## **S6 Table. Annotation of genes uniquely regulated by *PdsreA***

| ID | log2FC in △PdsreA | Pfam family | domain name(abbreviation) | domain name | nr_annotation |
|---|---|---|---|---|---|
| 133 elements included exclusively in "△PdsreA-down": | | | | | |
| PDIG_63570 | -1.10 | PF07690, | MFS_1, | Major Facilitator Superfamily, | Pc18g02960 [Penicillium chrysogenum Wisconsin 54-1255] |
| PDIG_71250 | -1.10 | PF00575, | S1, | S1 RNA binding domain, | RRNA biogenesis protein RRP5, putative |
| PDIG_35230 | -1.10 | | | | hypothetical protein PDIP_54780 |
| PDIG_30110 | -1.13 | PF00428, | Ribosomal_60s, | 60s Acidic ribosomal protein, | 60S acidic ribosomal protein P2 |
| PDIG_71520 | -1.13 | PF00583, | Acetyltransf_1, | Acetyltransferase (GNAT) family, | hypothetical protein PDIP_80820 |
| PDIG_84040 | -1.14 | PF00743,PF04082, | FMO-like,Fungal_trans, | Flavin-binding monooxygenase-like,Fungal specific transcription factor domain, | Fungal specific transcription factor, putative |
| PDIG_68480 | -1.15 | PF00636,PF03368, | Ribonuclease_3,Dicer_dimer, | Ribonuclease III domain,Dicer dimerisation domain, | Dicer-like protein 2 |
| PDIG_84710 | -1.15 | PF16198,PF01472,PF01509,PF04511,PF08068, | TruB_C_2,PUA,TruB_N,DER1,DKCLD, | tRNA pseudouridylate synthase B C-terminal domain,PUA domain,TruB family pseudouridylate synthase (N terminal domain),Der1-like family,DKCLD (NUC011) domain, | Centromere/microtubule-binding protein CBF5 |
| PDIG_88130 | -1.15 | PF08327,PF09229, | AHSA1,Aha1_N, | Activator of Hsp90 ATPase homolog 1-like protein,Activator of Hsp90 ATPase, N-terminal, | Pc22g05790 [Penicillium chrysogenum Wisconsin 54-1255] |
| PDIG_64000 | -1.16 | PF05178,PF12936, | Kri1,Kri1_C, | KRI1-like family,KRI1-like family C-terminal, | Ribosome biogenesis protein Kri1 |
| PDIG_15640 | -1.18 | PF11951, | Fungal_trans_2, | Fungal specific transcription factor domain, | hypothetical protein PDIG_15640 |
| PDIG_07260 | -1.18 | PF00043,PF02798, | GST_C,GST_N, | Glutathione S-transferase, C-terminal domain,Glutathione S-transferase, N-terminal | Translation elongation factor eEF-1B gamma subunit, putative |

| | | | | | |
|---|---|---|---|---|---|
| | | | | domain, | |
| PDIG_89420 | -1.19 | PF08238, | Sel1, | Sel1 repeat, | hypothetical protein PDIG_89420 |
| PDIG_12570 | -1.19 | PF03949,PF00390, | Malic_M,malic, | Malic enzyme, NAD binding domain,Malic enzyme, N-terminal domain, | malate dehydrogenase (oxaloacetate-decarboxylating) [Exophiala dermatitidis NIH/UT8656] |
| PDIG_84990 | -1.20 | | | | Protein kinase |
| PDIG_57320 | -1.21 | PF01269, | Fibrillarin, | Fibrillarin, | Fibrillarin, putative |
| PDIG_78490 | -1.21 | PF04588, | HIG_1_N, | Hypoxia induced protein conserved region, | hypothetical protein PDIG_78490 |
| PDIG_02290 | -1.21 | PF08241, | Methyltransf_11, | Methyltransferase domain, | hypothetical protein PDIG_02290 |
| PDIG_56300 | -1.22 | PF13561, | adh_short_C2, | Enoyl-(Acyl carrier protein) reductase, | hypothetical protein PDIP_65860 |
| PDIG_39900 | -1.23 | | | | Mitochondrial distribution and morphology protein 34 |
| PDIG_13640 | -1.24 | PF17125,PF01189, | Methyltr_RsmF_N, Methyltr_RsmB-F, | N-terminal domain of 16S rRNA methyltransferase RsmF,16S rRNA methyltransferase RsmB/F, | Nucleolar RNA methyltransferase (Nop2), putative |
| PDIG_91030 | -1.25 | PF00160, | Pro_isomerase, | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD, | Peptidyl-prolyl cis-trans isomerase D |
| PDIG_70480 | -1.26 | PF02780,PF02779, | Transketolase_C,Transket_pyr, | Transketolase, C-terminal domain,Transketolase, pyrimidine binding domain, | 3-methyl-2-oxobutanoate dehydrogenase, putative |
| PDIG_20950 | -1.27 | PF00645, | zf-PARP, | Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region, | PARP-type zinc finger-containing protein C2A9.07c |
| PDIG_18740 | -1.27 | | | | hypothetical protein PDIP_56570 |
| PDIG_73920 | -1.27 | PF00400, | WD40, | WD domain, G-beta repeat, | Pc22g03140 [Penicillium chrysogenum Wisconsin 54-1255] |
| PDIG_54410 | -1.28 | PF00650,PF03765, | CRAL_TRIO,CRAL_TRIO_N, | CRAL/TRIO domain,CRAL/TRIO, N-terminal domain, | Phosphatidylinositol transporter, putative |
| PDIG_47330 | -1.28 | PF00583, | Acetyltransf_1, | Acetyltransferase (GNAT) family, | Acetyltransferase, GNAT family |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| PDIG_12760 | -1.29 | PF00166, | Cpn10, | Chaperonin 10 Kd subunit, | Chaperonin, putative |
| PDIG_04330 | -1.29 | PF01965, | DJ-1_PfpI, | DJ-1/PfpI family, | ThiJ/PfpI family protein |
| PDIG_31790 | -1.30 | PF01039, | Carboxyl_trans, | Carboxyl transferase domain, | 3-methylcrotonyl-CoA carboxylase, beta subunit (MccB), putative |
| PDIG_39040 | -1.30 | PF13409,PF13410, | GST_N_2,GST_C_2, | Glutathione S-transferase, N-terminal domain,Glutathione S-transferase, C-terminal domain, | hypothetical protein PDIG_39040 |
| PDIG_56530 | -1.30 | PF01207, | Dus, | Dihydrouridine synthase (Dus), | tRNA dihydrouridine synthase, putative |
| PDIG_77380 | -1.32 | PF13561, | adh_short_C2, | Enoyl-(Acyl carrier protein) reductase, | Sorbitol/xylulose reductase Sou1-like, putative |
| PDIG_47770 | -1.33 |  |  |  | hypothetical protein PDIG_47770 |
| PDIG_17540 | -1.33 | PF10277, | Frag1, | Frag1/DRAM/Sfk1 family, | FK506 suppressor Sfk1, putative |
| PDIG_76930 | -1.33 | PF11951, | Fungal_trans_2, | Fungal specific transcription factor domain, | hypothetical protein PDIG_76930 |
| PDIG_40060 | -1.34 | PF00266, | Aminotran_5, | Aminotransferase class-V, | Kynureninase |
| PDIG_03890 | -1.34 | PF00561, | Abhydrolase_1, | alpha/beta hydrolase fold, | Pc20g03890 [Penicillium chrysogenum Wisconsin 54-1255] |
| PDIG_22360 | -1.34 | PF00004, | AAA, | ATPase family associated with various cellular activities (AAA), | AAA family ATPase, putative |
| PDIG_08090 | -1.38 | PF00676, | E1_dh, | Dehydrogenase E1 component, | 2-oxoisovalerate dehydrogenase complex alpha subunit, putative |
| PDIG_43630 | -1.39 | PF00107, | ADH_zinc_N, | Zinc-binding dehydrogenase, | Alcohol dehydrogenase, putative |
| PDIG_64350 | -1.39 |  |  |  | hypothetical protein PDIP_73690 |
| PDIG_87000 | -1.39 | PF05712,PF11717, | MRG,Tudor-knot, | MRG,RNA binding activity-knot of a chromodomain, | Histone acetylase complex subunit MRG15-2 |
| PDIG_64130 | -1.40 | PF00172, | Zn_clus, | Fungal Zn(2)-Cys(6) binuclear cluster domain, | hypothetical protein PDIP_73480 |
| PDIG_56750 | -1.41 | PF00400, | WD40, | WD domain, G-beta repeat, | WD repeat protein |
| PDIG_20110 | -1.41 |  |  |  | hypothetical protein PDIG_20110 |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_55550 | -1.41 | PF13434, | K_oxygenase, | L-lysine 6-monooxygenase (NADPH-requiring), | L-ornithine N5 monooxygenase |
| PDIG_22490 | -1.42 | PF02782,PF00370, | FGGY_C,FGGY_N, | FGGY family of carbohydrate kinases, C-terminal domain,FGGY family of carbohydrate kinases, N-terminal domain, | FGGY-family carbohydrate kinase, putative |
| PDIG_55470 | -1.42 | PF00291,PF00571, | PALP,CBS, | Pyridoxal-phosphate dependent enzyme,CBS domain, | Cystathionine beta-synthase, putative |
| PDIG_11700 | -1.42 | | | | hypothetical protein PDIG_11700 |
| PDIG_61640 | -1.43 | PF01246, | Ribosomal_L24e, | Ribosomal protein L24e, | hypothetical protein PDIP_71070 |
| PDIG_63620 | -1.43 | PF01474, | DAHP_synth_2, | Class-II DAHP synthetase family, | Phospho-2-dehydro-3-deoxyheptonate aldolase, class II |
| PDIG_66810 | -1.43 | PF01798,PF08156, | Nop,NOP5NT, | snoRNA binding domain, fibrillarin,NOP5NT (NUC127) domain, | Pre-rRNA processing nucleolar protein Sik1, putative |
| PDIG_48180 | -1.44 | | | | hypothetical protein PDIP_57560 |
| PDIG_55000 | -1.44 | | | | NADH-ubiquinone oxidoreductase 9.5 kDa subunit, putative |
| PDIG_83990 | -1.45 | PF08297, | U3_snoRNA_assoc, | U3 snoRNA associated, | hypothetical protein PDIP_89480 |
| PDIG_61240 | -1.46 | | | | hypothetical protein PDIG_61240 |
| PDIG_75870 | -1.46 | | | | hypothetical protein PDIG_75870 |
| PDIG_59730 | -1.48 | PF04427, | Brix, | Brix domain, | hypothetical protein PDIP_69150 |
| PDIG_41170 | -1.48 | PF00364,PF02817,PF00198, | Biotin_lipoyl,E3_binding,2-oxoacid_dh, | Biotin-requiring enzyme,e3 binding domain,2-oxoacid dehydrogenases acyltransferase (catalytic domain), | Biotin-dependent 2-oxo acid dehydrogenases acyltransferase, putative |
| PDIG_11360 | -1.48 | PF11274, | DUF3074, | Protein of unknown function (DUF3074), | hypothetical protein PDIP_82860 |
| PDIG_27920 | -1.49 | PF00463, | ICL, | Isocitrate lyase family, | Isocitrate lyase |
| PDIG_03200 | -1.49 | PF00625, | Guanylate_kin, | Guanylate kinase, | Guanylate kinase |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_36830 | -1.50 | PF10329, | DUF2417, | Region of unknown function (DUF2417), | Mitochondrial integral membrane protein |
| PDIG_24330 | -1.51 | | | | hypothetical protein PDIP_58810 |
| PDIG_75310 | -1.52 | PF01172, | SBDS, | Shwachman-Bodian-Diamond syndrome (SBDS) protein, | RNA binding protein, putative |
| PDIG_66090 | -1.54 | | | | hypothetical protein PDIP_75390 |
| PDIG_04810 | -1.54 | PF08883, | DOPA_dioxygen, | Dopa 4,5-dioxygenase family, | hypothetical protein PDIG_04810 |
| PDIG_07850 | -1.55 | | | | hypothetical protein PDIP_35890 |
| PDIG_23700 | -1.56 | PF00288,PF08544, | GHMP_kinases_N,GHMP_kinases_C, | GHMP kinases N terminal domain,GHMP kinases C terminal, | Mevalonate kinase |
| PDIG_58300 | -1.58 | PF01144, | CoA_trans, | Coenzyme A transferase, | succinyl-CoA:3-ketoacid-coenzyme A transferase [Neosartorya fischeri NRRL 181] |
| PDIG_23460 | -1.59 | PF00725,PF02737, | 3HCDH,3HCDH_N, | 3-hydroxyacyl-CoA dehydrogenase, C-terminal domain,3-hydroxyacyl-CoA dehydrogenase, NAD binding domain, | 3-hydroxybutyryl-CoA dehydrogenase, putative |
| PDIG_41570 | -1.60 | | | | hypothetical protein PDIG_41570 |
| PDIG_72980 | -1.60 | PF00153, | Mito_carr, | Mitochondrial carrier protein, | Mitochondrial carrier protein, putative |
| PDIG_22380 | -1.63 | | | | hypothetical protein PDIG_22380 |
| PDIG_56320 | -1.64 | | | | hypothetical protein PDIP_65880 |
| PDIG_78890 | -1.64 | PF00549,PF00755, | Ligase_CoA,Carn_acyltransf, | CoA-ligase,Choline/Carnitine o-acyltransferase, | Carnitine acetyl transferase |
| PDIG_53050 | -1.65 | | | | hypothetical protein PDIG_53050 |
| PDIG_29290 | -1.66 | PF00378, | ECH_1, | Enoyl-CoA hydratase/isomerase, | Enoyl-CoA hydratase/isomerase family protein |
| PDIG_44310 | -1.67 | PF00205,PF02775, | TPP_enzyme_M,TPP_enzyme_C, | Thiamine pyrophosphate enzyme, central domain,Thiamine pyrophosphate enzyme, C-terminal TPP binding domain, | acetolactate synthase [Aspergillus oryzae RIB40] |
| PDIG_55650 | -1.67 | | | | hypothetical protein PDIG_55650 |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_31800 | -1.67 | PF02771,PF00441,PF02770, | Acyl-CoA_dh_N,Acyl-CoA_dh_1,Acyl-CoA_dh_M, | Acyl-CoA dehydrogenase, N-terminal domain,Acyl-CoA dehydrogenase, C-terminal domain,Acyl-CoA dehydrogenase, middle domain, | Isovaleryl-CoA dehydrogenase IvdA, putative |
| PDIG_08310 | -1.70 | PF04209, | HgmA, | homogentisate 1,2-dioxygenase, | Homogentisate 1,2-dioxygenase (HmgA), putative |
| PDIG_31050 | -1.72 | PF01161, | PBP, | Phosphatidylethanolamine-binding protein, | Protease inhibitor (Tfs1), putative |
| PDIG_56920 | -1.73 | PF00081,PF02777, | Sod_Fe_N,Sod_Fe_C, | Iron/manganese superoxide dismutases, alpha-hairpin domain,Iron/manganese superoxide dismutases, C-terminal domain, | Superoxide dismutase |
| PDIG_08300 | -1.74 | PF01557,PF09298, | FAA_hydrolase,FAA_hydrolase_N, | Fumarylacetoacetate (FAA) hydrolase family,Fumarylacetoacetase N-terminal, | Fumarylacetoacetate hydrolase FahA |
| PDIG_70470 | -1.74 | PF05368, | NmrA, | NmrA-like family, | Isoflavone reductase, putative |
| PDIG_07390 | -1.78 | | | | hypothetical protein PDIG_07390 |
| PDIG_71010 | -1.79 | PF01556,PF00226,PF00684, | DnaJ_C,DnaJ,DnaJ_CXXCXGXG, | DnaJ C terminal domain,DnaJ domain,DnaJ central domain, | hypothetical protein PDIP_80330 |
| PDIG_08080 | -1.80 | | | | hypothetical protein PDIG_45050 |
| PDIG_45050 | -1.80 | PF14529,PF00078,PF00075, | Exo_endo_phos_2,RVT_1,RNase_H, | Endonuclease-reverse transcriptase,Reverse transcriptase (RNA-dependent DNA polymerase),RNase H, | hypothetical protein PDIG_45050 |
| PDIG_24510 | -1.81 | PF03239, | FTR1, | Iron permease FTR1 family, | Plasma membrane iron permease |
| PDIG_57140 | -1.81 | PF13489, | Methyltransf_23, | Methyltransferase domain, | hypothetical protein PDIP_66680 |
| PDIG_12190 | -1.82 | | | | hypothetical protein PDIP_38410 |
| PDIG_78090 | -1.85 | PF04427, | Brix, | Brix domain, | Imp4 protein, putative |
| PDIG_65470 | -1.86 | PF13236,PF13374,PF1280 | CLU,TPR_10,eIF3_p135,TPR_12,CL | Clustered mitochondria,Tetratricopeptide repeat,Translation initiation factor eIF3 subunit | hypothetical protein PDIP_74790 |

| | | | | | |
|---|---|---|---|---|---|
| | | 7,PF13424,PF15044, | U_N, | 135,Tetratricopeptide repeat,Mitochondrial function, CLU-N-term, | |
| PDIG_77450 | -1.88 | PF11700, | ATG22, | Vacuole effluxer Atg22 like, | hypothetical protein PDIG_77450 |
| PDIG_38170 | -1.88 | PF13418, | Kelch_4, | Galactose oxidase, central domain, | Kelch repeat protein |
| PDIG_02770 | -1.89 | PF00108,PF02803, | Thiolase_N,Thiolase_C, | Thiolase, N-terminal domain,Thiolase, C-terminal domain, | Sterol carrier protein, putative |
| PDIG_45340 | -1.91 | PF13561,PF07247, | adh_short_C2,AATase, | Enoyl-(Acyl carrier protein) reductase,Alcohol acetyltransferase, | hypothetical protein PDIP_17280 [Penicillium digitatum Pd1] |
| PDIG_83000 | -1.93 | PF07081, | DUF1349, | Protein of unknown function (DUF1349), | hypothetical protein PDIP_86790 |
| PDIG_60520 | -1.99 | | | | hypothetical protein PDIP_69930 |
| PDIG_27670 | -1.99 | PF00067, | p450, | Cytochrome P450, | Cytochrome P450 monooxygenase, putative |
| PDIG_03260 | -1.99 | PF00403, | HMA, | Heavy-metal-associated domain, | hypothetical protein PDIP_41920 |
| PDIG_32310 | -2.02 | | | | hypothetical protein PDIP_51900 |
| PDIG_51810 | -2.06 | PF04622, | ERG2_Sigma1R, | ERG2 and Sigma1 receptor like protein, | C-8 sterol isomerase (Erg-1), putative |
| PDIG_75680 | -2.07 | | | | hypothetical protein PDIG_75680 |
| PDIG_20140 | -2.12 | PF08547, | CIA30, | Complex I intermediate-associated protein 30 (CIA30), | hypothetical protein PDIG_20140 |
| PDIG_07340 | -2.16 | PF14683,PF14686, | CBM-like,fn3_3, | Polysaccharide lyase family 4, domain III,Polysaccharide lyase family 4, domain II, | hypothetical protein PDIG_07340 |
| PDIG_00260 | -2.18 | | | | hypothetical protein PDIG_00260 |
| PDIG_57550 | -2.20 | | | | hypothetical protein PDIP_67060 |
| PDIG_25230 | -2.21 | | | | hypothetical protein PDIP_59720 |
| PDIG_56950 | -2.23 | PF01425,PF00106, | Amidase,adh_short, | Amidase,short chain dehydrogenase, | General amidase, putative |
| PDIG_53070 | -2.26 | PF03328, | HpcH_HpaI, | HpcH/HpaI aldolase/citrate lyase family, | 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| PDIG_83260 | -2.27 | PF05063, | MT-A70, | MT-A70, | MT-A70 family |
| PDIG_42220 | -2.32 |  |  |  | hypothetical protein PDIG_42220 |
| PDIG_29970 | -2.36 | PF08538, | DUF1749, | Protein of unknown function (DUF1749), | Siderophore biosynthesis lipase/esterase, putative |
| PDIG_84380 | -2.36 | PF08570, | DUF1761, | Protein of unknown function (DUF1761), | hypothetical protein PDIG_84380 |
| PDIG_69650 | -2.37 |  |  |  | hypothetical protein PDIP_78940 |
| PDIG_62940 | -2.38 |  |  |  | hypothetical protein PDIP_72320 |
| PDIG_18400 | -2.42 | PF07992,PF00355, | Pyr_redox_2,Rieske, | Pyridine nucleotide-disulphide oxidoreductase,Rieske [2Fe-2S] domain, | AIF-like mitochondrial oxidoreductase (Nfrl), putative |
| PDIG_13300 | -2.43 | PF14033, | DUF4246, | Protein of unknown function (DUF4246), | hypothetical protein PDIP_40440 |
| PDIG_38270 | -2.56 |  |  |  | hypothetical protein PDIG_38270 |
| PDIG_24500 | -2.58 | PF01794,PF08022,PF08030, | Ferric_reduct,FAD_binding_8,NAD_binding_6, | Ferric reductase like transmembrane component,FAD-binding domain,Ferric reductase NAD binding domain, | Ferric reductase transmembrane component 5, putative |
| PDIG_38260 | -2.59 | PF07690, | MFS_1, | Major Facilitator Superfamily, | siderochrome-iron transporter (Sit1), putative [Aspergillus clavatus NRRL 1] |
| PDIG_53850 | -2.73 |  |  |  | hypothetical protein PDIG_53850 |
| PDIG_46910 | -3.19 | PF04116, | FA_hydroxylase, | Fatty acid hydroxylase superfamily, | Sterol delta 5,6-desaturase ERG3 |
| PDIG_22330 | -3.21 | PF04116, | FA_hydroxylase, | Fatty acid hydroxylase superfamily, | C-4 methyl sterol oxidase Erg25, putative |
| PDIG_77480 | -3.31 | PF00172, | Zn_clus, | Fungal Zn(2)-Cys(6) binuclear cluster domain, | hypothetical protein PDIG_77480 |
| PDIG_90350 | -3.67 | PF01284, | MARVEL, | Membrane-associating domain, | Non-classical export protein, putative |
| PDIG_71130 | -3.68 |  |  |  | hypothetical protein PDIG_71130 |
| PDIG_90150 | -9.40 | PF00010,PF09427, | HLH,DUF2014, | Helix-loop-helix DNA-binding domain,Domain of unknown function (DUF2014), | HLH transcription factor, putative |
| 259 elements included exclusively in "∆PdsreA-up": |  |  |  |  |  |
| PDIG_03030 | 6.30 | PF11951, | Fungal_trans_2, | Fungal specific transcription factor domain, | hypothetical protein PDIG_15640 |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_87530 | 4.36 | | | | hypothetical protein PDIG_87530 |
| PDIG_58090 | 4.10 | PF00199,PF06628, | Catalase,Catalase-rel, | Catalase,Catalase-related immune-responsive, | Catalase B |
| PDIG_33090 | 4.09 | PF14310,PF00933,PF01915, | Fn3-like,Glyco_hydro_3,Glyco_hydro_3_C, | Fibronectin type III-like domain,Glycosyl hydrolase family 3 N terminal domain,Glycosyl hydrolase family 3 C-terminal domain, | putative beta-glucosidase G |
| PDIG_60730 | 3.78 | PF00171, | Aldedh, | Aldehyde dehydrogenase family, | hypothetical protein PDIP_70160 |
| PDIG_59450 | 3.47 | PF07745, | Glyco_hydro_53, | Glycosyl hydrolase family 53, | Arabinogalactan endo-1,4-beta-galactosidase GalA |
| PDIG_64230 | 3.28 | | | | hypothetical protein PDIP_73570 |
| PDIG_87780 | 3.24 | | | | hypothetical protein PDIG_87780 |
| PDIG_49820 | 3.15 | | | | hypothetical protein PDIG_49820 |
| PDIG_44800 | 3.01 | PF00083, | Sugar_tr, | Sugar (and other) transporter, | MFS monosaccharide transporter, putative |
| PDIG_25750 | 2.97 | | | | GABA permease [Aspergillus fumigatus Af293] |
| PDIG_14830 | 2.93 | PF01095, | Pectinesterase, | Pectinesterase, | hypothetical protein PDIG_14830 |
| PDIG_60760 | 2.91 | PF01619, | Pro_dh, | Proline dehydrogenase, | Pyrroline-5-carboxylate reductase |
| PDIG_13580 | 2.90 | PF03442,PF00150, | CBM_X2,Cellulase, | Carbohydrate binding domain X2,Cellulase (glycosyl hydrolase family 5), | Extracellular endoglucanase, putative |
| PDIG_13830 | 2.88 | | | | hypothetical protein PDIP_39480 |
| PDIG_37780 | 2.84 | PF00324, | AA_permease, | Amino acid permease, | Amino acid permease (Dip5), putative |
| PDIG_84890 | 2.83 | | | | hypothetical protein PDIG_84890 |
| PDIG_87750 | 2.69 | PF01212, | Beta_elim_lyase, | Beta-eliminating lyase, | Threonine aldolase, putative |
| PDIG_44930 | 2.62 | PF07519, | Tannase, | Tannase and feruloyl esterase, | hypothetical protein PDIG_44930 |
| PDIG_32690 | 2.58 | PF03330, | DPBB_1, | Lytic transglycolase, | Expansin-like protein 1 |
| PDIG_26800 | 2.57 | PF06912, | DUF1275, | Protein of unknown function (DUF1275), | hypothetical protein PDIP_61250 |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_81120 | 2.54 | PF02133, | Transp_cyt_pur, | Permease for cytosine/purines, uracil, thiamine, allantoin, | hypothetical protein PDIG_81120 |
| PDIG_45070 | 2.53 | PF00295, | Glyco_hydro_28, | Glycosyl hydrolases family 28, | Polygalacturonase-2 |
| PDIG_03860 | 2.52 | PF04488, | Gly_transf_sug, | Glycosyltransferase sugar-binding region containing DXD motif, | hypothetical protein PDIG_03860 |
| PDIG_60740 | 2.47 | | | | hypothetical protein PDIP_70170 |
| PDIG_81130 | 2.43 | PF02133, | Transp_cyt_pur, | Permease for cytosine/purines, uracil, thiamine, allantoin, | hypothetical protein PDIG_81130 |
| PDIG_49470 | 2.40 | PF00282, | Pyridoxal_deC, | Pyridoxal-dependent decarboxylase conserved domain, | hypothetical protein PDIG_49470 |
| PDIG_13650 | 2.40 | PF00443,PF13920,PF02493, | UCH,zf-C3HC4_3,MORN, | Ubiquitin carboxyl-terminal hydrolase,Zinc finger, C3HC4 type (RING finger),MORN repeat, | putative MATH and UCH domain protein |
| PDIG_51040 | 2.40 | PF16815, | HRI1, | Protein HRI1, | hypothetical protein PDIG_51040 |
| PDIG_34250 | 2.38 | PF06422,PF00005,PF14510,PF01061, | PDR_CDR,ABC_tran,ABC_trans_N,ABC2_membrane, | CDR ABC transporter,ABC transporter,ABC-transporter extracellular N-terminal,ABC-2 type transporter, | ABC transporter, putative |
| PDIG_17100 | 2.37 | PF00083, | Sugar_tr, | Sugar (and other) transporter, | MFS monosaccharide transporter, putative |
| PDIG_67790 | 2.35 | PF13520, | AA_permease_2, | Amino acid permease, | hypothetical protein PDIP_77100 |
| PDIG_50110 | 2.31 | PF00857, | Isochorismatase, | Isochorismatase family, | Isochorismatase family protein |
| PDIG_89860 | 2.28 | PF13520, | AA_permease_2, | Amino acid permease, | hypothetical protein PDIG_89860 |
| PDIG_68670 | 2.28 | PF00232, | Glyco_hydro_1, | Glycosyl hydrolase family 1, | Beta-glucosidase |
| PDIG_15120 | 2.26 | | | | hypothetical protein PDIG_15120 |
| PDIG_54580 | 2.24 | | | | hypothetical protein PDIG_54580 |
| PDIG_31500 | 2.21 | PF09362, | DUF1996, | Domain of unknown function (DUF1996), | hypothetical protein PDIP_51080 [Penicillium digitatum Pd1] |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_83190 | 2.20 | PF00152,PF01336, | tRNA-synt_2,tRNA_anti-codon, | tRNA synthetases class II (D, K and N),OB-fold nucleic acid binding domain, | Cytoplasmic asparaginyl-tRNA synthetase, putative |
| PDIG_00570 | 2.19 | PF10282, | Lactonase, | Lactonase, 7-bladed beta-propeller, | hypothetical protein PDIG_00570 |
| PDIG_15490 | 2.19 | PF08669,PF01571, | GCV_T_C,GCV_T, | Glycine cleavage T-protein C-terminal barrel domain,Aminomethyltransferase folate-binding domain, | Aminomethyltransferase |
| PDIG_29560 | 2.11 | PF04371, | PAD_porph, | Porphyromonas-type peptidyl-arginine deiminase, | hypothetical protein PDIP_63960 |
| PDIG_42070 | 2.11 | | | | hypothetical protein UCREL1_8844 [Eutypa lata UCREL1] |
| PDIG_39440 | 2.11 | PF00202, | Aminotran_3, | Aminotransferase class-III, | hypothetical protein PDIG_39440 |
| PDIG_66580 | 2.10 | | | | hypothetical protein PDIP_75880 |
| PDIG_46690 | 2.10 | PF08244,PF00251, | Glyco_hydro_32C,Glyco_hydro_32N, | Glycosyl hydrolases family 32 C terminal,Glycosyl hydrolases family 32 N-terminal domain, | Putative intracellular invertase |
| PDIG_04910 | 2.10 | PF07690, | MFS_1, | Major Facilitator Superfamily, | MFS transporter, putative |
| PDIG_71680 | 2.08 | | | | Integral membrane protein |
| PDIG_15350 | 2.08 | PF00083, | Sugar_tr, | Sugar (and other) transporter, | hypothetical protein PDIG_15350 |
| PDIG_24110 | 2.07 | PF02776,PF00205,PF02775, | TPP_enzyme_N,TPP_enzyme_M,TPP_enzyme_C, | Thiamine pyrophosphate enzyme, N-terminal TPP binding domain,Thiamine pyrophosphate enzyme, central domain,Thiamine pyrophosphate enzyme, C-terminal TPP binding domain, | Ankyrin, putative |
| PDIG_36640 | 2.04 | PF01658,PF07994, | Inos-1-P_synth,NAD_binding_5, | Myo-inositol-1-phosphate synthase,Myo-inositol-1-phosphate synthase, | hypothetical protein PDIP_89710 |
| PDIG_52220 | 2.00 | PF04082, | Fungal_trans, | Fungal specific transcription factor domain, | hypothetical protein PDIG_52220 |
| PDIG_48560 | 2.00 | PF00860, | Xan_ur_permease, | Permease family, | Nucleoside transporter, putative |
| PDIG_20170 | 1.97 | PF00172, | Zn_clus, | Fungal Zn(2)-Cys(6) binuclear cluster domain, | hypothetical protein PDIG_20170 |
| PDIG_33200 | 1.95 | PF01137, | RTC, | RNA 3'-terminal phosphate cyclase, | RNA 3&apos;-terminal phosphate cyclase, |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | putative |
| PDIG_58220 | 1.95 | PF02347, | GDC-P, | Glycine cleavage system P-protein, | Glycine dehydrogenase |
| PDIG_36840 | 1.94 | PF00171, | Aldedh, | Aldehyde dehydrogenase family, | Aldehyde dehydrogenase |
| PDIG_58830 | 1.92 | PF01764, | Lipase_3, | Lipase (class 3), | Extracellular triacylglycerol lipase, putative |
| PDIG_79190 | 1.89 | PF13302, | Acetyltransf_3, | Acetyltransferase (GNAT) domain, | N-acetyltransferase, GNAT family, putative |
| PDIG_75190 | 1.88 | PF13561, | adh_short_C2, | Enoyl-(Acyl carrier protein) reductase, | hypothetical protein PDIG_75190 |
| PDIG_36960 | 1.88 | | | | hypothetical protein PDIP_83550 |
| PDIG_89390 | 1.87 | | | | putative beta-glucosidase btgE |
| PDIG_61970 | 1.85 | PF00580,PF13361, | UvrD-helicase,UvrD_C, | UvrD/REP helicase N-terminal domain,UvrD-like helicase C-terminal domain, | ATP-depentend DNA helicase, putative |
| PDIG_84160 | 1.85 | | | | hypothetical protein PDIG_84160 |
| PDIG_33750 | 1.84 | PF05730, | CFEM, | CFEM domain, | Extracellular serine-threonine rich protein |
| PDIG_43030 | 1.84 | PF09334, | tRNA-synt_1g, | tRNA synthetases class I (M), | Methionyl-tRNA synthetase |
| PDIG_61420 | 1.83 | PF00248, | Aldo_ket_red, | Aldo/keto reductase family, | Aldehyde reductase (GliO), putative |
| PDIG_34550 | 1.82 | | | | hypothetical protein PDIP_54110 |
| PDIG_43660 | 1.82 | PF00291,PF00290, | PALP,Trp_syntA, | Pyridoxal-phosphate dependent enzyme,Tryptophan synthase alpha chain, | Bifunctional tryptophan synthase TRPB |
| PDIG_53550 | 1.81 | PF00668,PF00501,PF07993,PF00550, | Condensation,AMP-binding,NAD_binding_4,PP-binding, | Condensation domain,AMP-binding enzyme,Male sterility protein,Phosphopantetheine attachment site, | HC-toxin synthetase |
| PDIG_48990 | 1.80 | PF08029,PF01634, | HisG_C,HisG, | HisG, C-terminal domain,ATP phosphoribosyltransferase, | hypothetical protein PDIP_58370 |
| PDIG_49390 | 1.80 | | | | hypothetical protein PDIG_49390 |
| PDIG_38810 | 1.80 | PF00078,PF00075,PF14529, | RVT_1,RNase_H,Exo_endo_phos_2, | Reverse transcriptase (RNA-dependent DNA polymerase),RNase H,Endonuclease-reverse transcriptase, | putative RNA-directed DNA polymerase from transposon X-element |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_83720 | 1.80 | | | | hypothetical protein PDIP_89220 |
| PDIG_30830 | 1.80 | PF00150,PF00734, | Cellulase,CBM_1, | Cellulase (glycosyl hydrolase family 5),Fungal cellulose binding domain, | putative endoglucanase/cellulase 1 [Penicillium digitatum] |
| PDIG_23080 | 1.79 | PF04389, | Peptidase_M28, | Peptidase family M28, | Aminopeptidase, putative |
| PDIG_10930 | 1.79 | PF03124, | EXS, | EXS family, | Protein-ER retention protein (Erd1), putative |
| PDIG_56600 | 1.78 | | | | hypothetical protein PDIP_66160 |
| PDIG_87700 | 1.77 | PF00501,PF07993,PF00550, | AMP-binding,NAD_binding_4,PP-binding, | AMP-binding enzyme,Male sterility protein,Phosphopantetheine attachment site, | L-aminoadipate-semialdehyde dehydrogenase |
| PDIG_58110 | 1.76 | PF01699, | Na_Ca_ex, | Sodium/calcium exchanger protein, | hypothetical protein PDIP_67600 |
| PDIG_06660 | 1.76 | PF00328, | His_Phos_2, | Histidine phosphatase superfamily (branch 2), | Acid phosphatase, putative |
| PDIG_23790 | 1.75 | PF02436,PF00289,PF02786,PF00364,PF00682,PF02785, | PYC_OADA,Biotin_carb_N,CPSase_L_D2,Biotin_lipoyl,HMGL-like,Biotin_carb_C, | Conserved carboxylase domain,Biotin carboxylase, N-terminal domain,Carbamoyl-phosphate synthase L chain, ATP binding domain,Biotin-requiring enzyme,HMGL-like,Biotin carboxylase C-terminal domain, | Pyruvate carboxylase, putative |
| PDIG_48400 | 1.74 | PF01425, | Amidase, | Amidase, | Amidase family protein |
| PDIG_29590 | 1.74 | PF13520, | AA_permease_2, | Amino acid permease, | Amino acid permease |
| PDIG_76170 | 1.73 | PF07690, | MFS_1, | Major Facilitator Superfamily, | MFS multidrug transporter, putative |
| PDIG_72690 | 1.73 | PF01988, | VIT1, | VIT family, | Calcium transporter, putative |
| PDIG_36170 | 1.73 | PF00445, | Ribonuclease_T2, | Ribonuclease T2 family, | Ribonuclease T2, putative |
| PDIG_00200 | 1.72 | PF13520, | AA_permease_2, | Amino acid permease, | Choline transporter Hnm1, putative |
| PDIG_30210 | 1.72 | PF02786,PF02787, | CPSase_L_D2,CPSase_L_D3, | Carbamoyl-phosphate synthase L chain, ATP binding domain,Carbamoyl-phosphate synthetase large chain, oligomerisation domain, | Carbamoyl-phosphate synthase, large subunit |
| PDIG_00100 | 1.72 | | | | hypothetical protein PDIG_00100 |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_84670 | 1.70 | PF13358,PF01498, | DDE_3,HTH_Tnp_Tc3_2, | DDE superfamily endonuclease,Transposase, | Transposable element tc3 transposase, putative |
| PDIG_87680 | 1.70 | PF00941,PF03450,PF00111,PF01799,PF01315,PF02738, | FAD_binding_5,CO_deh_flav_C,Fer2,Fer2_2,Ald_Xan_dh_C,Ald_Xan_dh_C2, | FAD binding domain in molybdopterin dehydrogenase,CO dehydrogenase flavoprotein C-terminal domain,2Fe-2S iron-sulfur cluster binding domain,[2Fe-2S] binding domain,Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain,Molybdopterin-binding domain of aldehyde dehydrogenase, | Xanthine dehydrogenase HxA, putative |
| PDIG_38950 | 1.69 | PF00464, | SHMT, | Serine hydroxymethyltransferase, | Serine hydroxymethyltransferase |
| PDIG_37200 | 1.69 | PF04193, | PQ-loop, | PQ loop repeat, | L-cystine transporter, putative |
| PDIG_25890 | 1.66 | PF00328, | His_Phos_2, | Histidine phosphatase superfamily (branch 2), | hypothetical protein PDIP_60370 |
| PDIG_52230 | 1.66 | | | | hypothetical protein PDIG_52230 |
| PDIG_42900 | 1.66 | | | | hypothetical protein PDIG_42900 |
| PDIG_00610 | 1.64 | | | | hypothetical protein PDIG_00610 |
| PDIG_32580 | 1.63 | PF03987,PF03986,PF10381, | Autophagy_act_C,Autophagy_N,Autophagy_C, | Autophagocytosis associated protein, active-site domain,Autophagocytosis associated protein (Atg3), N-terminal domain,Autophagocytosis associated protein C-terminal, | Autophagy-related protein 3 |
| PDIG_29740 | 1.63 | PF04139, | Rad9, | Rad9, | DNA repair protein rad9, putative |
| PDIG_32620 | 1.61 | PF01960, | ArgJ, | ArgJ family, | Arginine biosynthesis bifunctional protein ArgJ, mitochondrial |
| PDIG_03870 | 1.60 | PF07690, | MFS_1, | Major Facilitator Superfamily, | Amine transporter, putative |
| PDIG_14050 | 1.60 | | | | hypothetical protein PDIP_39700 |
| PDIG_01380 | 1.59 | | | | hypothetical protein PDIG_01380 |
| PDIG_34980 | 1.58 | PF03856, | SUN, | Beta-glucosidase (SUN family), | hypothetical protein PDIP_54540 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| PDIG_60710 | 1.57 | PF04082, | Fungal_trans, | Fungal specific transcription factor domain, | hypothetical protein PDIP_70140 |
| PDIG_84130 | 1.55 |  |  |  | hypothetical protein PDIG_84130 |
| PDIG_59840 | 1.54 |  |  |  | hypothetical protein PDIP_69260 |
| PDIG_82710 | 1.54 | PF07983,PF03198, | X8,Glyco_hydro_72, | X8 domain,Glucanosyltransferase, | 1,3-beta-glucanosyltransferase gel4 |
| PDIG_46700 | 1.53 | PF00083, | Sugar_tr, | Sugar (and other) transporter, | hypothetical protein PDIG_46700 |
| PDIG_51830 | 1.53 | PF07690, | MFS_1, | Major Facilitator Superfamily, | hypothetical protein PDIG_51830 |
| PDIG_85440 | 1.52 | PF05699, | Dimer_Tnp_hAT, | hAT family C-terminal dimerisation region, | hypothetical protein PDIG_86160 |
| PDIG_86160 | 1.52 | PF05699, | Dimer_Tnp_hAT, | hAT family C-terminal dimerisation region, | hypothetical protein PDIG_86160 |
| PDIG_43040 | 1.51 | PF09811, | Yae1_N, | Essential protein Yae1, N terminal, | hypothetical protein PDIG_43040 |
| PDIG_76200 | 1.50 | PF01490, | Aa_trans, | Transmembrane amino acid transporter protein, | hypothetical protein PDIG_76200 |
| PDIG_81100 | 1.50 |  |  |  | hypothetical protein PDIG_81100 |
| PDIG_48000 | 1.49 | PF13816, | Dehydratase_hem, | Haem-containing dehydratase, | hypothetical protein PDIP_57380 |
| PDIG_62410 | 1.48 | PF00083, | Sugar_tr, | Sugar (and other) transporter, | hypothetical protein PDIG_62410 |
| PDIG_57670 | 1.47 | PF03856, | SUN, | Beta-glucosidase (SUN family), | SUN family protein, putative |
| PDIG_29110 | 1.47 | PF04488, | Gly_transf_sug, | Glycosyltransferase sugar-binding region containing DXD motif, | SNARE complex subunit (Vam7) |
| PDIG_81560 | 1.47 |  |  |  | hypothetical protein PDIG_81560 |
| PDIG_72760 | 1.47 |  |  |  | hypothetical protein PDIG_72760 |
| PDIG_54660 | 1.47 | PF13813, | MBOAT_2, | Membrane bound O-acyl transferase family, | hypothetical protein PDIG_54660 |
| PDIG_17220 | 1.46 | PF00328, | His_Phos_2, | Histidine phosphatase superfamily (branch 2), | hypothetical protein PDIP_55120 |
| PDIG_19570 | 1.46 | PF01501, | Glyco_transf_8, | Glycosyl transferase family 8, | hypothetical protein PDIG_19570 |
| PDIG_87790 | 1.45 | PF00724, | Oxidored_FMN, | NADH:flavin oxidoreductase / NADH oxidase family, | 12-oxophytodienoate reductase, putative |
| PDIG_44840 | 1.44 | PF00120, | Gln-synt_C, | Glutamine synthetase, catalytic domain, | hypothetical protein PDE_04219 [Penicillium oxalicum 114-2] |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| PDIG_09300 | 1.44 | PF07690, | MFS_1, | Major Facilitator Superfamily, | Efflux pump antibiotic resistance protein, putative |
| PDIG_83180 | 1.44 | PF00076,PF10378, | RRM_1,RRM, | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain),Putative RRM domain, | Differentiation regulator (Nrd1), putative |
| PDIG_25990 | 1.43 | PF02115, | Rho_GDI, | RHO protein GDP dissociation inhibitor, | hypothetical protein PDIG_25990 |
| PDIG_45710 | 1.43 | PF00005,PF06422,PF14510,PF01061, | ABC_tran,PDR_CDR,ABC_trans_N,ABC2_membrane, | ABC transporter,CDR ABC transporter,ABC-transporter extracellular N-terminal,ABC-2 type transporter, | ABC drug exporter AtrF |
| PDIG_48040 | 1.42 | PF00995, | Sec1, | Sec1 family, | Sec1 family superfamily |
| PDIG_68550 | 1.42 | PF01975, | SurE, | Survival protein SurE, | hypothetical protein PDIP_77840 |
| PDIG_18030 | 1.42 | PF01704, | UDPGP, | UTP--glucose-1-phosphate uridylyltransferase, | UTP-glucose-1-phosphate uridylyltransferase Ugp1, putative |
| PDIG_66590 | 1.41 | PF01979, | Amidohydro_1, | Amidohydrolase family, | Allantoinase Dal1, putative |
| PDIG_63100 | 1.41 | PF00141, | peroxidase, | Peroxidase, | Cytochrome c peroxidase Ccp1, putative |
| PDIG_24730 | 1.40 | PF04909, | Amidohydro_2, | Amidohydrolase, | 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase, putative |
| PDIG_41940 | 1.40 | PF00162, | PGK, | Phosphoglycerate kinase, | Phosphoglycerate kinase |
| PDIG_33290 | 1.39 | PF11735, | CAP59_mtransfer, | Cryptococcal mannosyltransferase 1, | hypothetical protein PDIP_52870 |
| PDIG_65920 | 1.39 | PF00910, | RNA_helicase, | RNA helicase, | Para-Rep C2 |
| PDIG_70000 | 1.38 | PF00320, | GATA, | GATA zinc finger, | GATA transcription factor |
| PDIG_16670 | 1.38 | PF00005,PF00664, | ABC_tran,ABC_membrane, | ABC transporter,ABC transporter transmembrane region, | hypothetical protein PDIP_88180 |
| PDIG_37590 | 1.37 | PF00326, | Peptidase_S9, | Prolyl oligopeptidase family, | Dipeptidyl-peptidase 5 |
| PDIG_32180 | 1.37 | PF00735, | Septin, | Septin, | Septin AspA, putative |
| PDIG_77560 | 1.37 | PF03169, | OPT, | OPT oligopeptide transporter protein, | hypothetical protein PDIG_77560 |
| PDIG_73820 | 1.36 | PF04061, | ORMDL, | ORMDL family, | Unfolded protein response Orm1, putative |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_66140 | 1.36 | PF00025, | Arf, | ADP-ribosylation factor family, | ADP-ribosylation factor 6, putative |
| PDIG_10720 | 1.36 | PF00009,PF03143, | GTP_EFTU,GTP_EFTU_D3, | Elongation factor Tu GTP binding domain,Elongation factor Tu C-terminal domain, | hypothetical protein PDIP_82230 |
| PDIG_75470 | 1.35 | PF02990, | EMP70, | Endomembrane protein 70, | Multispanning membrane protein, putative |
| PDIG_31170 | 1.35 | | | | hypothetical protein PDIP_50750 |
| PDIG_13820 | 1.35 | | | | hypothetical protein PDIP_39470 |
| PDIG_22520 | 1.35 | | | | hypothetical protein PDIG_22520 |
| PDIG_48030 | 1.34 | PF00271,PF12513, | Helicase_C,SUV3_C, | Helicase conserved C-terminal domain,Mitochondrial degradasome RNA helicase subunit C terminal, | Mitochondrial ATP-dependent RNA helicase Suv3, putative |
| PDIG_81970 | 1.34 | PF03447,PF00742, | NAD_binding_3,Homoserine_dh, | Homoserine dehydrogenase, NAD binding domain,Homoserine dehydrogenase, | Homoserine dehydrogenase |
| PDIG_76610 | 1.33 | PF00724, | Oxidored_FMN, | NADH:flavin oxidoreductase / NADH oxidase family, | NADH oxidase |
| PDIG_25020 | 1.33 | PF00169, | PH, | PH domain, | hypothetical protein PDIG_25020 |
| PDIG_90060 | 1.33 | PF14698,PF00206, | ASL_C2,Lyase_1, | Argininosuccinate lyase C-terminal,Lyase, | Argininosuccinate lyase |
| PDIG_62770 | 1.32 | | | | hypothetical protein PDIP_72150 |
| PDIG_03510 | 1.32 | PF00795, | CN_hydrolase, | Carbon-nitrogen hydrolase, | Nitrilase, putative |
| PDIG_81980 | 1.31 | PF11927, | DUF3445, | Protein of unknown function (DUF3445), | hypothetical protein PDIG_81980 |
| PDIG_78350 | 1.31 | PF14604, | SH3_9, | Variant SH3 domain, | hypothetical protein PDIG_78350 |
| PDIG_21170 | 1.31 | PF01263, | Aldose_epim, | Aldose 1-epimerase, | Aldose 1-epimerase, putative |
| PDIG_52240 | 1.31 | PF05277, | DUF726, | Protein of unknown function (DUF726), | hypothetical protein PDIG_52240 |
| PDIG_40960 | 1.31 | PF07690, | MFS_1, | Major Facilitator Superfamily, | MFS transporter (Mch2), putative |
| PDIG_78430 | 1.31 | PF13520, | AA_permease_2, | Amino acid permease, | GabA permease, putative |
| PDIG_25160 | 1.30 | | | | hypothetical protein PDIP_59650 |
| PDIG_77890 | 1.30 | PF12223, | DUF3602, | Protein of unknown function (DUF3602), | hypothetical protein PDIG_77890 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| PDIG_62540 | 1.29 | PF00245, | Alk_phosphatase, | Alkaline phosphatase, | Alkaline phosphatase |
| PDIG_46330 | 1.27 | PF03641, | Lysine_decarbox, | Possible lysine decarboxylase, | hypothetical protein PDIG_46330 |
| PDIG_74520 | 1.27 | PF09333,PF13329, | ATG_C,ATG2_CAD, | Autophagy-related protein C terminal domain,Autophagy-related protein 2 CAD motif, | Autophagy regulatory protein Atg2, putative |
| PDIG_70690 | 1.27 | PF03928, | Haem_degrading, | Haem-degrading, | hypothetical protein PDIP_80010 |
| PDIG_74530 | 1.27 | PF00962, | A_deaminase, | Adenosine/AMP deaminase, | CECR1 family adenosine deaminase, putative |
| PDIG_40560 | 1.26 | PF03169, | OPT, | OPT oligopeptide transporter protein, | Oligopeptide transporter, putative |
| PDIG_25030 | 1.26 | PF00892, | EamA, | EamA-like transporter family, | Integral membrane protein, putative |
| PDIG_57890 | 1.26 | PF00133,PF08264, | tRNA-synt_1,Anticodon_1, | tRNA synthetases class I (I, L, M and V),Anticodon-binding domain of tRNA, | hypothetical protein DACRYDRAFT_20729 [Dacryopinax sp. DJM-731 SS1] |
| PDIG_24940 | 1.25 | PF03171, | 2OG-FeII_Oxy, | 2OG-Fe(II) oxygenase superfamily, | Oxidoreductase, 2OG-Fe(II) oxygenase family, putative |
| PDIG_18840 | 1.25 | PF07217, | Het-C, | Heterokaryon incompatibility protein Het-C, | NIMA-interacting protein TinC |
| PDIG_44850 | 1.25 | PF01274, | Malate_synthase, | Malate synthase, | Malate synthase |
| PDIG_27140 | 1.25 | PF07690, | MFS_1, | Major Facilitator Superfamily, | MFS transporter, putative |
| PDIG_79150 | 1.25 | PF07690, | MFS_1, | Major Facilitator Superfamily, | Protein HOL1, putative |
| PDIG_68500 | 1.24 | PF00171, | Aldedh, | Aldehyde dehydrogenase family, | Aldehyde dehydrogenase, putative |
| PDIG_24560 | 1.24 | PF07690, | MFS_1, | Major Facilitator Superfamily, | Pc21g07950 [Penicillium chrysogenum Wisconsin 54-1255] |
| PDIG_84660 | 1.24 | PF01490, | Aa_trans, | Transmembrane amino acid transporter protein, | Transporter, putative |
| PDIG_10550 | 1.23 | PF00026, | Asp, | Eukaryotic aspartyl protease, | Aspartic protease pep1 |
| PDIG_64720 | 1.23 | PF00503, | G-alpha, | G-protein alpha subunit, | G protein complex alpha subunit GanA |
| PDIG_66000 | 1.22 |  |  |  | pH-response transcription factor pacC/RIM101 |
| PDIG_58180 | 1.22 | PF05577, | Peptidase_S28, | Serine carboxypeptidase S28, | Serine peptidase, family S28, putative |
| PDIG_59830 | 1.22 | PF03950,PF00749, | tRNA-synt_1c_C,tRNA-synt_1c, | tRNA synthetases class I (E and Q), anti-codon binding domain,tRNA synthetases class I (E and Q), | Glutaminyl-tRNA synthetase |

| | | | | | |
|---|---|---|---|---|---|
| | | | | catalytic domain, | |
| PDIG_04490 | 1.22 | | | | hypothetical protein PDIG_04490 |
| PDIG_54050 | 1.22 | PF00735,PF00400, | Septin,WD40, | Septin,WD domain, G-beta repeat, | hypothetical protein THITE_2108385 [Thielavia terrestris NRRL 8126] |
| PDIG_61960 | 1.22 | PF03069, | FmdA_AmdA, | Acetamidase/Formamidase family, | Acetamidase/formamidase family protein |
| PDIG_53280 | 1.21 | PF04502, | DUF572, | Family of unknown function (DUF572), | MRNA splicing protein Yju2 |
| PDIG_79030 | 1.21 | | | | Ammonium transporter (Mep2), putative |
| PDIG_31160 | 1.21 | PF00561, | Abhydrolase_1, | alpha/beta hydrolase fold, | Homoserine O-acetyltransferase, putative |
| PDIG_52420 | 1.21 | PF00328, | His_Phos_2, | Histidine phosphatase superfamily (branch 2), | Phytase |
| PDIG_56670 | 1.21 | PF07690, | MFS_1, | Major Facilitator Superfamily, | MFS allantoate transporter, putative |
| PDIG_09390 | 1.20 | | | | hypothetical protein PDIG_09390 |
| PDIG_33490 | 1.20 | PF04982, | HPP, | HPP family, | HPP family protein |
| PDIG_32110 | 1.20 | PF00561, | Abhydrolase_1, | alpha/beta hydrolase fold, | hypothetical protein PDIP_51690 |
| PDIG_44830 | 1.20 | PF13561, | adh_short_C2, | Enoyl-(Acyl carrier protein) reductase, | Short-chain dehydrogenase/reductase family protein, putative |
| PDIG_68650 | 1.20 | PF01266, | DAO, | FAD dependent oxidoreductase, | hypothetical protein PDIP_77940 |
| PDIG_68180 | 1.19 | PF04982, | HPP, | HPP family, | HPP family protein |
| PDIG_67510 | 1.19 | PF01597, | GCV_H, | Glycine cleavage H-protein, | Glycine cleavage system H protein |
| PDIG_15680 | 1.19 | | | | hypothetical protein PDIG_15680 |
| PDIG_43170 | 1.19 | PF05572, | Peptidase_M43, | Pregnancy-associated plasma protein-A, | Extracellular metalloprotease [Penicillium digitatum Pd1] |
| PDIG_76030 | 1.19 | PF00225, | Kinesin, | Kinesin motor domain, | Kinesin family protein (KinA), putative |
| PDIG_67780 | 1.19 | PF09286,PF00082, | Pro-kuma_activ,Peptidase_S8, | Pro-kumamolisin, activation domain,Subtilase family, | Tripeptidyl-peptidase sed2 |
| PDIG_03210 | 1.19 | PF00735, | Septin, | Septin, | hypothetical protein PDIP_41870 |
| PDIG_31760 | 1.19 | PF07855, | DUF1649, | Protein of unknown function (DUF1649), | hypothetical protein AN2280.2 [Aspergillus |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
|  |  |  |  |  | nidulans FGSC A4] |
| PDIG_02540 | 1.18 | PF03456,PF02141,PF03455, | uDENN,DENN,dDENN, | uDENN domain,DENN (AEX-3) domain,dDENN domain, | hypothetical protein PDIG_02540 |
| PDIG_13280 | 1.18 | PF08303,PF08302,PF09511, | tRNA_lig_kinase,tRNA_lig_CPD,RNA_lig_T4_1, | tRNA ligase kinase domain,Fungal tRNA ligase phosphodiesterase domain,RNA ligase, | TRNA ligase |
| PDIG_09960 | 1.18 | PF00668,PF00550,PF00501, | Condensation,PP-binding,AMP-binding, | Condensation domain,Phosphopantetheine attachment site,AMP-binding enzyme, | HC-toxin synthetase |
| PDIG_24450 | 1.18 | PF01008, | IF-2B, | Initiation factor 2 subunit family, | hypothetical protein PDIP_58930 |
| PDIG_69380 | 1.18 | PF13302, | Acetyltransf_3, | Acetyltransferase (GNAT) domain, | hypothetical protein PDIP_78670 |
| PDIG_89580 | 1.18 | PF04082, | Fungal_trans, | Fungal specific transcription factor domain, | C6 transcription factor, putative |
| PDIG_67970 | 1.18 | PF00545, | Ribonuclease, | ribonuclease, | hypothetical protein PDIP_77270 |
| PDIG_69240 | 1.16 |  |  |  | hypothetical protein PDIP_78530 |
| PDIG_04450 | 1.16 | PF14823,PF14824,PF13241,PF00590, | Sirohm_synth_C,Sirohm_synth_M,NAD_binding_7,TP_methylase, | Sirohaem biosynthesis protein C-terminal,Sirohaem biosynthesis protein central,Putative NAD(P)-binding,Tetrapyrrole (Corrin/Porphyrin) Methylases, | Siroheme synthase, putative |
| PDIG_80280 | 1.15 | PF09816, | EAF, | RNA polymerase II transcription elongation factor, | hypothetical protein PDIG_80280 |
| PDIG_44730 | 1.15 | PF14661, | HAUS6_N, | HAUS augmin-like complex subunit 6 N-terminus, | hypothetical protein PDIG_44730 |
| PDIG_29320 | 1.15 | PF01764, | Lipase_3, | Lipase (class 3), | Autophagy related lipase Atg15, putative |
| PDIG_14140 | 1.15 | PF03198, | Glyco_hydro_72, | Glucanosyltransferase, | 1,3-beta-glucanosyltransferase gel2 |
| PDIG_22110 | 1.15 | PF01450,PF07991, | IlvC,IlvN, | Acetohydroxy acid isomeroreductase, catalytic domain,Acetohydroxy acid isomeroreductase, NADPH-binding domain, | Ketol-acid reductoisomerase |

| | | | | | |
|---|---|---|---|---|---|
| PDIG_22850 | 1.14 | PF00884,PF04987, | Sulfatase,PigN, | Sulfatase,Phosphatidylinositolglycan class N (PIG-N), | GPI ethanolamine phosphate transferase 1 |
| PDIG_47340 | 1.14 | PF04768, | NAT, | NAT, N-acetyltransferase, of N-acetylglutamate synthase, | Amino-acid acetyltransferase, mitochondrial |
| PDIG_58340 | 1.14 | PF05291, | Bystin, | Bystin, | RRNA processing protein Bystin, putative |
| PDIG_35580 | 1.13 | PF10415,PF00206, | FumaraseC_C,Lyase_1, | Fumarase C C-terminus,Lyase, | Fumarate hydratase |
| PDIG_17480 | 1.13 | PF00854, | PTR2, | POT family, | MFS peptide transporter Ptr2, putative |
| PDIG_80900 | 1.13 | PF10233, | Cg6151-P, | Uncharacterized conserved protein CG6151-P, | Clathrin-coated vesicle protein, putative |
| PDIG_85660 | 1.13 | PF00884, | Sulfatase, | Sulfatase, | hypothetical protein PDIG_85660 |
| PDIG_86490 | 1.12 | PF03372, | Exo_endo_phos, | Endonuclease/Exonuclease/phosphatase family, | Sphingomyelinase family protein, putative |
| PDIG_78380 | 1.12 | PF03169, | OPT, | OPT oligopeptide transporter protein, | Oligonucleotide transporter |
| PDIG_19560 | 1.12 | PF12859, | ANAPC1, | Anaphase-promoting complex subunit 1, | 20S cyclosome subunit (APC1/BimE), putative |
| PDIG_33890 | 1.12 | PF01406, | tRNA-synt_1e, | tRNA synthetases class I (C) catalytic domain, | Cysteinyl-tRNA synthetase |
| PDIG_17390 | 1.12 | PF03676, | UPF0183, | Uncharacterised protein family (UPF0183), | hypothetical protein PDIP_55290 |
| PDIG_89550 | 1.12 | PF03876,PF00575, | SHS2_Rpb7-N,S1, | SHS2 domain found in N terminus of Rpb7p/Rpc25p/MJ0397,S1 RNA binding domain, | Pc12g03390 [Penicillium chrysogenum Wisconsin 54-1255] |
| PDIG_46580 | 1.12 | PF01926,PF12631,PF10396, | MMR_HSR1,MnmE_helical,TrmE_N, | 50S ribosome-binding GTPase,MnmE helical domain,GTP-binding protein TrmE N-terminus, | Mitochondrial GTPase (Mss1), putative |
| PDIG_30890 | 1.12 | PF00202, | Aminotran_3, | Aminotransferase class-III, | 4-aminobutyrate transaminase |
| PDIG_84170 | 1.11 | PF00083, | Sugar_tr, | Sugar (and other) transporter, | MFS myo-inositol transporter, putative |
| PDIG_27090 | 1.11 | PF05653, | Mg_trans_NIPA, | Magnesium transporter NIPA, | hypothetical protein PDIP_61530 |
| PDIG_57150 | 1.11 | | | | hypothetical protein PDIP_66690 |
| PDIG_76110 | 1.11 | PF02872,PF0 | 5_nucleotid_C,Met | 5'-nucleotidase, C-terminal domain,Calcineurin-like | 5&apos;-nucleotidase, putative |

| | | | | | |
|---|---|---|---|---|---|
| | | 0149, | allophos, | phosphoesterase, | |
| PDIG_39770 | 1.11 | | | | hypothetical protein PDIG_39770 |
| PDIG_61880 | 1.11 | | | | Allergen Asp f 4 |
| PDIG_34910 | 1.11 | PF02265, | S1-P1_nuclease, | S1/P1 Nuclease, | Nuclease PA3, putative |
| PDIG_15690 | 1.10 | | | | hypothetical protein PDIG_15690 |
| PDIG_63150 | 1.10 | PF12063,PF00069, | DUF3543,Pkinase, | Domain of unknown function (DUF3543),Protein kinase domain, | Serine/threonine protein kinase (Pdd7p), putative |
| PDIG_69990 | 1.10 | PF06813, | Nodulin-like, | Nodulin-like, | hypothetical protein PDIP_79290 |
| PDIG_62340 | 1.09 | PF08229, | SHR3_chaperone, | ER membrane protein SH3, | Secretory component protein shr3, putative |
| PDIG_59710 | 1.09 | PF00677, | Lum_binding, | Lumazine binding domain, | Riboflavin synthase, alpha subunit |
| PDIG_06560 | 1.09 | PF00171, | Aldedh, | Aldehyde dehydrogenase family, | Aldehyde dehydrogenase |
| PDIG_88650 | 1.09 | PF10397,PF00206, | ADSL_C,Lyase_1, | Adenylosuccinate lyase C-terminus,Lyase, | Adenylosuccinate lyase Ade13, putative |
| PDIG_30980 | 1.09 | PF00117,PF00988, | GATase,CPSase_sm_chain, | Glutamine amidotransferase class-I,Carbamoyl-phosphate synthase small chain, CPSase domain, | Carbamoyl-phosphate synthase, small subunit |
| PDIG_14060 | 1.08 | | | | hypothetical protein PDIP_39710 |
| PDIG_28630 | 1.08 | PF00793, | DAHP_synth_1, | DAHP synthetase I family, | Phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited |
| PDIG_84840 | 1.08 | PF12929, | Mid1, | Stretch-activated Ca2+-permeable channel component, | Calcium channel subunit Mid1 |
| PDIG_15670 | 1.08 | | | | hypothetical protein PDIG_15670 |
| PDIG_36020 | 1.07 | PF00012, | HSP70, | Hsp70 protein, | Hsp70 family chaperone Lhs1/Orp150, putative |
| PDIG_66320 | 1.07 | PF00152, | tRNA-synt_2, | tRNA synthetases class II (D, K and N), | Aspartyl-tRNA synthetase Dps1, putative |