

Matching the proteome to the genome

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Supplementary Table 3. *In silico* identified *P. chrysogenum* PTS1 and PTS2 proteins

ORF code	Description of putative <i>P. chrysogenum</i> ORF		
		Species	Code
1. Secondary metabolism			
Pc16g03860	Acetylase / siderophore biosynthesis protein Sid3	<i>Ajellomyces capsulatus</i>	Sid3
Pc22g20380	Acetyltransferase SidF	<i>Penicillium marneffeii</i>	SidF
Pc21g21370	Acyl-coenzyme A:isopenicillin N acyltransferase	<i>Penicillium chrysogenum</i>	PenDE
Pc21g16080	Putative HypA-like protein / oxidase required for aflatoxin biosynthesis	<i>Neosartorya fischeri</i>	NFIA_038780
Pc22g13680	Isopenicillin N-CoA epimerase	<i>Acremonium chrysogenum</i>	CefD2
Pc22g24630	Putative isopenicillin N-CoA epimerase, partial	<i>Acremonium chrysogenum</i>	CefD2
Pc20g13500	Isopenicillin N-CoA synthetase	<i>Acremonium chrysogenum</i>	CefD1
Pc22g14900	Phenylacetyl-CoA ligase PclA	<i>Penicillium chrysogenum</i>	PclA
Pc22g20270	Phenylacetyl-CoA ligase PhIB	<i>Penicillium chrysogenum</i>	PhIB
Pc22g00460	Protein with dehydrogenase domain of non-ribosomal peptide synthetases	<i>Aspergillus niger</i>	An06g01070
2. C-metabolism: Beta oxidation related proteins			
Acyl CoA ligases/synthetases			
Pc13g01890	Putative acyl-CoA synthetase	<i>Aspergillus niger</i>	An18g03800
Pc13g05130	Putative acyl-CoA synthetase	<i>Aspergillus oryzae</i>	AO090011000917
Pc13g14420	Putative acyl-CoA synthetase	<i>Aspergillus terreus</i>	ATEG_05325
Pc15g00420	Putative bifunctional fatty acid transporter/acyl-CoA synthetase	<i>Aspergillus fumigatus</i>	AFUA_2G11360
Pc06g01160	Putative 4-coumarate-CoA ligase	<i>Aspergillus terreus</i>	ATEG_10234
Pc13g12270	Putative 4-coumarate-CoA ligase	<i>Neosartorya fischeri</i>	NFIA_012410
Pc21g20650	Putative 4-coumarate-CoA ligase	<i>Aspergillus nidulans</i>	AN9216.2
Pc21g22010	Putative 4-coumarate-CoA ligase	<i>Aspergillus fumigatus</i>	AFUB_025970
Pc22g24780	Putative 4-coumarate-CoA ligase	<i>Neosartorya fischeri</i>	NFIA_072630
Pc21g09470	Putative feruloyl-CoA synthetase	<i>Aspergillus nidulans</i>	AN5272.2
Pc21g23730	Putative feruloyl-CoA synthetase	<i>Aspergillus fumigatus</i>	AFUA_1G17190
Pc12g05520	Long-chain-fatty-acid-CoA ligase Faa2	<i>Saccharomyces cerevisiae</i>	Faa2
Pc20g10840	Putative long-chain-fatty-acid-CoA ligase	<i>Neurospora crassa</i>	NCU06063
Pc18g05710	Putative long-chain fatty acid transporter /acyl CoA synthetase	<i>Aspergillus fumigatus</i>	AFUA_6G07270
Acyl-CoA oxidases and dehydrogenases			
Pc22g07740	Putative acyl-CoA oxidase	<i>Aspergillus terreus</i>	ATEG_06082
Pc06g01180	Putative acyl-CoA dehydrogenase	<i>Glomus intraradices</i>	AAK63186
Pc14g00140	Putative acyl-CoA dehydrogenase	<i>Aspergillus nidulans</i>	AN3880_2
Pc21g09440	Putative acyl-CoA dehydrogenase	<i>Aspergillus nidulans</i>	AN5270_2

Pc21g17590 Putative acyl-CoA dehydrogenase
Pc21g19000 Putative acyl-CoA dehydrogenase
Pc12g08530 Putative long-chain acyl-CoA dehydrogenase
Pc16g07560 Putative long chain acyl-CoA dehydrogenase
Pc13g14410 Putative palmitoyl-CoA oxidase
Pc20g01800 Putative palmitoyl-CoA oxidase
Pc13g11930 Putative very-long-chain acyl-CoA dehydrogenase
Pc22g25150 Putative very-long-chain acyl-CoA dehydrogenase

Multifunctional enzyme and related proteins

Pc13g02710 Putative beta-oxidation protein/dehydratase
Pc21g21810 Putative levodione reductase / short chain dehydrogenase
Pc21g16840 Putative NAD+-dependent 15-hydroxyprostaglandin dehydrogenase
Pc16g14230 Putative NADPH-dependent beta-ketoacyl reductase
Pc22g03680 Putative NADPH-dependent beta-ketoacyl reductase
Pc22g15030 Peroxisomal 2,4-dienoyl-CoA reductase Sps19
Pc13g05940 Trifunctional enzyme Fox-2

Thiolasases, lipid transfer proteins and related proteins

Pc20g15010 Carnitine O-acetyltransferase
Pc20g12470 Delta3-cis-delta2-trans-enoyl-CoA isomerase Eci1
Pc12g01170 Putative enoyl-CoA hydratase/isomerase family protein
Pc12g14790 Putative enoyl-CoA hydratase/isomerase family protein
Pc13g14430 Putative enoyl-CoA hydratase/isomerase family protein
Pc13g15840 Putative enoyl-CoA hydratase/isomerase family protein
Pc22g20370 Putative enoyl-CoA hydratase/isomerase family protein
Pc22g22390 Putative enoyl-CoA hydratase/isomerase family protein
Pc22g25120 Putative enoyl-CoA hydratase/isomerase family protein
Pc21g09480 3-hydroxy-3-methylglutaryl CoA lyase HlyA
Pc13g12930 Putative 3-ketoacyl-CoA thiolase
Pc15g00410 Putative 3-ketoacyl-CoA thiolase
Pc22g06820 3-ketoacyl-CoA thiolase Pthik
Pc22g01300 Lipid transfer protein Scp2
Pc22g07280 Putative peroxisomal acyl-CoA thioesterase
Pc20g15660 Putative sterol carrier protein-2
Pc22g17070 Putative sterol carrier protein-2

3. Other C-metabolism

Pc12g09950 Alcohol oxidase Aox

Aspergillus niger An17g01150
Aspergillus fumigatus AFUA_2G16630
Neosartorya fischeri NFIA_003000
Aspergillus niger An04g03290
Aspergillus terreus ATEG_06288
Aspergillus fumigatus AFUB_091680
Aspergillus oryzae AO090005000482
Aspergillus oryzae AO090005000482

Aspergillus clavatus ACLA_004600
Neosartorya fischeri NFIA_056910
Aspergillus fumigatus AFUB_056830
Neosartorya fischeri NFIA_010890
Aspergillus terreus ATEG_03235
Saccharomyces cerevisiae Sps19
Neurospora crassa Fox-2

Candida tropicalis CT-Cat
Saccharomyces cerevisiae Eci1
Aspergillus oryzae AO090012000429
Neosartorya fischeri NFIA_022780
Aspergillus nidulans AN6767.2
Neosartorya fischeri NFIA_062740
Aspergillus niger An03g03550
Aspergillus fumigatus AFUA_1G01890
Phaeosphaeria nodorum SNOG_00491
Aspergillus nidulans HlyA
Aspergillus fumigatus AFUA_1G12650
Aspergillus terreus ATEG_01444
Podospira anserina Pthik
Yarrowia lipolytica Scp2
Aspergillus fumigatus AFUA_8G06680
Aspergillus oryzae O090003001431
Aspergillus oryzae AO090023000951

Penicillium chrysogenum Aox

Pc18g03000 Aldose 1-epimerase
 Pc12g05400 Citrate synthase CitA
 Pc06g01600 Putative FAD-dependent L-sorbose dehydrogenase / GMC oxidoreductase
 Pc22g10020 Putative FAD-dependent alcohol dehydrogenase / GMC oxidoreductase
 Pc12g13290 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
 Pc12g14280 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
 Pc21g12160 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
 Pc21g17810 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
 Pc22g00300 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
 Pc22g11470 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
 Pc22g18190 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
 Pc16g07070 Formate oxidase Fod1
 Pc18g01220 Fructose-bisphosphate aldolase Fba1
 Pc20g03330 Glucose-6-phosphate 1-dehydrogenase GsdA
 Pc18g01590 Putative glycolate oxidase-like protein / FMN-dependent dehydrogenase
 Pc22g19270 Putative glycolate oxidase-like protein / FMN-dependent dehydrogenase
 Pc21g23700 Long-chain-fatty-acid alcohol oxidase
 Pc20g13550 Malate synthase AcuE
 Pc12g11930 2-methylcitrate dehydratase, involved in propionate catabolism
 Pc20g03610 NADP-dependent isocitrate dehydrogenase lcdA
 Pc13g04510 NADP-dependent malate dehydrogenase MaeA
 Pc22g15170 Putative propionyl-CoA carboxylase
 Pc22g15180 Putative pyruvate carboxylase like protein
 Pc21g03400 Triose-phosphate-isomerase TpiA
 Pc21g22360 Vanillyl-alcohol oxidase VaoA

4. N-metabolism

Pc13g06300 Putative amidase
 Pc16g14240 Putative amidase
 Pc22g19440 Aspartate transaminase Aat2
 Pc13g03350 Putative copper amine oxidase
 Pc13g15940 Putative copper amine oxidase
 Pc16g11200 Putative copper amine oxidase
 Pc22g14860 Copper amine oxidase AMO
 Pc22g17240 Putative copper amine oxidase
 Pc14g00970 Putative D-amino-acid oxidase
 Pc18g01860 Putative D-amino-acid oxidase

Saccharomyces cerevisiae Ymr099c
Aspergillus niger CitA
Aspergillus clavatus ACLA_062810
Neosartorya fischeri NFIA_096800
Aspergillus terreus ATEG_06029
Aspergillus clavatus ACLA_055500
Magnaporthe grisea MGG_14264
Aspergillus oryzae AO090012000974
Pyrenophora tritici-repentis PTRG_08985
Aspergillus oryzae AO090012000974
Aspergillus oryzae AO090023000884
Debaryomyces vanriijiae Fod1
Saccharomyces cerevisiae Fba1
Aspergillus nidulans GsdA
Aspergillus oryzae AO090138000044
Aspergillus terreus ATEG_08297
Candida cloacae Fao1
Aspergillus nidulans AcuE
Salmonella enterica PrpD
Aspergillus niger lcdA
Aspergillus nidulans MaeA
Aspergillus niger An15g02830
Aspergillus niger An15g02820
Aspergillus nidulans TpiA
Penicillium simplicissimum VaoA

Aspergillus niger An14g00670
Aspergillus oryzae AO090003000475
Saccharomyces cerevisiae Aat2
Aspergillus nidulans AN1586.2
Aspergillus niger An09g01550
Aspergillus fumigatus AFUB_047750
Hansenula polymorpha AMO
Aspergillus oryzae AO090138000079
Chaetomium globosum CHGG_09439
Phaeosphaeria nodorum SNOG_08645

Pc20g06660 Putative D-amino-acid oxidase
 Pc21g05590 Putative D-amino-acid oxidase
 Pc13g04270 Dimethylglycine oxidase
 Pc16g07600 Putative FAD dependent oxidoreductase
 Pc16g11910 Putative FAD dependent oxidoreductase
 Pc18g03220 Putative FAD-dependent oxidoreductase
 Pc20g14920 Putative FAD dependent oxidoreductase
 Pc22g23700 Putative FAD dependent oxidoreductase, partial
 Pc12g09740 Putative fructosyl amine oxidase
 Pc13g01380 Putative fructosyl amine oxidase
 Pc16g11790 Putative fructosyl amine oxidase
 Pc21g09780 Putative fructosyl amine oxidase
 Pc22g00060 Putative fructosyl amine oxidase
 Pc22g23350 Putative fructosyl amine oxidase
 Pc13g09740 Fructosyl peptide oxidase FpoxE
 Pc12g13480 Putative glycine/D-amino acid oxidase
 Pc21g21120 Putative monoamine oxidase N
 Pc21g07490 Putative OHCU decarboxylase involved in purine catabolism
 Pc20g10700 Putative sarcosine oxidase / FAD-dependent oxidoreductase
 Pc22g20960 Urate oxidase Uaz
 Pc20g09430 Ureidoglycolate hydrolase Dal3

5. Antioxidants

Pc22g00860 Putative ascorbate-peroxidase
 Pc22g21240 Catalase CatC
 Pc16g07060 Putative catalase
 Pc12g13740 Catalase/oxidase KatG
 Pc13g11580 Putative epoxide hydrolase
 Pc21g19510 Epoxide hydrolase

6. Proteases/hydrolases/esterases

Pc13g09070 Putative esterase with alpha/beta hydrolase fold
 Pc21g14590 Insulin-degrading enzyme / a factor processing peptidase Ste23
 Pc06g01220 Putative lipase / hydrolase
 Pc18g03470 Lysine aminopeptidase ApsA
 Pc22g02620 Monoglyceride lipase
 Pc21g06860 Peroxisomal Lon protease
 Pc13g14580 Putative thioesterase

Aspergillus terreus ATEG_09513
Aspergillus nidulans AN0174.2
Arthrobacter globiformis Dmg
Neosartorya fischeri NFIA_059350
Aspergillus clavatus ACLA_061930
Aspergillus oryzae AO090038000193
Aspergillus nidulans AN7917.2
Phaeosphaeria nodorum SNOG_07579
Aspergillus nidulans AN2786.2
Aspergillus terreus ATEG_09887
Aspergillus terreus ATEG_07526
Aspergillus fumigatus AFUB_019110
Aspergillus oryzae AO090102000413
Aspergillus niger An08g01300
Eupenicillium terrenum FpoxE
Aspergillus terreus ATEG_07330
Aspergillus oryzae AO090023000011
Aspergillus clavatus ACLA_015330
Gibberella zeae FG02924.1
Aspergillus flavus Uaz
Saccharomyces cerevisiae Dal3

Aspergillus niger An08g08720
Aspergillus nidulans CatC
Aspergillus clavatus ACLA_077960
Penicillium marneffeii KatG
Aspergillus clavatus ACLA_022580
Rattus norvegicus cEH

Aspergillus clavatus ACLA_039450
Saccharomyces cerevisiae Ste23
Aspergillus terreus ATEG_10239
Aspergillus niger ApsA
Mus musculus Mgl1
Myxococcus xanthus LonD
Aspergillus terreus ATEG_04977

Pc21g01650 Putative thioesterase
Pc20g09660 Putative toxin biosynthesis protein / hydrolase
Pc22g05640 Putative toxin biosynthesis protein / hydrolase
Pc22g15400 Putative toxin biosynthesis protein / hydrolase

7. Peroxins and structural proteins

Pc13g04370 Intraperoxisomal peroxin Pex8p
Pc21g00970 Woronin body protein Hex1

8. Other enzymes

Pc20g15650 Putative acetyl-CoA acetyltransferase, partial
Pc18g05540 Putative alcohol dehydrogenase, class IV
Pc21g12260 Putative alcohol dehydrogenase, class V
Pc14g01040 Putative aldehyde dehydrogenase
Pc18g02760 Putative aldehyde dehydrogenase
Pc22g17230 Putative aldehyde dehydrogenase
Pc22g19300 Putative aldehyde dehydrogenase
Pc22g24860 Putative aldehyde dehydrogenase
Pc13g01530 Putative aldo/keto reductase
Pc22g25570 Putative aminoglycoside phosphotransferase
Pc13g12580 Putative aminotransferase
Pc20g13410 Putative aminotransferase
Pc12g11190 Argininosuccinate synthase Arg1
Pc22g10030 Betaine-aldehyde dehydrogenase
Pc15g01190 Putative catechol dioxygenase
Pc20g13690 Putative CoA-binding protein
Pc14g00560 Conserved hypothetical protein
Pc17g00720 Conserved hypothetical protein
Pc20g08300 Conserved hypothetical protein
Pc21g04910 Conserved hypothetical protein
Pc21g07210 Conserved hypothetical protein
Pc21g16040 Conserved hypothetical protein
Pc22g11520 Conserved hypothetical protein
Pc22g16280 Conserved hypothetical protein
Pc22g25190 Conserved hypothetical protein
Pc23g00390 Conserved hypothetical protein
Pc21g16710 Conserved protein with double-stranded beta helix domain
Pc21g22060 Conserved protein with DUF1446 domain of unknown function

Aspergillus oryzae AO090102000229
Neosartorya fischeri NFIA_103960
Aspergillus terreus ATEG_03116
Penicillium marneffeii PMAA_001860

Penicillium chrysogenum Pex8p
Aspergillus nidulans Hex1

Aspergillus oryzae AO090005000522
Aspergillus terreus ATEG_03722
Aspergillus clavatus ACLA_065540
Pyrenophora tritici-repentis PTRG_07120
Aspergillus terreus ATEG_05338
Gibberella zeae FG02273.1
Aspergillus terreus ATEG_08300
Aspergillus oryzae AO090701000318
Aspergillus terreus ATEG_09599
Aspergillus fumigatus AFUA_1G02880
Aspergillus niger An04g01140
Aspergillus terreus ATEG_07103
Saccharomyces cerevisiae Arg1
Escherichia coli BetB
Aspergillus niger An13g02000
Aspergillus oryzae AO090026000481
Aspergillus oryzae AO090124000070
Aspergillus terreus ATEG_04860
Aspergillus oryzae AO090020000033
Aspergillus clavatus ACLA_005650
Aspergillus oryzae AO090120000325
Aspergillus clavatus ACLA_001800
Aspergillus terreus ATEG_02643
Aspergillus niger An03g04610
Aspergillus clavatus ACLA_061100
Aspergillus clavatus ACLA_077930
Aspergillus oryzae AO090038000022
Neosartorya fischeri NFIA_057110

Pc13g05220	Putative cytochrome b5	<i>Neosartorya fischeri</i>	NFIA_083440
Pc20g15250	Putative dehydrogenase	<i>Neosartorya fischeri</i>	NFIA_055630
Pc22g20320	Putative dehydrogenase	<i>Aspergillus nidulans</i>	AN5984.2
Pc13g08330	3-dehydroshikimate dehydratase Qa-4	<i>Neurospora crassa</i>	Qa-4
Pc21g11780	Putative 4-hydroxyphenylpyruvate dioxygenase	<i>Neosartorya fischeri</i>	NFIA_047400
Pc21g14640	Putative dephospho-CoA kinase	<i>Saccharomyces cerevisiae</i>	Ydr196c
Pc21g05490	Dihydroxyacetone phosphate acyltransferase	<i>Homo sapiens</i>	DHAPAT
Pc13g07430	Putative dioxygenase	<i>Neosartorya fischeri</i>	NFIA_108240
Pc22g24590	Putative FAD binding domain protein	<i>Aspergillus clavatus</i>	ACLA_004100
Pc20g04300	Putative flavin-containing monooxygenase	<i>Aspergillus oryzae</i>	AO090005001317
Pc14g01270	Putative fumarylacetoacetate hydrolase family protein	<i>Aspergillus niger</i>	An18g06670
Pc20g15670	Glutathione-dependent formaldehyde-activating enzyme	<i>Paracoccus denitrificans</i>	Gfa
Pc22g05280	Putative histidine triad family hydrolase	<i>Ajellomyces capsulatus</i>	HCAG_01479
Pc16g05060	3-hydroxy-3-methylglutaryl coenzyme A reductase	<i>Sulfolobus solfataricus</i>	HmgA
Pc21g23650	D-lactate dehydrogenase	<i>Escherichia coli</i>	LdhA
Pc20g10430	D-mandelate dehydrogenase	<i>Rhodotorula graminis</i>	Dmdh
Pc21g08790	Putative NADP-dependent oxidoreductase	<i>Aspergillus terreus</i>	ATEG_04342
Pc21g11670	Putative NADPH:quinone reductase / Zn-dependent oxidoreductase	<i>Neosartorya fischeri</i>	NFIA_115150
Pc16g10070	Putative 2-nitropropane dioxygenase family oxidoreductase	<i>Aspergillus terreus</i>	ATEG_03597
Pc22g14270	Putative 2-nitropropane dioxygenase family oxidoreductase	<i>Aspergillus terreus</i>	ATEG_06490
Pc22g19490	Putative 2-nitropropane dioxygenase family oxidoreductase	<i>Aspergillus oryzae</i>	AO090011000650
Pc22g12040	Putative nitroreductase	<i>Aspergillus terreus</i>	ATEG_00752
Pc20g09670	Putative phosphotransferase	<i>Aspergillus oryzae</i>	AO090005000779
Pc13g02990	Protein phosphatase 2C Ptc5	<i>Saccharomyces cerevisiae</i>	Ptc5
Pc20g01980	Putative 2-polyprenyl-6-methoxyphenol hydroxylase	<i>Neosartorya fischeri</i>	NFIA_057170
Pc21g02970	Putative 2-polyprenyl-6-methoxyphenol hydroxylase	<i>Aspergillus oryzae</i>	AO090012000279
Pc13g06370	Protein weakly similar to ethanolamine utilization protein	<i>Phaeosphaeria nodorum</i>	SNOG_02939
Pc22g16620	Protein weakly similar to ethanolamine utilization protein	<i>Gibberella zeae</i>	FG03165.1
Pc13g12080	Putative protein with alpha/beta hydrolase fold	<i>Neosartorya fischeri</i>	NFIA_012240
Pc13g02660	Protein with Cupin barrel domain	<i>Aspergillus niger</i>	An11g08750
Pc16g02530	Protein with pentatricopeptide repeat	<i>Aspergillus terreus</i>	ATEG_08561
Pc13g10320	Putative short chain dehydrogenase	<i>Aspergillus terreus</i>	ATEG_04584
Pc16g08670	C-8 sterol isomerase Erg-1	<i>Neurospora crassa</i>	Erg-1
Pc22g24620	Putative sugar phosphate isomerases/epimerase	<i>Aspergillus terreus</i>	ATEG_08391
Pc13g03610	Putative YcaC-related amidohydrolase	<i>Aspergillus nidulans</i>	AN6066.2
Pc22g13390	Putative Zn-dependent alcohol dehydrogenase	<i>Aspergillus terreus</i>	ATEG_01304

Ortholog / Highest scoring Blast homolog description	Expect value	Putative PTS1	Putative PTS2
acetylase / siderophore biosynthesis protein	3e-129	sLKL*	
acetyltransferase	0.0	nAKL*	
acyl-coenzyme A:isopenicillin N acyltransferase	0.0	nARL*	
putative HypA-like protein	6e-172	qAHI*	
isopenicillin N-CoA epimerase	2e-139	kSKI*	
isopenicillin N-CoA epimerase	1e-13	aAKI*	
isopenicillin N-CoA synthetase	5e-164	sVRL*	
phenylacetyl-CoA ligase	0.0	gSKI*	
phenylacetyl-CoA ligase	0.0	kAKL*	
hypothetical protein	5e-149	kARI*	
acyl-CoA synthase like protein	0.0		6 / sRLsgllgHF
acyl-coenzyme A synthetase	0.0	kSKL*	
AMP-binding enzyme	0.0	kARL*	
bifunctional fatty acid transporter/acyl-CoA synthetase	0.0	kAKI*	
acyl-coenzyme A synthetases/AMP-(fatty) acid ligase	0.0	qTKI*	
4-coumarate-CoA ligase	0.0	tAKL*	
acyl-CoA synthetase	0.0	kARL*	
putative phenylacetyl-CoA ligase	9-e-138	pSKL*	
acyl-CoA synthetase	0.0	kAKL*	
acyl-CoA synthetase	0.0	rAKL*	
long-chain-fatty-acid-CoA ligase	0.0		8 / qRLqqtIsHV
long-chain-fatty-acid--CoA ligase	3e-108	kAKL*	
hypothetical protein	7e-137	aGKL*	
long-chain fatty acid transporter	0.0	qVRL*	
predicted protein	0.0	rAKL*	
probable acyl-CoA dehydrogenase	1e-85	sAKI*	
hypothetical protein	0.0	kARI*	
hypothetical protein	0.0	qSKL*	

acyl-CoA dehydrogenase like protein	0.0	kSHL*	
acyl-CoA dehydrogenase	0.0	qSKV*	
putative acyl-CoA dehydrogenase	0.0	nAKI*	
hypothetical protein	0.0	gMKL*	
conserved hypothetical protein	0.0	ISKL*	
putative fatty-acyl coenzyme A oxidase (Pox1)	0.0	kSKL*	
very-long-chain acyl-CoA dehydrogenase	0.0	sSKL*	
very-long-chain acyl-CoA dehydrogenase	0.0	gSKL*	
putative peroxisomal dehydratase	6e-141	kSKL*	
3-oxoacyl-(acyl-carrier-protein) reductase	7e-149		7 / qRLqalskQL
NAD-dependent 15-hydroxyprostaglandin dehydrogenase	3e-140	IPKL*	
oxidoreductase, short-chain dehydrogenase/reductase family	3e-130	kGRL*	
conserved hypothetical protein	6e-134	sAKL*	
peroxisomal 2,4-dienoyl-CoA reductase	3e-69	kSKL*	
trifunctional protein of beta-oxidation	0.0	kAKL*	
carnitine acetyl transferase	2e-153	kPKL*	
Peroxisomal delta3,delta2-enoyl-CoA isomerase	1e-41	rHKL*	
hypothetical protein	1e-115	kAKL*	
enoyl-CoA hydratase/isomerase family protein	1e-119	kAKL*	
hypothetical protein	1e-120	kVKI*	
enoyl-CoA hydratase/isomerase family protein	3e-128	fEKL*	
hypothetical protein	2e-133	nSKL*	
enoyl-CoA hydratase/isomerase family protein	4e-123	pSKL*	
hypothetical protein	9e-94	hSKL*	
3-hydroxy-3-methylglutaryl Coenzyme A lyase	0.0	kSKL*	
3-ketoacyl-CoA ketothiolase	0.0		4 / dRLssllsHL
3-ketoacyl-CoA thiolase	0.0		6 / qRLnsvanQL
peroxisomal 3-keto-acyl-CoA thiolase	0.0		6 / qRLsqvssHF
Fatty acid-binding protein	9e-29	gAKL*	
acyl-CoA thioesterase	2-e108	kVKL*	
hypothetical protein	0.0	kARI*	
hypothetical protein	0.0	IARF*	
alcohol oxidase	0.0	ISRL*	

Glucose-6-phosphate 1-epimerase	3e-54	kSRL*	
citrate synthase	0.0	gAKL*	
putative GMC oxidoreductase	0.0	yPRI*	
putative GMC oxidoreductase	0.0	qPRL*	
conserved hypothetical protein	0.0	sVKL*	
putative mitochondrial cytochrome b2	0.0	kPKL*	
hypothetical protein	3e-169	qVKL*	
hypothetical protein	2e-166	rPKL*	
L-lactate dehydrogenase	7e-143	nSKL*	
hypothetical protein	0.0	rARL*	
hypothetical protein	0.0	sSKL*	
formate oxidase 1	0.0	sSKL*	
fructose-bisphosphate aldolase	2e-145	aGQL*	
glucose-6-phosphate 1-dehydrogenase	0.0	pNRL*	
hypothetical protein	4e-169	lARL*	
conserved hypothetical protein	8e-170	lSKL*	
long chain fatty alcohol oxidase	1e-97	iARL*	
glyoxysomal malate synthase	0.0	aAKL*	
2-methylcitrate dehydratase	5e-110	kARF*	
precursor of mitochondrial isocitrate dehydrogenase	0.0	kARL*	
NADP-dependent malic enzyme	0.0	nAKL*	
hypothetical protein	0.0		19 / dRLhqyssHI
hypothetical protein	0.0	rGKL*	
triose-phosphate-isomerase	0.0	nARI*	
vanillyl-alcohol oxidase	1e-141	tTKL*	
hypothetical protein	0.0	hSKI*	
hypothetical protein	0.0	sAKL*	
cytosolic aspartate transaminase	8e-123	sAKL*	9 / dRLsslssHIM
hypothetical protein	0.0	cCRL*	
copper amine oxidase AO-I	0.0	kSHI*	
copper amine oxidase	0.0	qVKL*	
copper amine oxidase	0.0		4 / dRLqqlthQV
hypothetical protein	0.0	kPRM*	
predicted protein	5e-62	pSKL*	
hypothetical protein	3e-126	qSHL*	

predicted protein	2e-130	kSRL*
hypothetical protein	1-e-170	rAKL*
N,N-dimethylglycine oxidase	0.0	mSRL*
putative FAD dependent oxidoreductase	3e-177	rANL*
FAD dependent oxidoreductase superfamily	8e-152	gSKL*
hypothetical protein	5e-172	tIKL*
hypothetical protein	5e-145	qARL*
hypothetical protein	2e-07	ISRL*
hypothetical protein	2e-171	qAKL*
conserved hypothetical protein	3e-174	ISKL*
conserved hypothetical protein	0.0	gSKI*
fructosyl amine: oxygen oxidoreductase	0.0	aSRL*
hypothetical protein	0.0	aAKL*
hypothetical protein	0.0	aAKL*
fructosyl peptide oxidase	0.0	dAKL*
predicted protein	5e-164	nSKL*
hypothetical protein	1e-129	sSHL*
conserved hypothetical protein	1e-71	qSRI*
hypothetical protein	8e-148	sSKI*
urate oxidase	2e-147	kAKL*
ureidoglycolate hydrolase	1e-19	pAKL*
hypothetical protein	2e-147	rARL*
catalase	0.0	pARL*
putative catalase	0.0	sSRL*
catalase-peroxidase	0.0	rPRL*
putative epoxide hydrolase	1e-119	kARL*
epoxide hydrolase	2e-39	aGKL*
putative lipase/esterase	0.0	tARL*
metalloprotease involved in a-factor processing	0.0	dAKL*
predicted protein	1e-94	qSNL*
lysine aminopeptidase	0.0	qSKL*
monoglyceride lipase	5e-25	kAKL*
ATP-dependent protease La	6e-162	eSRL*
predicted protein	4e-61	tAKL*

hypothetical protein	5e-59	eAKL*
putative toxin biosynthesis protein	5e-128	kSRF*
conserved hypothetical protein	0.0	eSKL*
conserved hypothetical protein	1e-82	rSKI*
peroxin-8	0.0	eSKL*
Woronin body major protein	2e-77	gSRL*
hypothetical protein	1e-29	tARL*
maleylacetate reductase	0.0	IANL*
putative alcohol dehydrogenase	3e-155	qAKL*
aldehyde dehydrogenase	0.0	nARL*
retinal dehydrogenase 2	0.0	gTKL*
hypothetical protein	0.0	kSKL*
aldehyde dehydrogenase	0.0	gTRL*
hypothetical protein	0.0	IPRL*
hypothetical protein	4e-125	dCKI*
Phosphotransferase enzyme family domain protein	3e-164	eGKL*
hypothetical protein	9e-137	kARL*
hypothetical protein	6e-169	aWKL*
argininosuccinate synthase	5e-171	gERL*
betaine-aldehyde dehydrogenase	2e-158	fAKL*
hypothetical protein	8e-168	qGKL*
hypothetical protein	1e-73	sQRL*
hypothetical protein	1e-123	rAKL*
conserved hypothetical protein	2e-21	eARL*
hypothetical protein	1e-152	eSKI*
conserved hypothetical protein	2e-113	mEKL*
hypothetical protein	0.0	rSKL*
conserved hypothetical protein	2e-79	yANI*
conserved hypothetical protein	9e-58	kVRL*
hypothetical protein	1e-111	eGRL*
conserved hypothetical protein	3e-46	aVKL*
conserved hypothetical protein	9e-23	kAKL*
hypothetical protein	2e-97	sARL*
hypothetical protein	0.0	rGKL*

putative cytochrome b5	9e-38	aAKL*	
NAD-binding Rossmann fold oxidoreductase family protein	0.0	kAQL*	
hypothetical protein	5e-174	IARL*	
3-dehydroshikimate dehydratase	7e-83	qHRL*	
Putative AP endonuclease, family 2	9e-117	kSRI*	
putative dephospho-CoA kinase	1e-42	kAKL*	
peroxisomal acyl-CoA: dihydroxyacetonephosphate acyltransferase	5e-44	eAKL*	
putative oxidoreductase, 2-nitropropane dioxygenase family	3e-158	aSKL*	
FAD binding domain protein	0.0	qGRL*	
hypothetical protein	0.0	tARL*	
hypothetical protein	4e-142	sSKL*	
glutathione-dependent formaldehyde-activating enzyme	3e-60	fANL*	
predicted protein	3e-55	rGKL*	
hypothetical protein 3-hydroxy-3-methylglutaryl coenzyme A reductase	2e-55	aSKI*	
fermentative D-lactate dehydrogenase, NAD-dependent	2e-97	pVRL*	
D-mandelate dehydrogenase	9e-62	gSKL*	
hypothetical protein	3e-166	kAKL*	
alcohol dehydrogenase, zinc-containing	7e-159	kSKL*	
predicted protein	1e-110	vSKL*	
hypothetical protein	3e-167	sSKL*	
hypothetical protein	9e-172	vSKL*	
conserved hypothetical protein	4e-92	fGKL*	
hypothetical protein	2e-123	yYKL*	
protein phosphatase 2C homolog 5	1e-95	kSKL*	
putative phenol 2-monooxygenase	0.0	gSRL*	
hypothetical protein	0.0	qSRL*	
hypothetical protein	1e-49	kAKL*	
hypothetical protein	1e-60	tTKL*	
alpha/beta hydrolase fold protein	2e-109	aARL*	
hypothetical protein	2e-39	kAKL*	
predicted protein	0.0	kPKM*	
conserved hypothetical protein	6e-141		5 / dRLtqvneHL
C-8 sterol isomerase	4e-89	qLKL*	
predicted protein	3e-166	kHKL*	
hypothetical protein	5e-68	fSKI*	
conserved hypothetical protein	3e-171	gSKL*	