**Supplementary Table 1.** Mitochondrial proteins identified by mass spectrometry from mitochondrial extracts of wild type (JGY43) and PAS kinase-deficient yeast (JGY1244), but not CBF1-deficient yeast. Proteins are divided into functional categories and are listed by protein name, accession number, the number of times the protein was retrieved (out of three biological replicates), the average retrieval number of the protein as well as the standard deviation of the retrieval number for strains 43 and 1244, and the description of the protein. Retrieval numbers are included as an indication of confidence Protein functions were based off of their gi description in NCBI, or the description in the Saccharomyces Genome Database ([Cherry et al., 2012](#_ENREF_8); [Engel et al., 2014](#_ENREF_17)).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene/**  **protein** | **Accession #** | **# strain 43** | **Ave. # strain 43** | **Std. dev. strain 43** | **# strain 1244** | **Ave. # strain 1244** | **Std. dev. strain 1244** | **Description** |
| TCA/Respiration/Metabolism | | | | | | | | |
| Idh2 | gi|6324709 | 3 | 20.3 | 3.2 | 3 | 24.7 | 9.0 | isocitrate dehydrogenase |
| Nde1 | gi|6323794 | 3 | 56.0 | 31.5 | 3 | 64.0 | 18.4 | Mito. external NADH dehydro. |
| Leu4 | gi|6324225 | 3 | 26.3 | 7.2 | 3 | 43.3 | 20.6 | α-isopropylmalate synthase |
| Pda1 | gi|6321026 | 3 | 38.7 | 4.6 | 3 | 49.0 | 23.4 | α-subunit pyruvate dehydro. |
| Kgd2 | gi|6320352 | 3 | 35.0 | 10.8 | 3 | 50.3 | 8.4 | α-ketoglutarate dehydro. subunit |
| Cyt1 | gi|6324639 | 3 | 71.3 | 27.7 | 3 | 320.7 | 214.5 | Cytochrome c1 |
| Lat1 | gi|6324258 | 3 | 61.3 | 28.0 | 3 | 80.7 | 20.5 | pyruvate dehydro. component (E2) |
| Ald5 | gi|6320917 | 3 | 55.7 | 3.5 | 3 | 71.3 | 18.6 | Aldehyde dehydro. |
| Ilv1 | gi|6320930 | 3 | 56.7 | 8.3 | 3 | 65.7 | 15.5 | threonine deaminase |
| Alo1 | gi|6323553 | 3 | 67.7 | 19.4 | 3 | 81.0 | 16.8 | D-arabinono-1 |
| Cdc19 | gi|6319279 | 3 | 118.7 | 115.5 | 3 | 40.0 | 12.0 | Pyruvate kinase |
| Fat2 | gi|6319699 | 3 | 170.7 | 195.2 | 3 | 51.7 | 30.2 | Probable AMP-binding protein |
| Ilv6 | gi|6319837 | 3 | 53.0 | 11.5 | 3 | 76.3 | 28.3 | Acetolactate synthase reg.subunit |
| Sdh2 | gi|6322987 | 3 | 77.7 | 32.9 | 3 | 219.3 | 176.8 | Succinate dehydro. subunit |
| Lys4 | gi|6320440 | 3 | 88.3 | 20.6 | 3 | 192.0 | 96.1 | homoaconitase |
| Adh1 | gi|6324486 | 3 | 129.3 | 49.0 | 3 | 89.7 | 27.4 | Alcohol dehydro. |
| Ccp1 | gi|6322919 | 3 | 61.7 | 26.9 | 3 | 48.3 | 18.6 | Cytochrome-c peroxidase |
| Pdc1 | gi|6323073 | 3 | 132.0 | 101.8 | 3 | 88.3 | 48.2 | pyruvate decarboxylase |
| Gpd1 | gi|6320181 | 3 | 151.7 | 131.9 | 3 | 64.3 | 22.2 | glycerol-3-phosphate dehydro. |
| Pdh1 | gi|6325258 | 3 | 94.7 | 8.1 | 2 | 203.0 | 0.0 | putative 2-methylcitrate dehydratase |
| Eno2 | gi|6321968 | 2 | 201.0 | 120.2 | 3 | 72.0 | 32.9 | enolase |
| Aim45 | gi|6325261 | 3 | 99.7 | 35.9 | 1 | 69.0 | 0.0 | putative mammalian ETF-α ortholog |
| Cdc48 | gi|6320077 | 2 | 167.0 | 0.0 | 3 | 71.0 | 26.5 | microsomal ATPase |
| Gpm1 | gi|6322697 | 3 | 158.0 | 80.9 | 3 | 81.0 | 48.9 | Phosphoglycerate mutase |
| Gsy2 | gi|6323287 | 2 | 139.0 | 99.0 | 2 | 57.0 | 26.9 | Glycogen synthase |
| Cyb2 | gi|6323587 | 2 | 79.0 | 8.5 | 2 | 97.0 | 0.0 | Cytochrome b2 |
| **Protein Expression** | | | | | | | | |
| Mss51 | gi|6323232 | 3 | 91.3 | 18.5 | 2 | 128.5 | 75.6 | involved mRNA maturation of COX1 |
| Rps3 | gi|6324151 | 3 | 103.3 | 43.2 | 3 | 74.3 | 13.3 | Ribosomal protein S3 |
| Eft1 | gi|6324707 | 3 | 108.3 | 81.1 | 3 | 49.0 | 14.7 | translation elongation factor2 |
| Eft2 | gi|6320593 | 3 | 108.3 | 81.1 | 3 | 49.0 | 14.7 | translation elongation factor 2 |
| Ssb1 | gi|6319972 | 3 | 90.7 | 21.2 | 3 | 62.3 | 15.5 | cytoplasmic HSP70 family member |
| Scp160 | gi|6322381 | 2 | 408.5 | 122.3 | 2 | 99.0 | 17.0 | G-protein receptor of mating |
| Mrpl1 | gi|6320321 | 1 | 72.0 | 0.0 | 1 | 394.0 | 0.0 | Mito.large subunit ribosomal protein |
| **Secretion/Export/Import** | | | | | | | | |
| Mic60 | gi|6322868 | 3 | 99.7 | 70.1 | 2 | 172.0 | 0.0 | Component of the MICOS complex |
| Kar2 | gi|6322426 | 3 | 89.0 | 30.3 | 3 | 188.7 | 118.3 | mammalian BiP (GPR78) homolog |
| Tom70 | gi|6324208 | 3 | 60.7 | 11.9 | 3 | 45.3 | 8.1 | mito. specialized import receptor |
| Tim44 | gi|6322167 | 3 | 96.0 | 14.2 | 3 | 188.7 | 96.5 | 48.8 kDa mito. import protein |
| **Yeast Growth/Division** | | | | | | | | |
| Mmd1 | gi|6322138 | 3 | 51.7 | 14.4 | 3 | 78.3 | 33.4 | Deoxyhypusine hydroxylase |
| Cdc12 | gi|6321899 | 2 | 87.0 | 1.4 | 3 | 133.3 | 103.9 | 10nm filaments of septin component |
| **Structural** | | | | | | | | |
| Om45 | gi|6322055 | 3 | 29.0 | 18.0 | 3 | 64.7 | 20.6 | mito. outer membrane protein |
| Pex11 | gi|6324425 | 2 | 67.5 | 7.8 | 3 | 150.7 | 95.8 | Peroxisomal membrane protein |
| **Stress Response/Sporulation** | | | | | | | | |
| Ssb2 | gi|6324120 | 3 | 90.7 | 21.2 | 2 | 70.0 | 11.3 | Heat shock protein of HSP70 family |
| Hsp82 | gi|6325016 | 3 | 207.3 | 224.0 | 3 | 60.0 | 8.9 | 82 kDa heat shock protein |
| Hsc82 | gi|6323840 | 3 | 207.3 | 224.0 | 3 | 60.0 | 8.9 | constitutive heat shock protein |
| Ssa1 | gi|6319314 | 3 | 93.7 | 41.8 | 3 | 30.0 | 21.8 | Heat shock protein of HSP70 family |
| **Signal Transduction** | | | | | | | | |
| Rho1 | gi|6325423 | 2 | 99.5 | 36.1 | 3 | 85.3 | 51.0 | GTP-binding ras-like protein |
| **Amino Acid Synthesis** | | | | | | | | |
| Erg6 | gi|6323635 | 3 | 86.3 | 41.6 | 3 | 52.0 | 10.1 | Delta(24)-sterol C-methyltransferase |
| Bat1 | gi|6322002 | 3 | 81.0 | 7.8 | 3 | 135.0 | 73.0 | branched-chain amino acid trans. |
| **DNA Replication/Recombination** | | | | | | | | |
| Abf2 | gi|6323717 | 1 | 94.0 | 0.0 | 1 | 189.0 | 0.0 | HMG-1 homolog |
| **Unknown** | | | | | | | | |
| Aim9 | gi|6320924 | 3 | 60.3 | 11.5 | 3 | 85.0 | 48.5 | Yer080wp |

Abbreviations include dehydrogenase (dehydro.), regulatory (reg.), mitochondrial (mito), transaminase (trans.), methyltransferase (methyl.).

**Supplementary Table 2**. Mitochondrial proteins identified by mass spectrometry from mitochondrial extracts of CBF1-deficient yeast but not wild type (JGY43) and PAS kinase-deficient yeast (JGY1244). Proteins are divided into functional categories and are listed by protein name, accession number, the number of times the protein was retrieved (out of three biological replicates), the average retrieval number of the protein as well as the standard deviation of the retrieval number, and the description of the protein. Retrieval numbers are included as an indication of confidence. Protein functions were based off of their gi description in NCBI, or the description in the Saccharomyces Genome Database ([Cherry et al., 2012](#_ENREF_8); [Engel et al., 2014](#_ENREF_17)).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene/**  **Protein** | **Accession #** | **#** | **Ave.**  **#** | **Std.**  **dev.** | **Description** |
| TCA/Respiration/Metabolism | | | | | |
| Ale1 | gi|6324749 | 1 | 63 | 0 | Lysophospholipid acyltransferase |
| Sdh1 | gi|6322416 | 1 | 24 | 0 | Succinate dehydrogenase |
| Pgi1 | gi|6319673 | 1 | 85 | 0 | Glucose-6-phosphoate isomerase |
| Glt1 | gi|6320030 | 1 | 95 | 0 | Glutamate synthase |
| Protein Expression | | | | | |
| Aim10 | gi|6320931 | 1 | 40 | 0 | protein with similarity to tRNA synthetases |
| Rps25b | gi|6323365 | 1 | 89 | 0 | Ribosomal protein S25B (S31B) (rp45) (YS23) |
| Rps25a | gi|6321464 | 1 | 89 | 0 | Ribosomal protein S25A (S31A) (rp45) (YS23 |
| Hsh155 | gi|6323944 | 1 | 90 | 0 | U2-snRNP associated splicing factor |
| Secretion/Export/Import | | | | | |
| Sna1 | gi|6320482 | 3 | 53 | 0.7 | Hypothetical transmembrane protein |
| Structural | | | | | |
| Mas6 | gi|6324344 | 1 | 40 | 0 | Mitochondrial inner membrane protein of the Tim23 complex |
| Mdm20 | gi|6324497 | 1 | 96 | 0 | Subunit of the NatB N-terminal acetyltransferase |
| Stress Response/Sporulation | | | | | |
| Ynl194cp | gi|6324135 | 2 | 60 | 0 | sporulation and plasma membrane sphingolipid content |
| Signal Transduction | | | | | |
| Yel043wp | gi|6320792 | 1 | 98 | 0 | Cytoskeleton protein involved in intracellular signaling |
| Ypr097wp | gi|6325354 | 1 | 94 | 0 | Contains a PX domain and binds phoshoinositides |
| Vesicles/Endocytosis | | | | | |
| Pal1 | gi|6320555 | 1 | 91 | 0 | Protein of unknown function maybe involved in endocytosis |

Supplementary Table 3. Mitochondrial proteins identified by mass spectrometry from mitochondrial extracts of wild type (JGY43) yeast but not CBF1-deficient (JGY1277) or PAS kinase-deficient yeast (JGY1244). Proteins are divided into functional categories and are listed by protein name, accession number, the number of times the protein was retrieved (out of three biological replicates), the average retrieval number of the protein as well as the standard deviation of the retrieval number, and the description of the protein. Retrieval numbers are included as an indication of confidence. Protein functions were based off of their gi description in NCBI, or the description in the Saccharomyces Genome Database ([Cherry et al., 2012](#_ENREF_8); [Engel et al., 2014](#_ENREF_17)).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene/**  **Protein** | **Accession #** | **#** | **Ave. #** | **Std. dev.** | **Description** |
| TCA/Respiration/Metabolism | | | | | |
| Mcx1 | gi|6319704 | 2 | 331.5 | 6.4 | mitochondrial ClpX |
| Oac1 | gi|6322729 | 2 | 346.0 | 162.6 | mitochondrial oxaloacetate transport protein |
| Afg1 | gi|6320783 | 2 | 353.5 | 252.4 | ATPase family gene |
| Leu9 | gi|6324682 | 2 | 357.0 | 7.1 | isopropylmalate synthase |
| Pos5 | gi|6325068 | 2 | 371.5 | 2.1 | mitochondrial NADH kinase |
| Pex22 | gi|6319263 | 2 | 386.0 | 36.8 | peroxisomal membrane protein |
| Wbp1 | gi|6320835 | 3 | 387.3 | 22.4 | oligosaccharyl transferase glycoprotein complex |
| Ecm31 | gi|6319653 | 2 | 402.0 | 106.1 | 3-methyl-2-oxobutanoate hydroxymethyltransferase |
| Oar1 | gi|6322795 | 2 | 414.0 | 7.1 | 3-oxoacyl-[acyl-carrier-protein] reductase |
| Rpn7 | gi|6325365 | 2 | 415.5 | 106.8 | subunit of the regulatory particle of the proteasome |
| Coa1 | gi|6322034 | 2 | 419.5 | 38.9 | assembly of the cytochrome c oxidase complex |
| Gif1 | gi|6322215 | 2 | 430.0 | 26.9 | (putative) involved in cell cycle control; Gif1p |
| Lip5 | gi|6324770 | 2 | 448.5 | 122.3 | lipoic acid synthase |
| Pkp1 | gi|6322147 | 2 | 457.5 | 99.7 | mitochondrial protein kinase |
| Protein expression | | | | | |
| Cbp6 | gi|6319596 | 2 | 205.0 | 48.1 | translational activator of COB mRNA |
| Mrp20 | gi|6320613 | 2 | 244.0 | 169.7 | mitochondrial ribosomal large subunit protein |
| Mrpl22 | gi|6324152 | 3 | 271.3 | 127.2 | mitochondrial ribosomal large subunit protein |
| Mrpl49 | gi|6323472 | 3 | 297.7 | 123.1 | mitochondrial 60S ribosomal protein L4 |
| Mrpl31 | gi|6322711 | 2 | 298.0 | 130.1 | 15.5 kDa mitochondrial ribosomal protein YmL31 |
| Pet54 | gi|6321661 | 2 | 310.0 | 198.0 | translational activator of cytochrome c oxidase subunit III |
| Nuc1 | gi|6322253 | 2 | 320.0 | 168.3 | mitochondrial nuclease |
| Gas1 | gi|6323967 | 2 | 341.0 | 200.8 | cell surface glycoprotein 115-120 kDa |
| Mrpl36 | gi|6319598 | 3 | 369.0 | 171.5 | mitochondrial ribosomal protein MRPL36 (YmL36) |
| Rml2 | gi|6320785 | 2 | 375.0 | 120.2 | mitochondrial protein of the large ribosomal subunit |
| Cox11 | gi|6325125 | 2 | 403.5 | 105.4 | required for delivery of copper to Cox1p |
| Msw1 | gi|6320474 | 3 | 404.7 | 134.8 | mitochondrial tryptophanyl-tRNA synthetase |
| Mtf2 | gi|6320160 | 2 | 429.5 | 64.3 | involved in mRNA splicing |
| Ydr370c | gi|6320578 | 2 | 505.5 | 21.9 | mRNA 5'-end-capping quality-control protein |
| Secretion/Export/Import | | | | | |
| Mdl2 | gi|6324985 | 2 | 309.5 | 70.0 | ATP-binding cassette (ABC) transporter family member |
| Tim21 | gi|6321470 | 2 | 348.0 | 80.6 | component of the TIM23 complex |
| Cpr6 | gi|6323246 | 2 | 362.0 | 223.4 | cyclophilin related to the mammalian CyP-40 |
| Bfr1 | gi|6324772 | 2 | 421.0 | 110.3 | involved in secretion |
| Spc3 | gi|6323095 | 3 | 433.0 | 46.4 | signal peptidase subunit |
| Structural | | | | | |
| Aim24 | gi|6322540 | 2 | 288.0 | 162.6 | functions in determining mitochondrial architecture |
| Prp12 | gi|6323960 | 2 | 363.0 | 4.2 | Integral membrane mitochondrial protein |
| Snl1 | gi|6322173 | 2 | 403.5 | 82.7 | 18.3 kD integral membrane protein |
| Signal transduction | | | | | |
| Srp54 | gi|6325345 | 2 | 490.0 | 9.9 | Signal recognition particle subunit |
| Endocytosis | | | | | |
| Erv25 | gi|6323630 | 2 | 391.5 | 119.5 | vesicle coat component |
| Unknown | | | | | |
| Ypr063c | gi|6325320 | 2 | 379.0 | 43.8 | ER-localized protein of unknown function |
| Ydl157c | gi|6320044 | 2 | 395.0 | 228.1 | unknown function |
| Ykl053c-a | gi|6322797 | 2 | 399.0 | 4.2 | dubious ORF |
| Yil077c | gi|6322113 | 2 | 425.5 | 53.0 | unknown function |

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