BX649606_79	1e-12	-	-	-	-	No domain identified
CAF32142.1	Pc16g12850	strong similarity to possible transcription factor CAF32142.1 - Aspergillus fumigatus	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot project	BX649607_65	0.0	39.9	42.1	30.3	27.8	No domain identified
	Pc18g06690	weak similarity to possible transcription factor CAF32142.1 - Aspergillus fumigatus				19.6	10.0	12.4	9.8	No domain identified
CAF32162.1	Pc12g05450	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	1e-76	16.1	17.9	19.8	21.8	Fungal specific transcription factor domain
	Pc16g04620	strong similarity to putative transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	4e-25	170.0	143.9	89.8	86.8	Zn(II)2Cys6
	Pc18g00170	similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	6e-19	17.7	20.4	25.8	25.2	Fungal specific transcription factor domain
	Pc18g01480	strong similarity to putative transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	3e-25	33.9	25.8	14.1	16.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g03760	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	1e-42	90.4	97.1	56.0	75.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g05900	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	1e-100	30.9	31.0	45.9	45.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g12360	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	3e-36	3.3	3.2	13.2	15.3	Zn(II)2Cys6
	Pc21g22690	weak similarity to putative transcriptional regulator CAF32162.1 - Aspergillus fumigatus [putative pseudogene]				3.2	1.8	15.2	12.2	No domain identified
	Pc21g23810	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	8e-31	12.7	13.3	467.3	648.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g17120	strong similarity to putative transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	9e-25	8.9	5.3	4.9	4.5	Zn(II)2Cys6
	Pc23g00510	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus [putative sequencing error]	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	2e-40	1.1	0.7	2.2	3.1	Fungal specific transcription factor domain
	Pc23g00600	strong similarity to hypothetical transcriptional regulator CAF32162.1 - Aspergillus fumigatus	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	3e-97	325.0	364.7	266.7	289.2	Zn(II)2Cys6, Fungal specific transcription factor domain
CASP	Pc16g12820	strong similarity to CCAAT displacement protein CASP - Homo sapiens	product: "hypothetical protein, conserved"; Aspergillus fumigatus BAC	BX649607_61	0.0	167.4	116.9	119.5	90.7	CASP C terminal domain
CAT8	Pc13g07090	similarity to gluconeogenesis transcriptional regulator CAT8 - Kluyveromyces lactis	gene: "B11E5.150"; product: "related to transcriptional activator Mut3p";	BX842620_15	3e-13	19.4	15.1	14.0	13.7	Zn(II)2Cys6
	Pc16g05020	weak similarity to gluconeogenesis transcriptional regulator CAT8 - Kluyveromyces lactis [putative pseudogene]				20.3	38.3	31.6	30.1	Zn(II)2Cys6
	Pc18g04020	similarity to gluconeogenesis transcriptional regulator CAT8 - Kluyveromyces lactis	gene: "CAT8"; product: "Cat8"; Candida albicans Ntg1 (NTG1) gene,	AF222908_3	5e-08	5.9	2.4	5.2	5.5	Zn(II)2Cys6
CBF	Pc16g07450	strong similarity to CCAAT-binding transcription factor CBF - Homo sapiens [putative sequencing error]	hypothetical protein SPAC4F10.09c - fission yeast	T38813	1e-144	73.5	69.3	33.7	21.9	CBF/Mak21 family
CCR4	Pc22g02690	strong similarity to transcription regulator Ccr4 - Saccharomyces cerevisiae	gene: "104H10.120"; product: "related to CCR4 protein"; Neurospora	NC104H10_13	1e-162	529.2	433.5	322.5	299.8	Leucine Rich Repeat Endonuclease/Exonuclease/phosphatase family
CDC39	Pc13g10490	strong similarity to transcription regulator protein Cdc39 - Saccharomyces cerevisiae	gene: "H4H7.010"; product: "related to CDC39 protein"; Neurospora	BX908811_1	0.0	221.8	176.4	187.1	175.0	CCR4-Not complex component (Not1)
CIN5	Pc12g13890	similarity to transcription activator Cin5 - Saccharomyces cerevisiae	related to AP-1-like transcription factor [imported] - Neurospora crassa	T49700	1e-06	226.7	214.1	178.6	177.3	bZIP-like leucine zipper (bZIP 1)
	Pc13g08530	weak similarity to transcription activator Cin5 - Saccharomyces cerevisiae				1.8	2.3	7.4	8.9	bZIP-like leucine zipper (bZIP 1)
CMR1	Pc06g01890	similarity to transcription activator CMR1 - Colletotrichum lagenarium	gene: "B10D6.140"; product: "hypothetical protein"; Neurospora	BX842624_14	1e-13	44.8	47.3	42.1	51.3	C2H2, Zn(II)2Cys6
	Pc12g09540	similarity to melanin regulator CMR1 - Colletotrichum lagenarium	gene: "B10D6.140"; product: "hypothetical protein"; Neurospora	BX842624_14	8e-17	31.6	26.0	23.4	21.3	C2H2, Zn(II)2Cys6
	Pc16g05230	similarity to melanin regulator CMR1 - Colletotrichum lagenarium	gene: "B10D6.140"; product: "hypothetical protein"; Neurospora	BX842624_14	2e-18	9.0	9.1	12.0	13.3	C2H2, Zn(II)2Cys6
	Pc20g05960	similarity to hypothetical transcriptional activator CMR1 - Colletotrichum lagenarium	gene: "B10D6.140"; product: "hypothetical protein"; Neurospora	BX842624_14	1e-105	200.9	147.8	136.1	181.1	C2H2, Zn(II)2Cys6
	Pc21g07180	similarity to melanin regulator CMR1 - Colletotrichum lagenarium	Aspergillus fumigatus regA gene for transcription factor RegA,	AJ582911_1	2e-15	62.1	83.4	88.8	155.1	C2H2, Zn(II)2Cys6
	Pc21g07310	similarity to transcription activator CMR1 - Colletotrichum lagenarium	gene: "CMR1"; Colletotrichum lagenarium CMR1 gene, complete cds.	AB024516_1	1e-09	47.3	42.3	35.9	36.3	C2H2, Zn(II)2Cys6
	Pc22g15230	similarity to hypothetical transcriptional activator CMR1 - Colletotrichum lagenarium	gene: "B10D6.140"; product: "hypothetical protein"; Neurospora	BX842624_14	7e-12	335.4	300.1	223.9	239.8	C2H2, Zn(II)2Cys6
CON7	Pc22g20120	weak similarity to hypothetical transcriptional regulator CON7 - Magnaporthe grisea [truncated ORF][putative pseudogene]				7.3	2.7	1.1	1.7	No domain identified
	Pc22g21070	strong similarity to hypothetical transcriptional regulator CON7 - Magnaporthe grisea	gene: "CON7"; product: "putative transcriptional regulator";	AF015771_1	1e-36	43.2	42.4	31.4	25.6	C2H2
CREA	Pc20g13880	strong similarity to catabolite repressor creA - Aspergillus niger	Carbon catabolite repressor protein - Aspergillus niger	JN0785	1e-150	243.5	195.3	159.9	111.5	C2H2
	Pc20g13890	similarity to hypothetical DNA-binding protein creA - Aspergillus oryzae	product: "unknown"; Aspergillus oryzae DNA-binding protein CreA	AF322183_2	7e-10	72.9	91.9	65.2	64.3	No domain identified
	Pc22g17640	weak similarity to catabolite repressor creA - Aspergillus niger				45.4	52.8	73.2	36.7	No domain identified
CREC	Pc12g09670	strong similarity to hypothetical protein involved in carbon catabolite repression creC - Aspergillus nidulans	gene: "creC"; product: "CreC"; Emericella nidulans CreC (creC) gene,	AF136452_1	0.0	145.2	172.0	125.9	136.3	WD40 domain, G-beta repeat
CRZ1	Pc13g03120	strong similarity to calcineurin responsive zinc-finger transcription factor Crz1 - Saccharomyces cerevisiae	hypothetical protein YNL027w - yeast (Saccharomyces cerevisiae)	S62939	4e-39	49.6	36.7	31.0	27.3	C2H2
	Pc20g10390	similarity to calcineurin responsive zinc-finger transcription factor Crz1 - Saccharomyces cerevisiae	gene: "B9B15.140"; product: "conserved hypothetical protein";	NCB9B15_12	1e-104	61.7	39.1	44.8	36.1	C2H2
CTF1-α, CTF1-β	Pc12g02640	weak similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	product: "nitrogen regulatory protein OTam"; Aspergillus oryzae	AF272849_1	3e-05	79.1	83.0	78.3	97.1	Fungal specific transcription factor domain
	Pc12g07690	weak similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	gene: "amdR"; product: "regulatory protein"; Aspergillus oryzae	AOAMDR_1	1e-12	6.7	5.8	10.7	20.3	Fungal specific transcription factor domain
	Pc12g15560	weak similarity to cutinase transcription factor beta CTF1b - Fusarium solani				13.7	12.2	12.7	24.8	Zn(II)2Cys6
	Pc13g06050	strong similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani [putative sequencing error]	CUTINASE TRANSCRIPTION FACTOR 1 ALPHA.	CT1A_FUSSO	0.0	37.3	25.1	26.2	30.3	Fungal specific transcription factor domain
	Pc13g14440	strong similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	CUTINASE TRANSCRIPTION FACTOR 1 ALPHA.	CT1A_FUSSO	3e-29	6.5	13.3	13.1	29.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g00200	strong similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	gene: "B2N18.280"; product: "conserved hypothetical protein";	BX897674_27	3e-38	1.2	1.2	5.0	9.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g00220	similarity to cutinase transcription factor alpha CTF1a - Fusarium solani	gene: "B11N2.030"; product: "probable CUTINASE TRANSCRIPTION	NCB11N2_3	2e-14	2.6	2.8	16.2	40.3	Zn(II)2Cys6
	Pc16g02700	weak similarity to cutinase transcription factor beta CTF1b - Fusarium solani	probable regulatory protein - fission yeast (Schizosaccharomyces	T38690	7e-11	9.4	97.0	20.8	129.6	Fungal specific transcription factor domain
	Pc16g10430	strong similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani [putative sequencing error]	gene: "B2N18.280"; product: "conserved hypothetical protein";	BX897674_27	1e-35	13.3	11.2	12.6	10.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g13580	weak similarity to cutinase transcription factor beta CTF1b - Fusarium solani	gene: "amdR"; product: "regulatory protein"; Aspergillus oryzae	AOAMDR_1	2e-04	16.7	17.4	22.9	22.0	Fungal specific transcription factor domain
	Pc18g02700	strong similarity to cutinase transcription factor beta CTF1b - Fusarium solani	CUTINASE TRANSCRIPTION FACTOR 1 BETA.	CT1B_FUSSO	1e-46	113.2	121.6	140.2	163.8	Fungal specific transcription factor domain
	Pc18g05600	weak similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani				22.3	23.2	20.3	27.7	No domain identified
	Pc19g00550	strong similarity to cutinase transcription factor beta CTF1b - Fusarium solani	CUTINASE TRANSCRIPTION FACTOR 1 BETA.	CT1B_FUSSO	1e-56	226.3	450.3	165.4	332.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g06460	weak similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	product: "nitrogen regulatory protein OTam"; Aspergillus oryzae	AF272849_1	0.0	304.9	366.7	179.5	168.9	Fungal specific transcription factor domain
	Pc20g07170	weak similarity to cutinase transcription factor alpha CTF1a - Fusarium solani	gene: "B2N18.280"; product: "conserved hypothetical protein";	BX897674_27	1e-07	11.0	10.5	14.5	20.2	Zn(II)2Cys6
	Pc21g05320	similarity to cutinase transcription factor beta CTF1b - Fusarium solani	CUTINASE TRANSCRIPTION FACTOR 1 BETA.	CT1B_FUSSO	3e-42	29.0	15.0	66.9	11.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g11250	strong similarity to cutinase transcription factor beta CTF1b - Fusarium solani	CUTINASE TRANSCRIPTION FACTOR 1 BETA.	CT1B_FUSSO	1e-165	283.8	392.5	380.4	665.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g11260	weak similarity to cutinase transcription factor alpha CTF1a - Fusarium solani				46.8	43.4	53.1	47.8	Fungal specific transcription factor domain
	Pc21g12640	strong similarity to cutinase transcription factor beta CTF1b - Fusarium solani	CUTINASE TRANSCRIPTION FACTOR 1 BETA.	CT1B_FUSSO	8e-86	114.8	123.5	122.5	178.5	Fungal specific transcription factor domain
	Pc21g19570	similarity to cutinase transcription factor beta CTF1b - Fusarium solani	gene: "B2N18.280"; product: "conserved hypothetical protein";	BX897674_27	5e-24	24.1	40.0	41.8	86.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g19640	weak similarity to cutinase transcription factor alpha CTF1a - Fusarium solani	gene: "facB"; product: "FacB"; Aspergillus niger putative DNA binding	ANU56099_1	3e-13	20.5	21.5	17.3	23.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g23800	similarity to cutinase transcription factor alpha CTF1a - Fusarium solani	hypothetical protein SPBC530.05 - fission yeast	T40521	4e-20	58.5	56.7	67.6	81.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g00050	similarity to cutinase transcription factor 1 CTF1-alpha like protein An18g03930 - Aspergillus niger				21.5	41.9	32.8	61.8	No domain identified
	Pc22g10180	weak similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	gene: "B5K2.090"; product: "related to Cutinase transcription factor 1	BX842632_9	0.0	197.6	203.3	203.3	138.6	Zn(II)2Cys6
	Pc22g12400	weak similarity to cutinase transcription factor beta CTF1b - Fusarium solani				604.8	548.7	343.4	279.8	Zn(II)2Cys6
	Pc22g13610	weak similarity to cutinase transcription factor alpha CTF1a - Fusarium solani	probable transcription activator protein [imported] - fission yeast	T50198	7e-36	71.3	59.5	61.3	62.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g24790	similarity to cutinase transcription factor alpha CTF1a - Fusarium solani	probable transcription activator protein [imported] - fission yeast	T50198	3e-30	51.1	120.9	73.1	91.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g25130	similarity to cutinase transcription factor 1 CTF1-alpha - Fusarium solani	gene: "amdR"; product: "regulatory protein"; Aspergillus oryzae	AOAMDR_1	4e-24	42.2	49.2	47.3	50.1	Fungal specific transcription factor domain
CYS3	Pc18g06160	similarity to positive sulphur regulator CYS3 - Neurospora crassa	gene: "metR"; product: "positive sulphur transcription regulator METR";	AF148535_1	2e-20	451.8	439.9	397.2	539.7	bZIP 2 (Basic region leucine zipper)
	Pc22g17390	strong similarity to positive sulphur regulator CYS3 - Neurospora crassa	gene: "metR"; product: "positive sulphur transcription regulator METR";	AF148535_1	8e-58	296.4	383.6	413.5	475.2	bZIP 1 and bZIP 2 (Basic region leucine zipper)
DEP1	Pc21g05330	weak similarity to regulator of phospholipid metabolism Dep1 - Saccharomyces cerevisiae	hypothetical protein SPBC21C3.02c [imported] - fission yeast	T50346	5e-07	171.6	140.4	96.7	84.9	Sds3-like domain
DopA (Dopey)	Pc12g10390	strong similarity to developmental regulator of asexual and sexual reproduction dopA - Aspergillus nidulans	gene: "dopA"; product: "DopAp"; Emericella nidulans DopAp (dopA)	AF134206_1	0.0	287.9	240.4	237.6	244.6	Dopey, N-terminal domain
FACB	Pc06g01000	similarity to acetate regulatory DNA binding protein facB - Aspergillus niger	hypothetical protein B14D6.340 [imported] - Neurospora crassa	T49482	1e-116	1.6	3.6	0.9	6.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc13g12510	strong similarity to acetate regulatory DNA binding protein facB - Aspergillus nidulans	gene: "facB"; product: "FacB"; Aspergillus oryzae putative DNA binding	AOU56098_1	0.0	293.4	232.9	179.7	135.6	Zn(II)2Cys6, Fungal specific transcription factor domain
FCR1	Pc03g00300	similarity to hypothetical transcriptional regulator FCR1 - Candida albicans	gene: "FCR1"; product: "zinc cluster transcription factor Fcr1p";	AF057038_1	3e-11	1.9	1.6	5.5	3.8	Zn(II)2Cys6
	Pc16g14350	similarity to hypothetical transcriptional regulator FCR1 - Candida albicans	gene: "FCR1"; product: "zinc cluster transcription factor Fcr1p";	AF057038_1	7e-13	58.8	25.1	23.9	13.5	Zn(II)2Cys6
	Pc20g08400	similarity to hypothetical transcriptional regulator FCR1 - Candida albicans	gene: "FCR1"; product: "zinc cluster transcription factor Fcr1p";	AF057038_1	2e-12	26.4	63.4	58.0	95.1	Zn(II)2Cys6
	Pc22g26220	similarity to hypothetical transcriptional regulator FCR1 - Candida albicans	gene: "FCR1"; product: "zinc cluster transcription factor Fcr1p";	AF057038_1	9e-11	-	-	-	-	Zn(II)2Cys6
FET5p	Pc16g04390	strong similarity to transcription factor fet5p - Schizosaccharomyces pombe	gene: "B16B8.080"; product: "conserved hypothetical protein";	BX842634_8	1e-103	170.3	156.8	88.3	59.7	ATP bind domain 1
	Pc21g20460	strong similarity to purine nucleotide binding protein fet5p - Schizosaccharomyces pombe	probable membrane protein YOR262w - yeast (Saccharomyces	S67159	7e-96	40.2	37.9	44.0	32.9	ATP bind domain 1
FKH2	Pc18g00430	strong similarity to fork head 2 protein Fkh2 - Saccharomyces cerevisiae	gene: "YNL2403c"; product: "Ynl2403p"; Saccharomyces cerevisiae	SC12141_1	2e-50	27.3	24.6	14.4	16.2	Fork head domain, Fork head associated (FHA) domain
GAL4	Pc13g10600	similarity to transcription factor Gal4 - Saccharomyces cerevisiae	gene: "B2E7.100"; product: "related to lactose regulatory protein";	BX897675_10	8e-16	55.8	53.2	40.6	34.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc14g00920	similarity to transcription factor Gal4 - Saccharomyces cerevisiae	gene: "PRF"; product: "binuclear zinc transcription factor"; Nectria	AY218847_1	2e-11	79.0	76.6	26.8	24.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g10260	weak similarity to transcription factor Gal4 - Saccharomyces cerevisiae				13.3	24.2	19.9	18.9	Fungal specific transcription factor domain
	Pc16g11020	similarity to transcription factor Gal4 - Saccharomyces cerevisiae	product: "Unknown protein"; Arabidopsis thaliana Unknown protein	BT002460_1	1e-40	141.3	158.7	146.0	133.3	Zn(II)2Cys6, Fungal specific transcription factor domain
GATA factor	Pc12g09220	weak similarity to GATA transcription factor - Nematostella vectensis	gene: "Gata"; product: "GATA transcription factor"; Nematostella	AY465174_1	2e-06	3.5	3.0	23.7	8.5	GATA zinc finger
GCR3	Pc12g04560	similarity to transcription regulator CaGCR3 - Candida albicans	gene: "B13O20.110"; product: "related to cap binding protein 80	NCB13O20_8	0.0	202.3	200.9	152.2	140.1	MIF4G, MIF4G -like and MIF4G-like 2
GLCD	Pc16g06560	strong similarity to transcriptional activator glcD - Aspergillus nidulans	gene: "glcd"; product: "GLCD gamma"; Aspergillus nidulans GLCD	AF320978_1	6e-76	174.0	102.7	82.1	52.2	Helix-loop-helix DNA-binding domain (HLH)
HAA1	Pc12g09470	similarity to transcriptional activator Haa1 - Saccharomyces cerevisiae	COPPER RESISTANCE PROTEIN CRF1.	CRF1_YARLI	4e-14	540.9	420.6	429.5	314.3	Copper fist DNA binding domain
	Pc13g00890	similarity to transcriptional activator Haa1 - Saccharomyces cerevisiae	COPPER RESISTANCE PROTEIN CRF1.	CRF1_YARLI	4e-15	112.3	117.8	114.7	107.3	Copper fist DNA binding domain
	Pc13g12180	weak similarity to transcriptional activator Haa1 - Saccharomyces cerevisiae	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot project	BX649606_63	5e-53	142.0	157.3	113.7	137.3	Copper fist DNA binding domain
	Pc15g01300	similarity to transcriptional activator Haa1 - Saccharomyces cerevisiae	COPPER RESISTANCE PROTEIN CRF1.	CRF1_YARLI	1e-14	27.6	29.8	38.9	44.7	Copper fist DNA binding domain
	Pc20g05930	similarity to transcriptional activator Haa1 - Saccharomyces cerevisiae	product: "unknown"; S.cerevisiae chromosome XVI cosmid 9723.	SC9723_8	4e-10	16.1	12.9	8.3	10.8	Copper fist DNA binding domain
Helicase-like Transcription Factor	Pc12g11570	weak similarity to helicase-like transcription factor - Homo sapiens	product: "DNA repair protein-like"; Arabidopsis thaliana genomic DNA,	AB016875_2	2e-80	46.3	36.3	28.5	23.1	SNF2 family N-terminal domain, Helicase conserved C-terminal domain
	Pc21g17740	strong similarity to helicase-like transcription factor - Homo sapiens	product: "helicase-like transcription factor-like protein"; Arabidopsis	ATAB5245_26	1e-107	32.4	16.0	28.4	28.7	SNF2 family N-terminal domain, Helicase conserved C-terminal domain,
	Pc22g01270	weak similarity to helicase-like transcription factor - Homo sapiens	probable helicase - fission yeast (Schizosaccharomyces pombe)	T39936	1e-128	213.5	185.7	144.8	136.2	SNF2 family N-terminal domain, Helicase conserved C-terminal domain
Heterotrimeric CCAAT-binding complex HAP	Pc12g01590	strong similarity to protein hapB - Aspergillus nidulans	gene: "hapB"; product: "HapB"; Aspergillus niger HapB (hapB) mRNA,	AY324802_1	4e-83	167.7	149.5	119.9	86.6	CCAAT-binding transcription factors: CBF-B/NF-YA subunit B
	Pc12g04670	strong similarity to HAPE - Aspergillus oryzae	gene: "hapE"; product: "HAPE"; Aspergillus oryzae gene for HAPE,	AB010432_1	1e-106	330.5	311.2	310.2	269.8	Core histone H2A/H2B/H3/H4, Histone-like transcription factor (CBF/NF-Y) and
	Pc14g01630	strong similarity to CCAAT-binding protein hapC - Aspergillus oryzae	gene: "hapC"; product: "HAPC"; Aspergillus oryzae gene for HAPC,	AB010431_1	2e-78	339.7	388.1	289.1	316.3	Histone-like transcription factor (CBF/NF-Y) and archaeal histone
HFI1	Pc22g08060	strong similarity to transcriptional coactivator HFI1 related protein CAD71048.1 - Neurospora crassa	gene: "B7H23.230"; product: "related to transcriptional coactivator	NCB7H23_22	4e-92	144.2	132.3	94.5	107.1	No domain identified
HIR1	Pc16g06220	strong similarity to histone transcription regulator Hir1 - Saccharomyces cerevisiae	gene: "B10H18.120"; product: "related to histone transcription	BX897678_12	0.0	93.0	84.7	77.5	61.4	TUP1-like enhancer of split, WD40 domain, G-beta repeat
HPA3	Pc12g01260	strong similarity to hypothetical bHLH transcription factor hpa3 - Aspergillus nidulans	gene: "hpa3"; product: "putative bHLH transcription factor"; Emericella	ENI269479_1	4e-90	233.7	288.8	220.1	143.4	Helix-loop-helix DNA-binding domain
HSF	Pc21g14490	similarity to heat shock transcription factor HSF - Schizosaccharomyces pombe	Neurospora crassa DNA linkage group II BAC clone B18P7;	BX842594_12	4e-91	148.6	144.3	124.6	111.5	HSF-type DNA-binding domain

Hypothetical	Pc22g11850	strong similarity to hypothetical transcription factor - Schizosaccharomyces pombe	probable transcription factor - fission yeast (Schizosaccharomyces	T37859	4e-40	74.2	59.0	53.0	49.4	YEATS family
Hypothetical transcription regulator	Pc14g00020	weak similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	gene: "5E6.310"; product: "related to nitrate assimilation regulatory	NC5E6_27	4e-24	85.6	132.7	153.2	343.6	Zn(II)2Cys6
	Pc16g11780	weak similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	hypothetical protein SPBC530.11c - fission yeast	T40527	2e-05	55.0	55.7	49.6	75.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc18g01980	strong similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	gene: "SPAC1327.01c"; "SPAC18G6.16c"; "SPAC1783.09c";	SPAC1327_1	5e-60	81.3	89.0	71.9	78.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g09420	similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	gene: "SPAPB1A11.04c"; S.pombe chromosome I BAC pB1A11.	SPAPB1A11_4	4e-15	20.5	23.6	38.7	77.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g16480	weak similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	gene: "15E11.040"; product: "conserved hypothetical protein";	NC15E11_3	1e-54	41.0	38.0	28.4	39.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g20390	similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	hypothetical protein SPBC530.11c - fission yeast	T40527	6e-11	25.9	19.6	22.9	31.4	Fungal specific transcription factor domain
	Pc22g06240	weak similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	gene: "B15B3.150"; product: "related to general repressor of	BX842622_15	2e-14	41.3	23.9	65.3	31.9	Fungal specific transcription factor domain
	Pc22g11880	weak similarity to hypothetical transcription regulator protein - Schizosaccharomyces pombe	gene: "SPAPB1A11.04c"; S.pombe chromosome I BAC pB1A11.	SPAPB1A11_4	7e-09	21.9	28.4	34.4	50.3	Zn(II)2Cys6, Fungal specific transcription factor domain
ING1	Pc21g12750	weak similarity to growth regulator ING1 - Mus musculus	hypothetical protein SPAC3G9.08 - fission yeast	T11644	3e-15	59.4	56.3	54.4	36.2	PHD-finger
JLBA	Pc20g15070	similarity to JUN-like transcription factor jlbA - Aspergillus nidulans	gene: "jlbA"; product: "JUN-like bZIP transcription factor"; Emericella	AF361222_1	4e-11	17.2	17.4	13.0	16.5	bZIP 1 and bZIP 2 (Basic region leucine zipper)
LAC9	Pc16g06860	similarity to positive regulator of the lactose-galactose regulon LAC9 - Kluyveromyces lactis	gene: "B2E7.100"; product: "related to lactose regulatory protein";	BX897675_10	1e-103	253.6	257.1	275.1	338.7	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g03000	similarity to positive regulator of the lactose-galactose regulon LAC9 - Kluyveromyces lactis	product: "Unknown protein"; Arabidopsis thaliana Unknown protein	BT002460_1	0.0	150.0	125.5	143.6	118.4	Zn(II)2Cys6, Fungal specific transcription factor domain
LaeA	Pc16g14010	strong similarity to hypothetical methyltransferase AAO34671.1 - Gibberella zeae	Aspergillus fumigatus LaeA gene, complete cds;	AY422723_1	1e-130	365.6	361.9	373.8	395.3	Methyltransferase domain
LEU3	Pc12g00620	similarity to leucine-specific regulatory protein Leu3 - Saccharomyces cerevisiae	regulatory protein LEU3 - yeast (Saccharomyces cerevisiae)	RGBYL3	1e-14	26.8	19.0	29.0	20.4	Zn(II)2Cys6
	Pc18g04740	strong similarity to leucine-specific regulatory protein Leu3 - Saccharomyces cerevisiae	regulatory protein LEU3 - yeast (Saccharomyces cerevisiae)	RGBYL3	8e-44	238.5	211.1	174.3	194.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g07510	strong similarity to leucine-specific regulatory protein Leu3 - Saccharomyces cerevisiae	regulatory protein LEU3 - yeast (Saccharomyces cerevisiae)	RGBYL3	4e-31	141.5	117.7	119.5	124.7	Zn(II)2Cys6
LYS14	Pc06g01850	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	DNA centromeric region sequence from BAC DP26B06, DP34F04,	CNS09S4S_32	1e-31	27.1	15.0	31.1	32.7	Zn(II)2Cys6
	Pc12g01430	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae [putative pseudogene]	gene: "17E5.150"; product: "conserved hypothetical protein";	NC17E5_14	7e-09	2.2	2.8	4.1	2.3	Zn(II)2Cys6
	Pc12g10570	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	product: "putative cysteine-binding protein fliY"; Haloferax volcanii	AF315625_1	8e-58	84.5	82.5	59.5	61.7	Zn(II)2Cys6
	Pc13g02260	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	hypothetical fungal Zn(2)-Cys(6) zinc-finger protein - fission yeast	T41718	9e-06	89.4	50.3	42.5	33.7	Zn(II)2Cys6
	Pc13g05080	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	gene: "MPP1"; product: "ZnII/2cys6 transcription factor"; Pichia	AY190521_1	2e-16	14.0	8.4	11.8	16.4	Zn(II)2Cys6
	Pc14g00980	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	hypothetical fungal Zn(2)-Cys(6) zinc-finger protein - fission yeast	T41718	1e-06	44.2	69.4	153.7	182.8	Zn(II)2Cys6
	Pc20g01750	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	transcription activator LYS14 - yeast (Saccharomyces cerevisiae)	S61587	9e-04	24.3	18.2	37.9	39.3	Zn(II)2Cys6
	Pc20g02030	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	2e-06	73.0	69.1	99.5	138.1	Zn(II)2Cys6
	Pc20g10800	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	gene: "Ca20C1.12"; product: "possible zinc-finger protein"; C.albicans	CAC20C1_11	2e-04	6.5	6.2	11.8	13.7	Zn(II)2Cys6
	Pc20g15410	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	transcription activator LYS14 - yeast (Saccharomyces cerevisiae)	S61587	8e-05	44.6	37.0	40.2	46.2	Zn(II)2Cys6
	Pc21g00920	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	gene: "rosA"; product: "repressor of sexual development"; Aspergillus	ENI519682_1	1e-06	104.9	102.1	114.0	126.9	Zn(II)2Cys6
	Pc21g05540	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	gene: "ARCA"; product: "ARCA protein"; Emericella nidulans ARCA	ENI294750_1	1e-116	169.6	125.2	97.8	52.9	Zn(II)2Cys6
	Pc21g07600	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae				6.1	7.8	14.9	13.1	Zn(II)2Cys6
	Pc21g13260	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	gene: "5E6.190"; product: "related to ARCA protein"; Neurospora	NC5E6_17	1e-15	48.0	26.8	23.4	36.6	Zn(II)2Cys6
	Pc22g20680	similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot project	BX649605_122	1e-62	68.8	61.7	56.5	68.6	Zn(II)2Cys6
	Pc22g24260	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	gene: "AfA12H2.19c"; product: "hypothetical protein"; Aspergillus	AFA12H2_19	2e-64	2.9	2.9	15.2	11.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g24500	weak similarity to transcription activator of lysine pathway Lys14 - Saccharomyces cerevisiae	gene: "B1D14.250"; product: "hypothetical protein"; Neurospora	NCB1D14_25	2e-14	0.3	0.3	0.7	0.4	Zn(II)2Cys6
MAL13	Pc13g02490	similarity to maltose pathway regulatory protein Mal13 - Saccharomyces cerevisiae	hypothetical protein YGR288w - yeast (Saccharomyces cerevisiae)	S64623	4e-08	101.4	77.6	112.4	109.7	Zn(II)2Cys6
	Pc16g08120	similarity to maltose pathway regulatory protein Mal13 - Saccharomyces cerevisiae	gene: "104H10.220"; product: "related to transcription activator amyR";	NC104H10_21	3e-11	69.0	117.3	63.1	75.1	Zn(II)2Cys6
	Pc21g07200	similarity to maltose pathway regulatory protein Mal13 - Saccharomyces cerevisiae	gene: "AfA12H2.19c"; product: "hypothetical protein"; Aspergillus	AFA12H2_19	3e-07	209.2	180.3	161.7	134.7	Zn(II)2Cys6
MCM1	Pc22g24340	strong similarity to MADS-box domain transcription factor Mcm1 - Saccharomyces cerevisiae	Yeast (S.cerevisiae) FUN80 gene, complete cds.	SCFUN80_1	5e-33	568.4	622.8	697.9	673.1	MADS-box/SRF-type transcription factor (DNA-binding and dimerisation
MEAB	Pc18g00880	strong similarity to hypothetical transcription regulator meaB - Aspergillus nidulans	gene: "meaB"; product: "MEAB protein"; Aspegillus nidulans meaB	ANMEABG_1	1e-104	382.5	386.9	303.4	183.0	bZIP leucine zipper
MED8	Pc13g08130	similarity to transcription factor Med8 - Saccharomyces cerevisiae	hypothetical protein SPBC21.04 - fission yeast (Schizosaccharomyces	T39886	7e-12	153.5	117.8	166.9	190.6	No domain identified
MEDA (MEDUSA)	Pc22g13450	strong similarity to hypothetical Medusa medA - Aspergillus nidulans	gene: "medA"; product: "Medusa"; Emericella nidulans Medusa	AF080599_1	1e-162	137.5	124.6	65.7	52.7	No domain identified
	Pc22g13460	weak similarity to developmental regulator medusa - Aspergillus nidulans	gene: "medA"; product: "developmental regulator medusa"; Aspergillus	AF207903_1	1e-05	155.2	140.9	101.5	98.2	No domain identified
MPP1	Pc12g02890	similarity to hypothetical ZnII/2cys6 transcription factor MPP1 - Pichia angusta	gene: "MPP1"; product: "ZnII/2cys6 transcription factor"; Pichia	AY190521_1	4e-20	31.0	27.9	26.1	23.3	No domain identified
	Pc14g00200	strong similarity to hypothetical ZnII/2cys6 transcription factor MPP1 - Pichia angusta	gene: "MPP1"; product: "ZnII/2cys6 transcription factor"; Pichia	AY190521_1	1e-36	21.5	23.9	27.1	34.1	No domain identified
mtTFB	Pc20g03700	weak similarity to mitochondrial transcription factor mtTFB - Kluyveromyces lactis	gene: "SPAC1002.08c"; product: "RNA polymerase specificity factor	SPAC1002_8	1e-04	42.5	45.8	38.1	27.3	rRNAAD domain (Ribosomal RNA adenine dimethylase)
NC2	Pc12g13040	similarity to alpha chain of transcription regulator NC2 - Homo sapiens	probable transcription repressor - fission yeast	T37855	3e-18	158.5	138.0	146.4	86.5	Core histone H2A/H2B/H3/H4. Histone-like transcription factor (CBF/NF-Y)
NF-X1	Pc21g09140	strong similarity to cysteine-rich transcription factor NF-X1 - Homo sapiens	probable cysteine-rich transcription regulator - fission yeast	T41146	1e-144	41.4	41.6	34.7	25.3	NF-X1 type zinc finger, R3H domain
NIRA	Pc13g02000	weak similarity to nitrate assimilation regulatory protein nirA - Aspergillus nidulans	nitrate assimilation regulatory protein nirA - Emericella nidulans	A41697	6e-37	19.7	18.3	20.0	24.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc13g02410	similarity to nitrate assimilation regulatory protein nirA - Aspergillus nidulans	gene: "SPBC1683.13c"; Schizosaccharomyces pombe cosmids	SPBC1683_13	3e-22	41.8	43.6	52.3	42.6	Fungal specific transcription factor domain
	Pc21g07150	strong similarity to nitrate assimilation regulatory protein nirA - Aspergillus nidulans	nitrate assimilation regulatory protein nirA - Emericella nidulans	A41697	0.0	105.1	75.8	57.6	55.5	Zn(II)2Cys6, Fungal specific transcription factor domain
NIT-4	Pc06g01270	weak similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	related to pathway-specific nitrogen regulator [imported] - Neurospora	T51029	1e-137	426.4	335.9	112.8	100.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g00120	strong similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	regulatory protein nit-4 - Neurospora crassa	A41696	4e-30	70.5	86.6	112.1	170.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g09830	weak similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa [putative sequencing error]	regulatory protein nit-4 - Neurospora crassa	A41696	2e-37	179.5	167.9	133.2	107.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g11450	similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	regulatory protein nit-4 - Neurospora crassa	A41696	4e-08	299.2	258.7	332.3	283.6	Zn(II)2Cys6
	Pc13g15160	weak similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	gene: "MPP1"; product: "ZnII/2cys6 transcription factor"; Pichia	AY190521_1	3e-04	64.5	36.1	36.7	37.5	Zn(II)2Cys6
	Pc16g09100	strong similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	regulatory protein nit-4 - Neurospora crassa	A41696	3e-35	18.1	19.6	66.0	62.3	Fungal specific transcription factor domain
	Pc16g10210	weak similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	hypothetical protein SPBC530.05 - fission yeast	T40521	2e-06	48.5	39.4	56.3	62.9	Zn(II)2Cys6
	Pc16g13230	similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	regulatory protein nit-4 - Neurospora crassa	A41696	2e-35	23.1	17.7	16.5	11.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g12800	strong similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	regulatory protein nit-4 - Neurospora crassa	A41696	9e-45	0.5	0.8	1.5	2.6	Zn(II)2Cys6
	Pc22g09340	weak similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	gene: "SPAPB1A11.04c"; S.pombe chromosome I BAC pB1A11.	SPAPB1A11_4	2e-17	36.0	28.7	30.4	27.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g14440	similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	gene: "SPBC1683.13c"; Schizosaccharomyces pombe cosmids	SPBC1683_13	1e-33	18.5	23.1	20.6	32.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g14550	weak similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	gene: "X4G11.050"; product: "hypothetical protein"; Neurospora crassa	NCX4G11_5	2e-04	129.4	166.6	125.2	136.4	Fungal specific transcription factor domain
	Pc22g20620	strong similarity to nitrogen assimilation regulatory protein nit-4 - Neurospora crassa	regulatory protein nit-4 - Neurospora crassa	A41696	4e-33	131.5	153.6	116.3	98.4	Zn(II)2Cys6, Fungal specific transcription factor domain
NOT3	Pc20g04790	strong similarity to transcription regulator not3 - Homo sapiens	probable transcription regulator - fission yeast (Schizosaccharomyces	T38023	2e-94	172.6	183.4	116.4	99.8	Not3 (Not1 N-terminal domain, CCR4-Not complex component). NOT2 /
NREB	Pc12g11600	GATA transcription factor nreB - Penicillium chrysogenum	gene: "nreB"; product: "GATA transcription factor"; Penicillium	U96385_1	1e-146	76.4	78.6	68.1	43.3	GATA zinc finger
	Pc22g24480	regulator of nitrogen metabolite repression nre - Penicillium chrysogenum [putative sequencing error]	NITROGEN REGULATORY PROTEIN AREA (NITROGEN	AREA_PENRO	0.0	182.5	149.6	144.4	113.1	Nitrogen regulatory protein AreA N terminus, GATA zinc finger
NUC-1	Pc12g05460	strong similarity to transcription activator nuc-1 - Neurospora crassa	probable transcription activator nuc-1 - Neurospora crassa	A36378	3e-40	108.2	99.5	90.3	70.2	Helix-loop-helix DNA-binding domain
	Pc23g00570	similarity to transcription activator nuc-1 - Neurospora crassa [truncated ORF][putative sequencing error]	probable transcription activator nuc-1 - Neurospora crassa	A36378	5e-23	7.7	6.3	4.8	2.9	Helix-loop-helix DNA-binding domain
PAB1642	Pc18g00440	weak similarity to hypothetical transcription regulator PAB1642 - Pyrococcus abyssi	gene: "PF1337"; product: "transcriptional activator, putative";	AE010238_9	2e-11	58.5	35.7	33.3	33.5	TENA/THI-4/PQQC family
PACC	Pc18g00420	transcription factor pacC - Penicillium chrysogenum	gene: "pacC"; product: "transcription factor PacC"; Penicillium	PCU44726_1	0.0	211.5	171.5	219.2	151.2	C2H2
PAIB	Pc13g01950	similarity to transcription regulator 2 of pai operon paiB - Bacillus subtilis	gene: "mll0013"; product: "transcriptional regulator"; Mesorhizobium	AP002994_10	3e-30	4.8	3.4	7.1	5.5	FMN-binding domain 2
	Pc15g01210	similarity to transcription regulator 2 of pai operon paiB - Bacillus subtilis	gene: "mll0013"; product: "transcriptional regulator"; Mesorhizobium	AP002994_10	2e-26	88.3	83.5	174.2	169.7	FMN-binding domain 2
PBP	Pc13g15350	similarity to transcription factor PBP - Fusarium solani	gene: "nsdD"; product: "NsdD"; Aspergillus nidulans NsdD (nsdD)	ENU70043_1	1e-112	110.1	82.8	82.5	49.4	GATA zinc finger
	Pc22g02540	strong similarity to transcription factor PBP - Fusarium solani	gene: "lreB"; product: "GATA-factor"; Emericella nidulans ABC	AF082072_2	3e-65	49.1	51.4	70.2	73.2	GATA zinc finger, PAS fold domain
PHD	Pc18g00330	strong similarity to hypothetical phd finger transcription regulator - Schizosaccharomyces pombe	probable phd finger transcription regulator - fission yeast	T41449	2e-32	36.0	29.3	27.4	27.3	PHD-finger
PIP2	Pc12g13120	similarity to the transcription factor Pip2 - Saccharomyces cerevisiae	transcription factor PIP2 - yeast (Saccharomyces cerevisiae)	S70646	2e-05	43.0	70.2	66.1	127.8	Zn(II)2Cys6
	Pc13g00900	weak similarity to the transcription factor Pip2 - Saccharomyces cerevisiae				3.3	1.2	5.3	0.4	Zn(II)2Cys6
	Pc22g04150	weak similarity to the transcription factor Pip2 - Saccharomyces cerevisiae	product: "transcriptional regulator, putative"; Aspergillus fumigatus	BX649607_85	5e-04	36.9	27.6	30.5	34.4	Zn(II)2Cys6
PIRIN: Cofactor of	Pc20g09190	strong similarity to cofactor of NFI/CTF1 transcription activator pirin - Homo sapiens	gene: "B9B11.100"; product: "related to pirin"; Neurospora crassa DNA	NCB9B11_10	1e-132	101.7	101.4	130.7	132.7	Pirin, Pirin C-terminal cupin domain, Cupin domain
PREG	Pc06g02200	strong similarity to phosphorus acquisition transcriptional activator NUC-1 negative regulator PREG - Neurospora crassa	regulatory protein preg - Neurospora crassa	S52974	1e-45	4.4	3.2	3.8	2.4	Cyclin domain
	Pc13g00560	strong similarity to phosphorus acquisition transcriptional activator NUC-1 negative regulator PREG - Neurospora crassa	regulatory protein preg - Neurospora crassa	S52974	2e-46	13.2	9.3	7.1	5.7	Cyclin domain
	Pc22g11620	strong similarity to phosphorus acquisition transcriptional activator NUC-1 negative regulator PREG - Neurospora crassa	regulatory protein preg - Neurospora crassa	S52974	1e-49	129.0	99.3	131.3	108.2	Cyclin domain, Cyclin N-terminal domain
PPR1	Pc12g11430	similarity to regulator protein Ppr1 - Saccharomyces cerevisiae	gene: "B9I2.010"; product: "conserved hypothetical protein";	NCB9I2_1	4e-62	10.9	12.0	18.6	23.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g14500	similarity to regulator protein Ppr1 - Saccharomyces cerevisiae	probable membrane protein YLR278c - yeast (Saccharomyces	S50366	3e-41	2.5	2.6	2.6	10.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g07320	weak similarity to regulator protein Ppr1 - Saccharomyces cerevisiae	probable membrane protein YIL130w - yeast (Saccharomyces	S48404	2e-07	3.3	3.7	4.4	3.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g15510	similarity to regulator protein Ppr1 - Saccharomyces cerevisiae	probable regulatory protein YHR178w - yeast (Saccharomyces	S48917	5e-25	77.2	92.2	78.9	107.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g04590	similarity to regulator protein Ppr1 - Saccharomyces cerevisiae	regulatory protein PPR1 - yeast (Saccharomyces cerevisiae)	RGBYP1	3e-16	239.9	219.2	227.0	210.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g07030	weak similarity to regulator protein Ppr1 - Saccharomyces cerevisiae	transcription activator protein acu-15 [imported] - Neurospora crassa	T46651	2e-16	43.7	37.6	24.4	28.3	Fungal specific transcription factor domain
	Pc22g14950	weak similarity to transcription activator Ppr1 - Saccharomyces cerevisiae				11.4	1.2	24.7	7.6	Fungal specific transcription factor domain
	Pc22g15370	similarity to regulator protein Ppr1 - Saccharomyces cerevisiae	regulatory protein PPR1 - yeast (Saccharomyces cerevisiae)	RGBYP1	1e-12	12.5	40.8	16.1	49.2	Fungal specific transcription factor domain
	Pc22g16640	weak similarity to transcription activator Ppr1 - Saccharomyces cerevisiae				48.8	67.3	63.9	104.3	Zn(II)2Cys6
PRF	Pc21g16690	similarity to binuclear zinc transcription factor PRF - Nectria haematococca [putative pseudogene]	probable membrane protein YLR228c - yeast (Saccharomyces	S51451	3e-06	14.9	17.2	20.7	14.0	Zn(II)2Cys6
	Pc22g05320	strong similarity to hypothetical binuclear zinc transcription factor PRF - Nectria haematococca	gene: "PRF"; product: "binuclear zinc transcription factor"; Nectria	AY218847_1	9e-78	51.1	53.3	27.1	36.1	Zn(II)2Cys6, Fungal specific transcription factor domain
PREP-1	Pc22g06630	similarity to homeodomain protein Prep-1 - Homo sapiens	product: "chromosome 10 open reading frame 48"; Homo sapiens	BC036207_1	2e-09	111.3	93.5	91.5	71.0	Homeobox domain, C2H2
PRO1	Pc06g01440	weak similarity to zinc-finger transcription factor pro1 - Sordaria macrospora	gene: "pro1"; product: "PRO1 protein"; Sordaria brevicollis pro1 gene	SBR238536_1	5e-05	80.5	78.5	53.6	57.6	Zn(II)2Cys6
	Pc21g17540	similarity to zinc-finger transcription factor pro1 - Sordaria macrospora [putative sequencing error]	hypothetical protein SPBC530.05 - fission yeast	T40521	9e-06	73.9	87.1	67.7	50.5	Zn(II)2Cys6, Fungal specific transcription factor domain
PtaA	Pc13g15250	strong similarity to hypothetical transcriptional activator ptaA - Aspergillus nidulans	gene: "ptaA"; product: "PTAA"; Aspergillus nidulans PTAA (ptaA) gene,	AF320977_1	6e-37	39.1	39.2	23.3	16.0	No domain identified
PtaC	Pc22g23480	strong similarity to hypothetical transcriptional activator ptaC - Aspergillus nidulans	gene: "ptaC"; product: "PTAC beta"; Aspergillus nidulans PTAC (ptaC)	AF320980_1	4e-57	48.5	48.1	33.0	28.7	No domain identified
PUT3	Pc12g10710	similarity to transcription activator Put3 - Saccharomyces cerevisiae	transcription activator PUT3 - yeast (Saccharomyces cerevisiae)	A39792	4e-10	90.6	79.7	27.2	35.1	Fungal specific transcription factor domain
	Pc13g01390	strong similarity to transcription activator Put3 - Saccharomyces cerevisiae	transcription activator PUT3 - yeast (Saccharomyces cerevisiae)	A39792	4e-26	36.4	42.1	31.9	45.2	Fungal specific transcription factor domain
	Pc20g12130	weak similarity to transcription activator Put3 - Saccharomyces cerevisiae	probable regulatory protein - fission yeast (Schizosaccharomyces	T38690	2e-35	4.6	2.8	13.2	33.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g11980	weak similarity to transcription activator Put3 - Saccharomyces cerevisiae	gene: "B8G12.430"; product: "conserved hypothetical protein";	NCB8G12_44	1e-07	1.3	1.6	2.4	2.2	Zn(II)2Cys6
	Pc22g00270	strong similarity to transcription activator Put3 - Saccharomyces cerevisiae	transcription activator PUT3 - yeast (Saccharomyces cerevisiae)	A39792	3e-27	99.3	208.8	140.7	337.3	Fungal specific transcription factor domain
	Pc22g07340	weak similarity to transcription activator Put3 - Saccharomyces cerevisiae	gene: "ZFR1"; product: "Zfr1"; Gibberella moniliformis Zfr1 (ZFR1)	AY493199_1	5e-06	1.7	17.9	7.1	21.5	Fungal specific transcription factor domain
	Pc22g12330	weak similarity to transcription activator Put3 - Saccharomyces cerevisiae	gene: "SPAC1399.05c"; S.pombe chromosome II cosmid c1399.	SPAC1399_1	6e-23	100.6	199.7	245.8	424.6	Zn(II)2Cys6
QA-1F	Pc16g03100	weak similarity to positive regulator qa-1F - Neurospora crassa				3.3	1.8	3.1	4.9	Zn(II)2Cys6
	Pc21g05050	weak similarity to positive regulator qa-1F - Neurospora crassa	gene: "PRF"; product: "binuclear zinc transcription factor"; Nectria	AY218847_1	2e-16	480.5	770.1	1169.9	973.6	Fungal specific transcription factor domain
	Pc12g01790	similarity to regulator protein qutA - Aspergillus nidulans	gene: "5E6.310"; product: "related to nitrate assimilation regulatory	NC5E6_27	2e-26	49.6	45.2	77.6	80.8	Zn(II)2Cys6, Fungal specific transcription factor domain

QUTA	Pc13g08420	strong similarity to regulator protein qutA - Aspergillus nidulans	gene: "qutA"; product: "quinic acid utilization activator, putative";	BX649605_38	0.0	51.2	44.0	45.1	49.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g00930	strong similarity to regulator protein qutA - Aspergillus nidulans				134.5	125.0	107.4	107.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g04140	similarity to regulator protein qutA - Aspergillus nidulans	transcription regulator, binuclear cluster zinc-finger protein - fission	T39677	2e-04	272.6	286.3	400.3	452.9	Zn(II)2Cys6
	Pc21g21100	weak similarity to regulator protein qutA - Aspergillus nidulans	Sequence 1 from Patent WO0121779.	AX100446_1	6e-18	-	-	-	-	Zn(II)2Cys6
	Pc22g12620	weak similarity to regulator protein qutA - Aspergillus nidulans	gene: "MPP1"; product: "ZnII/2cys6 transcription factor"; Pichia	AY190521_1	2e-05	35.6	54.4	61.3	69.9	Zn(II)2Cys6
QUTR	Pc21g16820	strong similarity to repressor protein qutR - Aspergillus nidulans	product: "unknown"; Emericella nidulans negative-acting regulatory	ANQUTR_1	1e-113	613.1	640.8	689.7	632.1	Uncharacterised protein family UPF0005
RDR1	Pc12g02800	similarity to zinc-finger transcription factor Rdr1 - Saccharomyces cerevisiae	gene: "MPP1"; product: "ZnII/2cys6 transcription factor"; Pichia	AY190521_1	1e-10	12.4	9.8	15.7	16.4	Zn(II)2Cys6
	Pc12g16580	strong similarity to zinc-finger transcription factor Rdr1 - Saccharomyces cerevisiae	probable membrane protein YOR380w - yeast (Saccharomyces	S67292	2e-85	343.2	378.4	52.5	98.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g07840	weak similarity to transcription repressor Rdr1 - Saccharomyces cerevisiae				221.1	222.7	224.9	193.7	No domain identified
	Pc18g00100	strong similarity to zinc-finger transcription factor Rdr1 - Saccharomyces cerevisiae	probable membrane protein YOR380w - yeast (Saccharomyces	S67292	2e-85					Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc18g02280	strong similarity to transcription repressor Rdr1 - Saccharomyces cerevisiae	probable membrane protein YOR380w - yeast (Saccharomyces	S67292	7e-47	12.8	9.3	11.7	13.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g17990	strong similarity to hypothetical transcription repressor Rdr1 - Saccharomyces cerevisiae	probable membrane protein YOR380w - yeast (Saccharomyces	S67292	3e-45	13.0	12.1	11.0	15.3	Zn(II)2Cys6, Fungal specific transcription factor domain
RES2p	Pc12g06750	weak similarity to cell cycle regulator res2p - Schizosaccharomyces pombe	gene: "mbpA"; product: "MBPA protein"; Aspergillus nidulans MBPA	AF236665_1	5e-75	111.0	85.7	63.1	67.9	APSES domain
	Pc13g15400	strong similarity to cell cycle regulator res2p - Schizosaccharomyces pombe	CELL DIVISION CYCLE RELATED-PROTEIN RES2/PCT1.	RES2_SCHPO	3e-62	108.6	89.8	73.2	69.8	APSES domain, Ankyrin repeat
RFEH	Pc21g03670	transcription factor rfeH - Penicillium chrysogenum	gene: "rfeH"; product: "RfeH"; Penicillium chrysogenum RfeH (rfeH)	AY189831_1	0.0	85.9	103.4	87.4	131.5	GATA zinc finger
RFG1	Pc22g06930	similarity to transcription regulator Rfg1 - Candida albicans	gene: "B8L21.130"; product: "hypothetical protein"; Neurospora crassa	NCB8L21_14	2e-27	21.0	9.5	7.4	5.8	HMG (high mobility group) box
RFX	Pc20g01690	transcription factor like protein RFX - Penicillium chrysogenum	gene: "RFX1"; product: "putative RFX transcription factor"; Penicillium	PCH243296_1	0.0	189.0	153.5	95.4	92.5	RFX DNA-binding domain
RGR1	Pc21g11300	similarity to regulator protein Rgr1 - Saccharomyces cerevisiae	hypothetical protein SPBC1A4.10c SPBP23A10.01c - fission yeast	T50388	2e-28	240.8	222.6	218.2	187.4	Mediator complex subunit MED14
RPH1	Pc13g12780	strong similarity to regulator protein Rph1 - Saccharomyces cerevisiae	gene: "B12N19.070"; product: "related to regulator of	NCB12N19_6	0.0	9.3	6.5	6.8	5.3	JmjN domain, JmjC domain
RSC1	Pc20g08240	strong similarity to protein Rsc1 - Saccharomyces cerevisiae	DNA centromeric region sequence from BAC DP26B06, DP34F04,	CNS09S4S_87	1e-140	106.7	101.0	60.0	49.2	Bromodomain, Bromo adjacent homology (BAH) domain
RSC8	Pc12g06620	strong similarity to chromatin remodeling gene transcription regulator Rsc8 - Saccharomyces cerevisiae	gene: "B2N18.250"; product: "related to nucleosome remodeling	BX897674_24	1e-143	266.2	254.6	268.1	214.2	Myb-like DNA-binding domain, SWIRM domain
SAC3	Pc22g15830	strong similarity to potential regulator of leucine permease gene expression Sac3 - Saccharomyces cerevisiae	probable leucine permease transcription regulator - fission yeast	T41415	4e-64	57.6	52.4	29.1	27.0	SAC3 GANP domain
SART1	Pc22g13140	strong similarity to hypoxia-associated transcriptional activator SART1 - Tetraodon nigroviridis	hypothetical protein B5O22.40 [imported] - Neurospora crassa	T49622	5e-92	150.6	148.9	158.0	125.7	SART-1 family
SC5F2A.29	Pc20g03020	weak similarity to hypothetical transcription regulator SC5F2A.29 - Streptomyces coelicolor	product: "probable transcriptional regulator, AraC family";	BX572600_256	2e-09	15.6	4.9	9.3	7.4	DJ-1/PfpI family
SEP1P	Pc20g00650	strong similarity to hnf-3/forkhead transcription factor sep1p - Schizosaccharomyces pombe	hnf-3/forkhead transcription factor homolog sep1 - fission yeast	JC6500	8e-30	96.3	66.7	36.8	38.2	Forkhead domain
SIN3	Pc12g03120	strong similarity to regulator protein Sin3 - Saccharomyces cerevisiae	gene: "B5K2.070"; product: "related to transcription regulatory protein";	BX842632_7	0.0	126.5	118.1	75.6	50.0	Paired amphipathic helix repeat (PAH), Histone deacetylase (HDAC)
SIP3	Pc18g02400	weak similarity to Snf1 interacting protein Sip3 - Saccharomyces cerevisiae	product: "SipA3"; Aspergillus nidulans SipA3 gene, complete cds.	AY150563_1	0.0	169.1	141.4	180.7	181.2	PH domain
SKN7	Pc22g04440	strong similarity to transcription regulator Skn7 - Saccharomyces cerevisiae	product: "stress response regulator SrrA"; Emericella nidulans stress	AY168636_1	0.0	206.4	163.8	306.5	197.2	HSF-type DNA-binding domain, Response regulator receiver domain
	Pc22g26090	weak similarity to transcription regulator Skn7 - Saccharomyces cerevisiae	Neurospora crassa DNA linkage group II BAC clone B18P7;	BX842594_12	5e-04	75.6	66.8	67.0	55.4	No domain identified
	Pc22g26380	weak similarity to transcription regulator Skn7 - Saccharomyces cerevisiae	gene: "OSJNBb0036G09.9"; product: "putative heat shock transcription	AP003309_9	3e-05	38.5	36.4	22.9	19.0	HSF-type DNA-binding domain
SMARCD1	Pc13g02850	strong similarity to SWI SNF-related, matrix-associated, actin-dependent regulator of chromatin SMARCD1 - Homo sapiens	gene: "B23I4.120"; product: "related to SWI/SNF complex 60 KDa	NCB23I4_11	1e-109	236.2	243.3	179.3	184.7	SWIB/MDM2 domain
SNF2	Pc21g17380	strong similarity to transcription regulator Snf2 - Saccharomyces cerevisiae	probable transcription regulator - fission yeast (Schizosaccharomyces	T37561	0.0	428.6	394.3	348.8	317.9	QLQ domain, HSA domain, SNF2 family N-terminal domain, Helicase
SNF5	Pc21g19240	strong similarity to transcription activator Snf5 - Saccharomyces cerevisiae	gene: "B13B7.230"; product: "related to transcription factor snf5p";	BX908807_23	1e-108	188.5	161.1	173.3	138.3	SNF5/SMARCB1/ INI1
SPAC11D3.07c	Pc12g11150	weak similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe	probable regulatory protein YHR178w - yeast (Saccharomyces	S48917	7e-06	18.9	38.9	44.8	60.4	Fungal specific transcription factor domain
	Pc15g01850	weak similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe	probable transcription regulator, binuclear cluster zinc-finger - fission	T37518	3e-04	23.3	20.0	25.4	30.0	No domain identified
	Pc16g00110	weak similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe				6.0	7.1	17.8	16.6	No domain identified
	Pc16g12650	weak similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe	probable transcription regulator, binuclear cluster zinc-finger - fission	T37518	3e-07	7.0	0.6	2.2	4.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc18g05390	similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe	gene: "B11E5.150"; product: "related to transcriptional activator Mut3p";	BX842620_15	0.0	118.0	114.0	92.5	86.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g15350	weak similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe [putative sequencing error]	gene: "B11E5.150"; product: "related to transcriptional activator Mut3p";	BX842620_15	3e-40	74.2	71.2	63.2	69.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g02170	weak similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe	gene: "B11E5.150"; product: "related to transcriptional activator Mut3p";	BX842620_15	2e-17	40.2	31.5	48.4	42.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g16600	weak similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe	probable transcription regulator, binuclear cluster zinc-finger - fission	T37518	T37518	52.7	46.9	45.7	34.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g13810	similarity to hypothetical transcription regulator SPAC11D3.07c - Schizosaccharomyces pombe	gene: "B11E5.150"; product: "related to transcriptional activator Mut3p";	BX842620_15	1e-87	7.8	13.0	8.0	19.9	Fungal specific transcription factor domain
SPAC139.03	Pc12g09550	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	7e-27	18.3	13.1	22.5	21.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g14990	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	transcription activator protein acu-15 [imported] - Neurospora crassa	T46651	4e-04	39.2	37.1	44.0	45.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc13g04660	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	5e-22	24.7	48.6	13.9	15.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc13g11110	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	2e-41	8.6	14.8	21.0	34.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc13g12410	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	T37604	106.1	112.2	101.3	123.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc14g00280	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "ZFR1"; product: "Zfr1"; Gibberella moniliformis Zfr1 (ZFR1)	AY493199_1	8e-08	12.3	15.2	8.3	12.5	Zn(II)2Cys6
	Pc15g01860	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	2e-82	17.2	19.4	21.9	20.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g00410	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	8e-12	51.5	55.3	103.9	89.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g00790	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "B11E5.250"; product: "conserved hypothetical protein";	BX842620_25	2e-45	35.2	89.0	53.8	98.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g01070	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	4e-43	28.5	25.4	38.9	52.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g04880	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "B23H20.120"; product: "conserved hypothetical protein";	NCB23H20_12	2e-06	375.1	389.1	381.9	377.1	Fungal specific transcription factor domain
	Pc16g07770	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "B11B23.130"; product: "conserved hypothetical protein";	NCB11B23_12	2e-19	10.7	13.6	12.8	13.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g08180	strong similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	4e-60	134.2	127.9	133.0	120.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g10140	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	5e-57	3.1	5.5	7.8	7.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc17g01190	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	5e-07	122.5	2.3	1.3	1.8	Zn(II)2Cys6, Zn(II)2Cys6
	Pc18g03150	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe [putative sequencing error]	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	1e-08	20.3	30.1	44.9	82.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc18g03810	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator protein [imported] - fission yeast	T50198	3e-35	142.3	136.1	207.1	189.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc18g05680	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	2e-24	35.8	28.5	38.0	41.7	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g04260	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "B11B23.130"; product: "conserved hypothetical protein";	NCB11B23_12	1e-48	40.1	33.8	37.9	43.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g11250	strong similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	2e-25	92.1	76.6	91.8	72.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g02230	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	7e-08	381.1	344.1	593.9	617.8	Zn(II)2Cys6
	Pc21g05300	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	9e-18	38.0	27.5	43.6	40.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g05840	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	2e-07	211.2	254.0	267.2	316.7	Zn(II)2Cys6
	Pc21g12340	similarity to hypothetical transcription regulator SPAC139.03 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	1e-19	5.8	4.6	81.2	57.5	Fungal specific transcription factor domain, Zn(II)2Cys6
	Pc21g23510	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	7e-20	124.7	130.1	131.0	149.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g03330	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	product: "unknown"; Nectria haematococca unknown gene.	AY165030_1	6e-17	12.3	12.4	15.7	15.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g06580	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	gene: "29E8.250"; product: "conserved hypothetical protein";	BX908809_25	2e-44	10.0	6.0	16.4	16.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g12580	similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	2e-12	15.6	13.8	15.4	18.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc24g01630	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	7e-09	109.1	1.8	0.5	0.2	Zn(II)2Cys6, Zn(II)2Cys6
	Pc24g02740	weak similarity to hypothetical transcription activator SPAC139.03 - Schizosaccharomyces pombe	probable transcription activator - fission yeast (Schizosaccharomyces	T37604	8e-09					Zn(II)2Cys6, Zn(II)2Cys6
SPBC530.05	Pc06g01190	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "facB"; product: "acetate regulatory DNA binding protein FacB,	BX649606_102	5e-17	140.6	184.3	211.0	244.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g09500	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	probable finger protein YKL038w - yeast (Saccharomyces cerevisiae)	S30010	2e-14	76.9	63.4	61.6	45.9	Zn(II)2Cys6
	Pc12g09750	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein SPBC530.05 - fission yeast	T40521	6e-05	2.2	2.7	2.1	3.5	Zn(II)2Cys6
	Pc12g13570	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein SPBC530.05 - fission yeast	T40521	2e-11	22.7	22.1	24.8	29.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g14400	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe				2.7	1.2	0.6	3.5	No domain identified
	Pc13g05420	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe [putative sequencing error]	hypothetical protein SPBC530.05 - fission yeast	T40521	7e-08	43.7	51.7	56.9	63.1	Zn(II)2Cys6
	Pc13g07830	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "B11E5.150"; product: "related to transcriptional activator Mut3p";	BX842620_15	2e-15	66.8	58.3	78.1	85.6	No domain identified
	Pc13g15930	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "facB"; product: "acetate regulatory DNA binding protein FacB";	ENU56097_1	6e-09	34.4	149.9	22.8	165.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g05870	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "grt1"; product: "zinc finger protein Grt1"; Schizosaccharomyces	AF236387_1	2e-27	48.6	64.8	57.3	61.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g09070	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein SPBC530.05 - fission yeast	T40521	9e-09	1.8	1.4	0.2	0.3	Zn(II)2Cys6
	Pc16g11760	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	probable trancription factor - fission yeast (Schizosaccharomyces	T37601	2e-04	92.4	197.9	187.7	217.1	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc17g00650	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	probable transcription regulator - fission yeast (Schizosaccharomyces	T40824	4e-05	3.8	3.3	7.7	4.9	No domain identified
	Pc18g00400	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	finger protein YJL206c - yeast (Saccharomyces cerevisiae)	S46625	1e-55	197.6	174.3	178.0	122.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g02380	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein B14D6.340 [imported] - Neurospora crassa	T49482	6e-10	15.0	6.6	15.0	24.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g06570	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein SPBC530.05 - fission yeast	T40521	6e-15	13.2	7.5	14.1	24.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g07910	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe				81.7	101.5	108.5	149.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g03950	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein SPBC530.05 - fission yeast	T40521	6e-06	21.6	14.9	23.5	16.0	Zn(II)2Cys6
	Pc21g04390	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "B11E5.150"; product: "related to transcriptional activator Mut3p";	BX842620_15	8e-12	91.7	74.6	80.3	75.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g14270	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein SPBC530.05 - fission yeast	T40521	2e-16	67.2	256.1	91.8	245.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g18890	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "B9I2.010"; product: "conserved hypothetical protein";	NCB9I2_1	5e-77	11.5	13.9	9.2	16.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g22750	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe				36.3	29.8	28.1	48.1	Zn(II)2Cys6
	Pc22g08140	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein SPBC530.05 - fission yeast	T40521	5e-09	121.6	106.9	86.5	90.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g16820	weak similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	hypothetical protein SPBC530.08 - fission yeast	T40524	8e-14	155.8	898.3	177.8	1502.1	Fungal specific transcription factor domain
	Pc22g21500	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "18A7.170"; product: "transcription activator protein acu-15";	NC18A7_18	1e-11	15.9	9.1	20.1	19.1	Fungal specific transcription factor domain
	Pc24g00780	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "X4G11.050"; product: "hypothetical protein"; Neurospora crassa	NCX4G11_5	7e-40	111.9	1.7	2.3	0.6	Zn(II)2Cys6
	Pc24g01310	similarity to hypothetical transcription regulator SPBC530.05 - Schizosaccharomyces pombe	gene: "X4G11.050"; product: "hypothetical protein"; Neurospora crassa	NCX4G11_5	1e-53	-	-	-	-	Zn(II)2Cys6
SPBC530.08	Pc16g05270	weak similarity to hypothetical transcription regulatory protein SPBC530.08 - Schizosaccharomyces pombe	transcription regulator SPBC16G5.17 - fission yeast	T39609	1e-07	1.7	1.1	0.9	0.7	Zn(II)2Cys6
SPCC4F11.01	Pc21g08640	weak similarity to hypothetical transcription regulator SPCC4F11.01 - Schizosaccharomyces pombe	gene: "B11C21.040"; product: "conserved hypothetical protein";	NCB11C21_4	2e-38	584.0	695.0	546.9	60.1	No domain identified
SPCC18.13	Pc16g10110	similarity to hypothetical WD-repeat transcription regulation protein SPCC18.13 - Schizosaccharomyces pombe	probable WD repeat transcription regulation protein - fission yeast	T41156	2e-24	189.1	180.7	206.4	204.6	WD domain, G-beta repeat
SPCC126.07c	Pc21g19540	strong similarity to hypothetical PHD-type zinc finger protein SPCC126.07c - Schizosaccharomyces pombe	probable PHD-type zinc finger - fission yeast (Schizosaccharomyces	T40911	3e-30	78.1	49.9	45.0	23.3	PHD-finger, C3HC4 type (RING finger)
SPCC417.09c	Pc06g00110	weak similarity to hypothetical transcriptional regulator SPCC417.09c - Schizosaccharomyces pombe [putative sequencing error]	probable membrane protein YIL130w - yeast (Saccharomyces	S48404	7e-10	67.8	112.0	62.7	70.1	Fungal specific transcription factor domain, Zn(II)2Cys6
	Pc12g08840	similarity to hypothetical transcriptional regulator SPCC417.09c - Schizosaccharomyces pombe	gene: "prnA"; product: "PrnA protein"; Aspergillus nidulans prnD, prnX,	ANAJ3459_3	0.0	90.2	80.9	72.4	63.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g14870	strong similarity to hypothetical transcriptional regulator SPCC417.09c - Schizosaccharomyces pombe [putative sequencing error]	gene: "prnA"; product: "PrnA protein"; Aspergillus nidulans prnD, prnX,	ANAJ3459_3	1e-130	19.5	27.1	62.1	78.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g15300	weak similarity to hypothetical transcriptional regulator SPCC417.09c - Schizosaccharomyces pombe	product: "unknown"; Nectria haematococca unknown gene.	AY165030_1	1e-13	92.6	83.5	70.3	67.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g19940	similarity to hypothetical transcriptional regulator SPCC417.09c - Schizosaccharomyces pombe	probable zinc-finger protein - fission yeast (Schizosaccharomyces	T41344	6e-18	32.9	26.2	38.6	42.0	Zn(II)2Cys6, Fungal specific transcription factor domain
SPT3	Pc16g12560	strong similarity to regulator protein Spt3 - Saccharomyces cerevisiae	product: "transcription factor spt3, putative"; Aspergillus fumigatus	BX649607_36	1e-138	70.7	58.2	37.6	32.3	Transcription initiation factor IID, 18kD subunit

SPT7	Pc13g09210	strong similarity to transcription factor Spt7 - Saccharomyces cerevisiae	gene: "B13D24.060"; product: "related to transcription regulator SPT7";	BX908789_6	0.0	7.2	6.8	18.9	9.7	Bromodomain, Bromo TP (bromodomain associated domain)
SPT10	Pc13g01600	strong similarity to regulator protein Spt10 - Saccharomyces cerevisiae	regulatory protein SPT10 - yeast (Saccharomyces cerevisiae)	S47865	7e-56	157.8	174.0	143.9	162.2	Acetyltransferase (GNAT) family, H2C2
SPT23	Pc13g13130	similarity to transcription suppressor protein Spt23 - Saccharomyces cerevisiae	product: "suppressor protein spt23-related, with ankyrin repeats";	BX649606_2	0.0	173.3	145.8	95.9	76.5	IPT/TIG domain, Ankyrin repeat
SREA	Pc16g03740	weak similarity to siderophore biosynthesis repressor sREA - Aspergillus nidulans	GATA-transcription factor - Penicillium chrysogenum	JC6170	8e-07	2.2	1.8	0.6	2.2	No domain identified
SREbp-1	Pc20g05880	similarity to sterol regulatory element binding protein-1 srebp-1 - Homo sapiens	gene: "B8I24.060"; product: "related to myc-type bHLH transcription	BX897676_6	4e-90	210.9	182.8	154.9	182.7	Helix-loop-helix DNA-binding domain
SREP	Pc21g05640	GATA transcription factor sreP - Penicillium chrysogenum	GATA-transcription factor - Penicillium chrysogenum	JC6170	0.0	221.4	169.5	122.1	76.1	GATA zinc finger
STE11	Pc18g06680	similarity to transcription factor ste11p - Schizosaccharomyces pombe	gene: "mat1-2"; product: "mating type 1-2 protein"; Mycosphaerella	AF440398_4	3e-10	17.6	4.5	8.4	6.7	HMG (high mobility group) box
	Pc22g05580	similarity to transcription factor ste11p - Schizosaccharomyces pombe	product: "HMG-box protein STE11"; Pneumocystis carinii HMG-box	AY257481_1	7e-10	2.2	1.3	3.3	2.4	HMG (high mobility group) box
STE12	Pc12g07060	strong similarity to homeodomain DNA-binding transcription factor ste12 - Aspergillus nidulans	gene: "ste12"; product: "homeodomain DNA-binding transcription	AF080600_1	0.0	283.8	234.4	184.6	127.9	STE like transcription factor, C2H2
STUA	Pc13g04920	strong similarity to transcription factor involved in differentiation stuA - Aspergillus nidulans	gene: "StuA"; product: "cell pattern formation-associated protein";	ENSTUA_1	1e-143	255.5	192.5	125.3	69.0	APSES domain
SWI4p	Pc21g08840	strong similarity to mating-type switching protein swi4p - Schizosaccharomyces pombe	gene: "MSH3"; product: "mutS homolog 3 (E. coli)"; Homo sapiens	AY275681_1	0.0	64.5	70.6	40.5	49.6	MutS domain I, II, III and V
SWI5	Pc13g09500	similarity to transcription factor Swi5 - Saccharomyces cerevisiae	hypothetical zinc-finger protein - fission yeast (Schizosaccharomyces	T39062	3e-22	305.3	251.1	166.3	89.0	C2H2
TAO3	Pc21g20900	strong similarity to transcription activator Tao3 - Saccharomyces cerevisiae	gene: "AfA12H2.01"; product: "conserved hypothetical protein";	AFA12H2_1	0.0	142.0	191.6	108.6	142.6	No domain identified
THI1p	Pc13g01210	similarity to transcription activator thi1p - Schizosaccharomyces pombe	probable transcription regulator - fission yeast (Schizosaccharomyces	T40824	3e-08	4.1	1.6	4.0	5.5	Zn(II)2Cys6
	Pc13g04200	similarity to thiamine repressible gene thi1p - Schizosaccharomyces pombe	gene: "facB"; product: "acetate regulatory DNA binding protein FacB";	ENU56097_1	4e-17	8.4	6.4	16.1	19.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc13g14910	weak similarity to thiamine repressible gene thi1p - Schizosaccharomyces pombe	gene: "grt1"; product: "zinc finger protein Grt1"; Schizosaccharomyces	AF236387_1	1e-14	34.5	31.1	46.2	57.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g03560	similarity to thiamine repressible gene thi1p - Schizosaccharomyces pombe	hypothetical protein SPBC530.05 - fission yeast	T40521	8e-17	19.2	8.1	21.7	43.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g14530	similarity to thiamine-repressible protein thi1p - Schizosaccharomyces pombe	gene: "nft1+"; product: "transcription factor"; Schizosaccharomyces	SPNTF1X_1	3e-19	3.5	2.9	8.8	3.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc18g06190	similarity to thiamine repressible gene thi1p - Schizosaccharomyces pombe	gene: "B11E5.150"; product: "related to transcriptional activator Mut3p";	BX842620_15	6e-89	38.5	31.6	41.5	41.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g02500	weak similarity to thiamine repressible gene thi1p - Schizosaccharomyces pombe	probable regulatory protein - fission yeast (Schizosaccharomyces	T38690	1e-15	36.5	33.3	29.4	44.5	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g12810	similarity to thiamine repressible gene thi1p - Schizosaccharomyces pombe	gene: "B2E7.100"; product: "related to lactose regulatory protein";	BX897675_10	1e-14	14.4	5.2	13.1	3.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc21g13820	similarity to thiamine-repressible protein thi1p - Schizosaccharomyces pombe	gene: "B2E7.100"; product: "related to lactose regulatory protein";	BX897675_10	1e-124	417.4	419.9	473.1	794.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g06450	similarity to thiamine-repressible protein thi1p - Schizosaccharomyces pombe	thiamin repressible genes regulatory protein thi1 [imported] - fission	S41962	1e-18	430.0	459.9	267.0	224.4	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g09250	similarity to thiamine-repressible protein thi1p - Schizosaccharomyces pombe	gene: "nft1+"; product: "transcription factor"; Schizosaccharomyces	SPNTF1X_1	6e-18	47.1	39.6	46.3	31.0	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g17630	similarity to thiamine repressible gene thi1p - Schizosaccharomyces pombe	gene: "facB"; product: "FacB"; Aspergillus niger putative DNA binding	ANU56099_1	2e-24	9.9	10.3	9.3	13.0	Zn(II)2Cys6, Fungal specific transcription factor domain
TRI6	Pc22g25600	strong similarity to transcription activator Tri6 - Fusarium cerealis	gene: "TRI6"; product: "regulatory protein"; Gibberella zeae strain	AY102589_3	9e-22	3.0	2.3	3.9	4.9	No domain identified
TRI10	Pc22g01630	similarity to transcription regulator TRI10 - Fusarium sporotrichioides	gene: "TRI10"; product: "regulatory protein"; Gibberella zeae strain	AY102584_5	1e-22	13.2	8.3	10.2	21.3	Zn(II)2Cys6
UAY	Pc06g01740	strong similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	purine utilization positive regulator - Emericella nidulans	S54779	0.0	85.5	79.1	50.5	62.2	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc12g10080	weak similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	DNA centromeric region sequence from BAC DP26B06, DP34F04,	CNS09S4S_32	3e-18	26.8	20.5	41.4	29.1	Zn(II)2Cys6
	Pc13g04550	strong similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	probable membrane protein YLR278c - yeast (Saccharomyces	S50366	3e-38	29.3	25.9	24.7	28.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc15g01100	similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	gene: "PRF"; product: "binuclear zinc transcription factor"; Nectria	AY218847_1	2e-26	12.0	1.7	14.6	2.9	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc16g05770	weak similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans [putative pseudogene]				2.2	2.8	1.8	6.4	Zn(II)2Cys6
	Pc16g13540	similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans [putative sequencing error]	purine utilization positive regulator - Emericella nidulans	S54779	4e-30	6.7	39.3	9.1	46.8	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc20g03640	weak similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans				3.6	0.7	2.0	24.0	Zn(II)2Cys6
	Pc20g07370	strong similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	purine utilization positive regulator - Emericella nidulans	S54779	5e-34	2.2	1.1	2.3	3.0	Zn(II)2Cys6
	Pc21g05090	weak similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot project	BX649605_28	7e-10	117.8	181.5	128.6	128.1	Fungal specific transcription factor domain
	Pc22g02170	weak similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	purine utilization positive regulator - Emericella nidulans	S54779	4e-12	2.3	4.6	17.0	42.6	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g04580	similarity to positive regulator of purine utilisation uaY - Aspergillus nidulans	gene: "CLTA1"; product: "putative GAL4-like transcriptional activator";	AF190427_1	1e-106	199.9	170.8	158.1	142.3	Zn(II)2Cys6, Fungal specific transcription factor domain
UGA3	Pc12g15860	weak similarity to regulator protein Uga3 - Saccharomyces cerevisiae	hypothetical fungal Zn(2)-Cys(6) zinc-finger protein - fission yeast	T41718	8e-12	283.3	209.8	160.3	145.5	Zn(II)2Cys6
UME6	Pc18g04480	similarity to transcription factor Ume6 - Saccharomyces cerevisiae	gene: "rosA"; product: "repressor of sexual development"; Aspergillus	ENI519682_1	1e-157	437.9	229.9	157.0	148.6	Zn(II)2Cys6
UPC2	Pc06g01390	similarity to RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	2e-11	0.6	2.2	1.8	2.4	Zn(II)2Cys6
	Pc12g04050	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	5e-08	101.7	107.2	124.7	131.9	Zn(II)2Cys6
	Pc12g12360	weak similarity to hypothetical RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	5e-16	7.0	4.7	10.2	7.2	Zn(II)2Cys6
	Pc13g01970	similarity to RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	gene: "pro1"; product: "PRO1"; Neurospora crassa pro1 gene for	NCR238440_1	6e-06	180.6	178.7	96.6	83.2	Zn(II)2Cys6
	Pc13g06530	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	gene: "17E5.150"; product: "conserved hypothetical protein";	NC17E5_14	2e-24	12.0	17.4	17.0	22.3	Zn(II)2Cys6
	Pc13g11250	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	4e-04	23.0	15.2	28.0	28.1	Zn(II)2Cys6
	Pc14g00210	weak similarity to transcription activator Upc2 - Saccharomyces cerevisiae [putative sequencing error]	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	3e-06	16.5	8.9	9.0	12.1	Zn(II)2Cys6
	Pc14g01000	similarity to transcription factor Upc2 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	1e-07	3.3	4.4	6.0	6.5	Zn(II)2Cys6
	Pc14g01370	similarity to transcription factor Upc2 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	6e-08	94.7	144.9	235.0	320.1	Zn(II)2Cys6
	Pc16g02960	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	1e-18	29.9	29.7	39.3	53.5	Zn(II)2Cys6
	Pc16g04030	weak similarity to RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	8e-06	10.8	12.1	18.6	23.6	No domain identified
	Pc16g05350	weak similarity to transcription activator Upc2 - Saccharomyces cerevisiae [putative pseudogene]				0.6	2.4	1.6	1.3	No domain identified
	Pc16g11730	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	zinc finger protein 1 homolog [imported] - Neurospora crassa	T49729	5e-09	219.1	161.9	119.7	80.8	Zn(II)2Cys6
	Pc16g13160	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	2e-14	11.4	15.1	16.5	18.6	Zn(II)2Cys6
	Pc18g05880	weak similarity to RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae				12.9	13.5	18.3	14.8	Zn(II)2Cys6
	Pc20g05430	weak similarity to RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	1e-04	4.3	10.1	2.9	7.5	Zn(II)2Cys6
	Pc21g00640	similarity to hypothetical RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	6e-13	78.8	88.1	98.1	99.0	Zn(II)2Cys6
	Pc21g08710	weak similarity to transcription activator Upc2 - Saccharomyces cerevisiae				52.5	33.2	42.9	34.6	Zn(II)2Cys6
	Pc21g09290	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	zinc finger protein 1 homolog [imported] - Neurospora crassa	T49729	5e-12	74.0	40.1	67.8	52.6	Zn(II)2Cys6
	Pc21g12280	similarity to RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	2e-12	89.0	55.3	66.8	33.9	Zn(II)2Cys6
	Pc21g15030	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	gene: "pro1"; product: "PRO1 protein"; Sordaria macrospora pro1	SAJ10151_1	6e-06	13.1	13.9	36.2	50.1	Zn(II)2Cys6
	Pc21g17760	weak similarity to transcription activator Upc2 - Saccharomyces cerevisiae	gene: "17E5.150"; product: "conserved hypothetical protein";	NC17E5_14	1e-16	78.6	70.3	82.0	72.5	Zn(II)2Cys6
	Pc21g18560	similarity to RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	hypothetical fungal Zn(2)-Cys(6) zinc-finger protein - fission yeast	T41718	2e-08	54.0	44.8	36.8	33.7	Zn(II)2Cys6
	Pc21g21670	weak similarity to hypothetical RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	probable membrane protein YLR228c - yeast (Saccharomyces	S51451	2e-07	2.8	1.0	3.9	2.1	Zn(II)2Cys6
	Pc22g00480	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	4e-15	38.3	40.5	84.6	87.3	Zn(II)2Cys6
	Pc22g06200	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	gene: "B9B15.005"; product: "putative protein"; Neurospora crassa	NCB9B15_1	6e-11	24.8	21.3	30.2	39.9	Zn(II)2Cys6
	Pc22g07590	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	2e-10	30.1	29.7	36.6	40.8	No domain identified
	Pc22g16910	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	product: "hypothetical protein"; Aspergillus fumigatus BAC pilot project	BX649605_122	2e-97	87.7	112.8	128.8	130.1	Zn(II)2Cys6
	Pc22g20530	weak similarity to hypothetical RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	probable membrane protein YLR228c - yeast (Saccharomyces	S51451	4e-05	18.2	20.2	41.4	75.6	No domain identified
	Pc22g22350	weak similarity to hypothetical RNA polymerase II transcription factor Upc2 - Saccharomyces cerevisiae	probable membrane protein YLR228c - yeast (Saccharomyces	S51451	7e-06	52.0	35.9	82.8	72.3	No domain identified
	Pc22g26430	similarity to transcription activator Upc2 - Saccharomyces cerevisiae	gene: "CAT8"; product: "Cat8"; Candida albicans Ntg1 (NTG1) gene,	AF222908_3	3e-07	5.6	6.7	9.0	10.5	Zn(II)2Cys6
	Pc24g00540	weak similarity to transcription activator Upc2 - Saccharomyces cerevisiae	probable membrane protein YDR213w - yeast (Saccharomyces	S61580	8e-06	15.2	10.2	21.5	28.7	No domain identified
USF2	Pc22g15870	weak similarity to upstream stimulatory factor of transcription USF2 - Homo sapiens	gene: "penR2"; product: "PENR2 protein"; Emericella nidulans penR2	ENI17331_1	2e-50	406.4	337.3	221.6	212.6	Helix-loop-helix DNA-binding domain
WC-1	Pc20g08380	strong similarity to central regulator of blue light responses wc-1 - Neurospora crassa	gene: "lreA"; product: "GATA-factor"; Emericella nidulans GATA-factor	AF515628_1	1e-172	32.8	33.9	29.5	31.9	PAS 3 domain, GATA domain
WETA	Pc22g03220	regulator protein wetA - Penicillium chrysogenum	wetA protein - Penicillium chrysogenum	S46660	0.0	10.3	4.2	14.9	13.6	No domain identified
XBP1	Pc22g00710	similarity to transcription repressor Xbp1 - Saccharomyces cerevisiae	probable membrane protein YIL101c - yeast (Saccharomyces	S48471	7e-05	9.9	6.1	12.8	11.3	No domain identified
XLNR	Pc21g02790	strong similarity to xylanolytic transcriptional activator xlnR - Aspergillus niger	gene: "AoxlnR"; product: "transcription activator"; Aspergillus oryzae	AB042843_1	0.0	159.2	139.8	118.8	150.3	Zn(II)2Cys6, Fungal specific transcription factor domain
	Pc22g22560	strong similarity to xylanolytic transcriptional activator xlnR - Aspergillus niger	gene: "xlnR"; product: "transcriptional activator"; Aspergillus niger xlnR	ANAJ1909_1	1e-136	118.4	93.5	90.5	81.6	Zn(II)2Cys6, Fungal specific transcription factor domain
YAP1	Pc06g00310	weak similarity to transcription factor YAP1 - Kluyveromyces lactis				38.8	23.5	25.4	25.4	No domain identified
	Pc21g01350	weak similarity to transcription factor YAP1 - Kluyveromyces lactis (no domain identified)				47.2	30.5	26.9	29.0	No domain identified
	Pc21g05670	weak similarity to transcription factor YAP1 - Kluyveromyces lactis (no domain identified)				1.7	2.1	5.4	5.2	No domain identified
YAP2	Pc22g19250	similarity to AP-1-like stress-induced transcriptional activator Yap2 - Saccharomyces cerevisiae	gene: "YAP2"; YAP2=AP-1-like stress-induced transcriptional activator	S68847_1	7e-05	29.9	26.2	26.4	32.6	No domain identified
YAP3	Pc12g16510	weak similarity to bZIP transcription factor Yap3 - Saccharomyces cerevisiae	gene: "B13D15.040"; product: "hypothetical protein"; Neurospora	BX842630_4	4e-40	941.4	823.2	152.1	111.8	bZIP-like leucine zipper (bZIP 1and bZIP 2)
	Pc18g00030	weak similarity to bZIP transcription factor Yap3 - Saccharomyces cerevisiae	gene: "B13D15.040"; product: "hypothetical protein"; Neurospora	BX842630_4	4e-40	-	-	-	-	bZIP-like leucine zipper (bZIP 1and bZIP 2)
ZFM1	Pc18g00800	strong similarity to transcription factor ZFM1 - Homo sapiens	gene: "94C8.060"; product: "related to branch point bridging protein	NC94C8_6	1e-164	245.1	226.6	148.0	89.7	KH domain, Zinc knuckle (CCHC)

@ Values given are the average of three independent experiments

Supplementary Table 27. Probe set characteristics of DSM_PENa520255F, hybridized with Wis54-1255 genomic DNA

	#	%	Average Signal
Total Probe Sets:	15525		107.7
Number Present:	15346	98.80%	108.9
Number Absent:	158	1.00%	3
Number Marginal:	21	0.10%	14.5
Annotated ORFs probe sets	13704		105
Number Present:	13615	99.40%	-
Number Absent:	76	0.60%	-
Number Marginal:	13	0.10%	-