

Matching the proteome to the genome

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Supplementary Table 5. *P. chrysogenum* proteins identified by LC-MS/MS analysis in microbody matrix fraction

ORF code	Description of putative <i>P. chrysogenum</i> ORF		
		Species	code
a. Secondary metabolism			
Pc22g20380	Acetyltransferase SidF	<i>Penicillium marneffei</i>	SidF
Pc21g21370	Acyl-coenzyme A:isopenicillin N acyltransferase	<i>Penicillium chrysogenum</i>	PenDE
Pc22g14900	Phenylacetyl-CoA ligase PclA	<i>Penicillium chrysogenum</i>	PclA
Pc22g20270	Phenylacetyl-CoA ligase PhIB	<i>Penicillium chrysogenum</i>	PhIB
b. Beta-oxidation related			
Pc21g17590	Putative acyl-CoA dehydrogenase	<i>Aspergillus niger</i>	An17g01150
Pc21g19000	Putative acyl-CoA dehydrogenase	<i>Aspergillus fumigatus</i>	AFUA_2G16630
Pc21g20710	Putative acyl-CoA dehydrogenase	<i>Neosartorya fischeri</i>	NFIA_056640
Pc13g01890	Putative acyl-CoA synthetase	<i>Aspergillus niger</i>	An18g03800
Pc13g05130	Putative acyl-CoA synthetase	<i>Aspergillus oryzae</i>	AO090011000917
Pc13g02710	Putative beta-oxidation protein/dehydratase	<i>Aspergillus clavatus</i>	ACLA_004600
Pc20g15010	Carnitine O-acetyltransferase	<i>Candida tropicalis</i>	CT-Cat
Pc22g24780	Putative 4-coumarate-CoA ligase	<i>Neosartorya fischeri</i>	NFIA_072630
Pc20g12470	Delta3-cis-delta2-trans-enoyl-CoA isomerase Eci1	<i>Saccharomyces cerevisiae</i>	Eci1
Pc22g20810	Putative enoyl-CoA hydratase	<i>Aspergillus clavatus</i>	ACLA_069640
Pc12g01170	Putative enoyl-CoA hydratase/isomerase family protein	<i>Aspergillus oryzae</i>	AO090012000429
Pc13g15840	Putative enoyl-CoA hydratase/isomerase family protein	<i>Neosartorya fischeri</i>	NFIA_062740
Pc22g22390	Putative enoyl-CoA hydratase/isomerase family protein	<i>Aspergillus fumigatus</i>	AFUA_1G01890
Pc13g12930	Putative 3-ketoacyl-CoA thiolase	<i>Aspergillus fumigatus</i>	AFUA_1G12650
Pc15g00410	Putative 3-ketoacyl-CoA thiolase	<i>Aspergillus terreus</i>	ATEG_01444
Pc21g04680	Putative 3-ketoacyl-CoA thiolase	<i>Aspergillus niger</i>	An13g00590
Pc22g06820	3-ketoacyl-CoA thiolase Pthik	<i>Podospira anserina</i>	Pthik
Pc21g21810	Putative levodione reductase / short chain dehydrogenase	<i>Neosartorya fischeri</i>	NFIA_056910
Pc12g08530	Putative long-chain acyl-CoA dehydrogenase	<i>Neosartorya fischeri</i>	NFIA_003000
Pc22g19950	Long chain fatty acyl-CoA synthetase	<i>Saccharomyces cerevisiae</i>	Faa1
Pc22g03680	Putative NADPH-dependent beta-ketoacyl reductase	<i>Aspergillus terreus</i>	ATEG_03235
Pc20g01800	Putative palmitoyl-CoA oxidase	<i>Aspergillus fumigatus</i>	AFUB_091680
Pc22g15030	Peroxisomal 2,4-dienoyl-CoA reductase Sps19	<i>Saccharomyces cerevisiae</i>	Sps19
Pc22g17070	Putative sterol carrier protein-2	<i>Aspergillus oryzae</i>	AO090023000951
Pc13g05940	Trifunctional enzyme Fox-2	<i>Neurospora crassa</i>	Fox-2
c. Glyoxylate cycle related			
Pc12g05400	Citrate synthase CitA	<i>Aspergillus niger</i>	CitA
Pc22g03660	Isocitrate lyase ICL1	<i>Aspergillus nidulans</i>	AcuD
Pc12g04750	Malate dehydrogenase	<i>Aspergillus niger</i>	An15g00070
Pc20g13550	Malate synthase AcuE	<i>Aspergillus nidulans</i>	AcuE
Pc20g03610	NADP-dependent isocitrate dehydrogenase lcdA	<i>Aspergillus niger</i>	lcdA
d. N-metabolism			
Pc16g14240	Putative amidase	<i>Aspergillus oryzae</i>	AO090003000475
Pc22g19440	Aspartate transaminase Aat2	<i>Saccharomyces cerevisiae</i>	Aat2
Pc21g04560	Putative copper amine oxidase	<i>Neosartorya fischeri</i>	NFIA_025150

Pc21g03120 Putative D-amino-acid oxidase
Pc21g05590 Putative D-amino-acid oxidase
Pc12g09740 Putative fructosyl amine oxidase
Pc22g00060 Putative fructosyl amine oxidase
Pc13g10660 Putative fructosyl amino acid oxidase
Pc22g20960 Urate oxidase Uaz
Pc20g09430 Ureidoglycolate hydrolase Dal3

e. Antioxidants

Pc16g07060 Putative catalase
Pc22g21240 Catalase CatC
Pc12g13740 Catalase/oxidase KatG
Pc13g11580 Putative epoxide hydrolase
Pc22g24640 Putative peroxiredoxin

6. Proteases/hydrolases/esterases

Pc06g01040 Putative acyl CoA thioesterase
Pc12g15100 Putative acyl-CoA thioesterase
Pc21g01650 Putative thioesterase
Pc15g00630 Putative thioesterase
Pc21g04900 Putative thioesterase family protein

g. Other

Pc18g02760 Putative aldehyde dehydrogenase
Pc18g03000 Aldose 1-epimerase
Pc22g25570 Putative aminoglycoside phosphotransferase
Pc22g10030 Betaine-aldehyde dehydrogenase
Pc20g13690 Putative CoA-binding protein
Pc16g03120 Conserved hypothetical protein
Pc20g08300 Conserved hypothetical protein
Pc21g04910 Conserved hypothetical protein
Pc13g07430 Putative dioxygenase
Pc20g04300 Putative flavin-containing monooxygenase
Pc12g14280 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
Pc22g11470 Putative flavocytochrome b2 protein / FMN-dependent dehydrogenase
Pc16g07070 Formate oxidase Fod1
Pc18g01220 Fructose-bisphosphate aldolase Fba1
Pc12g03090 Fumarate reductase Osm1 with cytochrome B5 domain
Pc14g01270 Putative fumarylacetoacetate hydrolase family protein
Pc20g03330 Glucose-6-phosphate 1-dehydrogenase GsdA
Pc22g22110 Glycerol 3-phosphate dehydrogenase GfdA
Pc14g00990 Putative GMC-family oxidoreductase
Pc21g08790 Putative NADP-dependent oxidoreductase
Pc21g11670 Putative NADPH:quinone reductase / Zn-dependent oxidoreductase
Pc16g14230 Putative NADPH-dependent beta-ketoacyl reductase
Pc22g14270 Putative 2-nitropropane dioxygenase family oxidoreductase
Pc22g19490 Putative 2-nitropropane dioxygenase family oxidoreductase
Pc21g02970 Putative 2-polyprenyl-6-methoxyphenol hydroxylase

Neosartorya fischeri NFIA_073030
Aspergillus nidulans AN0174.2
Aspergillus nidulans AN2786.2
Aspergillus oryzae AO090102000413
Aspergillus fumigatus AFUA_3G10130
Aspergillus flavus Uaz
Saccharomyces cerevisiae Dal3

Aspergillus clavatus ACLA_077960
Aspergillus nidulans CatC
Penicillium marnettei KatG
Aspergillus clavatus ACLA_022580
Aspergillus niger An16g00920

Aspergillus fumigatus AFUA_1G15170
Aspergillus oryzae AO090001000339
Aspergillus oryzae AO090102000229
Aspergillus clavatus ACLA_070120
Aspergillus fumigatus AFUA_7G03960

Aspergillus terreus ATEG_05338
Saccharomyces cerevisiae Ymr099c
Aspergillus fumigatus AFUA_1G02880
Escherichia coli BetB
Aspergillus oryzae AO090026000481
Neosartorya fischeri NFIA_090690
Aspergillus oryzae AO090020000033
Aspergillus clavatus ACLA_005650
Neosartorya fischeri NFIA_108240
Aspergillus oryzae AO090005001317
Aspergillus clavatus ACLA_055500
Aspergillus oryzae AO090012000974
Debaryomyces vanriijiae Fod1
Saccharomyces cerevisiae Fba1
Saccharomyces cerevisiae Osm1
Aspergillus niger An18g06670
Aspergillus nidulans GsdA
Aspergillus nidulans GfdA
Aspergillus fumigatus AFUA_8G04090
Aspergillus terreus ATEG_04342
Neosartorya fischeri NFIA_115150
Neosartorya fischeri NFIA_010890
Aspergillus terreus ATEG_06490
Aspergillus oryzae AO090011000650
Aspergillus oryzae AO090012000279

Pc13g06370 Protein weakly similar to ethanolamine utilization protein
Pc13g12080 Putative protein with alpha/beta hydrolase fold
Pc16g03770 Protein with cupin domain
Pc13g10320 Putative short chain dehydrogenase
Pc20g09970 Putative short chain dehydrogenase
Pc16g08670 C-8 sterol isomerase Erg-1
Pc21g03400 Triose-phosphate-isomerase TpiA
Pc21g00970 Woronin body protein Hex1
Pc13g03610 Putative YcaC-related amidohydrolase
Pc22g13390 Putative Zn-dependent alcohol dehydrogenase

2. Peroxisins and peroxisome-associated proteins

Pc13g08710 Component of COPII vesicles Emp24
Pc16g01180 Dynamin-like GTPase Dnm1
Pc14g01930 GTPase RhoA
Pc22g20190 Peroxin Pex1p
Pc20g06300 Peroxin Pex6p
Pc12g09400 Peroxin Pex11p

3. non-microbody proteins involved in penicillin metabolism

Pc21g21390 ACV synthetase (ACVS)
Pc21g21380 Isopenicillin N synthase (IPNS)
Pc20g04080 Regulatory protein SUAPRGA1

4. Cytoskeletal proteins

Pc13g15710 Actin-associated protein Rvs167
Pc13g05480 Actin-bundling protein Sac6
Pc22g08080 Putative actin cortical patch component
Pc21g10090 Putative actin filament depolymerizing protein
Pc21g06430 Actin-related protein Arp-3
Pc15g00800 ARP2/3 actin-organizing complex subunit Arc34
Pc14g01330 ARP2/3 actin-organizing complex subunit Sop2
Pc18g00580 Putative Arp2/3 complex subunit Arc16
Pc22g11760 Chaperonin-containing T-complex theta subunit involved in assembly of actin and tubulin Cct8
Pc13g11750 Cytoskeletal adaptor protein SagA
Pc20g15430 Putative F-actin-capping protein subunit alpha
Pc20g11630 Gamma-actin Act2
Pc22g19040 Microtubule associated protein Ytm1
Pc18g00550 Microtubule integrity protein Mal3
Pc20g00800 Protein with a possible role in folding of beta-tubulin
Pc22g21650 Tubulin alpha-1 chain Tba1
Pc13g13470 Tubulin beta-1 Tbb1

5. Proteins involved in translation

Pc13g14510 40S ribosomal protein S0
Pc20g00440 40S ribosomal protein S1
Pc21g13620 40S ribosomal protein S2
Pc18g02110 40S ribosomal protein S3
Pc20g02900 40S ribosomal protein S4

Phaeosphaeria nodorum SNOG_02939
Neosartorya fischeri NFIA_012240
Ochrobactrum anthropi Oant_0448
Aspergillus terreus ATEG_04584
Neosartorya fischeri NFIA_008770
Neurospora crassa Erg-1
Aspergillus nidulans TpiA
Aspergillus nidulans Hex1
Aspergillus nidulans AN6066.2
Aspergillus terreus ATEG_01304

Saccharomyces cerevisiae Emp24
Saccharomyces cerevisiae Dnm1
Aspergillus nidulans RhoA
Penicillium chrysogenum Pex1p
Penicillium chrysogenum Pex6p
Penicillium chrysogenum Pex11p

Penicillium chrysogenum PcbAB
Penicillium chrysogenum PcbC
Aspergillus nidulans SUAPRGA1

Saccharomyces cerevisiae Rsv167
Saccharomyces cerevisiae Sac6p
Aspergillus clavatus ACLA_068290
Aspergillus fumigatus AFUA_5G10570
Neurospora crassa Arp-3
Schizosaccharomyces pombe Arc2
Schizosaccharomyces pombe Sop2
Neosartorya fischeri NFIA_066590
Saccharomyces cerevisiae Cct8
Aspergillus nidulans SagA
Gallus gallus CapZA1
Penicillium chrysogenum Act2
Saccharomyces cerevisiae Ytm1
Schizosaccharomyces pombe Mal3
Aspergillus terreus ATEG_09456
Aspergillus nidulans Tba1
Aspergillus nidulans Tbb1

Candida albicans Yst1
Saccharomyces cerevisiae Rps1a
Saccharomyces cerevisiae Rps2
Saccharomyces cerevisiae Rps3
Saccharomyces cerevisiae Rps4b

Pc21g23270 40S ribosomal protein S5
 Pc22g06950 40S ribosomal protein S6
 Pc18g00610 40S ribosomal protein S7
 Pc16g08960 40S ribosomal protein S8
 Pc18g06210 40S ribosomal protein S11
 Pc18g02330 40S ribosomal protein S12
 Pc12g05940 40S ribosomal protein S13
 Pc22g20650 40S ribosomal protein S14
 Pc22g20260 40S ribosomal protein S15
 Pc22g20980 40S ribosomal protein S16
 Pc22g20470 40S ribosomal protein S17
 Pc22g00880 40S ribosomal protein S18
 Pc18g02490 40S ribosomal protein S19
 Pc20g04380 40S ribosomal protein S20
 Pc18g05330 40S ribosomal protein S21 (fusion protein)
 Pc21g12010 40S ribosomal protein S24
 Pc21g22970 40S ribosomal protein S25
 Pc13g01630 40S ribosomal protein S26E
 Pc16g02610 40S ribosomal protein S28
 Pc13g03870 40S ribosomal protein S30
 Pc16g10120 60S acidic ribosomal protein P0
 Pc13g03050 60S acidic ribosomal protein P1
 Pc22g20250 60S acidic ribosomal protein P2
 Pc13g11000 60S ribosomal protein L1
 Pc21g17430 60S ribosomal protein L2
 Pc20g14180 60S ribosomal protein L3
 Pc21g16520 60S ribosomal protein L4
 Pc13g11570 60S ribosomal protein L5
 Pc13g08880 60S ribosomal protein L6
 Pc13g05920 60S ribosomal protein L7
 Pc22g02060 60S ribosomal protein L8
 Pc16g02160 60S ribosomal protein L9
 Pc16g10560 60S ribosomal protein L10
 Pc13g07190 60S ribosomal protein L11
 Pc13g03190 60S ribosomal protein L12
 Pc13g06740 60S ribosomal protein L13
 Pc16g09160 60S ribosomal protein L15
 Pc16g12990 60S ribosomal protein L17
 Pc13g05540 60S ribosomal protein L18
 Pc13g04880 60S ribosomal protein L19
 Pc16g09260 60S ribosomal protein L20
 Pc20g02750 60S ribosomal protein L21
 Pc18g01750 60S ribosomal protein L22
 Pc18g03860 60S ribosomal protein L23
 Pc20g00680 60S ribosomal protein L23

Saccharomyces cerevisiae Rps5
Saccharomyces cerevisiae Rps6b
Saccharomyces cerevisiae Rps7a
Saccharomyces cerevisiae Rps8b
Saccharomyces cerevisiae Rps11b
Homo sapiens Rps12
Saccharomyces cerevisiae Rps13
Homo sapiens RPS14
Podospora anserina As1
Saccharomyces cerevisiae Rps16a
Saccharomyces cerevisiae Rps17a
Homo sapiens RPS18
Aspergillus nidulans Rps19
Homo sapiens RPS20
Saccharomyces cerevisiae Rps21a
Saccharomyces cerevisiae Rps24a
Saccharomyces cerevisiae Rps25b
Neurospora crassa Crp5
Aspergillus niger Rps28
Saccharomyces cerevisiae Rps30a
Saccharomyces cerevisiae Rpp0
Schizosaccharomyces pombe Rpa1
Schizosaccharomyces pombe Rpp2-2
Saccharomyces cerevisiae Rpl1b
Saccharomyces cerevisiae Rpl2b
Saccharomyces cerevisiae Rpl3
Saccharomyces cerevisiae Rpl4a
Saccharomyces cerevisiae Rpl5
Saccharomyces cerevisiae Rpl6b
Saccharomyces cerevisiae Rpl7a
Saccharomyces cerevisiae Rpl8b
Saccharomyces cerevisiae Rpl9b
Saccharomyces cerevisiae Rpl10
Saccharomyces cerevisiae Rpl11a
Mus musculus Rpl12
Danio rerio Rpl13
Saccharomyces cerevisiae Rpl15b
Saccharomyces cerevisiae Rpl17a
Saccharomyces cerevisiae Rpl18b
Saccharomyces cerevisiae Rpl19b
Saccharomyces cerevisiae Rpl20b
Saccharomyces cerevisiae Rpl21a
Mus musculus Rpl22
Saccharomyces cerevisiae Rpl23a
Homo sapiens RPL23A

Pc18g05370	60S ribosomal protein L24	<i>Saccharomyces cerevisiae</i>	Rlp24
Pc22g23790	60S ribosomal protein L24	<i>Saccharomyces cerevisiae</i>	Rpl24b
Pc18g03440	Putative 60S ribosomal protein L25	<i>Aspergillus oryzae</i>	AO090023000632
Pc21g21880	60S ribosomal protein L26	<i>Saccharomyces cerevisiae</i>	Rpl26b
Pc13g02890	60S ribosomal protein L27	<i>Saccharomyces cerevisiae</i>	Rpl27a
Pc20g08290	60S ribosomal protein L27a	<i>Saccharomyces cerevisiae</i>	Rpl28
Pc12g04760	Putative 60S ribosomal protein L28	<i>Aspergillus niger</i>	An15g00080
Pc22g01480	60S ribosomal protein L31	<i>Saccharomyces cerevisiae</i>	Rpl31b
Pc21g01520	60S ribosomal protein L32	<i>Saccharomyces cerevisiae</i>	Rpl32
Pc20g02980	60S ribosomal protein L37	<i>Saccharomyces cerevisiae</i>	Rpl35a
Pc13g07380	60S ribosomal protein L38	<i>Homo sapiens</i>	RPL38
Pc21g19530	60S ribosomal protein L43	<i>Saccharomyces cerevisiae</i>	Rpl43a
Pc22g14770	Putative ATPase involved in ribosome biogenesis Arb1	<i>Saccharomyces cerevisiae</i>	Arb1
Pc22g05790	Chaperone activator Aha1	<i>Saccharomyces cerevisiae</i>	Aha1
Pc22g23430	Cyclophilin-like peptidyl prolyl cis-trans isomerase	<i>Homo sapiens</i>	PPIL-1
Pc18g05190	Cyclophilin-like peptidyl prolyl cis-trans isomerase CypA	<i>Aspergillus niger</i>	CypA
Pc21g01740	DnaJ domain protein Mas5	<i>Saccharomyces cerevisiae</i>	Ydj1
Pc16g10080	DnaJ family chaperone Ydj1	<i>Saccharomyces cerevisiae</i>	Ydj1
Pc13g02940	Elongation factor 1-alpha	<i>Podospora anserina</i>	EF1A
Pc13g08810	Elongation factor 1-beta	<i>Xenopus laevis</i>	EF1B
Pc12g12040	Elongation factor 2 (EF-2) Etf1	<i>Saccharomyces cerevisiae</i>	Etf1
Pc20g11850	Elongation factor eEF-1 subunit gamma Tef4	<i>Saccharomyces cerevisiae</i>	Tef4
Pc18g00730	Putative eukaryotic translation initiation factor 3 subunit	<i>Aspergillus oryzae</i>	AO090003000629
Pc16g08430	Eukaryotic translation initiation factor 5A	<i>Saccharomyces cerevisiae</i>	Anb1
Pc13g06110	Putative FKBP-type peptidyl-prolyl isomerase	<i>Aspergillus clavatus</i>	ACLA_054400
Pc22g03140	G-protein complex beta subunit CpcB	<i>Aspergillus nidulans</i>	CpcB
Pc12g05640	Heat shock protein 90 Mod-E	<i>Podospora anserina</i>	Mod-E
Pc13g12990	Heat shock protein Hsp88	<i>Neurospora crassa</i>	Hsp-88
Pc21g18000	HSP40 co-chaperone Sis1	<i>Saccharomyces cerevisiae</i>	Sis1
Pc22g10220	Hsp70 chaperone HscA	<i>Aspergillus nidulans</i>	HscA
Pc12g16290	Hsp70 protein that interacts with the ribosome Ssz1	<i>Saccharomyces cerevisiae</i>	Ssz1
Pc22g11240	Molecular chaperone Hsp70	<i>Ajellomyces capsulatus</i>	Hsp70
Pc16g12680	mRNP component associated with polyribosomes Bfr1	<i>Saccharomyces cerevisiae</i>	Bfr1
Pc21g05900	NADP(+)-dependent dehydrogenase Tma29	<i>Saccharomyces cerevisiae</i>	Tma29
Pc20g13270	Nascent polypeptide-associated complex (NAC), alpha subunit	<i>Mus musculus</i>	Naca
Pc22g23300	Putative nascent polypeptide-associated complex subunit beta	<i>Homo sapiens</i>	BTF3
Pc20g00710	Peptide chain release factor eRF/aRF, subunit 1 Erf1	<i>Podospora anserina</i>	Erf1
Pc20g04810	Peptidyl prolyl cis-trans isomerase	<i>Rattus norvegicus</i>	PpiD
Pc16g13060	Peptidyl-prolyl cis-trans isomerase Cyp2	<i>Schizosaccharomyces pombe</i>	Cyp2
Pc22g19060	Peptidyl-prolyl cis-trans isomerase CypB	<i>Aspergillus nidulans</i>	CypB
Pc21g23500	Protein associated with ribosomes Tma19	<i>Saccharomyces cerevisiae</i>	Tma19
Pc12g01240	Protein involved in translation termination efficiency, mRNA poly(A) tail length and mRNA stability Tpa1	<i>Saccharomyces cerevisiae</i>	Tpa1
Pc13g06220	Putative ribonuclease responsible for the inhibition of translation	<i>Aspergillus clavatus</i>	ACLA_054320
Pc22g02470	Putative ribosomal protein Rps10a	<i>Saccharomyces cerevisiae</i>	Rps10a
Pc12g06170	Putative ribosome biogenesis protein Utp30	<i>Saccharomyces cerevisiae</i>	Utp30

Pc18g00860 Putative ribosome-associated protein Stm1
 Pc21g03130 Ribosome associated protein Tma46
 Pc21g08900 Ribosome biogenesis protein Rrs1
 Pc18g02190 Ribosome interacting GTPase Rbg1
 Pc12g10310 Putative RNA binding protein
 Pc22g23450 Putative RNase PH-related exoribonuclease
 Pc21g10360 Topoisomerase II associated protein Pat1
 Pc22g19890 Translation initiation factor 3 subunit
 Pc20g03590 Translation initiation factor 3 subunit 2 Tif34
 Pc12g01650 Translation initiation factor 3 subunit D Moe1
 Pc16g02480 Translation initiation factor 3 subunit eIF3f
 Pc21g01490 Translation initiation factor 4B
 Pc21g13600 Translation initiation factor 4E-1
 Pc22g23860 Translation initiation factor eIF-1A subunit
 Pc20g06740 Translation initiation factor eIF4A
 Pc21g15180 Translation initiation factor eIF-4A subunit
 Pc21g16240 Translation initiation factor eIF4E3
 Pc20g01120 Translation initiation factor eIF-6
 Pc16g04800 Translation initiation factor Rli1
 Pc20g08010 Translation initiation factor subunit eIF2A
 Pc22g19160 Translation initiation factor subunit eIF-4F
 Pc12g06650 Translational elongation factor EF-3 Hef3
 Pc20g03540 Translational initiation factor 2 beta Sui3
6. ER-proteins / ER dependent degradation
 Pc21g19270 Cdc48 protein
 Pc20g03970 Coatomer subunit alpha Ret1
 Pc13g13550 Coatomer subunit beta Sec26
 Pc16g14540 Coatomer subunit delta
 Pc12g16530 Coatomer subunit gamma
 Pc21g07430 Disulfide isomerase TigA
 Pc12g10670 ER Hsp70 chaperone BipA
 Pc06g00710 ER lumen located Hsp70 chaperone
 Pc18g05040 FKBP-type peptidyl-prolyl isomerase Fkbp22
 Pc22g11180 GTP-binding protein Ypt1
 Pc22g18030 Integral ER membrane protein Scs2
 Pc20g12700 Mannosyl-oligosaccharide glucosidase Cwh41
 Pc21g01130 Membrane organization and biogenesis-related protein Yop1
 Pc21g11280 Protein disulfide isomerase PdiA
 Pc13g03420 Protein disulfide isomerase PrpA
 Pc13g03200 Protein transport protein Sec23
 Pc22g00730 Putative reticulon-like protein Cwl1
 Pc12g00300 C-3 sterol dehydrogenase/C-4 decarboxylase Erg26
7. Mitochondrial proteins
 Pc12g03130 Acetyl-CoA hydrolase Ach1
 Pc22g23250 Acetylglutamate kinase Arg-6

Saccharomyces cerevisiae Stm1
Saccharomyces cerevisiae Tma46
Saccharomyces cerevisiae Rrs1
Saccharomyces cerevisiae Rbg1
Aspergillus nidulans AN2089_2
Homo sapiens EXOSC8
Saccharomyces cerevisiae Pat1
Homo sapiens EIF3G
Saccharomyces cerevisiae Tif34
Schizosaccharomyces pombe Moe1
Schizosaccharomyces pombe eIF3F
Homo sapiens EIF4H
Schizosaccharomyces pombe Tif1
Homo sapiens EIF1AY
Schizosaccharomyces pombe Tigf1
Mus musculus Eif4a
Homo sapiens EIF4E2
Saccharomyces cerevisiae Tif6
Saccharomyces cerevisiae Rli1
Homo sapiens EIF-2A
Saccharomyces cerevisiae Tif4631
Saccharomyces cerevisiae Hef3
Saccharomyces cerevisiae Sui3

Saccharomyces cerevisiae Cdc48
Saccharomyces cerevisiae Ret1
Saccharomyces cerevisiae Sec26
Bos taurus ARCN1
Homo sapiens COPG2
Aspergillus niger TigA
Aspergillus niger BipA
Homo sapiens HYOU1
Neurospora crassa Fkbp22
Aspergillus niger SrgB
Saccharomyces cerevisiae Scs2
Saccharomyces cerevisiae Cwh41
Saccharomyces cerevisiae Yop1
Aspergillus niger PdiA
Aspergillus niger PrpA
Saccharomyces cerevisiae Sec23
Schizosaccharomyces pombe Cwl1
Saccharomyces cerevisiae Erg26

Saccharomyces cerevisiae Ach1
Neurospora crassa Arg-6

Pc20g14810	Acetylornithine aminotransferase Arg8	<i>Kluyveromyces lactis</i>	Arg8
Pc16g13490	Acyl-CoA dehydrogenase	<i>Homo sapiens</i>	ACADSB
Pc12g09430	Putative alanine aminotransferase Alt1	<i>Saccharomyces cerevisiae</i>	Alt1
Pc16g07470	Aminomethyltransferase Gcv1	<i>Saccharomyces cerevisiae</i>	Gcv1
Pc22g15960	Arginine biosynthesis bifunctional protein Ecm40	<i>Saccharomyces cerevisiae</i>	Ecm40
Pc22g13130	Aspartate aminotransferase	<i>Mus musculus</i>	Got-2
Pc12g03370	ATP synthase alpha chain Atp1	<i>Saccharomyces cerevisiae</i>	Atp1
Pc21g10070	ATP synthase beta chain AtpB	<i>Neurospora crassa</i>	AtpB
Pc13g03260	ATP synthase gamma chain Atp3	<i>Saccharomyces cerevisiae</i>	Atp3
Pc22g16780	Branched-chain-amino-acid aminotransferase Bat1	<i>Saccharomyces cerevisiae</i>	Bat1
Pc13g01690	Conserved mitochondrial protein with unknown function Aim18	<i>Saccharomyces cerevisiae</i>	Aim18
Pc12g05380	Coproporphyrinogen III oxidase Hem13	<i>Saccharomyces cerevisiae</i>	Hem13
Pc21g14890	Cysteine synthase CysB	<i>Aspergillus nidulans</i>	CysB
Pc12g07280	Cytochrome c	<i>Aspergillus niger</i>	Cyc
Pc18g03560	Cytochrome c peroxidase Ccp1	<i>Saccharomyces cerevisiae</i>	Ccp1
Pc20g04720	Dihydrolipoyl dehydrogenase component of pyruvate dehydrogenase Lpd1	<i>Saccharomyces cerevisiae</i>	Lpd1
Pc20g01630	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase Lat1	<i>Saccharomyces cerevisiae</i>	Lat1
Pc20g08570	Dihydrolipoamide succinyltransferase Kgd2	<i>Saccharomyces cerevisiae</i>	Kgd2
Pc22g22710	Dihydroxy acid dehydratase Ilv3	<i>Saccharomyces cerevisiae</i>	Ilv3
Pc22g23810	Fumarase Fum1	<i>Saccharomyces cerevisiae</i>	Fum1
Pc20g06720	Putative fumarylacetoacetate hydrolase family protein Fmp41	<i>Saccharomyces cerevisiae</i>	Fmp41
Pc16g11070	Heat shock protein 60 Hsp60	<i>Saccharomyces cerevisiae</i>	Hsp60
Pc22g19990	Heat shock protein Ssc1	<i>Saccharomyces cerevisiae</i>	Ssc1
Pc18g05890	Homo-isocitrate dehydrogenase Lys12	<i>Saccharomyces cerevisiae</i>	Lys12
Pc13g06830	3-hydroxybutyryl-CoA dehydrogenase	<i>Homo sapiens</i>	HADH
Pc14g01170	Isocitrate dehydrogenase subunit 1 Idh1	<i>Ajellomyces capsulatus</i>	Idh1
Pc13g11380	Isocitrate dehydrogenase subunit 2	<i>Saccharomyces cerevisiae</i>	Idh2
Pc13g15810	Ketol-acid reductoisomerase Ilv-2	<i>Neurospora crassa</i>	Ilv-2
Pc20g01610	Malate dehydrogenase Mdh1	<i>Saccharomyces cerevisiae</i>	Mdh1
Pc20g13510	2-methylcitrate synthase McsA	<i>Aspergillus nidulans</i>	McsA
Pc22g23150	Methylisocitrate lyase Icl2	<i>Saccharomyces cerevisiae</i>	Icl2
Pc22g02810	Methylmalonate-semialdehyde dehydrogenase	<i>Rattus norvegicus</i>	MMSDH
Pc22g18410	Mitochondrial acetolactate synthase small subunit Ilv6	<i>Saccharomyces cerevisiae</i>	Ilv6
Pc22g02000	Mitochondrial aconitate hydratase Aco1	<i>Saccharomyces cerevisiae</i>	Aco1
Pc18g02420	Mitochondrial ADP/ATP carrier	<i>Penicillium chrysogenum</i>	BAC82547
Pc12g12500	Mitochondrial carrier protein family member with unknown function	<i>Aspergillus clavatus</i>	ACLA_073780
Pc14g00670	Mitochondrial enoyl reductase Etr1	<i>Saccharomyces cerevisiae</i>	Etr1
Pc16g06000	Mitochondrial inner membrane translocase subunit Tim44	<i>Saccharomyces cerevisiae</i>	Tim44
Pc18g02780	Putative mitochondrial peroxiredoxin	<i>Neosartorya fischeri</i>	NFIA_107600
Pc13g10820	Mitochondrial processing peptidase alpha subunit Mpp	<i>Neurospora crassa</i>	Mpp
Pc16g12780	Mitochondrial processing peptidase beta subunit Pep	<i>Neurospora crassa</i>	Pep
Pc22g15660	Putative mitochondrial ss DNA-binding protein Rim1	<i>Saccharomyces cerevisiae</i>	Rim1
Pc22g25220	NADH-quinone oxidoreductase	<i>Phanerochaete chrysosporium</i>	Qr
Pc21g15880	Nucleoside diphosphate kinase Ndk-1	<i>Neurospora crassa</i>	Ndk-1
Pc22g17950	Outer mitochondrial membrane protein porin Por1	<i>Saccharomyces cerevisiae</i>	Por1

Pc22g04770 2-oxoglutarate dehydrogenase Kgd1
Pc12g08790 2-oxoisovalerate dehydrogenase complex alpha subunit
Pc14g00690 Pyruvate dehydrogenase E1 B-subunit Pdb1
Pc22g11710 Pyruvate dehydrogenase E1 component alpha subunit Pda1
Pc20g14220 Pyruvate dehydrogenase kinase
Pc22g18450 37S ribosomal protein Rsm25
Pc21g15750 Putative ribosomal subunit protein L1
Pc22g14050 54S ribosomal protein L2
Pc13g11310 54S ribosomal protein L3
Pc20g00200 50S ribosomal protein L3
Pc15g00650 Putative ribosomal protein L4
Pc21g17510 50S ribosomal subunit L7
Pc21g19430 54S ribosomal protein L17
Pc21g06850 Ribosomal protein L23
Pc14g01910 Putative mitochondrial ribosomal protein L40
Pc21g11920 Putative ribosomal small subunit assembly protein Rrp7
Pc21g17970 Small subunit of carbamoyl phosphate synthetase Cpa1
Pc20g06030 Succinate dehydrogenase flavoprotein subunit Sdh1
Pc12g06870 Succinyl-CoA synthetase alpha subunit
Pc13g06650 Succinyl-CoA synthetase beta subunit Lsc2
Pc16g05560 Sulfide:quinone oxidoreductase
Pc12g15010 Translation elongation factor EF-Tu Tuf1
Pc12g05480 Ubiquinol-cytochrome C reductase complex core protein 2 Qcr2
Pc22g05840 Putative ubiquinol-cytochrome-c reductase complex subunit Qcr6
Pc21g10160 Ubiquinol-cytochrome c reductase iron-sulfur subunit precursor Rip1
Pc12g08680 Ubiquinone biosynthesis methyltransferase Coq5

8. Vacuole-related proteins

Pc21g00870 Aminopeptidase Y Lap1
Pc13g09680 Aspartic endopeptidase PepE
Pc22g00890 Carboxypeptidase CpyA/Prc1
Pc18g00620 RAB GTPase Vps21/Ypt51
Pc22g05200 Vacuolar protein sorting-associated protein Vps26
Pc18g03300 Vacuolar protein sorting-associated protein Vps74
Pc22g24360 Vacuolar proton pump subunit E Vma-4
Pc21g16970 Vacuolar serine protease
Pc22g13480 V-type ATPase, B subunit Vma2

9. Nuclear-associated proteins

Pc18g03940 14-3-3 family protein ArtA
Pc18g02770 AT DNA binding protein
Pc22g24000 ATP dependent RNA helicase Sub2
Pc22g19070 ATP-dependent RNA helicase Dbp1
Pc22g21030 ATP-dependent RNA helicase Dbp2
Pc20g08510 ATP-dependent RNA helicase Dhh1
Pc12g04670 CCAAT-binding factor complex subunit HapE
Pc21g03340 Cell cycle control protein Cwf8

Saccharomyces cerevisiae Kgd1
Homo sapiens BCHEL1
Saccharomyces cerevisiae Pdb1
Saccharomyces cerevisiae Pda1
Zea mays PDK2
Saccharomyces cerevisiae Rsm25
Aspergillus niger An09g05980
Saccharomyces cerevisiae Mrp7
Saccharomyces cerevisiae Mrpl3
Saccharomyces cerevisiae Mrpl9
Saccharomyces cerevisiae Mrpl4
Saccharomyces cerevisiae Mrpl7
Saccharomyces cerevisiae Mrpl17
Saccharomyces cerevisiae Mrp20
Saccharomyces cerevisiae Mrpl40
Saccharomyces cerevisiae Rrp7
Neurospora crassa Cpa-1
Saccharomyces cerevisiae Sdh1
Rattus norvegicus Suc1g1
Saccharomyces cerevisiae Lsc2
Schizosaccharomyces pombe SPBC2G5.06c
Saccharomyces cerevisiae Tuf1
Saccharomyces cerevisiae Qcr2
Saccharomyces cerevisiae Qcr6
Saccharomyces cerevisiae Rip1
Saccharomyces cerevisiae Coq5

Aspergillus fumigatus Lap1
Aspergillus niger PepE
Aspergillus nidulans CpyA
Saccharomyces cerevisiae Vps21
Saccharomyces cerevisiae Pep8/Vps26
Saccharomyces cerevisiae Vps74
Neurospora crassa Vma-4
Penicillium chrysogenum Pen ch 18
Saccharomyces cerevisiae Vma2

Aspergillus nidulans ArtA
Mus musculus Thyn1
Saccharomyces cerevisiae Sub2
Saccharomyces cerevisiae Dbp1
Saccharomyces cerevisiae Dbp2
Saccharomyces cerevisiae Dhh1
Aspergillus nidulans HapE
Schizosaccharomyces pombe Cwf8

Pc22g07050	Chromatin remodeling complex component Rvb1	<i>Saccharomyces cerevisiae</i>	Rvb1
Pc16g11940	Chromatin structure-remodeling complex protein Arp9	<i>Saccharomyces cerevisiae</i>	Arp9
Pc21g14600	Cleavage and polyadenylation specific factor 5	<i>Homo sapiens</i>	NUDT21
Pc22g18880	Component of small ribosomal subunit (SSU) processosome Rrp9	<i>Saccharomyces cerevisiae</i>	Rrp9
Pc21g19210	Curved DNA-binding protein 42 kDa Cdb4	<i>Schizosaccharomyces pombe</i>	Cdb4
Pc22g03430	DEAD box ATP-dependent RNA helicase	<i>Homo sapiens</i>	DDX18
Pc22g22320	Developmental regulator VelB	<i>Aspergillus nidulans</i>	VelB
Pc16g04650	DNA repair protein Rad51	<i>Aspergillus nidulans</i>	UvsC
Pc21g11440	DNA replication factor A1 Ssb1	<i>Schizosaccharomyces pombe</i>	Ssb1
Pc20g07200	DNA replication factor C subunit Rfc2	<i>Saccharomyces cerevisiae</i>	Rfc2
Pc20g05810	Putative exosome complex exonuclease	<i>Homo sapiens</i>	RRP46
Pc12g07260	Exosome complex exonuclease Rrp42	<i>Saccharomyces cerevisiae</i>	Rrp42
Pc16g12800	Fibrillarin Nop1	<i>Saccharomyces cerevisiae</i>	Nop1
Pc22g02290	Filament-forming protein Tpr/p270	<i>Homo sapiens</i>	TPR
Pc12g11330	Putative FKBP-type peptidyl-prolyl isomerase	<i>Aspergillus nidulans</i>	AN3908_2
Pc20g03510	Putative glycine-rich RNA-binding protein	<i>Aspergillus nidulans</i>	AN2989_2
Pc22g01260	GTP-binding nuclear protein Gsp1/Ran	<i>Candida albicans</i>	Gsp1
Pc21g02200	Heterokaryon incompatibility protein HetC	<i>Neurospora crassa</i>	Het-C
Pc20g07890	Histone H1 HhoA	<i>Aspergillus nidulans</i>	HhoA
Pc21g14540	Histone H2A variant Htz1	<i>Saccharomyces cerevisiae</i>	Htz1
Pc20g08600	Histone H2B Htb1	<i>Aspergillus nidulans</i>	Htb1
Pc16g12260	Histone H4 Hhf1	<i>Saccharomyces cerevisiae</i>	Hhf1
Pc16g09240	Putative HMG box protein	<i>Aspergillus clavatus</i>	ACLA_030120
Pc16g05450	Putative HMG box protein	<i>Aspergillus terreus</i>	ATEG_00182
Pc21g03140	Hsp90 binding co-chaperone regulating telomerase activity Sba1	<i>Saccharomyces cerevisiae</i>	Sba1
Pc21g01970	Karyopherin alpha Srp1	<i>Saccharomyces cerevisiae</i>	Srp1
Pc18g04820	KH domain RNA-binding protein Rnc1	<i>Schizosaccharomyces pombe</i>	Rnc1
Pc22g24340	MADS box transcription factor Mcm1	<i>Saccharomyces cerevisiae</i>	Mcm1
Pc21g11890	mRNA binding post-transcriptional regulator Nam8	<i>Saccharomyces cerevisiae</i>	Nam8
Pc18g03450	mRNA splicing protein Prp39	<i>Saccharomyces cerevisiae</i>	Prp39
Pc21g03380	mRNA turnover protein Mrt4	<i>Saccharomyces cerevisiae</i>	Mrt4
Pc13g09020	Non-histone chromatin protein Nhp6	<i>Saccharomyces cerevisiae</i>	Nhp6b
Pc12g15120	Nuclear and cytoplasmic polyadenylated RNA-binding protein Pub1	<i>Saccharomyces cerevisiae</i>	Pub1
Pc22g01070	Nuclear mRNA splicing factor	<i>Homo sapiens</i>	SF3B3
Pc20g00300	Nuclear peroxiredoxin Dot5	<i>Saccharomyces cerevisiae</i>	Dot5
Pc16g02050	Nuclear pore complex protein SonA	<i>Aspergillus nidulans</i>	SonA
Pc13g14680	Nucleolar protein Nop58	<i>Saccharomyces cerevisiae</i>	Nop58
Pc21g19320	Nucleolar protein required for 60S ribosome subunit biogenesis Nip7	<i>Saccharomyces cerevisiae</i>	Nip7
Pc15g01230	Nucleolin protein Gar2	<i>Schizosaccharomyces pombe</i>	Gar2
Pc21g20590	Putative nucleoporin Nup49	<i>Saccharomyces cerevisiae</i>	Nup49
Pc20g00560	Nucleosome assembly protein Nap1	<i>Saccharomyces cerevisiae</i>	Nap1
Pc21g16630	Nucleosome assembly protein NapB	<i>Aspergillus nidulans</i>	NapB
Pc06g01240	Poly(A) polymerase Pla1	<i>Schizosaccharomyces pombe</i>	Pla1
Pc16g09030	Polyadenylate-binding protein Pab1	<i>Saccharomyces cerevisiae</i>	Pab1
Pc20g09410	Pre-mRNA splicing factor Brr2	<i>Saccharomyces cerevisiae</i>	Brr2

Pc12g14830 Pre-mRNA splicing factor Cwf5
 Pc16g04580 Pre-mRNA splicing factor Rrp5
 Pc13g10700 Pre-mRNA splicing factor Srp2
 Pc13g05520 Putative pre-mRNA splicing factor Srp1
 Pc12g15950 Pre-rRNA processing nucleolar protein Sik1
 Pc13g05660 Ran GTPase exchange factor Srm1
 Pc22g17020 Putative ribosomal biogenesis protein
 Pc22g22040 60S ribosome biogenesis protein Brx1
 Pc21g03160 RNA annealing protein Yra1
 Pc14g01320 RNA binding domain protein
 Pc21g18310 Putative RNA binding domain protein Tcg
 Pc22g03990 Putative RNA binding protein
 Pc22g16240 Putative RNA binding protein
 Pc21g14870 Putative RNA binding protein Arp1
 Pc22g21370 Putative RNA polymerase-associated factor Paf1
 Pc22g08700 RNA exonuclease possibly involved in pre-rRNA processing Rex4
 Pc20g09320 RNA-3'-phosphate cyclase family protein Rcl1
 Pc13g13010 RNA-binding La domain protein Sla1
 Pc22g20070 RNA-binding protein Vip1
 Pc21g02010 rRNA biogenesis protein Rrp5
 Pc14g00640 rRNA processing protein Enp1
 Pc15g00770 rRNA-processing protein Utp23
 Pc12g12300 Putative SAP domain protein
 Pc13g12010 SAGA complex component Sgf29
 Pc16g09820 Serine/threonine protein phosphatase type 1 BimG
 Pc22g04990 Serine/threonine-protein kinase CotA
 Pc13g12610 Small nuclear ribonucleoprotein complex protein Nhp2
 Pc13g07180 Small nuclear ribonucleoprotein SmB
 Pc21g07040 Small nuclear ribonucleoprotein U1
 Pc13g04070 Small subunit of nuclear cap-binding protein complex
 Pc12g05100 Transcription elongation complex subunit Cdc68
 Pc12g05980 Transcription elongation complex subunit Pob3
 Pc21g01240 Transcription initiation factor TFIID complex 60 kDa subunit Taf6
 Pc20g03580 Transcriptional coactivator Mbf1
 Pc21g16450 Transcriptional regulator Cwf13/SkiP
 Pc22g21830 Transcriptional regulator Rvb2
 Pc12g04590 Transcriptional repressor TupA/RocA
 Pc12g05910 Transformer-SR ribonucleoprotein
 Pc22g14170 tRNA methyltransferase subunit Gcd14
 Pc21g03370 U1 small nuclear ribonucleoprotein 70 kDa Snp1
 Pc22g00370 U3 small nucleolar ribonucleoprotein protein Lcp5

10. Proteasome-associated proteins

Pc13g09540 Alpha subunit of the 20S core complex of the 26S proteasome Scl1
 Pc15g00320 Alpha subunit of the 20S proteasome Pup2
 Pc14g01140 20S proteasome alpha-type subunit Pre10

Schizosaccharomyces pombe Cwf5
Schizosaccharomyces pombe Rrp5
Schizosaccharomyces pombe Srp2
Schizosaccharomyces pombe Srp1
Saccharomyces cerevisiae Sik1
Saccharomyces cerevisiae Srm1
Neosartorya fischeri NFIA_109800
Saccharomyces cerevisiae Brx1
Saccharomyces cerevisiae Yra1
Homo sapiens SNRPA
Schizosaccharomyces pombe Tcg
Ajellomyces capsulatus HCAG_05306
Neosartorya fischeri NFIA_078970
Saccharomyces cerevisiae Arp1
Saccharomyces cerevisiae Paf1
Saccharomyces cerevisiae Rex4
Saccharomyces cerevisiae Rcl1
Schizosaccharomyces pombe Sla1
Schizosaccharomyces pombe Vip1
Saccharomyces cerevisiae Rrp5
Saccharomyces cerevisiae Enp1
Saccharomyces cerevisiae Utp23
Aspergillus oryzae AO090026000192
Saccharomyces cerevisiae Sgf29
Aspergillus nidulans BimG
Aspergillus nidulans CotA
Saccharomyces cerevisiae Nhp2
Homo sapiens SmB
Homo sapiens SNRPA
Homo sapiens NCBP2
Saccharomyces cerevisiae Spt16/Cdc68
Saccharomyces cerevisiae Pob3
Saccharomyces cerevisiae Taf6
Saccharomyces cerevisiae Mbf1
Homo sapiens SNW1
Saccharomyces cerevisiae Rvb2
Saccharomyces cerevisiae Tup1
Aspergillus niger An07g02990
Saccharomyces cerevisiae Gcd14
Saccharomyces cerevisiae Snp1
Saccharomyces cerevisiae Lcp5

Saccharomyces cerevisiae Scl1
Saccharomyces cerevisiae Pup2
Saccharomyces cerevisiae Pre10

Pc20g11580 20S proteasome alpha-type subunit Pre5
Pc20g01470 20S proteasome beta-type subunit Pre8
Pc12g10270 proteasome component Pup1 precursor
Pc20g06040 26S protease regulatory subunit Rpt1
Pc12g09420 26S proteasome regulatory subunit Rpn7
Pc12g05300 26S proteasome regulatory subunit Rpn8
Pc22g23600 Ubiquitin C-terminal hydrolase Ubp6
Pc13g09510 Ubiquitin/S27a fusion protein Ubi1

11. Other proteins

Pc22g10140 Acetyl-CoA acetyltransferase Erg10
Pc13g03920 Acetyl-CoA carboxylase Acc1
Pc12g05420 O-acetylhomoserine (thiol)-lyase CysD
Pc22g14240 Adaptor-related protein complex AP-1, mu subunit 1
Pc16g05080 S-adenosyl-L-homocysteine hydrolase Sah1
Pc16g04380 S-adenosylmethionine synthetase MetK
Pc12g05310 Adenylate kinase Adk1
Pc21g22820 Alcohol dehydrogenase AlcA
Pc06g00180 Aldehyde dehydrogenase ALDH
Pc12g01130 Putative aldehyde reductase II
Pc21g20480 ATP citrate lyase, subunit Acl1
Pc20g07710 ATP sulfurylase Aps
Pc21g21940 Bifunctional pyrimidine biosynthesis protein Ura2
Pc16g00170 Putative BNR/Asp-box repeat domain protein
Pc22g20150 Carbamoyl phosphate synthetase large subunit Cpa2
Pc12g16500 Putative casein kinase I
Pc12g08280 Conserved hypothetical protein
Pc13g05450 Conserved hypothetical protein
Pc13g06930 Conserved hypothetical protein
Pc13g08890 Conserved hypothetical protein
Pc15g00300 Conserved hypothetical protein
Pc16g02070 Conserved hypothetical protein
Pc18g02660 Conserved hypothetical protein
Pc20g03660 Conserved hypothetical protein
Pc20g04140 Conserved hypothetical protein
Pc21g18130 Conserved hypothetical protein
Pc22g10200 Conserved hypothetical protein
Pc22g14390 Conserved hypothetical protein
Pc22g16300 Conserved hypothetical protein
Pc22g19790 Conserved hypothetical protein
Pc06g01640 Conserved protein with DUF1014 domain of unknown function
Pc22g23560 Conserved protein with DUF1690 domain
Pc22g11220 Conserved protein with DUF2012 domain
Pc22g03150 Conserved protein with DUF339 domain of unknown function
Pc12g04460 Conserved protein with DUF410 domain of unknown function
Pc22g18040 Conserved protein with UBX domain protein

Saccharomyces cerevisiae Pre5
Saccharomyces cerevisiae Pre8
Saccharomyces cerevisiae Pup1
Saccharomyces cerevisiae Rpt1
Saccharomyces cerevisiae Rpn7
Saccharomyces cerevisiae Rpn8
Saccharomyces cerevisiae Ubp6
Aspergillus nidulans Ubi1

Saccharomyces cerevisiae Erg10
Saccharomyces cerevisiae Acc1
Aspergillus nidulans CysD
Mus musculus AP47
Saccharomyces cerevisiae Sah1
Neurospora crassa MetK
Saccharomyces cerevisiae Adk1
Aspergillus nidulans AlcA
Aspergillus nidulans AldA
Penicillium marneffeii PMAA_102060
Sordaria macrospora Acl1
Penicillium chrysogenum Aps
Saccharomyces cerevisiae Ura2
Aspergillus clavatus ACLA_008170
Saccharomyces cerevisiae Cpa2
Aspergillus niger An07g06080
Aspergillus clavatus ACLA_064290
Aspergillus clavatus ACLA_079520
Aspergillus nidulans AN0493_2
Aspergillus clavatus ACLA_024430
Aspergillus clavatus ACLA_070370
Aspergillus nidulans AN1378.2
Aspergillus niger An18g04090
Aspergillus fumigatus AFUA_3G08690
Aspergillus niger An16g02650
Aspergillus fumigatus AFUB_054830
Aspergillus niger An16g09240
Aspergillus oryzae AO090020000577
Aspergillus oryzae AO070325000105
Aspergillus terreus ATEG_04407
Aspergillus clavatus ACLA_019940
Aspergillus fumigatus AFUB_096070
Neosartorya fischeri NFIA_037810
Aspergillus niger An01g08860
Aspergillus fumigatus AFUA_6G05050
Aspergillus terreus ATEG_05537

Pc21g16940 Cu,Zn superoxide dismutase SodC
 Pc21g04710 3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase AroF
 Pc20g03170 Putative deoxyribose-phosphate aldolase
 Pc14g01740 Enolase Eno
 Pc13g03280 Putative epimerase/dehydratase family protein
 Pc22g04400 Epsin-like protein Ent1
 Pc12g05820 Esterase
 Pc21g23210 Putative extracellular cell wall glucanase
 Pc22g24130 FMN dependent dehydrogenase
 Pc22g05750 Fructose-1,6-bisphosphatase FbpA
 Pc12g09190 GDP-mannose pyrophosphorylase A
 Pc22g10040 Glucosamine-6-phosphate deaminase
 Pc13g05350 Glutamate 5-kinase Pro1
 Pc22g00970 Glutamate decarboxylase GadA
 Pc22g08300 Glutamate dehydrogenase Gdh-1
 Pc20g08320 Probable glutathione degrading peptidase Dug1
 Pc22g25070 Glutathione dependent formaldehyde dehydrogenase Sfa1
 Pc16g13280 Glutathione reductase Glr1
 Pc13g07540 Putative glutathione (GSH) S-transferase Kappa (GSTK) family protein
 Pc21g14560 Glyceraldehyde-3-phosphate dehydrogenase GpdA
 Pc21g08590 Hydroxyacylglutathione hydrolase Glo2
 Pc20g07230 Inorganic diphosphatase lpp1
 Pc12g13280 Putative ketopantoate reductase family protein
 Pc13g02200 Putative lipase/hydrolase
 Pc22g20800 Mannitol-1-phosphate dehydrogenase
 Pc22g06040 Mannose-1-phosphate guanyltransferase Psa1/Mpg1
 Pc22g01670 MAP kinase MpkB
 Pc18g01840 Putative methyltransferase
 Pc21g02940 Putative molybdenum cofactor biosynthesis protein
 Pc12g04310 NAD-dependent formate dehydrogenase Fdh
 Pc21g01510 Putative NAD-binding Rossmann fold oxidoreductase family protein
 Pc12g00830 Putative NADP-dependent mannitol/sorbitol/xylulose dehydrogenase
 Pc20g09400 Putative oligopeptidase family protein
 Pc13g05260 L-ornithine N5-oxygenase SidA involved in siderophore biosynthesis SidA
 Pc18g01280 Oxysterol binding protein Kes1
 Pc16g07680 Putative pantetheine-phosphate adenyltransferase
 Pc21g05500 Pantothenate synthase Pan6
 Pc12g09360 Phosphoenolpyruvate carboxykinase acuF
 Pc12g10940 6-phosphogluconate dehydrogenase, decarboxylating Gnd1
 Pc16g04730 Phosphoglycerate kinase PgkA
 Pc21g01360 Putative phospholipase D (PLD)
 Pc21g02210 Putative phytanoyl-CoA dioxygenase family protein
 Pc13g08760 Protein phosphatase Ssd1
 Pc12g13180 Protein with xylose isomerase-like TIM barrel
 Pc13g07230 Pyruvate carboxylase Pyc

Aspergillus fumigatus SodC
Aspergillus nidulans AroF
Aspergillus niger An11g09730
Penicillium chrysogenum Eno
Aspergillus fumigatus AFUA_1G03490
Saccharomyces cerevisiae Ent1
Homo sapiens ESD
Neosartorya fischeri NFIA_009250
Mycobacterium smegmatis LA2M
Aspergillus oryzae FbpA
Homo sapiens GMPPA
Homo sapiens GNPDA1
Saccharomyces cerevisiae Pro1
Aspergillus oryzae GadA
Neurospora crassa Gdh-1
Saccharomyces cerevisiae Dug1
Saccharomyces cerevisiae Sfa1
Saccharomyces cerevisiae Glr1
Neosartorya fischeri NFIA_108300
Aspergillus niger GpdA
Saccharomyces cerevisiae Glo2
Saccharomyces cerevisiae lpp1
Aspergillus fumigatus AFUA_2G14497
Ustilago maydis UM02236.1
Streptococcus mutans MtlD
Saccharomyces cerevisiae Psa1
Aspergillus nidulans MpkB
Aspergillus fumigatus AFUA_8G01930
Aspergillus fumigatus AFUA_2G15550
Neurospora crassa Fdh
Neosartorya fischeri NFIA_091650
Aspergillus clavatus ACLA_074390
Aspergillus fumigatus AFUA_8G04730
Aspergillus fumigatus SidA
Saccharomyces cerevisiae Kes1
Saccharomyces cerevisiae Ygr277c
Saccharomyces cerevisiae Pan6
Aspergillus nidulans AcuF
Saccharomyces cerevisiae Gnd1
Penicillium chrysogenum PgkA
Aspergillus fumigatus AFUA_2G16520
Aspergillus fumigatus AFUA_2G15850
Saccharomyces cerevisiae Ssd1
Gibberella zeae FG03879.1
Aspergillus niger Pyc

Pc21g06300 Probable quinone oxidoreductase Zta1
 Pc22g21440 Ribose-5-phosphate isomerase
 Pc13g14570 Ribose-phosphate pyrophosphokinase Prs5
 Pc22g06690 Putative Rossmann-fold NAD(P)(+)-binding protein
 Pc22g16470 Septin AspA
 Pc16g01850 Septin Cdc10
 Pc12g16020 Serine hydroxymethyltransferase Shm2
 Pc12g04550 Serine/threonine protein kinase Gsk3
 Pc20g15270 Putative Ser/Thr protein phosphatase family protein
 Pc16g08740 Siderophore biosynthesis protein
 Pc12g14020 Synaptobrevin homolog Ykt6
 Pc12g10250 Putative TAM domain methyltransferase
 Pc22g02940 Thioredoxin reductase TrxB
 Pc21g16950 Transaldolase Tal1
 Pc13g12450 Transketolase Tkl1
 Pc16g02420 Type 2C protein phosphatase Ptc2
 Pc21g10370 UDP-glucose 4-epimerase Gal10
 Pc21g12790 UDP-glucose pyrophosphorylase Ugp1
 Pc21g01990 Putative urease accessory protein
 Pc12g07580 Urease accessory protein UreG
 Pc22g02900 Vacuolar targeting protein Atg24/Snx4
 Pc12g04720 Weakly conserved hypothetical protein
 Pc21g11540 Putative xylitol dehydrogenase
 Pc13g07960 Putative zinc-containing alcohol dehydrogenase
 Pc16g08460 Zinc containing alcohol dehydrogenase Mad2
 Pc16g12970 Putative zinc-dependent alcohol dehydrogenase
 Pc20g01390 Zinc metalloproteinase MepB

Saccharomyces cerevisiae Zta1
Escherichia coli RpiB
Saccharomyces cerevisiae Prs5
Aspergillus niger An16g06270
Aspergillus nidulans AspA
Saccharomyces cerevisiae Cdc10
Saccharomyces cerevisiae Shm2
Schizosaccharomyces pombe Gsk3
Neosartorya fischeri NFIA_055650
Escherichia coli lucB
Saccharomyces cerevisiae Ykt6
Aspergillus clavatus ACLA_089760
Penicillium chrysogenum TrxB
Saccharomyces cerevisiae Tal1
Saccharomyces cerevisiae Tkl1
Saccharomyces cerevisiae Ptc2
Saccharomyces cerevisiae Gal10
Saccharomyces cerevisiae Ugp1
Aspergillus clavatus ACLA_075040
Glycine max Eu3
Saccharomyces cerevisiae Snx4/Atg24
Aspergillus oryzae AO090701000010
Neosartorya fischeri NFIA_115270
Aspergillus niger An04g02690
Uromyces viciae-fabae Mad2
Aspergillus oryzae AO090011000369
Aspergillus fumigatus MepB

Ortholog / Highest scoring Blast homolog description	Expect value	C-terminal signal	Putative PTS2	Mr (kDa)	# of unique peptides	Protein probability (%)	Protein coverage
acetyltransferase	0.0	nAKL*		51	2	100	7%
acyl-coenzyme A:isopenicillin N acyltransferase	0.0	nARL*		40	16	100	58%
phenylacetyl-CoA ligase	0.0	gSKI*		63	3	100	11%
phenylacetyl-CoA ligase	0.0	kAKL*		63	5	100	13%
acyl-CoA dehydrogenase like protein	0.0	kSHL*		49	27	100	73%
acyl-CoA dehydrogenase	0.0	qSKV*		48	2	99	7%
acyl-CoA dehydrogenase family protein	0.0			57	7	100	21%
acyl-CoA synthase like protein	0.0		6 / sRLsgllgHF	63	10	100	24%
acyl-coenzyme A synthetase	0.0	kSKL*		75	13	100	27%
putative peroxisomal dehydratase	6e-141	kSKL*		36	14	100	56%
carnitine acetyl transferase	2e-153	kPKL*		73	15	100	31%
acyl-CoA synthetase	0.0	kAKL*		61	3	100	8%
Peroxisomal delta3,delta2-enoyl-CoA isomerase	1e-41	rHKL*		31	2	99	12%
enoyl-CoA hydratase	3e-113	[dSKL*]		32	2	99	13%
hypothetical protein	1e-115	kAKL*		30	3	100	13%
enoyl-CoA hydratase/isomerase family protein	3e-128	fEKL*		31	4	100	22%
enoyl-CoA hydratase/isomerase family protein	4e-123	pSKL*		34	2	99	11%
3-ketoacyl-CoA ketothiolase	0.0		4 / dRLsllsHL	44	15	100	51%
3-ketoacyl-CoA thiolase	0.0		6 / qRLnsvanQL	44	11	100	36%
hypothetical protein	0.0			43	3	100	10%
peroxisomal 3-keto-acyl-CoA thiolase	0.0		6 / qRLsqvssHF	43	12	100	40%
3-oxoacyl-(acyl-carrier-protein) reductase	7e-149		7 / qRLqalskQL	33	17	100	68%
putative acyl-CoA dehydrogenase	0.0	nAKI*		48	3	100	9%
long chain fatty acyl:CoA synthetase	5e-168			76	2	100	4%
conserved hypothetical protein	6e-134	sAKL*		28	12	100	58%
putative fatty-acyl coenzyme A oxidase (Pox1)	0.0	kSKL*		78	4	100	8%
peroxisomal 2,4-dienoyl-CoA reductase	3e-69	kSKL*		33	15	100	57%
hypothetical protein	0.0	IARF*		49	15	100	43%
trifunctional protein of beta-oxidation	0.0	kAKL*		97	34	100	48%
citrate synthase	0.0	gAKL*		52	9	100	24%
isocitrate lyase	0.0		222 / nRLvairaQA	60	30	100	70%
hypothetical protein	9e-159			34	19	100	72%
glyoxysomal malate synthase	0.0	aAKL*		61	13	100	30%
precursor of mitochondrial isocitrate dehydrogenase	0.0	kARL*		54	15	100	29%
hypothetical protein	0.0	sAKL*		63	18	100	42%
cytosolic aspartate transaminase	8e-123	sAKL*	9 / dRLsllsHIM	48	13	100	42%
amine oxidase	0.0			77	5	100	10%

FAD dependent oxidoreductase superfamily	2e-147		38	8	100	28%
hypothetical protein	1-e-170	rAKL*	40	6	100	19%
hypothetical protein	2e-171	qAKL*	46	5	100	15%
hypothetical protein	0.0	aAKL*	49	2	99	5%
fructosyl amino acid oxidase/sarcosine oxidase	0.0		48	9	100	29%
urate oxidase	2e-147	kAKL*	34	14	100	60%
ureidoglycolate hydrolase	1e-19	pAKL*	28	5	100	28%
putative catalase	0.0	sSRL*	55	3	100	12%
catalase	0.0	pARL*	57	6	100	16%
catalase-peroxidase	0.0	rPRL*	82	19	100	32%
putative epoxide hydrolase	1e-119	kARL*	29	2	100	14%
hypothetical protein	2e-76		18	3	100	19%
acyl-CoA thioesterase II	5e-163	[ISKI*]	40	8	100	29%
hypothetical protein	4e-137	[aANL*]	40	5	100	20%
hypothetical protein	5e-59	eAKL*	21	2	99	12%
thioesterase family protein	7e-69		19	3	100	22%
thioesterase family protein	3e-57	(dSKL*)	25	3	100	14%
retinal dehydrogenase 2	0.0	gTKL*	54	3	100	10%
Glucose-6-phosphate 1-epimerase	3e-54	kSRL*	35	2	99	14%
phosphotransferase enzyme family domain protein	3e-164	eGKL*	40	4	100	14%
betaine-aldehyde dehydrogenase	2e-158	fAKL*	53	4	100	20%
hypothetical protein	1e-73	sQRL*	16	3	100	18%
hypothetical protein	7e-90	[iSKM*]	31	5	100	23%
hypothetical protein	1e-152	eSKI*	39	6	100	21%
conserved hypothetical protein	2e-113	mEKL*	37	5	100	19%
putative oxidoreductase, 2-nitropropane dioxygenase family	3e-158	aSKL*	36	3	100	15%
hypothetical protein	0.0	tARL*	54	15	100	47%
putative mitochondrial cytochrome b2	0.0	kPKL*	55	8	100	27%
hypothetical protein	0.0	rARL*	55	5	100	13%
formate oxidase 1	0.0	sSKL*	66	10	100	26%
fructose-bisphosphate aldolase	2e-145	aGQL*	39	11	100	46%
fumarate reductase	1e-86		67	31	100	54%
hypothetical protein	4e-142	sSKL*	31	7	100	35%
glucose-6-phosphate 1-dehydrogenase	0.0	pNRL*	58	3	100	7%
glycerol 3-phosphate dehydrogenase (NAD+)	0.0	(aARL*)	48	4	100	16%
choline oxidase (CodA)	1e-178		61	2	99	6%
hypothetical protein	3e-166	kAKL*	38	2	99	9%
alcohol dehydrogenase, zinc-containing	7e-159	kSKL*	36	12	100	46%
oxidoreductase, short-chain dehydrogenase/reductase family	3e-130	kGRL*	29	8	100	37%
hypothetical protein	3e-167	sSKL*	36	4	100	17%
hypothetical protein	9e-172	vSKL*	38	11	100	44%
hypothetical protein	0.0	qSRL*	71	3	100	7%

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hypothetical protein	1e-49	kAKL*	17	4	100	30%
alpha/beta hydrolase fold protein	2e-109	aARL*	40	2	99	7%
hypothetical protein	9e-147	(ISRL*)	31	5	100	25%
conserved hypothetical protein	6e-141		31	5	100	33%
short chain dehydrogenase family protein	3e-135	[rAKI*]	34	6	100	26%
C-8 sterol isomerase	4e-89	qLKL*	26	2	100	12%
triose-phosphate-isomerase	0.0	nARI*	27	5	100	27%
Woronin body major protein	2e-77	gSRL*	60*	10	100	22%*
hypothetical protein	5e-68	fSKI*	27	2	99	13%
conserved hypothetical protein	3e-171	gSKL*	39	19	100	59%
integral membrane component of endoplasmic reticulum-derived COPII-coated vesicles	6e-43		24	3	100	17%
dynamamin-related protein Dnm1	0.0		88	2	99	3%
rho GTPase	1e-97		22	2	99	12%
peroxin-1	0.0		130	5	100	6%
peroxin-6	0.0		157	5	100	5%
peroxin-11	4e-135		26	2	99	10%
alpha-aminoadipyl-cysteinyl-valine synthetase	0.0		426	72	100	27%
isopenicillin N synthase	0.0		38	10	100	31%
protein involved in the regulation of penicillin biosynthesis	6e-91		32	3	100	13%
actin-associated protein	2e-111		48	2	99	7%
fimbrin, actin-bundling protein	0.0		71	4	100	11%
putative actin cortical patch component	0.0		65	5	100	14%
cofilin	3e-58		17	3	100	22%
actin-related protein 3	0.0		47	9	100	27%
ARP2/3 actin-organizing complex subunit Arc34	4e-75		37	5	100	17%
ARP2/3 actin-organizing complex subunit Sop2	7e-112		40	7	100	23%
putative Arp2/3 complex subunit Arc16	9e-93		20	3	100	22%
Subunit of the cytosolic chaperonin Cct ring complex	9e-129		46	3	100	6%
cytoskeletal adaptor protein	6e-177		47	3	100	11%
F-actin capping protein alpha-1 subunit	2e-38		30	2	100	10%
gamma-actin	0.0		42	12	100	47%
Constituent of 66S pre-ribosomal particles	2e-100		52	2	99	7%
EB1 family Mal3	3e-58		27	4	100	15%
conserved hypothetical protein	6e-61		25	2	99	9%
tubulin alpha-1 chain	0.0		50	10	100	41%
tubulin beta chain	0.0		50	12	100	43%
40S ribosomal protein S0	8e-91		32	5	100	19%
ribosomal protein 10 (rp10) of the small (40S) subunit	1e-104		29	12	100	48%
protein component of the small (40S) subunit	2e-94		28	6	100	32%
protein component of the small (40S) ribosomal subunit	2e-95		29	10	100	48%
protein component of the small (40S) ribosomal subunit	8e-113		29	5	100	20%

protein component of the small (40S) ribosomal subunit	3e-88	23	8	100	33%
protein component of the small (40S) ribosomal subunit	8e-89	27	7	100	37%
protein component of the small (40S) ribosomal subunit	9e-55	23	4	100	19%
protein component of the small (40S) ribosomal subunit	3e-78	23	7	100	50%
protein component of the small (40S) ribosomal subunit	4e-65	18	6	100	41%
ribosomal protein S12	1e-39	16	6	100	47%
protein component of the small (40S) ribosomal subunit	1e-63	17	7	100	34%
ribosomal protein S14	9e-60	16	8	100	62%
40S ribosomal protein S15 (S12)	1e-76	18	2	99	17%
protein component of the small (40S) ribosomal subunit	5e-63	16	6	100	45%
ribosomal protein 51 (rp51) of the small (40s) subunit	7e-51	16	3	100	26%
ribosomal protein S18	4e-64	18	10	100	55%
40S ribosomal protein S19	1e-71	16	7	100	47%
ribosomal protein S20	4e-35	13	2	99	17%
protein component of the small (40S) ribosomal subunit	3e-30	50*	3	100	8 %*
protein component of the small (40S) ribosomal subunit	2e-45	15	4	100	26%
protein component of the small (40S) ribosomal subunit	2e-13	12	4	100	31%
40S ribosomal protein S26E	8e-56	13	4	100	36%
ribosomal protein S28	1e-71	16	3	100	21%
protein component of the small (40S) ribosomal subunit	3e-12	7	2	100	32%
ribosomal protein L10e	7e-104	33	7	100	31%
60S acidic ribosomal protein P1-alpha 1	1e-19	11	2	100	40%
ribosomal protein A4	1e-19	11	2	100	38%
N-terminally acetylated protein component of the large (60S) ribosomal subunit	1e-80	24	3	100	19%
protein component of the large (60S) ribosomal subunit	1e-107	27	7	100	45%
protein component of the large (60S) ribosomal subunit	3e-165	44	22	100	53%
N-terminally acetylated protein component of the large (60S) ribosomal subunit	2e-110	40	13	100	53%
protein component of the large (60S) ribosomal subunit	2e-99	35	9	100	35%
protein component of the large (60S) ribosomal subunit	9e-47	22	9	100	44%
protein component of the large (60S) ribosomal subunit	4e-80	32	7	100	25%
ribosomal protein L4 of the large (60S) ribosomal subunit	1e-100	29	10	100	35%
protein component of the large (60S) ribosomal subunit	6e-59	22	8	100	46%
protein component of the large (60S) ribosomal subunit	1e-89	25	11	100	36%
protein component of the large (60S) ribosomal subunit	4e-74	20	5	100	29%
60S ribosomal protein L12	9e-67	18	4	100	36%
60S ribosomal protein L13	2e-43	26	11	100	43%
protein component of the large (60S) ribosomal subunit	1e-97	24	10	100	42%
protein component of the large (60S) ribosomal subunit	3e-58	20	3	100	17%
protein component of the large (60S) ribosomal subunit	7e-60	21	5	100	32%
protein component of the large (60S) ribosomal subunit	2e-54	23	8	100	37%
protein component of the large (60S) ribosomal subunit	2e-63	21	7	100	40%
protein component of the large (60S) ribosomal subunit	4e-52	18	3	100	22%
ribosomal protein L22	2e-18	14	4	100	40%
protein component of the large (60S) ribosomal subunit	4e-58	15	2	100	11%
ribosomal protein L23a	9e-40	16	8	100	47%

ribosome biogenesis protein RLP24	5e-41	22	2	99	9%
ribosomal protein L30 of the large (60S) ribosomal subunit	3e-41	18	8	100	42%
hypothetical protein	2e-58	36	5	100	16%
protein component of the large (60S) ribosomal subunit	2e-40	15	6	100	38%
cytoplasmic ribosomal protein of the large subunit	1e-47	23	6	100	27%
ribosomal protein of the large (60S) ribosomal subunit	6e-61	17	10	100	60%
hypothetical protein	1e-67	17	8	100	57%
protein component of the large (60S) ribosomal subunit	1e-34	14	4	100	31%
protein component of the large (60S) ribosomal subunit	3e-40	15	7	100	42%
protein component of the large (60S) ribosomal subunit	5e-30	10	2	100	25%
ribosomal protein L38	5e-14	9	2	100	19%
protein component of the large (60S) ribosomal subunit	9e-33	10	2	100	28%
ATPase of the ATP-binding cassette (ABC) family involved in 40S and 60S ribosome biogenesis	0.0	68	9	99	21%
co-chaperone that binds to Hsp82p and activates its ATPase activity	2e-58	36	8	100	40%
peptidylprolyl isomerase-like 1	2e-58	18	2	99	15%
cyclophilin-like peptidyl prolyl cis-trans isomerase	9e-82	19	9	100	65%
protein chaperone involved in regulation of the HSP90 and HSP70 functions	4e-64	47	2	99	8%
protein chaperone involved in regulation of the HSP90 and HSP70 functions	2e-115	46	6	100	24%
translation elongation factor1 subunit alpha	0.0	50	14	100	41%
elocation factor 1 beta	4e-55	25	2	99	13%
elongation factor 2 (EF-2),	0.0	94	11	100	15%
translation elongation factor EF-1 gamma	1e-84	46	3	100	11%
hypothetical protein	0.0	138	10	100	12%
translation initiation factor eIF-5A	7e-58	18	6	99	34%
putative FKBP-type peptidyl-prolyl isomerase	1e-38	13	2	99	20%
guanine nucleotide-binding protein beta subunit-like protein	2e-180	35	14	100	50%
heat shock protein 90 homolog	0.0	80	9	100	17%
heat shock protein Hsp88	0.0	79	3	100	6%
type II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1	2e-47	39	9	100	31%
heat shock protein 70	0.0	67	17	100	42%
Hsp70 protein that interacts with Zuo1p	2e-123	61	4	100	12%
heat shock protein 70	0.0	70	15	100	48%
component of mRNP complexes associated with polyribosomes	7e-16	56	6	100	17%
NADP(+)-dependent dehydrogenase, associated to translation machinery	1e-72	29	4	100	23%
nascent polypeptide-associated complex alpha subunit	3e-36	22	2	99	13%
basic transcription factor 3 isoform B	1e-38	17	4	100	28%
eukaryotic peptide chain release factor subunit 1	0.0	55	5	100	13%
peptidylprolyl isomerase D	7e-87	41	2	99	7%
cyclophilin family peptidyl-prolyl cis-trans isomerase	2e-56	18	3	100	19%
peptidyl-prolyl cis-trans isomerase B	2e-92	29	6	100	21%
protein that associates with ribosomes	9e-19	21	5	100	38%
protein involved in translation termination efficiency, mRNA poly(A) tail length and mRNA stability	1e-105	74	4	100	8%
L-PSP endoribonuclease family protein	1e-53	15	2	100	29%
protein component of the small (40S) ribosomal subunit	2e-36	18	7	100	35%
Possible U3 snoRNP protein involved in maturation of pre-18S rRNA	9e-08	44	6	100	21%

(sSRL*)

protein that interacts with ribosomes and acts with Cdc13p to maintain telomere structure	2e-11		35	13	100	46%
protein of unknown function that associates with ribosomes	2e-71		40	4	100	13%
regulator of ribosome synthesis	3e-36		25	5	100	28%
member of the DRG family of GTP-binding proteins, interacts with translating ribosomes	4e-152		42	4	100	16%
hypothetical protein	0.0		49	4	100	14%
exosome component 8	3e-22		42	2	99	9%
topoisomerase II-associated deadenylation-dependent mRNA-decapping factor	3e-42		91	2	99	4%
eukaryotic translation initiation factor 3, subunit 4 delta	6e-43		32	4	100	14%
subunit of the core complex of translation initiation factor 3(eIF3)	4e-102		37	4	100	11%
eukaryotic translation initiation factor 3 subunit D homolog	1e-153		65	3	100	10%
translation initiation factor eIF3f	1e-88		37	3	100	14%
eukaryotic translation initiation factor 4H	2e-15		53	4	100	9%
translation initiation factor eIF-4E	1e-56		27	5	100	22%
eukaryotic translation initiation factor 1A	4e-58		17	4	100	25%
translation initiation factor eIF4A	0.0		44	7	100	24%
eukaryotic translation initiation factor 4A	0.0		47	2	100	8%
eukaryotic translation initiation factor 4E type 2	6e-44		36	4	100	11%
constituent of 66S pre-ribosomal particles	2e-104		26	6	100	40%
essential iron-sulfur protein required for ribosome biogenesis and translation initiation	0.0		81	2	100	4%
eukaryotic translation initiation factor 2A	6e-96		70	2	99	4%
translation initiation factor eIF4G	9e-66		138	3	100	5%
elongation factor 3B	0.0		117	4	100	6%
beta subunit of the translation initiation factor eIF2	2e-51		34	3	100	9%
cell division control protein 48	0.0		90	10	100	21%
alpha subunit of the coatamer complex (COPI)	0.0		135	7	100	8%
essential beta-coat protein of the COPI coatamer	0.0		106	2	99	3%
coatamer subunit delta	2e-98		59	5	100	12%
coatamer protein complex, subunit gamma 2	0.0		100	3	100	5%
disulfide isomerase	3e-153	HDEL*	40	2	100	6%
dnaK-type molecular chaperone	0.0	HDEL*	74	15	100	28%
hypoxia up-regulated 1 precursor	2e-72	KDEL*	108	2	100	3%
peptidyl-prolyl isomerase	1e-43	KDEL*	14	3	100	22%
secretion related GTPase	3e-115		22	3	100	17%
integral ER membrane protein that regulates phospholipid metabolism	1e-20		30	2	99	9%
processing alpha glucosidase I	1e-150	HDEL*	93	4	100	8%
membrane protein that interacts with Yip1p to mediate membrane traffic	3e-29		19	2	99	13%
protein disulfide isomerase A	0.0	HDEL*	56	8	100	21%
PDI related protein A	4e-161	HDEL*	54	2	99	7%
GTPase-activating protein	0.0		85	3	100	5%
reticulon-like protein	5e-12		38	2	100	7%
C-3 sterol dehydrogenase	6e-47		46	2	100	6%
acetyl-coA hydrolase	0.0		58	6	100	17%
N-acetyl-gamma-glutamyl-phosphate reductase	0.0		97	3	100	5%

acetylnithine aminotransferase	7e-104	52	2	99	6%
acyl-Coenzyme A dehydrogenase, short/branched chain precursor	2e-123	47	2	99	6%
Probable alanine aminotransferase, mitochondrial	2e-146	60	2	99	6%
T subunit of the mitochondrial glycine decarboxylase complex	1e-85	51	4	100	13%
mitochondrial ornithine acetyltransferase	1e-109	51	6	100	17%
aspartate aminotransferase, mitochondrial	2e-153	47	11	100	34%
alpha subunit of the F1 sector of mitochondrial F1F0 ATP synthase	0.0	60	6	100	16%
ATP synthase beta chain, mitochondrial precursor	0.0	55	15	100	50%
gamma subunit of the F1 sector of mitochondrial F1F0 ATP synthase	8e-67	32	2	99	8%
mitochondrial branched-chain amino acid aminotransferase	2e-133	46	2	100	7%
putative protein of unknown function	4e-16	45	3	100	12%
coproporphyrinogen III oxidase	8e-95	50	12	100	28%
cysteine synthase (o-acetylserine (thiol)-lyase)	0.0	40	10	100	48%
cytochrome c	3e-52	14	2	99	19%*
mitochondrial cytochrome-c peroxidase	5e-70	40	6	100	19%
dihydrolipoamide dehydrogenase component (E3) of the pyruvate dehydrogenase complex	6e-171	54	5	100	14%
dihydrolipoamide acetyltransferase component (E2) of the pyruvate dehydrogenase complex	1e-116	71	7	100	20%
dihydrolipoyl transsuccinylase, component of the alpha-ketoglutarate dehydrogenase complex	1e-133	50	3	100	13%
dihydroxyacid dehydratase	0.0	65	2	99	5%
fumarase, converts fumaric acid to L-malic acid in the TCA cycle	0.0	58	10	100	23%
Putative mitochondrial protein of the fumarylacetoacetate (FAA) hydrolase family	3e-53	26	2	99	9%
heat shock protein 60	0.0	62	9	100	25%
matrix ATPase, subunit of the presequence translocase-associated protein import motor	0.0	73	10	100	22%
homo-isocitrate dehydrogenase	1e-128	38	6	100	20%
3-hydroxyacyl-CoA dehydrogenase	2e-48	34	2	99	11%
isocitrate dehydrogenase [NAD] subunit 1, mitochondrial	0.0	42	14	100	45%
subunit of mitochondrial NAD(+)-dependent isocitrate dehydrogenase	2e-131	42	10	100	36%
ketol-acid reductoisomerase	0.0	44	9	100	30%
mitochondrial malate dehydrogenase	2e-116	36	12	100	61%
2-methylcitrate synthase, mitochondrial precursor	0.0	51	5	100	12%
2-methylisocitrate lyase of the mitochondrial matrix	6e-150	66	3	100	9%
methylmalonate-semialdehyde dehydrogenase	0.0	63	4	100	10%
regulatory subunit of acetolactate synthase	3e-100	35	3	100	12%
mitochondrial aconitate hydratase	0.0	85	15	100	25%
mitochondrial ADP/ATP carrier	8e-180	34	8	100	26%
putative mitochondrial carrier protein	3e-158	54	2	99	7%
2-enoyl thioester reductase	2e-54	45	4	100	16%
peripheral mitochondrial membrane protein involved in mitochondrial protein import	4e-79	57	5	100	16%
antioxidant protein LsfA	3e-98	25	3	100	13%
matrix processing peptidase	0.0	38	2	99	8%
mitochondrial-processing peptidase subunit beta	0.0	53	2	99	7%
single-stranded DNA-binding protein essential for mitochondrial genome maintenance	2e-09	16	3	100	27%
1,4-benzoquinone reductase	3e-78	21	2	99	11%
nucleoside-diphosphate kinase	1e-68	17	5	100	39%
mitochondrial porin (voltage-dependent anion channel)	3e-47	36	5	100	19%

2-oxoglutarate dehydrogenase, component of the alpha-ketoglutarate dehydrogenase complex	0.0	119	14	100	20%
branched-chain alpha-keto acid dehydrogenase	3e-116	50	4	100	11%
E1 beta subunit of the pyruvate dehydrogenase (PDH) complex	1e-115	39	3	100	12%
alpha subunit (E1) of the pyruvate dehydrogenase complex	2e-144	45	9	100	31%
pyruvate dehydrogenase kinase isoform 2	3e-66	50	2	99	5%
mitochondrial ribosomal protein of the small subunit	2e-31	30	5	100	25%
hypothetical protein	6e-129	32	3	100	11%
mitochondrial ribosomal protein of the large subunit	5e-22	30	4	100	22%
mitochondrial ribosomal protein of the large subunit	7e-43	42	3	100	10%
54S ribosomal protein L9, mitochondrial	4e-60	32	4	100	19%
mitochondrial ribosomal protein of the large subunit	3e-09	27	2	100	12%
mitochondrial ribosomal protein of the large subunit	1e-32	39	2	100	6%
mitochondrial ribosomal protein of the large subunit	1e-29	38	2	99	6%
mitochondrial ribosomal protein of the large subunit	4e-14	26	3	100	17%
mitochondrial ribosomal protein of the large subunit	1e-07	41	2	99	9%
essential protein involved in rRNA processing and ribosome biogenesis	2e-09	41	4	100	15%
Small subunit of carbamoyl phosphate synthetase	0.0	49	3	100	8%
flavoprotein subunit of succinate dehydrogenase	0.0	71	14	100	31%
succinate-CoA ligase, GDP-forming, alpha subunit	1e-107	34	10	100	40%
beta subunit of succinyl-CoA ligase	2e-132	48	7	100	20%
sulfide:quinone oxidoreductase, mitochondrial	2e-103	48	2	99	8%
mitochondrial translation elongation factor Tu	8e-167	48	12	100	31%
subunit 2 of the ubiquinol cytochrome-c reductase complex	1e-27	48	5	100	18%
subunit 6 of the ubiquinol cytochrome-c reductase complex	3e-06	19	3	100	21%
ubiquinol-cytochrome-c reductase, a Rieske iron-sulfur protein of the cytochrome bc1 complex	3e-69	26	4	100	25%
2-hexaprenyl-6-methoxy-1,4-benzoquinone methyltransferase	1e-77	35	2	100	8%
leucine aminopeptidase 1	0.0	53	4	100	9%
aspartic protease	0.0	43	10	100	34%
carboxypeptidase Y	0.0	61	4	100	9%
GTPase required for transport during endocytosis and for correct sorting of vacuolar hydrolases	1e-65	27	2	99	10%
vacuolar protein sorting protein	2e-75	41	6	100	21%
non-essential protein of unknown function involved in vacuolar protein sorting	2e-96	40	4	100	18%
V-type proton ATPase subunit E	6e-69	26	3	100	14%
vacuolar serine protease	0.0	52	7	100	18%
subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase	0.0	56	2	99	6%
14-3-3 protein important for polarized growth	5e-127	29	2	99	10%
thymocyte nuclear protein 1	2e-42	36	5	100	25%
ATP-dependent RNA helicase	0.0	50	3	100	10%
ATP-dependent RNA helicase	0.0	73	11	100	21%
ATP-dependent RNA helicase	0.0	59	6	100	17%
ATP-dependent RNA helicase DHH1	0.0	59	8	100	18%
component of CCAAT binding complex	1e-114	29	2	99	7%
cell cycle control protein	2e-63	50	2	99	9%

essential protein involved in transcription regulation	0.0	50	7	100	25%
component of both the SWI/SNF and RSC chromatin remodeling complexes	3e-21	70	2	99	5%
cleavage and polyadenylation specific factor 5	1e-56	32	5	100	22%
ribosomal RNA-processing protein 9	7e-72	66	2	100	4%
curved DNA-binding protein	9e-61	44	8	100	30%
ATP-dependent RNA helicase	0.0	67	2	99	4%
developmental regulator	2e-77	39	4	100	15%
DNA repair protein RAD51	0.0	37	2	100	9%
replication factor A protein 1	2e-169	68	2	99	5%
replication factor C subunit 2	9e-99	42	2	99	11%
exosome component	1e-09	26	2	99	9%
protein involved in rRNA processing	3e-21	41	2	99	8%
U3 small nucleolar RNA-associated protein	1e-102	34	12	100	41%
nuclear pore complex-associated protein	2e-163	226	3	100	2%
FK506-binding protein 4	3e-151	53	2	99	8%
hypothetical protein	8e-34	16	2	100	25%
GTP-binding nuclear protein GSP1/Ran	2e-108	24	5	100	18%
heterokaryon incompatibility protein	0.0	86	5	99	8%
histone H1	2e-33	24	3	100	17%
histone variant H2AZ	6e-44	15	2	99	14%
histone H2B	5e-70	15	4	100	21%
histone required for chromatin assembly and chromosome function	2e-40	15	2	100	16%*
putative HMG box protein	1e-49	32	3	100	12%
predicted protein	7e-35	35	2	99	14%
co-chaperone that binds to and regulates Hsp90 family chaperones	3e-21	22	2	99	11%
importin subunit alpha	0.0	61	5	100	11%
RNA-binding protein that suppresses calcineurin deletion	7e-87	39	6	100	23%
pheromone receptor transcription factor	1e-35	23	2	99	15%
RNA binding protein, component of the U1 snRNP protein	1e-67	44	8	100	26%
pre-mRNA-processing factor 39	4e-39	67	3	100	7%
protein involved in mRNA turnover and ribosome assembly	8e-48	28	2	99	13%
nonhistone chromosomal protein 6B	4e-27	12	3	100	26%
poly(A)+ RNA-binding protein	2e-42	54	2	100	5%
splicing factor 3b, subunit 3	0.0	134	5	100	6%
thioredoxin reductase	2e-21	23	2	99	13%
nuclear pore complex protein	0.0	39	6	100	25%
protein involved in pre-rRNA processing	9e-153	63	5	100	13%
nucleolar protein required for 60S ribosome subunit biogenesis	6e-51	28	3	100	17%
nucleolar protein	3e-51	53	4	100	12%
nuclear pore complex protein Nup49	5e-06	49	2	100	7%
nucleosome assembly protein I	1e-74	46	4	100	9%
nucleosome assembly protein	8e-91	40	3	100	10%
poly(A) polymerase	1e-172	66	4	100	10%
poly(A) binding protein	1e-146	80	3	100	5%
pre-mRNA-splicing helicase BRR2	0.0	249	4	100	3%

RNA-binding protein	3e-60	42	2	100	8%
pre-mRNA-processing protein 5	5e-153	50	4	100	15%
pre-mRNA splicing factor	1e-25	35	6	100	23%
pre-mRNA-splicing factor	1e-26	44	5	100	14%
ribosome biosynthesis protein Sik1	2e-168	57	3	100	7%
regulator of chromosome condensation	5e-81	61	3	100	9%
ribosomal biogenesis protein Gar2	4e-126	51	3	100	11%
ribosome biogenesis protein	1e-70	40	3	100	12%
RNA annealing protein	5e-21	26	4	100	24%
small nuclear ribonucleoprotein polypeptide A	2e-23	20	2	99	16%
single-stranded telomeric binding protein	3e-15	40	7	100	25%
predicted protein	4e-111	54	6	100	16%
RNA binding domain protein	2e-66	35	5	100	23%
protein of unknown function, rich in asparagine residues	3e-68	65	5	100	9%
RNA polymerase II-associated protein 1	3e-12	54	3	100	9%
RNA exonuclease possibly involved in pre-rRNA processing and ribosome assembly	1e-53	33	2	99	8%
RNA terminal phosphate cyclase-like protein involved in rRNA processing	3e-49	42	5	100	16%
La autoantigen homolog	2e-33	45	3	100	11%
RNA-binding protein	4e-33	28	4	100	18%
ribosomal RNA processing protein	0.0	199	5	100	4%
essential nuclear protein 1	7e-85	59	2	99	5%
rRNA-processing protein	2e-22	36	2	99	7%
hypothetical protein	1e-65	31	5	100	21%
SAGA histone acetyltransferase complex 29 kDa subunit	4e-21	36	3	100	9%
phosphoprotein phosphatase	0.0	37	3	100	11%
serine/threonine protein kinase required for polar growth and hyphal elongation	0.0	73	2	100	4%
H/ACA ribonucleoprotein complex subunit 2	1e-32	24	4	100	26%
small nuclear ribonucleoprotein polypeptides B and B1	9e-22	21	2	99	18%
small nuclear ribonucleoprotein polypeptide A	5e-35	27	7	100	34%
nuclear cap binding protein subunit 2	5e-46	21	5	100	35%
subunit of the heterodimeric FACT complex	0.0	115	3	100	4%
subunit of the heterodimeric FACT complex	4e-133	62	2	99	5%
transcription initiation factor TFIID subunit 6	3e-91	48	2	99	6%
multiprotein bridging factor 1	4e-30	17	4	100	27%
SKI-interacting protein	1e-106	65	3	100	7%
essential protein involved in transcription regulation	0.0	51	6	100	18%
general repressor of transcription	1e-106	64	9	100	22%
hypothetical protein	4e-86	37	4	100	15%
tRNA (adenine-N(1)-)-methyltransferase catalytic subunit TRM61	8e-59	57	2	99	6%
U1 small nuclear ribonucleoprotein 70 kDa homolog	4e-29	44	7	99	26%
U3 small nucleolar ribonucleoprotein protein	1e-16	42	2	99	7%
proteasome component C7-alpha	6e-78	28	6	100	25%
alpha subunit of the 20S proteasome	3e-99	27	4	100	24%
proteasome component C1	3e-70	29	5	100	17%

20S proteasome alpha-type subunit	2e-71	28	3	100	16%
20S proteasome beta-type subunit	8e-99	30	2	100	8%
beta-type subunit of 20S proteasome	2e-93	30	6	100	26%
26S protease regulatory subunit 7 homolog	0.0	49	2	100	5%
essential, non-ATPase regulatory subunit of the 26S proteasome	2e-77	55	2	99	7%
essential, non-ATPase regulatory subunit of the 26S proteasome	8e-107	39	6	100	24%
ubiquitin carboxyl-terminal hydrolase 6	4e-77	65	5	100	11%
ubiquitin / ribosomal protein S27a	1e-67	18	3	100	21%
cytosolic acetyl-CoA C-acetyltransferase	2e-130	41	4	100	13%
acetyl-CoA carboxylase	0.0	253	12	100	7%
O-acetylhomoserine (thiol)-lyase	0.0	47	3	100	11%
adaptor-related protein complex AP-1, mu subunit 1	2e-174	51	4	100	13%
S-adenosyl-L-homocysteine hydrolase	0.0	49	5	100	13%
S-adenosylmethionine synthase	0.0	42	11	100	41%
adenylate kinase	4e-94	28	2	99	11%
alcohol dehydrogenase I (ADH I)	4e-180	37	8	100	36%
aldehyde dehydrogenase ALDH	0.0	54	2	99	7%
aldehyde reductase II	6e-87	39	5	100	18%
ATP citrate lyase	0.0	72	8	100	15%
Atp Sulfurylase	0.0	64	6	100	13%
bifunctional carbamoylphosphate synthetase-aspartate transcarbamylase	0.0	247	5	100	3%
BNR/Asp-box repeat domain protein	3e-146	40	7	100	25%
carbamoyl phosphate synthetase large subunit	0.0	128	7	100	9%
hypothetical protein	0.0	42	6	100	18%
hypothetical protein	0.0	27	3	100	8%
conserved hypothetical protein	5e-75	32	4	100	20%
hypothetical protein	2e-46	15	2	99	21%
conserved hypothetical protein	3e-155	41	2	99	10%
conserved hypothetical protein	3e-63	30	2	99	9%
hypothetical protein	9e-71	21	6	100	45%
hypothetical protein	6e-100	32	3	100	14%
hypothetical protein	4e-56	37	2	99	7%*
hypothetical protein	0.0	61	3	100	9%
conserved hypothetical protein	3e-59	27	2	99	12%
hypothetical protein	4e-67	38	3	100	10%
hypothetical protein	0.0	61	2	99	6%
hypothetical protein	3e-119	44	4	100	13%
conserved hypothetical protein	1e-58	30	3	100	14%
DUF1014 domain protein	1e-76	24	5	100	27%
conserved hypothetical protein	6e-70	22	2	99	10%
hypothetical protein	5e-80	27	2	99	7%
hypothetical protein	1e-117	35	2	99	6%
DUF410 domain protein	4e-169	38	8	100	35%
conserved hypothetical protein	1e-124	35	2	99	17%

Cu,Zn superoxide dismutase	2e-74	16	5	100	38%
3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase	9e-178	40	3	100	15%
2-deoxyribose-5-phosphate aldolase family protein	2e-80	46	3	100	9%
enolase	0.0	47	16	100	57%
epimerase/dehydratase family protein	2e-173	42	2	99	7%
epsin-like protein required for endocytosis and actin patch assembly	8e-47	63	2	100	7%
esterase D	3e-86	31	5	100	17%
extracellular cell wall glucanase Crf1/allergen Asp F9	6e-98	36	2	99	8%
L-lactate 2-monoxygenase	5e-78	44	10	100	31%
fructose-1,6-bisphosphatase	4e-178	38	7	100	20%
mannose-1-phosphate guanyltransferase alpha	6e-99	48	3	100	8%
glucosamine-6-phosphate deaminase 1	2e-97	40	11	100	34%
glutamate 5-kinase	1e-116	47	4	100	12%
glutamate decarboxylase	0.0	59	3	100	8%
NAD-specific glutamate dehydrogenase	0.0	123	10	100	15%
probable glutathione degrading di- and tri-peptidase	1e-155	53	2	99	4%
glutathione-dependent formaldehyde dehydrogenase	1e-145	40	7	100	22%
glutathione oxidoreductase	3e-127	51	5	100	23%
putative 2-hydroxychromene-2-carboxylate isomerase	4e-86	24	3	100	17%
glyceraldehyde-3-phosphate dehydrogenase	3e-171	36	13	100	55%
hydroxyacylglutathione hydrolase, cytoplasmic isozyme	3e-61	31	3	100	15%*
cytoplasmic inorganic pyrophosphatase	2e-113	33	6	100	21%
ketopantoate reductase family protein	4e-134	35	3	100	11%
hypothetical protein	5e-40	27	3	100	16%
mannitol-1-phosphate 5-dehydrogenase	2e-74	42	7	100	21%
mannose-1-phosphate guanyltransferase	7e-155	40	8	100	31%
mitogen-activated protein kinase	0.0	41	2	99	5%
methyltransferase LaeA-like	3e-128	38	4	100	13%
molybdenum cofactor biosynthesis protein Gephyrin	0.0	75	3	100	7%
formate dehydrogenase	5e-179	50	5	100	15%
hypothetical protein	1e-130	36	11	100	34%
putative sorbitol/xylulose reductase	4e-130	29	5	100	23%
oligopeptidase family protein	0.0	79	4	100	6%
L-ornithine N5-oxygenase SidA	0.0	55	4	100	12%
member of the oxysterol binding protein family	1e-92	46	2	100	9%
putative pantetheine-phosphate adenyllyltransferase involved in the biosynthesis of coenzyme A	2e-17	44	4	100	14%
pantothenate synthase	2e-56	39	2	99	5%
phosphoenolpyruvate carboxykinase	0.0	66	3	100	8%
6-phosphogluconate dehydrogenase, decarboxylating	0.0	56	17	100	41%
phosphoglycerate kinase	0.0	44	3	100	11%
phospholipase D	0.0	128	2	99	2%
phytanoyl-CoA dioxygenase family protein	5e-135	35	5	100	24%
protein with a role in maintenance of cellular integrity	0.0	151	6	100	7%
hypothetical protein	1e-75	28	2	99	7%
pyruvate carboxylase	0.0	131	16	100	19%

probable quinone oxidoreductase	6e-80	35	6	100	26%
ribose 5-phosphate isomerase B	3e-25	17	2	100	15%
ribose-phosphate pyrophosphokinase 5	1e-113	47	3	100	10%
hypothetical protein	3e-113	26	5	100	24%
septin	0.0	43	4	100	13%
component of the septin ring of the mother-bud neck that is required for cytokinesis	8e-106	39	3	100	13%
cytosolic serine hydroxymethyltransferase	0.0	52	3	100	8%
protein kinase	4e-156	45	2	99	5%
Ser/Thr protein phosphatase family protein	0.0	73	10	100	25%
aerobactin siderophore biosynthesis protein lucB	4e-34	54	2	99	5%
vesicle membrane protein (v-SNARE) with acyltransferase activity	3e-61	24	2	99	10%
putative TAM domain methyltransferase	2e-138	40	2	99	8%
thioredoxin reductase	0.0	36	3	100	13%
transaldolase	1e-110	35	4	100	14%
transketolase 1	0.0	74	2	99	4%
protein phosphatase type 2C	3e-80	48	2	99	7%
UDP-glucose 4-epimerase	2e-117	40	2	99	6%
UDP-glucose pyrophosphorylase	0.0	58	2	99	7%
urease accessory protein UreD	1e-131	44	3	100	12%
Ni-binding urease accessory protein UreG	5e-84	29	4	100	24%
sorting nexin protein/autophagy-related protein 24	3e-70	56	2	100	8%
hypothetical protein	3e-22	37	2	99	7%
xylitol dehydrogenase	9e-176	38	6	100	19%
hypothetical protein	3e-160	37	6	100	19%
major alcohol dehydrogenase	4e-117	37	5	100	19%
hypothetical protein	2e-170	43	3	100	11%
zinc metalloproteinase	0.0	81	4	100	10%

Notes

Protein has a C-terminal kSML*; some orthologs in other fungi have a PTS1

Orthologs have a PTS1; Intron incorrectly spliced; corrected protein sequence has the indicated PTS1

Highly conserved protein without a PTS

Possible internal PTS2 sequence

Protein has a C-terminal KASL*; orthologs in other fungi have a related C-terminus or a PTS1

Protein has a C-terminal sSML*; orthologs in other fungi have a related C-terminus or a PTS1

Protein has C-terminal IASL*; orthologs in *Aspergilli* have a PTS1

Orthologs have a PTS1; Intron incorrectly spliced; corrected protein sequence has the indicated PTS1

Orthologs have a PTS1; Intron incorrectly spliced; corrected protein sequence has the indicated PTS1

C-terminus is tQRI*; orthologs in other fungi have C-termini related to PTS1

Orthologs have no PTS1; only *Coccidioides immitis* has a nEKL*

Orthologs have a PTS1; Intron incorrectly spliced; corrected protein sequence has the indicated PTS1

Possible internal PTS2 sequence

Orthologs in other fungi have no PTS1, but manual annotation reveals a conserved additional intron in *Aspergillus* sequences in Genbank that reveals a PTS1

C-terminus is rAVL*; Orthologs in other fungi have a PTS1

Mainly present in bacteria; PTS1 not conserved in the few available fungal orthologs

Orthologs have a PTS1; Intron incorrectly spliced; corrected protein sequence has the indicated PTS1

*ORF should be only the C-terminal 207 aa; all peptides come from this part of the protein; coverage = 56%

membrane protein

Peroxisomal membrane protein

*Fusion protein caused by incorrect splicing; only peptides were identified from the C-terminal 88 aa protein; coverage = 42 %. This represents the ribosomal protein.

membrane protein
membrane protein

membrane protein

*protein is too long, orthologs are ca. 111 aa; coverage = 23 %

membrane protein
membrane protein

peripheral membrane protein

membrane protein

*protein is too long at N-terminus, orthologs are ca. 103 aa; coverage = 21 %

Only N-terminal part of the protein shows similarity to putative orthologs

*Protein is too long at N-terminus, orthologs are ca. 212 aa; coverage = 12 %

*N-terminal 22 amino acids are not present in orthologs; coverage = 16 %