Specific changes in mitochondrial lipidome alter mitochondrial proteome and increase the geroprotective efficiency of lithocholic acid in chronologically aging yeast

Supplementary Material

Supplemental Figure S1. LCA exhibits age-related differential effects on the concentrations of different classes of mitochondrial membrane phospholipids in chronologically aging wild-type (WT) yeast. WT cells were cultured in the nutrient-rich YP medium initially containing 0.2% glucose with 50 µM LCA or without it. Mitochondria were purified from cells recovered on day 2, 4 or 7 of cell culturing. Extraction of mitochondrial membrane lipids, and mass spectrometric identification and quantitation of the extracted phospholipid classes were carried out as described in Materials and methods. The concentrations of phospholipids were calculated as nmoles phospholipid/mg protein. (A) PS, PI and PC are phospholipid classes that exhibit the bilayer forming shape of a cylinder; they decrease the extent of membrane curving for the IMM. (B) PA, PE and CL are phospholipid classes that have the non-bilayer forming shape of a cone; they increase the extent of membrane curving for the IMM. Data are presented as means ± SEM (n = 3; *p < 0.05; ns, not significant). Abbreviations: CL, cardiolipin; PA, phosphatidic acid; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PA, phosphatidic acid; PI, phosphatidylinositol; PS, phosphatidylserine.
Supplemental Figure S2. LCA exhibits age-related differential effects on the concentrations of different classes of mitochondrial membrane phospholipids in chronologically aging ups1Δ yeast. Cells of the ups1Δ mutant strain were cultured in the nutrient-rich YP medium initially containing 0.2% glucose with 50 µM LCA or without it. Mitochondria were purified from cells recovered on day 2, 4 or 7 of cell culturing. Extraction of mitochondrial membrane lipids, and mass spectrometric identification and quantitation of the extracted phospholipid classes were carried out as described in Materials and methods. The concentrations of phospholipids were calculated as nmoles phospholipid/mg protein. (A) PS, PI and PC are phospholipid classes that exhibit the bilayer forming shape of a cylinder; they decrease the extent of membrane curving for the IMM. (B) PA, PE and CL are phospholipid classes that have the non-bilayer forming shape of a cone; they increase the extent of membrane curving for the IMM. Data are presented as means ± SEM (n = 3; *p < 0.05; ns, not significant). Abbreviations: CL, cardiolipin; PA, phosphatidic acid; PC, phosphatidylincholine; PE, phosphatidylethanolamine; PA, phosphatidic acid; PI, phosphatidylinositol; PS, phosphatidylserine.
Supplemental Figure S3. LCA exhibits age-related differential effects on the concentrations of different classes of mitochondrial membrane phospholipids in chronologically aging *ups2Δ* yeast. Cells of the *ups2Δ* mutant strain were cultured in the nutrient-rich YP medium initially containing 0.2% glucose with 50 µM LCA or without it. Mitochondria were purified from cells recovered on day 2, 4 or 7 of cell culturing. Extraction of mitochondrial membrane lipids, and mass spectrometric identification and quantitation of the extracted phospholipid classes were carried out as described in Materials and methods. The concentrations of phospholipids were calculated as nmoles phospholipid/mg protein. (A) PS, PI and PC are phospholipid classes that exhibit the bilayer forming shape of a cylinder; they decrease the extent of membrane curving for the IMM. (B) PA, PE and CL are phospholipid classes that have the non-bilayer forming shape of a cone; they increase the extent of membrane curving for the IMM. Data are presented as means ± SEM (n = 3; *p < 0.05; ns, not significant). Abbreviations: CL, cardiolipin; PA, phosphatidic acid; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PA, phosphatidic acid; PI, phosphatidylinositol; PS, phosphatidylserine.
Supplemental Figure S4. LCA exhibits age-related differential effects on the concentrations of different classes of mitochondrial membrane phospholipids in chronologically aging psd1Δ yeast. Cells of the psd1Δ mutant strain were cultured in the nutrient-rich YP medium initially containing 0.2% glucose with 50 µM LCA or without it. Mitochondria were purified from cells recovered on day 2, 4 or 7 of cell culturing. Extraction of mitochondrial membrane lipids, and mass spectrometric identification and quantitation of the extracted phospholipid classes were carried out as described in Materials and methods. The concentrations of phospholipids were calculated as nmoles phospholipid/mg protein. (A) PS, PI and PC are phospholipid classes that exhibit the bilayer forming shape of a cylinder; they decrease the extent of membrane curving for the IMM. (B) PA, PE and CL are phospholipid classes that have the non-bilayer forming shape of a cone; they increase the extent of membrane curving for the IMM. Data are presented as means ± SEM (n = 3; *p < 0.05; ns, not significant). Abbreviations: CL, cardiolipin; PA, phosphatidic acid; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PA, phosphatidic acid; PI, phosphatidylinositol; PS, phosphatidylserine.
Supplemental Figure S5. Scatter plots comparing the relative concentrations of proteins in mitochondria purified from WT or ups1Δ (short-lived) cells cultured with or without LCA. Mitochondria were purified from WT or ups1Δ cells recovered on day 2, 4 or 7 of cell culturing. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. Scatter plots comparing the relative abundance of mitochondrial proteins between specified datasets were plotted on a log-log scale spanning six orders of magnitude. Data on the relative abundance of mitochondrial proteins are presented as means of 2 independent experiments.
Supplemental Figure S6. The ups1Δ mutation alters the concentrations of many mitochondrial proteins in yeast cultured with or without LCA. (A – F) Venn diagrams showing a comparison of the datasets of relative concentrations of mitochondrial proteins that are statistically significantly downregulated or upregulated by LCA in WT, by the ups1Δ mutation in the absence of LCA, and by LCA in ups1Δ cells; WT cells were recovered on day 2, 4 or 7 of culturing. (G and J) Venn diagrams showing a comparison of the datasets of relative concentrations of mitochondrial proteins that are statistically significantly downregulated or upregulated by LCA in WT cells recovered on day 2, 4 or 7 of culturing. (H and K) Venn diagrams showing a comparison of the datasets of relative concentrations of mitochondrial proteins that are statistically significantly downregulated or upregulated by the ups1Δ mutation in the absence of LCA; ups1Δ cells were recovered on day 2, 4 or 7 of culturing. (I and L) Venn diagrams showing a comparison of the datasets of relative concentrations of mitochondrial proteins that are statistically significantly downregulated or upregulated by LCA in ups1Δ cells recovered on day 2, 4 or 7 of culturing.
Supplemental Figure S7. Scatter plots comparing the relative concentrations of proteins in mitochondria purified from WT or ups2Δ (long-lived) cells cultured with or without LCA. Mitochondria were purified from WT or ups2Δ cells recovered on day 2, 4 or 7 of cell culturing. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. Scatter plots comparing the relative abundance of mitochondrial proteins between specified datasets were plotted on a log-log scale spanning six orders of magnitude. Data on the relative abundance of mitochondrial proteins are presented as means of 2 independent experiments.
Supplemental Figure S8. The *ups2Δ* mutation alters the concentrations of many mitochondrial proteins in yeast cultured with or without LCA. (A – F) Venn diagrams showing a comparison of the datasets of relative concentrations of mitochondrial proteins that are statistically significantly downregulated or upregulated by LCA in WT, by the *ups2Δ* mutation in the absence of LCA, and by LCA in *ups2Δ* cells; WT cells were recovered on day 2, 4 or 7 of culturing. (G and J) Venn diagrams showing a comparison of the datasets of relative concentrations of mitochondrial proteins that are statistically significantly downregulated or upregulated by LCA in WT cells recovered on day 2, 4 or 7 of culturing. (H and K) Venn diagrams showing a comparison of the datasets of relative concentrations of mitochondrial proteins that are statistically significantly downregulated or upregulated by the *ups2Δ* mutation in the absence of LCA; *ups2Δ* cells were recovered on day 2, 4 or 7 of culturing. (I and L) Venn diagrams showing a comparison of the datasets of relative concentrations of mitochondrial proteins that are statistically significantly downregulated or upregulated by LCA in *ups2Δ* cells recovered on day 2, 4 or 7 of culturing.
Supplemental Table S1. The relative concentrations of proteins in mitochondria purified from WT cells cultured with or without LCA. Mitochondria were purified from WT cells recovered on day 2 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI WT + LCA | Rati o WT + LCA /WT |
|-----------|-------------|---------------|---------|--------------------|-------------------|-------------------|----------|----------------|---------------------|
| P01972    | ATPase inhibitor, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 851347 | INH1; YDL181W | metabolic process;regulation of biological process | mitochondrion | catalytic activity;enzyme regulator activity;protein binding | 2.162 | 0.468 | 0.22 |
| P00420    | Cytochrome c oxidase subunit 3 [OS=Saccharomyces cerevisiae S288c] | 854627 | COX3; Q0275 | metabolic process;transport | membrane/mitochondrion | catalytic activity;transporter activity | 3.642 | 1.154 | 0.32 |
| P40784    | MIOREX complex component 12 [OS=Saccharomyces cerevisiae S288c] | 853459 | MRX12; YJR003C | mitochondrion | | | 0.403 | 0.145 | 0.36 |
| P39726    | Glycine cleavage system H protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 851254 | GCV3; YAL044C | metabolic process | mitochondrion | catalytic activity | 9 | 3.642 | 0.40 |
| P07255    | Cytochrome c oxidase subunit 7A [OS=Saccharomyces cerevisiae S288c] | 851492 | COX9; YDL067C | metabolic process;transport | membrane/mitochondrion | catalytic activity;transporter activity | 9 | 3.642 | 0.40 |
| Q04041    | Succinate dehydrogenase assembly factor 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 852123 | ACN9; SDH7; YDR511W | cell organization and biogenesis;regulation of biological process | mitochondrion;organelle lumen | | 0.931 | 0.389 | 0.42 |
| P49954    | Probable hydrolyase NIT3 [OS=Saccharomyces cerevisiae S288c] | 851065 | NIT3; YLR351C | metabolic process | cytoplasm/mitochondrion | catalytic activity | 0.624 | 0.274 | 0.44 |
| P23180    | Probable oxidoreductase AIM17 [OS=Saccharomyces cerevisiae S288c] | 856365 | AIM17; YHL021C | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;metal ion binding | 9 | 4.012 | 0.45 |
| P10507    | mitochondrial processing peptidase subunit beta [OS=Saccharomyces cerevisiae S288c] | 850869 | MAS1; YLR363C | metabolic process;transport | mitochondrion;organelle lumen | catalytic activity;metal ion binding;protein binding | 2.481 | 1.154 | 0.47 |
| P38884    | Altered inheritance of mitochondria protein 18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 856605 | AIM18; YHR198C | | mitochondrion | catalytic activity | 0.311 | 0.145 | 0.47 |
| Q03028    | Mitochondrial 2-oxoacid decarboxylase carrier 1 [OS=Saccharomyces cerevisiae S288c] | 855969 | ODC1; YPL124C | metabolic process;transport | membrane/mitochondrion | structural molecule activity;transporter activity | 7.799 | 3.642 | 0.47 |
| P00445    | Superoxide dismutase [Cu-Zn] [OS=Saccharomyces cerevisiae S288c] | 853568 | SOD1; YJR040C | cell organization and biogenesis;cellular homeostasis;metabolic process;regulation of biological process;response to stimulus | cytoplasm;cytosol/mitochondrion;nucleus | antioxidant activity;catalytic activity;metal ion binding;protein binding | 1.848 | 0.874 | 0.47 |
| Q00605    | Octanoyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 850940 | LIP2; YLR239C | metabolic process | cytoplasm/mitochondrion | catalytic activity | 0.245 | 0.116 | 0.47 |
| P32799    | Cytochrome c oxidase subunit 6A, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 852684 | COX13; YGL191W | cell organization and biogenesis;metabolic process;regulation of biological process;transport | membrane/mitochondrion | catalytic activity;enzyme regulator activity;transporter activity | 18.953 | 9 | 0.47 |
| P38880    | GIPIase MTG1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 856573 | MTG1; YHR168W | metabolic process;transport | membrane/mitochondrion | catalytic activity;metal ion binding;nucleotide binding;transporter activity | 0.145 | 0.07 | 0.48 |
| P40008    | Protein FMP52, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 856721 | FMP52; YER004W | endoplasmic reticulum;membrane/mitochondrion | catalytic activity | 2.162 | 1.054 | 0.49 |
| Gene Name | Description | Function | Localization | Similarity Score |
|-----------|-------------|----------|--------------|------------------|
| ATP synthase subunit beta, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, nucleotide binding | membrane, mitochondrion | 0.968 | 0.501 | 0.52 |
| Tryptophan--RNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, metal ion binding | cytoplasm, mitochondrion | 0.896 | 0.468 | 0.52 |
| Citrate/organic acid carrier protein [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | DNA binding, structural molecule activity, transporter activity | membrane, mitochondrion | 3.467 | 1.818 | 0.52 |
| Protein YIM1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, metal ion binding | cytoplasm, endoplasmic reticulum, mitochondrion | 0.833 | 0.438 | 0.53 |
| Cytochrome c iso-1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | metal ion binding, protein binding | mitochondrion | 12.335 | 6.499 | 0.53 |
| Mitochondrial peculiar membrane protein 1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | antioxidant activity, catalytic activity, nucleotide binding | membrane, mitochondrion | 3.642 | 1.929 | 0.53 |
| Superoxide dismutase (Mn), mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity | mitochondrion, organelle lumen | 9 | 4.878 | 0.54 |
| Glutamyl-tRNA synthetase subunit A, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, transporter activity | mitochondrion | 5.31 | 2.981 | 0.56 |
| Cytochrome b-c1 complex subunit 8 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, protein binding, structural molecule activity | mitochondrion, ribosome | 15.681 | 9 | 0.57 |
| tricatin-1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | metal ion binding, protein binding | mitochondrion | 0.191 | 0.11 | 0.58 |
| Succinate:fumarate oxidoreductase transporter [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | structural molecule activity, transporter activity | mitochondrion | 17.957 | 10.365 | 0.58 |
| S45 ribosomal protein L3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, RNA binding, structural molecule activity | mitochondrion, nucleus, ribosome | 1.043 | 0.61 | 0.58 |
| Glyceroldehyde-3-phosphate dehydrogenase 3 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, nucleotide binding, RNA binding | cytoplasm, cytosol, membrane, mitochondrion, nucleus | 3.962 | 2.325 | 0.59 |
| Ammonia transport outward protein 2 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | transporter activity | mitochondrion, vacuole | 0.874 | 0.52 | 0.59 |
| 40S ribosomal protein S18-A [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | RNA binding, structural molecule activity | mitochondrion, ribosome | 0.874 | 0.52 | 0.59 |
| S45 ribosomal protein L32, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | RNA binding, structural molecule activity | mitochondrion, ribosome | 0.638 | 0.389 | 0.61 |
| Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | structural molecule activity, transporter activity | mitochondrion | 7.111 | 4.337 | 0.61 |
| mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, DNA binding, structural molecule activity | mitochondrion, nucleus | 0.585 | 0.359 | 0.61 |
| mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | structural molecule activity, transporter activity | mitochondrion | 0.54 | 0.334 | 0.62 |
| mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, nucleotide binding | membrane, mitochondrion | 7.111 | 4.337 | 0.61 |
| mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | structural molecule activity, transporter activity | mitochondrion | 0.54 | 0.334 | 0.62 |
| mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c] | catalytic activity, nucleotide binding | membrane, mitochondrion | 99 | 62.096 | 0.63 |
| Gene ID | Description | Localization | Function | Biological Process | Molecular Function | GO ID | Location | Expression | p-value |
|--------|-------------|--------------|----------|--------------------|--------------------|-------|----------|------------|----------|
| P35088 | Stationary phase gene 1 protein | [OS=Saccharomyces cerevisiae S288c] | mitochondrial | process, transport | endoplasmic reticulum, membrane, mitochondrion | 853151 | YPR121W | 250.18 | 0.63 |
| P37292 | Serine hydroxymethyltransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial | metabolic process | mitochondrion | 852565 | SHM41; YBR263W | 12.219 | 0.63 |
| Q01163 | 37S ribosomal protein S23, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | catalytic activity | 85274B | RSM03; YGL129C | 2.695 | 0.63 |
| P04806 | Hexokinase-1 | [OS=Saccharomyces cerevisiae S288c] | cytoplasm, cytosol, mitochondrion | catalytic activity, nucleotide binding, RNA binding, structural molecule activity | 850164 | HXK1; YFR053C | 0.289 | 0.64 |
| P4051 | Intermediate dehydrogenase subunit | [OS=Saccharomyces cerevisiae S288c] | membrane, mitochondrion, nucleus | catalytic activity, metal ion binding | 856118 | ICP55; YER078C | 0.25 | 0.64 |
| P71518 | Putative transferase CAF17, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, organelle lumen | catalytic activity | 853586 | IBA57; YIR122W | 0.241 | 0.64 |
| P38714 | Arginine–RNA ligase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | cytoplasm, mitochondrion, organelle lumen | catalytic activity, nucleotide binding | 856491 | MRS1; YHR091C | 0.174 | 0.65 |
| Q06965 | MIM5 complex subunit Mic10 | [OS=Saccharomyces cerevisiae S288c] | membrane organization and biogenesis, metabolic process | membrane, mitochondrion | 850300 | MO51; M10; YCL057C-A | 4.179 | 0.65 |
| Q00711 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | membrane, mitochondrion | catalytic activity, nucleotide binding, protein binding | 853709 | SDH1; YKL148C | 18.619 | 0.66 |
| P00431 | Cytochrome c peroxidase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrion, organelle lumen | antioxidant activity, catalytic activity, metal ion binding, protein binding | 853940 | CCP1; YKR066C | 2.162 | 0.66 |
| P40961 | Prohibitin-1 | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | membrane, mitochondrion | protein binding | 853033 | PHB1; YGR132C | 9 | 0.66 |
| P39926 | Protein S102 | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | cytoplasm, endoplasmic reticulum, membrane | protein binding | 855221 | S102; YMR183C | 3.642 | 0.66 |
| P38072 | Protein SCO2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | membrane, mitochondrion | antioxidant activity, catalytic activity, metal ion binding | 852312 | SCO2; YBR024W | 1.404 | 0.66 |
| P40710 | ADP, ATP carrier protein 1 | [OS=Saccharomyces cerevisiae S288c] | mitochondrial | metabolic process | structural molecule activity, transport activity | 855078 | AAC1; YMR056C | 10.288 | 0.67 |
| P71695 | Glutaredoxin-2 | [OS=Saccharomyces cerevisiae S288c] | cellular homeostasis, metabolic process | cytoplasm, cytosol, mitochondrion, nucleus | antioxidant activity, catalytic activity | 852124 | GRX2; YDR513W | 1.31 | 0.67 |
| P14832 | Peptidyl-prolyl cis-trans isomerase | [OS=Saccharomyces cerevisiae S288c] | cell differentiation, cell organization and biogenesis, metabolic process | cytoplasm, mitochondrion, nucleus | catalytic activity, RNA binding | 851733 | CPR1; YDR155C | 1.31 | 0.67 |
| P23641 | Mitochondrial phosphate carrier protein | [OS=Saccharomyces cerevisiae S288c] | metabolic process | membrane, mitochondrion | protein binding, structural molecule activity, transport activity | 853540 | MIR1; YJR077C | 26.826 | 0.67 |
| P25642 | 54S ribosomal protein IMG2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 850434 | IMG2; YCR071C | 1.154 | 0.67 |
| P36151 | Uncharacterized protein YKR070W | [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion | 853944 | YKR070W | 1.976 | 0.68 |
| Q04887 | Mitochondrial inner membrane protein SHH3 | [OS=Saccharomyces cerevisiae S288c] | metabolic process | membrane, mitochondrion | catalytic activity, metal ion binding | 855145 | SHM3; YMR118C | 1.031 | 0.68 |
| Q22428 | Probable 2-methylcitrate dehydratase | [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, membrane, mitochondrion | catalytic activity | 856108 | PDH1; YPR002W | 19.935 | 0.68 |
| Protein Name | Description | GO Terms | Localization | Function | Localization | Molecular Role | Catalytic Activity | Binding Type | Binding Type | Binding Type |
|--------------|-------------|----------|--------------|----------|--------------|----------------|------------------|--------------|--------------|--------------|
| P10823       | Guanine nucleotide-binding protein alpha-2 subunit 2 | [OS=Saccharomyces cerevisiae] | 528B        | cell differentiation; cell growth; cell organization and biogenesis; cellular homeostasis; regulation of biological process; response to stimulus | cytosol; membrane; mitochondrion | catalytic activity; metal ion binding; nucleotide binding | 0.978           | 0.668        | 0.68         |
| P07143       | Cytochrome c1, heme protein, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; transport | cytosol; membrane; mitochondrion | metal ion binding | 19.309          | 13.251       | 0.69         |
| P16517       | S4S ribosomal protein L4, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 1.565           | 1.081        | 0.69         |
| P38523       | GrpE protein homolog, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; regulation of biological process; transport | membrane; mitochondrion; organelle lumen | enzyme regulator activity; nucleotide binding; protein binding | 2.36            | 1.637        | 0.69         |
| P32316       | 4-acetyl-CoA hydrolase | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process | cytoplasm; cytosol; mitochondrion | catalytic activity | 29.539          | 20.544       | 0.70         |
| P36017       | Vacular protein sorting-associated protein 21 | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; transport | cytosol; endosome; membrane; mitochondrion | catalytic activity; transporter activity | 0.719           | 0.501        | 0.70         |
| P32860       | Nfu1-like protein, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | cell organization and biogenesis; cellular homeostasis; metabolic process | mitochondrion; organelle lumen | metal ion binding | 5.494           | 3.87         | 0.70         |
| P38122       | 3-methyl-2-oxobutanoate hydroxymethyltransferase | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process | mitochondrion | catalytic activity | 0.585           | 0.413        | 0.71         |
| P00425       | Cytochrome c oxidase polypeptide 5B, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 1.648           | 1.31         | 0.71         |
| P06168       | Ketol-acid reductoisomerase, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | cell organization and biogenesis; metabolic process | mitochondrion | catalytic activity; DNA binding; metal ion binding | 28.126          | 19.962       | 0.71         |
| P03538       | Glyceraldehyde-3-phosphate dehydrogenase 2 | [OS=Saccharomyces cerevisiae] | 528B        | cell death; metabolic process | cytoplasm; cytosol; membrane; mitochondrion; nucleus | catalytic activity; nucleotide binding | 1.721           | 1.228        | 0.71         |
| P23440       | Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; regulation of biological process | membrane; mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 22.95           | 16.433       | 0.72         |
| P09950       | 5-aminoimidazole synthase, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process | mitochondrion; organelle lumen | catalytic activity | 0.389           | 0.28         | 0.72         |
| P26449       | ATP synthase subunit e, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; transport | membrane; mitochondrion | catalytic activity; structural molecule activity; transporter activity | 9               | 6.499        | 0.72         |
| P08425       | Phenylalanine-SRNA ligase, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process | cytoplasm; mitochondrion; organelle lumen | catalytic activity; metal ion binding; nucleotide binding; RNA binding | 0.346           | 0.25         | 0.72         |
| P19882       | Heat shock protein 60, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrion | catalytic activity; DNA binding; protein binding | 23.816          | 17.33        | 0.73         |
| P18239       | ADP/ATP carrier protein 2 | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; transport | membrane; mitochondrion | structural molecule activity; transporter activity | 135.88          | 7            | 0.73         |
| Q04368       | Stationary phase protein 4 | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; transport | membrane; mitochondrion | catalytic activity; nucleotide binding | 4.995           | 3.642        | 0.73         |
| P23117       | Protein AF01 | [OS=Saccharomyces cerevisiae] | 528B        | cell organization and biogenesis; metabolic process; response to stimulus; transport | mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 1.154           | 0.848        | 0.73         |
| Q06892       | NADH kinase 50S, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | metabolic process; response to stimulus | mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 2.311           | 1.848        | 0.74         |
| P32445       | Single-stranded DNA-binding protein Rim1, mitochondrial | [OS=Saccharomyces cerevisiae] | 528B        | cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrion | DNA binding | 6.743           | 4.995        | 0.74         |
| Q02127 | Protein ARG5,6, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 856800 | ARG5,6; YEBO69W | metabolic process;regulation of biological process | cytoplasm; mitochondrion; organelle lumen | catalytic activity; nucleotide binding; protein binding | 0.458 | 0.341 | 0.74 |
| P00401 | Cytochrome c oxidase subunit 1 [OS=Saccharomyces cerevisiae 528C] | 854598 | COX1; Q0045 | metabolic process; transport | mitochondrial | catalytic activity; metal ion binding; transporter activity | 2.162 | 1.61 | 0.74 |
| P43167 | Uncharacterized mitochondrial carrier YFR045W | 850606 | YFR045W; YFR045W | metabolic process; transport | membrane; mitochondrial | structural molecule activity; transporter activity | 0.378 | 0.585 | 0.75 |
| P32898 | Mitochondrial pressequence protein [OS=Saccharomyces cerevisiae 528C] | 852041 | CFM1; YDR430C | metabolic process | mitochondrial | catalytic activity; metal ion binding | 2.162 | 1.626 | 0.75 |
| P21801 | Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 850685 | SDH2; YL041C | metabolic process; transport | membrane; mitochondrial | catalytic activity; metal ion binding | 32.839 | 24.809 | 0.76 |
| P51719 | Aspartate–tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 856000 | MS01; YPL104W | metabolic process | cytoplasm; mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 0.708 | 0.531 | 0.76 |
| Q12031 | Mitochondrial 2-methylisocitrinate lyase [OS=Saccharomyces cerevisiae 528C] | 856114 | ICL2; YPR006C | metabolic process | mitochondrial; organelle lumen | catalytic activity | 7.859 | 5.952 | 0.76 |
| P40047 | Aldehyde dehydrogenase 5, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 856804 | ALD5; YER073W | metabolic process | mitochondrial; organelle lumen | catalytic activity | 3.146 | 2.384 | 0.76 |
| P40341 | Mitochondrial respiratory chain complexes assembly protein YTA12 [OS=Saccharomyces cerevisiae 528C] | 851114 | YTA12; YMR088C | cell organization and biogenesis; metabolic process; response to stimulus; transport | cytoplasm; membrane; mitochondrial | catalytic activity; metal ion binding; nucleotide binding; protein binding | 1.795 | 1.371 | 0.76 |
| P25605 | Acetolactate synthase I subunit, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 850348 | ILV6; YCL009C | metabolic process; regulation of biological process | mitochondrial | catalytic activity; enzyme regulator activity | 11.743 | 9 | 0.77 |
| P40185 | Protein mmf1, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 854760 | MMF1; YL051C | cell organization and biogenesis; metabolic process | mitochondrial; organelle lumen | 9 | 6.943 | 0.77 |
| P40600 | NADH-cytochrome b5 reductase 2 [OS=Saccharomyces cerevisiae 528C] | 853707 | MCR1; YKL150W | metabolic process; response to stimulus | membrane; mitochondrial | catalytic activity; protein binding | 19.691 | 15.238 | 0.77 |
| P37293 | N-terminal acetyltransferase 2 [OS=Saccharomyces cerevisiae 528C] | 853050 | NAT2; YGR147C | metabolic process | cytoplasm; mitochondrial | catalytic activity | 0.931 | 0.73 | 0.78 |
| Q07651 | SUR7 family protein FMP45 [OS=Saccharomyces cerevisiae 528C] | 851304 | FMP45; YDL223C | cell differentiation; cell organization and biogenesis | membrane; mitochondrial | catalytic activity | 3.125 | 2.455 | 0.79 |
| P18797 | Protein phosphatase 2C homolog 7, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 856475 | PTC7; YHR076W | metabolic process | mitochondrial | catalytic activity; metal ion binding; protein binding | 0.874 | 0.688 | 0.79 |
| P00360 | glyceraldehyde-3-phosphate dehydrogenase 1 [OS=Saccharomyces cerevisiae 528C] | 851395 | TDH1; YLG029W | metabolic process | cytoplasm; cytosol; membrane; mitochondrial | catalytic activity; nucleotide binding | 0.823 | 0.65 | 0.79 |
| P53312 | Succinyl-CoA ligase (ADP-forming) subunit beta, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 853159 | LSC3; YGR244C | metabolic process | mitochondrial | catalytic activity; nucleotide binding | 20.017 | 15.819 | 0.79 |
| P07253 | cytochrome b 8 pre-mRNA processing protein 6 [OS=Saccharomyces cerevisiae 528C] | 852417 | CBP6; YBR120C | cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrial; ribosome | catalytic activity; metal ion binding; protein binding | 2.728 | 2.162 | 0.79 |
| P00175 | Cytochrome b2, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 854950 | CYB2; YML054C | metabolic process; transport | cytosol; membrane; mitochondrial; nucleus | catalytic activity; metal ion binding; nucleotide binding | 1.113 | 0.884 | 0.79 |
| P25646 | Pyruvate dehydrogenase [acetyl-transferring]- phosphatase 2, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 850441 | PTC6; YCR079W | cell communication; metabolic process; regulation of biological process; response to stimulus | mitochondrial; organelle lumen | catalytic activity | 0.61 | 0.487 | 0.80 |
| P05660 | Phosphoglycerate kinase [OS=Saccharomyces cerevisiae 528C] | 850370 | PGK1; YCR012W | metabolic process | cytoplasm; membrane; mitochondrial | catalytic activity; nucleotide binding | 2.415 | 1.929 | 0.80 |
| P38891 | Branched-chain amino acid aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae 528C] | 856615 | BAT1; YHR208W | metabolic process; regulation of biological process; response to stimulus | mitochondrial; organelle lumen | catalytic activity | 15.876 | 12.689 | 0.80 |
P47052  succinate dehydrogenase (ubiquinone) flavoprotein subunit 2, mitochondrial [Os=Saccharomyces cerevisiae S288c]  8513405  YIL045W; YIL045W  metabolic process;transport  membrane;mitochondrion  catalytic activity;nucleotide binding  5.884  4.712  0.80

P32891  D-lactate dehydrogenase [cytochrome] 1, mitochondrial [Os=Saccharomyces cerevisiae S288c]  851380  OLD1; YDL174C  metabolic process;transport  membrane;mitochondrion  catalytic activity;nucleotide binding  13.03  10.45  0.80

P37356  Uncharacterized protein YNR040W [Os=Saccharomyces cerevisiae S288c]  855776  YNR040 W; YNR040 W  mitochondrial  1.154  0.931  0.81

P36059  ATP-dependent (S)-NAD(P)H:pyruvate hydratase dehydratase [Os=Saccharomyces cerevisiae S288c]  8513706  YKL151C; YKL151C  metabolic process  cytoplasm  catalytic activity;nucleotide binding  1.081  0.874  0.81

P23833  Protein SCO1, mitochondrial [Os=Saccharomyces cerevisiae S288c]  852325  SCO1; YBR037C  cell organization and biogenesis;cellular homeostasis;response to stimulus;transport  membrane;mitochondrion  antioxidant activity;catalytic activity  1.783  1.448  0.81

P33416  Heat shock protein 78, mitochondrial [Os=Saccharomyces cerevisiae S288c]  851845  HSP78; YDR258C  cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus  mitochondrion;organellar lumen  catalytic activity;nucleotide binding;protein binding  12.525  10.199  0.81

P36335  Citrate synthase 3, mitochondrial [Os=Saccharomyces cerevisiae S288c]  856107  CIT3; YPR001W  metabolic process  mitochondrion  catalytic activity  6.11  4.995  0.82

P12686  37S ribosomal protein MRP13, mitochondrial [Os=Saccharomyces cerevisiae S288c]  852975  MRP13; YGR084C  cell organization and biogenesis;metabolic process  mitochondrion;ribosome  structural molecule activity  1.512  1.239  0.82

P07251  ATP synthase subunit alpha, mitochondrial [Os=Saccharomyces cerevisiae S288c]  852177  ATP1; YBL099W  metabolic process;transport  cytosol;membrane;mitochondrion  catalytic activity;nucleotide binding;transporter activity  34.938  28.663  0.82

P53219  Aldehyde oxidase domain-containing protein IMD32 [Os=Saccharomyces cerevisiae S288c]  852919  IMD32; YGR031 W  metabolic process;transport  mitochondrion  catalytic activity  1.404  1.154  0.82

P09294  Endola 1 [Os=Saccharomyces cerevisiae S288c]  853169  ENO1; YGR254 W  metabolic process;regulation of biological process  cytoplasm;cytosol;membrane;mitochondrion;vacuole  catalytic activity;metal ion binding;protein binding  0.711  0.585  0.82

P08539  Guanine nucleotide-binding protein alpha-1 subunit [Os=Saccharomyces cerevisiae S288c]  856394  GPA1; YHR005C  cell organization and biogenesis;cellular component movement;regulation of biological process;response to stimulus;transport  cytosol;endosome;membrane  catalytic activity;nucleotide binding;protein binding  0.682  0.562  0.82

P32902  37S ribosomal protein MRPA, mitochondrial [Os=Saccharomyces cerevisiae S288c]  856384  MRPA; YHL004W  cell organization and biogenesis;metabolic process  mitochondrion;ribosome  structural molecule activity  1.154  0.957  0.83

P18496  Mitochondrial ATPase complex subunit ATP10 [Os=Saccharomyces cerevisiae S288c]  851109  ATP10; YLR383W  cell organization and biogenesis  cytoplasm;membrane;mitochondrion  protein binding  1.818  1.512  0.83

P21560  Protein CBP3, mitochondrial [Os=Saccharomyces cerevisiae S288c]  858886  CBP3; YPL215W  cell organization and biogenesis;regulation of biological process  membrane;mitochondrion;ribosome  1.031  0.859  0.83

P35191  Dna1 homolog 1, mitochondrial [Os=Saccharomyces cerevisiae S288c]  850530  MD11; YFL016C  cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus  mitochondrion;organellar lumen  enzyme regulator activity;metal ion binding;nucleotide binding;protein binding  4.722  3.977  0.84

P49095  Glycine dehydrogenase (Decarboxylating), mitochondrial [Os=Saccharomyces cerevisiae S288c]  852227  GCC2; YMR118P W  metabolic process  cytosol;mitochondrion  catalytic activity  2.884  2.433  0.84

P33310  ATP-dependent permease MOD11, mitochondrial [Os=Saccharomyces cerevisiae S288c]  850885  MOD11; YLR188W  transport  membrane;mitochondrion  catalytic activity;nucleotide binding;transporter activity  0.624  0.528  0.85

Q01574  acetyl-coenzyme A synthetase 1 [Os=Saccharomyces cerevisiae S288c]  851245  ACS1; YAL054C  cell organization and biogenesis;metabolic process  cytoplasm;cytosol;endoplasmic reticulum;mitochondrion;nucleus  catalytic activity;nucleotide binding  0.624  0.528  0.85

P53170  (Pyruvate dehydrogenase (acetyl-transferring) kinase 2, mitochondrial [Os=Saccharomyces cerevisiae S288c]  852821  PKP2; YGL059W  metabolic process;regulation of biological process  mitochondrion;organellar lumen  catalytic activity;metal ion binding;protein binding  1.096  0.931  0.85
| Gene   | YPR136W | Description                                                                 | Location                        | Interaction                                                                 | Activity                                                                 | Value   | SD   |
|--------|---------|------------------------------------------------------------------------------|---------------------------------|----------------------------------------------------------------------------|----------------------------------------------------------------------------|---------|------|
| P23291 | Casein kinase I homolog 1 (OS=S. cerevisiae)                                | cell organization and biogenesis | cytoplasm; endoplasmic reticulum; membrane; mitochondrion; nucleus          | catalytic activity; nucleotide binding; protein binding                   | 1.043   | 0.887| 0.85|
| P00925 | Enolase 2 (OS=S. cerevisiae)                                                | metabolic process               | cytoplasm; cytosol; membrane; mitochondrion; vacuole                      | catalytic activity; metal ion binding; protein binding                   | 1.043   | 0.887| 0.85|
| Q06678 | S45 ribosomal protein L35, mitochondrial (OS=S. cerevisiae)                 | cell organization and biogenesis| mitochondrion; ribosome                                                   | structural molecule activity                                             | 1.424   | 1.219| 0.86|
| P23549 | Flavoprotein-like protein (OS=S. cerevisiae)                                | metabolic process               | cytoplasm; membrane; mitochondrion                                         | catalytic activity; nucleotide binding; protein binding                  | 6.743   | 5.813| 0.86|
| P35252 | Sphingolipid long chain base-responsive protein (OS=S. cerevisiae)          | cell organization and biogenesis| mitochondrion; ribosome                                                   | structural molecule activity                                             | 14.013  | 12.111| 0.86|
| P40086 | Cytochrome c oxidase (OS=S. cerevisiae)                                     | metabolic process               | mitochondrion; organelle lumen                                             | catalytic activity                                                      | 1.555   | 1.346| 0.87|
| P09457 | ATP synthase subunit 5, mitochondrial (OS=S. cerevisiae)                     | metabolic process               | membrane; mitochondrion                                                   | catalytic activity; transporter activity                                 | 9       | 7.799| 0.87|
| P46367 | Potassium-activated aldehyde dehydrogenase, mitochondrial (OS=S. cerevisiae) | metabolic process               | mitochondrion; organelle lumen                                             | catalytic activity                                                      | 58.078  | 50.795| 0.87|
| P04840 | Mitochondrial outer membrane protein porin 1 (OS=S. cerevisiae)             | cell death; cell organization and biogenesis; cellular homeostasis; regulation of biological process | cytoplasm; membrane; mitochondrion                                      | transporter activity                                                      | 15.238  | 13.384| 0.88|
| P28424 | Isocitrate dehydrogenase (NAD) subunit 2, mitochondrial (OS=S. cerevisiae)  | metabolic process               | mitochondrion; organelle lumen                                             | catalytic activity; metal ion binding; nucleotide binding; protein binding | 6.197   | 5.449| 0.88|
| P05085 | Prohibitin 2 (OS=S. cerevisiae)                                             | cell organization and biogenesis| mitochondrial; organelle lumen                                             | catalytic activity; protein binding                                      | 4.926   | 4.337| 0.88|
| P07246 | Alcohol dehydrogenase 3, mitochondrial (OS=S. cerevisiae)                   | metabolic process               | mitochondrial; organelle lumen                                             | catalytic activity; metal ion binding                                    | 10.159  | 9     | 0.89|
| P46681 | D-lactate dehydrogenase (cytochrome c) 1, mitochondrial (OS=S. cerevisiae)  | metabolic process               | mitochondrial; organelle lumen                                             | catalytic activity; metal ion binding                                    | 1.829   | 1.626| 0.89|
| P40495 | Homoisocitrate dehydrogenase, mitochondrial (OS=S. cerevisiae)              | metabolic process               | mitochondrial; organelle lumen                                             | catalytic activity; metal ion binding                                    | 6.499   | 5.813| 0.89|
| P17505 | Malate dehydrogenase, mitochondrial (OS=S. cerevisiae)                      | metabolic process               | mitochondrial; organelle lumen                                             | catalytic activity; protein binding; RNA binding                        | 99      | 88.615| 0.90|
| P40815 | Aminomethyltransferase, mitochondrial (OS=S. cerevisiae)                    | metabolic process               | mitochondrial                                                                | catalytic activity; protein binding                                      | 11.217  | 10.053| 0.90|
| P33266 | Uncharacterized protein (OS=S. cerevisiae)                                  | response to stimulus            | membrane; mitochondrion                                                   | catalytic activity; nucleotide binding; transporter activity             | 1.233   | 1.116| 0.91|
| P33311 | ATP-dependent permease MLD2, mitochondrial (OS=S. cerevisiae)               | cell organization and biogenesis| cytosol; mitochondrial; organelle lumen                                    | catalytic activity                                                      | 13.785  | 12.554| 0.91|
| P20967 | 2-oxoglutarate dehydrogenase, mitochondrial (OS=S. cerevisiae)             | metabolic process               | cytosol; mitochondrial; organelle lumen                                    | catalytic activity                                                      | 2.35    | 2.162| 0.92|
cerevisiae S288c]

Q22166
2-isopropylmalate synthase 2, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
854275
LEUR; YOR108W
metabolic process
mitochondrion
catalytic activity;protein binding
3.739 3.453 0.92

P16387
Pyruvate dehydrogenase EI component subunit alpha, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
856925
PDA1; YER178W
cell growth;metabolic process
mitochondrion;organelle lumen
catalytic activity
25.264 23.384 0.93

P09297
Threonine dehydratase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
856819
ILV1; YER086W
metabolic process
cytoplasm;mitochondrion
catalytic activity
3.375 3.125 0.93

P32795
Mitochondrial inner membrane i-AAA protease supercomplex subunit YME1
[OS=Saccharomyces cerevisiae S288c]
856135
YME1; YPR024W
metabolic process;response to stimulus;transport
membrane;mitochondrion
catalytic activity;metal ion binding;nucleotide binding;protein binding
1.938 1.798 0.93

P39522
Dihydroy-acid dehydratase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
853473
ILV1; YIR016C
metabolic process
mitochondrion
catalytic activity;metal ion binding
39.37 36.649 0.93

Q08179
Mitochondrial distribution and morphology protein 38
[OS=Saccharomyces cerevisiae S288c]
854130
MDM38; YDL027C
cell organization and biogenesis;cellular homeostasis;regulation of biological process;transport
membrane;mitochondrion
catalytic activity
5.683 5.31 0.93

P19657
Plasma membrane ATPase 2
[OS=Saccharomyces cerevisiae S288c]
856071
PMA2; YPL038W
membrane;mitochondrion
9 8.427 0.94

P40053
Altered inheritance of mitochondria protein 9, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
856813
AIM9; YER086W
mitochondrion
catalytic activity
4.289 4.036 0.94

P32191
Glycerol-3-phosphate dehydrogenase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
854651
GLT2; YIL155C
metabolic process
membrane;mitochondrion
catalytic activity
9.502 9 0.95

P32843
Mitochondrial escape protein 2
[OS=Saccharomyces cerevisiae S288c]
855348
YME2; YMR320C
cell organization and biogenesis;metabolic process;transport
membrane;mitochondrion
nucleotide binding;RNA binding
3.112 2.949 0.95

P19414
Aconitate hydratase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
851013
ACO1; YLR034C
cell organization and biogenesis;metabolic process;transport
cytoplasm;cytosol;mitochondrion;organelle lumen
catalytic activity;DNA binding;metal ion binding
66.002 66.002 1.00

P05930
Heat shock protein SSC1, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
853503
SSC1; YDR45C
cell organization and biogenesis;metabolic process;transport
membrane;mitochondrion;nucleus;organelle lumen
catalytic activity;enzyme regulator activity;nucleotide binding;protein binding
51.75 51.75 1.00

P09624
Dihydrolipoyl dehydrogenase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
850527
LPD1; YFL038C
cellular homeostasis;metabolic process;regulation of biological process;transport
mitochondrion;organelle lumen
catalytic activity;nucleotide binding
30.623 30.623 1.00

Q07500
External NADH-ubiquinone oxidoreductase 2, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
851474
NDE2; YDL285W
metabolic process
mitochondrion
catalytic activity;protein binding
12.594 12.594 1.00

P00890
Citrate synthase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
853732
CT1; YNR001C
metabolic process;transport
cytoplasm;mitochondrion;organelle lumen
catalytic activity
11.798 11.798 1.00

P07275
Delta 1-pyrroline-5-carboxylate dehydrogenase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
856432
PUT2; YHR037W
metabolic process
membrane;mitochondrion;organelle lumen
catalytic activity
6.565 6.565 1.00

P28834
Isocitrate dehydrogenase (NAD) subunit 1, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
855691
IDH1; YNL037C
metabolic process;transport
cytoplasm;mitochondrion;organelle lumen
catalytic activity;metal ion binding;protein binding;RNA binding
15.238 15.238 1.00

Q08222
Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
854538
CIR2; YOR356W
metabolic process;transport
membrane;mitochondrion
catalytic activity;metal ion binding;nucleotide binding
3.019 3.019 1.00

P34273
Pyruvate dehydrogenase EI component subunit beta, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
852522
PDB1; YBR221C
metabolic process
mitochondrion;organelle lumen
catalytic activity
10.288 10.288 1.00
Mitochondrial peroxiredoxin PRX1 (Saccharomyces cerevisiae S288c) 852215 PRX1; YBL046C cellular homeostasis; metabolic process; regulation of biological process; response to stimulus mitochondrial antioxidant activity; catalytic activity 6.848 6.848 1.00

Altered inheritance of mitochondria protein 24; mitochondrial (Saccharomyces cerevisiae S288c) 853543 AIM24; YIR098C cell organization and biogenesis mitochondrial 3.175 3.175 1.00

Mitochondrial respiratory chain complexes assembly protein AFG3 (Saccharomyces cerevisiae S288c) 856737 AFG3; YER071C cell organization and biogenesis; metabolic process; response to stimulus membrane; mitochondrial catalytic activity; metal ion binding; nucleotide binding; protein binding 1.228 1.228 1.00

ATP synthase subunit 4; mitochondrial (Saccharomyces cerevisiae S288c) 856027 ATP4; YPL078C cell organization and biogenesis; metabolic process; transport membrane; mitochondrial catalytic activity; transporter activity 3.642 3.642 1.00

Probable electron transfer flavoprotein subunit beta (Saccharomyces cerevisiae S288c) 853121 CIR1; YGR207C metabolic process; transport mitochondrial; organelle lumen 7.66 7.66 1.00

Mitochondrial oxoacetate transport protein (Saccharomyces cerevisiae S288c) 853739 OAC1; YKL120W metabolic process; transport membrane; mitochondrial structural molecule activity; transporter activity 5.813 5.813 1.00

Probable alanine aminotransferase, mitochondrial (Saccharomyces cerevisiae S288c) 850778 ALT1; YLR089C metabolic process mitochondrial; organelle lumen catalytic activity 1.438 1.438 1.00

Elongation factor G, mitochondrial (Saccharomyces cerevisiae S288c) 850758 MEF1; YLR069C cell organization and biogenesis; metabolic process cytosol; mitochondrial catalytic activity; nucleotide binding; RNA binding 1.024 1.024 1.00

Mitochondrial genome maintenance protein MGM101 (Saccharomyces cerevisiae S288c) 853609 MGM101; YIR144W cell organization and biogenesis; metabolic process; response to stimulus chromosone; mitochondrial DNA binding 4.456 4.456 1.00

Accumulation of dyads protein 2 (Saccharomyces cerevisiae S288c) 850368 ADY2; YCR010C transport membrane; mitochondrial; vacuole transporter activity 12.895 12.895 1.00

ATP synthase subunit d; mitochondrial (Saccharomyces cerevisiae S288c) 853853 ATP7; YKL016C metabolic process; transport membrane; mitochondrial catalytic activity; transporter activity 5.105 5.105 1.00

Mitochondrial phosphate carrier protein 2 (Saccharomyces cerevisiae S288c) 856779 PIC2; YEB035C cellular homeostasis; metabolic process; transport membrane; mitochondrial structural molecule activity; transporter activity 2.793 2.793 1.00

Non-classical export protein 2 (Saccharomyces cerevisiae S288c) 856272 NCE102; YPR149W cell organization and biogenesis; regulation of biological process cytoplasm; endoplasmic reticulum; membrane; mitochondrial 12.895 12.895 1.00

Glycine–tRNA ligase 1, mitochondrial (Saccharomyces cerevisiae S288c) 853808 GLS1; YER116C metabolic process cytoplasm; mitochondrial; organelle lumen catalytic activity; nucleotide binding; protein binding 0.468 0.468 1.00

Mitochondrial import inner membrane translocase subunit Tim23 (Saccharomyces cerevisiae S288c) 855751 TIM23; YNR017W transport membrane; mitochondrial protein binding; transporter activity 5.31 5.31 1.00

Mitochondrial acidic protein MAM33 (Saccharomyces cerevisiae S288c) 854740 MAM33; YIL070C metabolic process; regulation of biological process mitochondrial; organelle lumen translation regulator activity 3.642 3.642 1.00

Cytochrome c oxidase subunit 2 (Saccharomyces cerevisiae S288c) 854622 COX2; QO210 metabolic process; transport membrane; mitochondrial catalytic activity; metal ion binding; protein binding; transporter activity 3.642 3.642 1.00

37S ribosomal protein MRP51, mitochondrial (Saccharomyces cerevisiae S288c) 855985 MRP51; YPL118W cell organization and biogenesis; metabolic process mitochondrial; ribosome structural molecule activity 1.154 1.154 1.00

MIOREX complex component 9 (Saccharomyces cerevisiae S288c) 851535 YDL027C; YMR099; YDL027C endoplasmic reticulum; membrane; mitochondrial 1.913 1.913 1.00

Mitochondrial inner membrane protein SHH4 (Saccharomyces cerevisiae S288c) 850861 SHH4; YLR064W metabolic process membrane; mitochondrial catalytic activity; metal ion binding 6.499 6.499 1.00

Carrier protein YMC1, mitochondrial (Saccharomyces cerevisiae S288c) 856171 YMC1; YPR058W metabolic process; transport membrane; mitochondrial; vacuole structural molecule activity; transporter activity 2.384 2.384 1.00
Q12029  Probable mitochondrial transport protein ffs1  
[OS=Saccharomyces cerevisiae 5288c]  
854445  FSF1; YOR271C  
transport  
membrane,mitochondrion  
transporter activity  
2.36 2.36 1.00

P39952  Mitochondrial inner membrane protein Oxa1  
[OS=Saccharomyces cerevisiae 5288c]  
856898  OXA1; YER154W  
cell organization and biogenesis;transport  
membrane,mitochondrion  
transporter activity  
1.738 1.738 1.00

P35292  37S ribosomal protein S35, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
853075  MRPS35; YGR165W  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
structural molecule activity  
1.512 1.512 1.00

P11325  Leucine--tRNA ligase, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
851098  NAM2; YLR382C  
cell organization and biogenesis;metabolic process;regulation of biological process  
cytoplasm,mitochondrion,organelle lumen  
catalytic activity; nucleotide binding; RNA binding  
0.353 0.353 1.00

P35889  uncharacterized mitochondrial hydrolase FMP41  
[OS=Saccharomyces cerevisiae 5288c]  
855533  FMP41; YNL168C  
metabolic process  
mitochondrion  
catalytic activity;metal ion binding  
1.254 1.254 1.00

Q2165  ATP synthase subunit delta, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
851560  ATP6; YDL004W  
metabolic process;transport  
membrane,mitochondrion  
catalytic activity;transporter activity  
4.623 4.623 1.00

P36141  Putative reox protein fmp46, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
853923  FMP46; YKR049C  
metabolic process  
mitochondrion  
catalytic activity; protein binding  
4.337 4.337 1.00

P32664  Mitochondrial import receptor subunit TOM40  
[OS=Saccharomyces cerevisiae 5288c]  
855243  TOM40; YMR203W  
transport  
cytoplasm,membrane,mitochondrion  
protein binding;transporter activity  
1.154 1.154 1.00

Q2117  Protein Mrpl11  
[OS=Saccharomyces cerevisiae 5288c]  
851597  MRPL11; YDR033W  
transport  
endoplasmic reticulum;membrane,mitochondrion  
transporter activity  
2.831 2.831 1.00

Q20643  LETM1 domain-containing protein Yuh47, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
856243  YUH47; YPR125W  
cell organization and biogenesis  
membrane,mitochondrion  
1.043 1.043 1.00

P43594  MICOS complex subunit Mic19  
[OS=Saccharomyces cerevisiae 5288c]  
850663  AIM13; MIC19; YPR011C  
cell organization and biogenesis  
cytoplasm,membrane,mitochondrion  
3.329 3.329 1.00

P36534  54S ribosomal protein L40, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
855930  MRPL40; YPL173W  
cell organization and biogenesis;metabolic process  
mitochondrion; ribosome  
protein binding;structural molecule activity  
1.512 1.512 1.00

Q22024  54S ribosomal protein L13, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
853875  MRPL13; YKR066C  
cell organization and biogenesis;metabolic process  
mitochondrion; ribosome  
structural molecule activity  
1.371 1.371 1.00

P40508  Uncharacterized protein Yll077c  
[OS=Saccharomyces cerevisiae 5288c]  
854733  YIL077C; YIL077C  
mitochondrion  
1.448 1.448 1.00

Q5892  MIOREX complex component 2  
[OS=Saccharomyces cerevisiae 5288c]  
850997  YLR290C; COG11; YLR290C  
metabolic process  
mitochondrion  
3.217 3.217 1.00

P37298  Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
851758  SDH4; YDR178W  
metabolic process;transport  
membrane,mitochondrion  
catalytic activity;metal ion binding  
4.995 4.995 1.00

Q23734  Nuclear control of ATPase protein 2  
[OS=Saccharomyces cerevisiae 5288c]  
856278  NCA2; YPR155C  
metabolic process  
membrane,mitochondrion  
0.565 0.565 1.00

P74045  mitochondrial import inner membrane translocase subunit Tim54  
[OS=Saccharomyces cerevisiae 5288c]  
853392  TIM54; YIL054W  
cell organization and biogenesis;transport  
cytoplasm,membrane,mitochondrion  
transporter activity  
0.655 0.655 1.00

P39965  probable proline--tRNA ligase, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
856820  AIM10; YER087W  
metabolic process  
cytoplasm,mitochondrion  
catalytic activity; nucleotide binding; RNA binding  
0.343 0.343 1.00

P40582  Glutathione S-transferase 1  
[OS=Saccharomyces cerevisiae 5288c]  
854856  GTS1; YHR038C  
metabolic process  
endoplasmic reticulum;membrane,mitochondrion; nucleus  
antioxidant activity; catalytic activity; protein binding; RNA binding  
1.683 1.683 1.00

P38910  10-kDa heat shock protein, mitochondrial  
[OS=Saccharomyces cerevisiae 5288c]  
854185  HSP10; YOR020C  
cell organization and biogenesis;metabolic process;response to stimulus;transport  
cytoplasm,mitochondrion,organelle lumen  
metal ion binding; nucleotide binding; protein binding  
4.623 4.623 1.00

Q24782  Mitochondrial aspartate-glutamate transporter Agc1  
[OS=Saccharomyces cerevisiae 5288c]  
856132  AGC1; YPR021C  
metabolic process;transport  
membrane,mitochondrion  
structural molecule activity;transporter activity  
0.407 0.407 1.00

Q06143  mitochondrial diatrizoate transporter  
[OS=Saccharomyces cerevisiae 5288c]  
851063  DTC1; YLR348C  
metabolic process;transport  
membrane,mitochondrion  
structural molecule activity;transporter activity  
1.154 1.154 1.00
Q2349 ATP synthase subunit H, mitochondrial [OS=Saccharomyces cerevisiae S288c] 851002 ATP14; YLR295C cell organization and biogenesis; metabolic process; transport membrane, mitochondrion catalytic activity, transporter activity 2.728 2.728 1.00

P35996 345 ribosomal protein L38, mitochondrial [OS=Saccharomyces cerevisiae S288c] 853684 MRPL38; YKL170W cell organization and biogenesis; metabolic process mitochondrion; ribosome RNA binding; structural molecule activity 2.594 2.594 1.00

Q3824 Uncharacterized protein YOR020W-A [OS=Saccharomyces cerevisiae S288c] 146648 YOR020 W-A; YOR020 W-A metabolic process; transport membrane, mitochondrion 5.813 5.813 1.00

P29204 345 ribosomal protein L6, mitochondrial [OS=Saccharomyces cerevisiae S288c] 856552 MRPL6; YHR147C cell organization and biogenesis; metabolic process mitochondrion; ribosome RNA binding; structural molecule activity 1.371 1.371 1.00

P40416 iron-sulfur clusters transporter ATM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 853447 ATM1; YMR301C cellular homeostasis; metabolic process; transport membrane, mitochondrion catalytic activity; activity; nucleotide binding; transporter activity 0.453 0.453 1.00

P2453 Protein ATP11, mitochondrial [OS=Saccharomyces cerevisiae S288c] 855401 ATP11; YNL315C cell organization and biogenesis mitochondrion protein binding 1.512 1.512 1.00

P25626 345 ribosomal protein IMG1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 850413 IMG1; YCR046C cell organization and biogenesis; metabolic process mitochondrion; ribosome structural molecule activity 1.424 1.424 1.00

P50945 MICO complex subunit MCIC7 [OS=Saccharomyces cerevisiae S288c] 856263 AIM37; MC27; YNL100W cell organization and biogenesis membrane, mitochondrion 1.254 1.254 1.00

P10834 protein PET54 [OS=Saccharomyces cerevisiae S288c] 853147 PET54; YGR222 W metabolic process; regulation of biological process membrane, mitochondrion; organelle lumen nucleotide binding; RNA binding; translation regulator activity 0.874 0.874 1.00

Q08970 Mitochondrial metal transporter 2 [OS=Saccharomyces cerevisiae S288c] 85877 MMM72; YPL224C cellular homeostasis; regulation of biological process; response to stimulus membrane, mitochondrion transporter activity 0.532 0.532 1.00

Q03201 375 ribosomal protein S10, mitochondrial [OS=Saccharomyces cerevisiae S288c] 851611 RSM10; YDR041 W cell organization and biogenesis; metabolic process mitochondrion; ribosome structural molecule activity 1.424 1.424 1.00

P46521 345 ribosomal protein L11, mitochondrial [OS=Saccharomyces cerevisiae S288c] 851325 MRPL11; YDL022W cell organization and biogenesis; metabolic process mitochondrion; ribosome structural molecule activity 1.069 1.069 1.00

P23572 Thioredoxin-3, mitochondrial [OS=Saccharomyces cerevisiae S288c] 850444 TKK9; YCR083W cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport cytoplasm, mitochondrion catalytic activity 2.511 2.511 1.00

P33759 375 ribosomal protein S5, mitochondrial [OS=Saccharomyces cerevisiae S288c] 852553 MRPS5; YBR251W cell organization and biogenesis; metabolic process mitochondrion; ribosome RNA binding; structural molecule activity 0.995 0.995 1.00

P32387 345 ribosomal protein L41, mitochondrial [OS=Saccharomyces cerevisiae S288c] 852014 MRPL20; YDR405 W cell organization and biogenesis; metabolic process mitochondrion; ribosome nucleotide binding; protein binding; RNA binding; structural molecule activity 1.254 1.254 1.00

Q40172 Sensitive to high expression protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c] 852002 SHER9; YDR393 W cell organization and biogenesis membrane, mitochondrion 0.374 0.374 1.00

P27697 Atypical kinase COQ8, mitochondrial [OS=Saccharomyces cerevisiae S288c] 852758 COQ8; YGL119W metabolic process membrane, mitochondrion; organelle lumen catalytic activity; nucleotide binding 0.453 0.453 1.00

Q08245 protein ZEO1 [OS=Saccharomyces cerevisiae S288c] 854040 ZEO1; YDL109W cell organization and biogenesis membrane, mitochondrion protein binding 2.162 2.162 1.00

P66519 345 ribosomal protein L7, mitochondrial [OS=Saccharomyces cerevisiae S288c] 851823 MRPL17; YDR237 W cell organization and biogenesis; metabolic process mitochondrion; ribosome RNA binding; structural molecule activity 0.468 0.468 1.00

P33111 Mitochondrial pyruvate carrier 3 [OS=Saccharomyces cerevisiae S288c] 853158 FMP43; MPC3; YGR243 W transport membrane, mitochondrion transporter activity 1.154 1.154 1.00

Q12305 Thioulate sulfurtransferase RD11, mitochondrial [OS=Saccharomyces cerevisiae S288c] 854459 RD11; YOR285 W endoplasmic reticulum; membrane, mitochondrion catalytic activity 1.154 1.154 1.00

Q12204 Probable phospholipase YOR022C, mitochondrial [OS=Saccharomyces cerevisiae S288c] 854187 YOR022C; YOR022C metabolic process mitochondrion catalytic activity; metal ion binding 0.233 0.233 1.00
P51903  Peroxosomal acyl-coenzyme A thioester hydrolase 1 [Os-Saccharomyces cerevisiae 52B8c]  
854477  TES1; YLR019C  
metabolic process; transport  
membrane; mitochondrion  
catalytic activity  
0.931 0.931 1.00

P74140  Altered inheritance rate of mitochondria protein 25 [Os-Saccharomyces cerevisiae 52B8c]  
853563  AIM025; YIR500C  
cell organization and biogenesis  
membrane; mitochondrion  
transporter activity  
0.369 0.369 1.00

P32839  Mitochondrial chaperone BC51 [Os-Saccharomyces cerevisiae 52B8c]  
851981  BCS1; YDR375C  
cell organization and biogenesis; metabolic process; response to stimulus; transport  
cytosol; membrane; mitochondrion  
catalytic activity; nucleotide binding; transporter activity  
0.425 0.425 1.00

P05159  Cytochrome c oxidase subunit 6b [Os-Saccharomyces cerevisiae 52B8c]  
850727  COX12; YLR083C  
cell organization and biogenesis; metabolic process; transport  
membrane; mitochondrion  
catalytic activity; transporter activity  
3.642 3.642 1.00

P02888  Inner membrane assembly complex subunit 17 [Os-Saccharomyces cerevisiae 52B8c]  
856005  AIM43; INA17; YPL099C  
cell organization and biogenesis  
membrane; mitochondrion  
protein binding  
0.701 0.701 1.00

P06567  ABC1 family protein MCP2 [Os-Saccharomyces cerevisiae 52B8c]  
850955  YLR253W; MCP1; YLE235W  
cell organization and biogenesis  
membrane; mitochondrion  
0.218 0.218 1.00

P49017  2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial [Os-Saccharomyces cerevisiae 52B8c]  
854930  COQ5; YML110C  
metabolic process  
membrane; mitochondrion; organelle lumen  
catalytic activity  
0.551 0.551 1.00

Q12359  Altimoria transport outward protein J [Os-Saccharomyces cerevisiae 52B8c]  
851992  ATO3; YDR383C  
transport  
membrane; mitochondrion  
transporter activity  
0.995 0.995 1.00

P37299  Cytochrome b-c1 complex subunit 10 [Os-Saccharomyces cerevisiae 52B8c]  
856990  OCR10; YHR001 W-A  
metabolic process; transport  
membrane; mitochondrion  
catalytic activity; transporter activity  
5.31 5.31 1.00

P38079  Protein YRO2 [Os-Saccharomyces cerevisiae 52B8c]  
852343  YRO2; YBR054W  
transport  
endoplasmic reticulum; membrane; mitochondrion  
transporter activity  
1.424 1.424 1.00

P53305  Mitochondrial 37S ribosomal protein S27 [Os-Saccharomyces cerevisiae 52B8c]  
853129  RSM27; YGR215 W  
cell organization and biogenesis; metabolic process  
mitochondrion; ribosome  
structural molecular activity  
2.162 2.162 1.00

P46948  mitochondrial membrane protein FMP33 [Os-Saccharomyces cerevisiae 52B8c]  
853279  FMP33; YIL161W  
metabolic process  
membrane; mitochondrion  
2.162 2.162 1.00

P00485  Autophagy-related protein 33 [Os-Saccharomyces cerevisiae 52B8c]  
851070  ATG33; YLR356W  
cell communication; metabolic process; response to stimulus  
membrane; mitochondrion  
2.162 2.162 1.00

P12233  ATP synthase subunit g, mitochondrial [Os-Saccharomyces cerevisiae 52B8c]  
856131  ATP20; YPL020W  
cell organization and biogenesis; metabolic process; transport  
membrane; mitochondrion  
catalytic activity; transporter activity  
1.371 1.371 1.00

P32611  54S ribosomal protein RML2, mitochondrial [Os-Saccharomyces cerevisiae 52B8c]  
856660  RML2; YEL050C  
cell organization and biogenesis; metabolic process  
mitochondrion; ribosome  
catalytic activity; RNA binding; structural molecular activity  
0.389 0.389 1.00

P38300  Inner membrane mitobosome receptor MBA1, mitochondrial [Os-Saccharomyces cerevisiae 52B8c]  
852483  MBA1; YBR185C  
cell organization and biogenesis; regulation of biological process  
membrane; mitochondrion  
0.995 0.995 1.00

P08020  Iron sulfur cluster assembly protein 1, mitochondrial [Os-Saccharomyces cerevisiae 52B8c]  
855968  ISU1; YPL139W  
cell organization and biogenesis; cellular homeostasis; metabolic process  
cytosol; mitochondrion; organelle lumen  
catalytic activity; metal ion binding; protein binding  
0.778 0.778 1.00

P14540  Fuctose-bisphosphate aldolase [Os-Saccharomyces cerevisiae 52B8c]  
853805  FBAL; YKL060C  
metabolic process  
cytosol; cytosol; membrane; mitochondrion  
catalytic activity; metal ion binding  
0.292 0.292 1.00

P20608  37S ribosomal protein S16, mitochondrial [Os-Saccharomyces cerevisiae 52B8c]  
856094  MRPS16; YPL013C  
cell organization and biogenesis; metabolic process  
mitochondrion; ribosome  
structural molecular activity  
1.683 1.683 1.00

P04159  Uncharacterized protein YNL206W [Os-Saccharomyces cerevisiae 52B8c]  
855153  YNL206W  
membrane; mitochondrion; ribosome  
0.668 0.668 1.00

P53732  37S ribosomal protein S12, mitochondrial [Os-Saccharomyces cerevisiae 52B8c]  
853772  MRPS12; YNR036C  
cell organization and biogenesis; metabolic process  
mitochondrion; ribosome  
structural molecular activity  
1.154 1.154 1.00

P23369  54S ribosomal protein L25, mitochondrial [Os-Saccharomyces cerevisiae 52B8c]  
852967  MRPL25; YGR076C  
cell organization and biogenesis; metabolic process  
mitochondrion; ribosome  
structural molecular activity  
1.31 1.31 1.00
| Gene ID | Description | Cellular Location | Activity, Protein Binding | Log2Fold Change | p-Value |
|---------|-------------|-------------------|--------------------------|----------------|---------|
| Q07560 | Protein isd11 | mitochondrial | catalytic activity, protein binding | 1.783 | 1.783 |
| P41911 | Glycerol-3-phosphate dehydrogenase | mitochondrial | catalytic activity, nucleotide binding, protein binding | 0.186 | 0.186 |
| P32220 | Mitochondrial import inner membrane translocase subunit TIM21 | mitochondrial | protein binding | 0.719 | 0.719 |
| P34321 | Succinate dehydrogenase (ubiquinone) cytochrome b subunit | mitochondrial | catalytic activity, metal ion binding | 1.276 | 1.276 |
| P37244 | 54S ribosomal protein L50 | mitochondrial | structural molecule activity | 1.512 | 1.512 |
| P38702 | Mitochondrial carrier protein LEU8 | mitochondrial | structural molecule activity, transporter activity | 0.334 | 0.334 |
| P36147 | Presequence translocated-associated motor subunit pm17 | mitochondrial | catalytic activity, metal ion binding | 0.425 | 0.425 |
| Q02886 | N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D | mitochondrial | catalytic activity, metal ion binding | 0.995 | 0.995 |
| P46526 | 54S ribosomal protein L27 | mitochondrial | structural molecule activity | 0.995 | 0.995 |
| P31663 | 45S ribosomal protein L12 | mitochondrial | RNA binding, structural molecule activity | 1.31 | 1.31 |
| P31614 | ATP-dependent RNA helicase mnh4 | mitochondrial | catalytic activity, nucleotide binding, RNA binding | 0.145 | 0.145 |
| Q07914 | mitochondrial import inner membrane translocase subunit TIM14 | mitochondrial | enzyme regulator activity, protein binding, transporter activity | 0.778 | 0.778 |
| P36531 | 54S ribosomal protein L30 | mitochondrial | structural molecule activity | 0.668 | 0.668 |
| P21306 | ATP synthase subunit epsilon | mitochondrial | catalytic activity, transporter activity | 2.162 | 2.162 |
| Q01976 | ADP-ribose pyrophosphatase | mitochondrial | catalytic activity, metal ion binding | 0.425 | 0.425 |
| P38169 | Kinurenine 3-monoxygenase | mitochondrial | catalytic activity, nucleotide binding | 0.269 | 0.269 |
| P32785 | MethylylRNA formyltransferase, mitochondrial | mitochondrial | catalytic activity | 0.179 | 0.179 |
| P81451 | ATP synthase subunit K | mitochondrial | catalytic activity, transporter activity | 3.642 | 3.642 |
| P81450 | ATP synthase subunit J | mitochondrial | catalytic activity, transporter activity | 9 | 9 |
| P36671 | Ribosome missing factor 2 | mitochondrial | catalytic activity, nucleotide binding, RNA binding | 0.334 | 0.334 |
| P32445 | Asparagine-tRNA ligase, mitochondrial | mitochondrial | catalytic activity, nucleotide binding | 0.137 | 0.137 |
| Q07534 | Solute carrier family 25 member 38 homolog | mitochondrial | structural molecule activity, transporter activity | 0.389 | 0.389 |
| ID       | Gene Name                          | Function                      | Location                  | Activity                              | PMI   |
|----------|------------------------------------|-------------------------------|---------------------------|---------------------------------------|-------|
| P2084    | 54S ribosomal protein L33, mitochondrial | cell organization and biogenesis | mitochondrial ribosome    | structural molecule activity           | 2.162 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P47141   | 37S ribosomal protein S26, mitochondrial | cell organization and biogenesis; response to stimulus | mitochondrial ribosome    | antioxidant activity; catalytic activity; RNA binding; structural molecule activity | 0.425 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P40858   | 54S ribosomal protein L49, mitochondrial | cell organization and biogenesis | mitochondrial ribosome    | RNA binding; structural molecule activity | 0.468 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P36523   | 54S ribosomal protein L15, mitochondrial | cell organization and biogenesis | mitochondrial ribosome    | catalytic activity; RNA binding; structural molecule activity | 0.334 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P37297   | ULM1 protein YSC83                   |                                | membrane, mitochondrial   |                                       | 0.233 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P34224   | Uncharacterized protein YBL059W      |                                | membrane, mitochondrial   |                                       | 0.468 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| Q08230   | Succinate dehydrogenase assembly factor 2, mitochondrial | cell differentiation; cell organization and biogenesis; metabolic process | mitochondrial; organelle lumen | protein binding                        | 0.468 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P0087    | MICOS subunit MCl2                   | cell organization and biogenesis | membrane, mitochondrial   |                                       | 0.638 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P03787   | Intron-encoded RNA maturation b4     | metabolic process              | membrane, mitochondrial   | catalytic activity; RNA binding       | 0.28  |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| Q03429   | Mitochondrial zinc maintenance protein 1, mitochondrial | cell organization and biogenesis; metabolic process | mitochondrial; organelle lumen | protein binding                        | 0.334 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P53785   | 54S ribosomal protein L19, mitochondrial | cell organization and biogenesis; metabolic process | mitochondrial ribosome    | RNA binding; structural molecule activity | 0.874 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| Q01802   | Aspartate aminotransferase, mitochondrial | metabolic process              | mitochondrial; organelle lumen | catalytic activity; protein binding   | 0.155 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P01098   | ATPase-stabilizing factor 9 kDa, mitochondrial | metabolic process; regulation of biological process | mitochondrial             | catalytic activity; enzyme regulator activity; protein binding | 2.162 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P05779   | Ubiquinone biosynthesis protein COQ9, mitochondrial | metabolic process              | membrane, mitochondrial   |                                       | 0.359 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P33212   | Probable transcriptional regulatory protein MHI1 | metabolic process              | mitochondrial             |                                       | 0.359 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P00942   | Trisphosphate isomerase               | metabolic process              | cytoplasm; cytosol; membrane; mitochondrial | catalytic activity                   | 0.194 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P32378   | 4-hydroxybenzoate polyphenoltransferase, mitochondrial | metabolic process; transport | membrane, mitochondrial   | catalytic activity                    | 0.292 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| P07680   | Ubiquinone biosynthesis O-methyltransferase, mitochondrial | metabolic process              | membrane, mitochondrial   | catalytic activity                    | 0.274 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| Q2V299   | Uncharacterized protein YDL110W-A    |                                | membrane, mitochondrial   |                                       | 1.154 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| Q0690    | 54S ribosomal protein L51, mitochondrial | cell organization and biogenesis; metabolic process | mitochondrial; ribosome    | RNA binding; structural molecule activity | 0.292 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
| Q06886   | Thiosulfate sulfurtransferase TUM1 | metabolic process              | cytoplasm, mitochondrial   | catalytic activity; protein binding   | 0.212 |
|          | [OS=Saccharomyces cerevisiae 528Bc] |                               |                           |                                       | 1.00  |
Q36E5 uncharacterised mitochondrial outer membrane protein YDR381C-A [OS=Saccharomyces cerevisiae 528Bc]

Q2463 Acyl carrier protein, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P40581 peroxiredoxin HYR1 [OS=Saccharomyces cerevisiae 528Bc]

Q8058 Coenzyme D-binding protein COQ10, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P20821 tRNA-lysyl assembly protein 1 [OS=Saccharomyces cerevisiae 528Bc]

Q07821 37S ribosomal protein rmlA, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

Q08645 polyphosphate synthase [OS=Saccharomyces cerevisiae 528Bc]

G2328 Mitochondrial import inner membrane translocase subunit Timm2 [OS=Saccharomyces cerevisiae 528Bc]

P40990 Protein Mss2, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P4039 Cytochrome c oxidase polypeptide VIII, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P38812 Phosphatidylglycerophosphatase GEP4, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P10174 cytochrome c oxidase subunit 7 [OS=Saccharomyces cerevisiae 528Bc]

P3915 mitochondrial import inner membrane translocase subunit Tim17 [OS=Saccharomyces cerevisiae 528Bc]

P53733 37S ribosomal protein s19, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P07635-1 Histidine-RNA ligase, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P40751 putative lipase protein ligase A [OS=Saccharomyces cerevisiae 528Bc]

G24887 54S ribosomal protein L23, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P52720 rRNA methyltransferase 1, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P39940 E3 ubiquitin-protein ligase Rps5 [OS=Saccharomyces cerevisiae 528Bc]

Q04598 54S ribosomal protein L34, mitochondrial [OS=Saccharomyces cerevisiae 528Bc]

P4693 sorting assembly machinery 35 kDa subunit [OS=Saccharomyces cerevisiae 528Bc]

P25578 CDP-diacylglycerol-glycerol 3-phosphate 3-phosphatidyltransferase [OS=Saccharomyces cerevisiae 528Bc]
| Gene ID | Description                          | Function/Location                      | Subunit | Molecule | Value 1 | Value 2 |
|---------|--------------------------------------|----------------------------------------|---------|----------|---------|---------|
| 57414   | COX assembly mitochondrial protein   | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57415   | Long-chain fatty-acid-CoA ligase 2    | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57416   | Altered inheritance of mitochondrial | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57417   | ATP synthase subunit f, mitochondrial| [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57418   | Ubiquitin carboxyl-terminal hydrolase 16| [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57419   | Cytochrome c iso-2                   | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57420   | Mitochondrial Rhf GTPase 1           | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57421   | Cytochrome c oxidase assembly protein| [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57422   | Protein COX12                        | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57423   | Autophagy-related protein 52         | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57424   | Mitochondrial COX                  | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57425   | Cytochrome c import factor CYC2      | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57426   | C-1-tetrahydrofolate synthase       | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57427   | Z-isopropylmalate synthase           | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57428   | Aminopeptidase 2                    | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57429   | Long-chain fatty-acid-CoA ligase 1   | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57430   | External NADH-ubiquinone oxidoreductase 1 | [OS=Saccharomyces cerevisiae 528Bc] | |          |         |         |
| 57431   | Valine--tRNA ligase, mitochondrial  | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57432   | Isocitrate dehydrogenase [NADP], mitochondrial | [OS=Saccharomyces cerevisiae 528Bc] | |          |         |         |
| 57433   | Fumarate hydratase, mitochondrial   | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57434   | Heat shock protein 56, mitochondrial | [OS=Saccharomyces cerevisiae 528Bc]    |         |          |         |         |
| 57435   | Cytochrome b-c1 complex subunit 1, mitochondrial | [OS=Saccharomyces cerevisiae 528Bc] | |          |         |         |
| 57436   | Cytochrome b-c1 complex subunit 2, mitochondrial | [OS=Saccharomyces cerevisiae 528Bc] | |          |         |         |
| Gene ID | Description                                                                 | Function                  | Subcellular Location            | GO Terms                                                                 |
|--------|------------------------------------------------------------------------------|---------------------------|---------------------------------|--------------------------------------------------------------------------|
| P16547 | Mitochondrial outer membrane protein OMA45                                  | mem protein; mitochr      | membrane,mitochondr             | catalytic activity,transporter activity                                  |
| P54783 | D-arnolino-1, L-lactone oxidase                                              | metabolic process         | membrane,mitochr                | catalytic activity,nucleotide binding                                    |
| P16451 | Pyruvate dehydrogenase complex protein X component, mitochondrial            | metabolic process         | mitochr; organelle lumen        | catalytic activity,structural molecule activity                          |
| P33982 | Isocitrate dehydrogenase [NADP]                                              | metabolic process         | cytoplasm,mitochr               | catalytic activity,metal ion binding,nucleotide binding                 |
| Q05931 | Heat shock protein SSQ1, mitochondrial                                       | cell org and biogenesis,metabolic process | mitochr; organelle lumen | nucleotide binding,protein binding                                        |
| P38077 | ATP synthase subunit gamma, mitochondrial                                     | metabolic process, transport | mem protein,mitochr             | catalytic activity,transporter activity                                  |
| P25374 | Cysteine desulfurase, mitochondrial                                          | metabolic process         | mitochr; nucleus                | catalytic activity,metal ion binding,protein binding                    |
| P38071 | Enoyl-[acyl-carrier-protein] reductase [NADPH, B-specific], mitochondrial    | metabolic process         | mitochr; organelle lumen        | catalytic activity,DNA binding,metal ion binding                         |
| P01120 | Ras-like protein 2                                                           | cell communication,cell differentiation,metabolic process | mem protein,mitochr; nucleus | catalytic activity,nucleotide binding,protein binding                   |
| P16622 | Ferrochelatase, mitochondrial                                               | metabolic process         | mem protein,mitochr             | catalytic activity                                                       |
| P48527 | Tyrosine-3-hydroxy-Ligase, mitochondrial                                     | metabolic process         | cytoplasm,mitochr;organelle lumen | catalytic activity,metal ion binding,protein binding                    |
| Q04558 | Fatty aldehyde dehydrogenase HFD1                                             | metabolic process         | endoplasmic reticulum; endosome;membrane,mitochr | catalytic activity                                                       |
| P32666 | Cytochrome oxidase assembly protein SHY1                                      | cell org and biogenesis    | mem protein,mitochr             | protein binding                                                          |
| P27929 | 37S ribosomal protein NAM9, mitochondrial                                    | cell org and biogenesis,metabolic process,regulation of biological process | mitochr; ribosome | RNA binding,structural molecule activity                                 |
| P35457 | Alanine--glyoxylate aminotransferase 1                                       | metabolic process         | cytosol,mitochr                 | catalytic activity                                                       |
| P38988 | Mitochondrial CTP/GDP carrier protein 1                                      | mem protein               |                                 | structural molecule activity,transporter activity                        |
| P43616 | Cytochrome oxidase assembly protein SHY1                                      | cell org and biogenesis    |                                 | catalytic activity,metal ion binding,protein binding                    |
| P28817 | 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial                            | metabolic process         |                                 | catalytic activity                                                       |
| Q12480 | Probable electron transfer flavoprotein subunit alpha, mitochondrial         | metabolic process,transport |                                 | catalytic activity,transporter activity                                   |
| P10662 | 37S ribosomal protein MRP3, mitochondrial                                    | cell org and biogenesis,metabolic process | mitochr; ribosome | antioxidant activity,catalytic activity,metal ion binding,protein binding |
| P39525 | 3-oxoacyl-[acyl-carrier-protein] synthase homolog                            | metabolic process         |                                 | catalytic activity                                                       |
| Gene ID | Protein Name                  | Description                                                                 | Localization                      | Subcellular Localization       | Molecular Function         | GO Term                      | Gene List                                                                 |
|--------|------------------------------|------------------------------------------------------------------------------|-----------------------------------|--------------------------------|---------------------------|------------------------------|---------------------------------------------------------------------------|
| Q04599 | 54S ribosomal protein l1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | mitochondrion, ribosome          | RNA binding, structural molecule activity | 1.069 | 1.336 | 1.25 |
| P19516 | Cytochrome c oxidase assembly protein COX11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | membrane, mitochondrion, ribosome | metal ion binding            | 1.069 | 1.336 | 1.25 |
| P39006 | Phosphatidylserine decarboxylase proenzyme 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process                         | membrane, mitochondrion          | catalytic activity           | 0.487 | 0.61  | 1.25 |
| P16046 | Mitochondrial intermembrane space import and assembly protein 40 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis                                            | membrane, mitochondrion          | catalytic activity, protein binding, transporter activity | 2.3 | 2.914 | 1.27 |
| P17267 | Assembly factor clp4 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis                                            | membrane, mitochondrion          |                                   | 5.579 | 7.111 | 1.27 |
| P2335  | Protein 55S1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process                         | membrane, mitochondrion          | protein binding, translation regulator activity | 1.512 | 1.929 | 1.28 |
| P14908 | Mitochondrial transcription factor 1 [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process                         | mitochondrion, organelle lumen   | catalytic activity, DNA binding, RNA binding | 0.778 | 0.995 | 1.28 |
| P15375 | Saccharolysin, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process                                                           | cytoplasm, golgi, mitochondrion, vacuole | catalytic activity, metal ion binding | 0.216 | 0.278 | 1.29 |
| P19194 | Mitochondrial processing peptidase subunit alpha [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport                                                 | membrane, mitochondrion, organelle lumen | catalytic activity, metal ion binding, protein binding | 2.311 | 2.981 | 1.29 |
| Q04935 | Cytochrome c oxidase protein 20, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | membrane, mitochondrion          | protein binding               | 1.894 | 2.455 | 1.30 |
| P42847 | 37S ribosomal protein 51B, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | mitochondrion, ribosome          | RNA binding, structural molecule activity | 1.054 | 1.371 | 1.30 |
| P53969 | Sorting assembly machinery 50 kDa subunit [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, transport                                  | membrane, mitochondrion          | protein binding, transporter activity | 0.374 | 0.487 | 1.30 |
| P07213 | Mitochondrial import receptor subunit TOM70 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, transport                                  | membrane, mitochondrion          | protein binding, transporter activity | 1.728 | 2.257 | 1.31 |
| P01852 | Mitochondrial import inner membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c] | transport                                                                  | membrane, mitochondrion          | nucleotide binding, protein binding | 4.125 | 5.404 | 1.31 |
| P07266 | Mitochondrial RNA-splicing protein MR51 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | mitochondrion, organelle lumen   | catalytic activity, DNA binding, RNA binding | 0.425 | 0.557 | 1.31 |
| P03227 | Mitochondrial fusion and transport protein lgp1 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | membrane, mitochondrion          | protein binding, structural molecule activity | 0.425 | 0.557 | 1.31 |
| P08968 | UPR560, protein FM460 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | mitochondrion                    | protein binding               | 2.495 | 3.27  | 1.31 |
| P02776 | Mitochondrial import inner membrane translocase subunit TIM50 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process, transport              | membrane, mitochondrion          | catalytic activity, protein binding, transporter activity | 7.483 | 9.857 | 1.32 |
| P36258 | 34S ribosomal protein l17, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | mitochondrion, ribosome          | structural molecule activity   | 0.52  | 0.688 | 1.32 |
| P36163 | mitochondrial metalloendopeptidase OMA1 [OS=Saccharomyces cerevisiae S288c] | metabolic process                                                           | membrane, mitochondrion          | catalytic activity, metal ion binding | 0.551 | 0.73  | 1.32 |
| P03799 | 37S ribosomal protein 58, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process                         | mitochondrion, ribosome          | structural molecule activity   | 1.424 | 1.894 | 1.33 |
| P12288 | Malonyl CoA:acyl carrier protein transacylase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process                                                           | mitochondrial                     | catalytic activity             | 0.668 | 0.896 | 1.34 |
P1735 S-demethoxyubiquinone
hydroxylase, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

854292 CATS; YOR125C metabolic process membrane/mitochondrion catalytic activity;metal ion binding 0.54 0.778 1.44

Q0623 Protein FMP25, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

850766 FMP25; YLR077W cell organization and biogenesis membrane/mitochondrion 0.968 1.412 1.46

P3127 mitochondrial carrier protein
RIM2 [OS=Saccharomyces
cerevisiae S288c]

852491 RIM2; YBR192W cell organization and biogenesis;transport membrane/mitochondrion structural molecule activity;transporter activity 1.239 1.818 1.47

P25573 Mitochondrial inner membrane i-AAP protease supercomplex subunit MGR1 [OS=Saccharomyces
cerevisiae S288c]

850313 MGR1; YCL044C metabolic process membrane/mitochondrion protein binding 0.701 1.031 1.47

P35180 mitochondrial import receptor subunit Tom20 [OS=Saccharomyces
cerevisiae S288c]

852973 TOM20; YGR082W cell organization and biogenesis;transport membrane/mitochondrion protein binding;transporter activity 0.701 1.031 1.47

P08466 mitochondrial nuclease
[Pyruvate dehydrogenase
(acetyl-transferring) kinase 1, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

851222 NUC1; YIL208C cell death;metabolic process membrane/mitochondrion;nucleus catalytic activity;metal ion binding;protein binding 1.336 1.976 1.48

P40530 [Protein
854769 PKP1; YIL042C metabolic process mitochondrial;organelle lumen catalytic activity;nucleotide binding;protein binding 0.931 1.404 1.51

P48237 Mitochondrial group I intron
splicing factor CCM1
[OS=Saccharomyces
cerevisiae S288c]

853053 CCM1; YGR1500C cell organization and biogenesis;metabolic process mitochondrial RNA binding 0.089 0.136 1.53

Q00153 ATPase synthesis protein 25, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

851123 ATP25; YMR098C cell organization and biogenesis;regulation of biological process membrane/mitochondrion 0.116 0.179 1.54

P46525 44S ribosomal protein L24, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

855211 MRPL24; YMR193W cell organization and biogenesis;metabolic process mitochondrial;ribosome RNA binding;structural molecule activity 1.929 2.981 1.55

P32048 Lysine--tRNA ligase, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

855651 MSK1; YNL073W cell organization and biogenesis;metabolic process cytoplasm/mitochondrion;organelle lumen catalytic activity;nucleotide binding;RNA binding 0.122 0.189 1.55

P38393 Glutamyl-tRNA synthetase
[OS=Saccharomyces
cerevisiae S288c]

852198 PET112; YBL080C cell organization and biogenesis;metabolic process mitochondrial catalytic activity;nucleotide binding 0.15 0.233 1.55

P36101 tRNA threonylcarbamoyladenosine
dehydratase 2
[OS=Saccharomyces
cerevisiae S288c]

853841 TCD2; YKL027W metabolic process cytosol;membrane/mitochondrion catalytic activity;nucleotide binding;protein binding 0.616 0.957 1.55

P47150 37S ribosomal protein S7, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

853578 RPS7; YIR313C cell organization and biogenesis;metabolic process mitochondrial RNA binding;structural molecule activity 0.616 0.957 1.55

P38771 Ribosome-recycling factor, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

856433 RRF1; YHR038W cell organization and biogenesis;metabolic process mitochondrial RNA binding 1.254 1.955 1.56

P49630 Lysozyme
[OS=Saccharomyces
cerevisiae S288c]

856262 TAZ1; YPR140W cell organization and biogenesis;metabolic process membrane/mitochondrion catalytic activity 0.194 0.304 1.57

P00427 Cytochrome c oxidase
subunit 6, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

856448 COX6; YHR051W metabolic process membrane/mitochondrion catalytic activity;metal ion binding;transporter activity 4.623 7.254 1.57

Q12467 MIOREX complex component 4
[OS=Saccharomyces
cerevisiae S288c]

855935 YPL168W; MIO4; YPL168W membrane/mitochondrion 0.202 0.318 1.57

P40102 proteophosphorin oxidase
[OS=Saccharomyces
cerevisiae S288c]

856733 HEM14; YER014W membrane/mitochondrion catalytic activity 1.482 2.36 1.59

P32266 Dynamin-like GTPase
[OS=Saccharomyces
cerevisiae S288c]

854386 MGM1; YGR211C cell organization and biogenesis membrane/mitochondrion catalytic activity;nucleotide binding;protein binding 0.28 0.448 1.60

P13334 54S ribosomal protein L9, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

851135 MRPL9; YGR220C cell organization and biogenesis;metabolic process mitochondrial;ribosome structural molecule activity 0.311 0.501 1.61

P40998 uncharacterized mitochondrial membrane protein [OS=Saccharomyces
cerevisiae S288c]

856931 FMP10; YER182W membrane/mitochondrion 2.36 3.833 1.62

P22353 54S ribosomal protein L8, mitochondrial
[OS=Saccharomyces
cerevisiae S288c]

853382 MRPL8; YIL063C cell organization and biogenesis;metabolic process mitochondrial;ribosome structural molecule activity 0.359 0.585 1.63
| Accession   | Description                                                                 | Cellular Location/Process                                                                 | Function/Activity                      | K1011 | K1091 | K1092 |
|-------------|-----------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|----------------------------------------|-------|-------|-------|
| P34222      | Peptidyl-tRNA hydrolase 2                                                   | cytoplasm; cytosol; membrane; mitochondrion                                              | catalytic activity; protein binding    | 0.425 | 0.701 | 1.65 |
| P18175      | 375 ribosomal protein MRP21, mitochondrial                                  | cell organization and biogenesis; metabolic process                                      | mitochondrion; ribosome                | 0.425 | 0.701 | 1.65 |
| P12195      | Protein ATP12, mitochondrial                                               | cell organization and biogenesis                                                          | mitochondrion                          | 0.468 | 0.778 | 1.66 |
| P40515      | Mitochondrial fission 1 protein                                            | cell death; cell organization and biogenesis; regulation of biological process           | membrane; mitochondrion               | 0.468 | 0.778 | 1.66 |
| Q04330      | 375 ribosomal protein RSM28, mitochondrial                                  | cell organization and biogenesis; metabolic process                                      | mitochondrion; ribosome                | 2.675 | 4.484 | 1.68 |
| P29489      | Mitochondrial import inner membrane translocase subunit TIM16               | transport                                                                                  | protein binding                        | 0.52  | 0.874 | 1.68 |
| P66520      | 345 ribosomal protein L10, mitochondrial                                    | cell organization and biogenesis; metabolic process                                      | mitochondrion; ribosome                | 0.551 | 0.931 | 1.69 |
| P28321      | monoglyceride lipase                                                        | metabolic process; regulation of biological process                                      | cytoplasm; endoplasmic reticulum; membrane; mitochondrion | 0.551 | 0.931 | 1.69 |
| P35986      | Succinyl-CoA ligase [ADP-forming] subunit alpha, mitochondrial              | cell organization and biogenesis; metabolic process                                      | mitochondrion; ribosome                | 1.276 | 2.162 | 1.69 |
| P22354      | 345 ribosomal protein L20, mitochondrial                                    | cell organization and biogenesis; metabolic process                                      | mitochondrion; ribosome                | 0.585 | 0.995 | 1.70 |
| P40471      | NADPH-dependent 1-acylglutaryne reductase                                   | cytoplasm; endoplasmic reticulum; membrane; mitochondrion                                | catalytic activity; nucleotide binding | 9     | 15.238| 1.69 |
| P42844      | Mitochondrial protein import protein ZIM17                                   | cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport | mitochondrion; organelle lumen; membrane; mitochondrion; organelle lumen | 0.585 | 0.995 | 1.70 |
| P00128      | Cytochrome b-c1 complex subunit 7                                           | cell organization and biogenesis; metabolic process; transport                            | membrane; mitochondrion               | 15.681| 26.826| 1.71 |
| P40165      | NAD(P)H-hydration epimerase [OS=Saccharomyces cerevisiae 5288c]              | cell organization and biogenesis; metabolic process; transport                            | membrane; mitochondrion               | 1.61  | 2.831 | 1.76 |
| Q03190      | Mitochondrial 2-oxoglutarate carrier 2                                     | cell organization and biogenesis; metabolic process                                      | mitochondrion                          | 0.778 | 1.371 | 1.76 |
| P19262      | Dihydropicolylamine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial  | cell organization and biogenesis; metabolic process                                      | mitochondrion                          | 5.7   | 10.053| 1.76 |
| P54003      | Protein SUR7                                                                | cell differentiation; transport                                                           | membrane; mitochondrion               | 0.848 | 1.512 | 1.78 |
| P15424      | ATP-dependent RNA helicase MMS116, mitochondrial                            | cell organization and biogenesis; regulation of biological process                       | mitochondrion; organelle lumen         | 1.154 | 2.082 | 1.80 |
| P10849      | mitochondrial transcription factor 2 [OS=Saccharomyces cerevisiae 5288c]      | cell organization and biogenesis; metabolic process                                      | mitochondrion; organelle lumen         | 0.259 | 0.468 | 1.81 |
| Q22896      | mitochondrial carnitine carrier [OS=Saccharomyces cerevisiae 5288c]          | cell organization and biogenesis; metabolic process                                      | mitochondrion; ribosome                | 0.931 | 1.683 | 1.81 |
| P51998      | 345 ribosomal protein Yml8, mitochondrial                                   | cell organization and biogenesis; metabolic process                                      | mitochondrion; ribosome                | 0.931 | 1.683 | 1.81 |
| P53230      | Phosphatidate cytidylyltransferase, mitochondrial                           | cell organization and biogenesis; metabolic process                                      | mitochondrion; organelle lumen         | 0.292 | 0.532 | 1.82 |

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| Gene ID | Gene Name                    | Description                                                                 | Subcellular Location       | GO Terms                                                                 | Interaction Type | p-value 1 | p-value 2 | Odds Ratio |
|---------|------------------------------|------------------------------------------------------------------------------|---------------------------|--------------------------------------------------------------------------|------------------|-----------|-----------|------------|
| P3122   | tRNA-M6-adenosine threonylcarbamoyltransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity; metal ion binding                                     |                  | 0.334     | 0.616     | 1.84       |
| P38626  | NADH-cytochrome b5 reductase 1 | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity                                                      |                  | 0.334     | 0.616     | 1.84       |
| Q06484  | MIOREX complex component 10 | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | membrane, mitochondrial                                                |                  | 0.35      | 0.65      | 1.86       |
| P02771  | Protein PET117, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity; DNA binding; RNA binding                            |                  | 1.154     | 2.162     | 1.87       |
| P36775  | Lon protease homolog, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | cytoplasm; mitochondrial; nucleosome                                          |                  | 1.222     | 2.311     | 1.89       |
| P31820  | 375 ribosomal protein 59, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | RNA binding; structural molecule activity                                |                  | 1.254     | 2.384     | 1.90       |
| P40496  | 375 ribosomal protein 252, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | structural molecule activity                                              |                  | 0.468     | 0.896     | 1.91       |
| Q06668  | Methyltransferase DMS1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity                                                      |                  | 0.484     | 0.931     | 1.92       |
| P21771  | 375 ribosomal protein 528, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | RNA binding; structural molecule activity                                |                  | 0.833     | 1.637     | 1.97       |
| P25038  | Translation initiation factor IF-2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity; nucleotide binding; RNA binding                    |                  | 0.054     | 0.11      | 2.04       |
| P53848  | Folic acid synthesis protein fol1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity; metal ion binding; nucleotide binding                |                  | 0.045     | 0.093     | 2.07       |
| Q08222  | Genetic interactor of prohibitin 3, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity; nucleotide binding; transporter activity             |                  | 0.059     | 0.122     | 2.07       |
| P34231  | Uncharacterized protein YKL187C, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity; nucleotide binding; RNA binding                  |                  | 0.093     | 0.194     | 2.09       |
| P38746  | Oligo-ATPase homolog, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | nucleotide binding                                                      |                  | 0.093     | 0.194     | 2.09       |
| P38756  | tRNA threonylcarbamoyltransferase dehydratase 1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity; nucleotide binding                                  |                  | 0.093     | 0.194     | 2.09       |
| P40452  | Cytochrome c oxidase assembly factor 1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | protein binding                                                         |                  | 0.874     | 1.848     | 2.11       |
| P42384  | Thiosulfate sulfatransferase RD1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity                                                      |                  | 0.874     | 1.848     | 2.11       |
| Q12393  | Genetic interactor of prohibitin 5, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity                                                      |                  | 0.122     | 0.259     | 2.12       |
| P28377  | Protein MSP1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | membrane, mitochondrial; nucleus                                          |                  | 0.122     | 0.259     | 2.12       |
| Q04472  | Mitochondrial inner membrane I-AAP protease supercomplex subunit MGR3, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | catalytic activity; nucleotide binding; protein binding                |                  | 0.15      | 0.322     | 2.15       |
| P38816  | thioredoxin reductase 2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | mitochondrial              | antioxidant activity; catalytic activity                                |                  | 0.136     | 0.292     | 2.15       |
| P21375 | Fumarate reductase 2 [OS=Saccharomyces cerevisiae S288c] | 853510 | OSM1; YJR051W | metabolic process | endoplasmic reticulum;mitochondrion | catalytic activity;nucleotide binding | 0.16 | 0.346 | 2.16 |
| P40502 | Altered inheritance of mitochondria protein 39, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 854722 | AIM19; YL067C | membrane;mitochondrion | | | 0.995 | 2.162 | 2.17 |
| Q01532-1 | Cysteine proteinase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 853701 | AIQ1; YPL091W | metabolic process;regulation of biological process;response to stimulus | cytoplasm;mitochondrion | catalytic activity;DNA binding;RNA binding | 0.179 | 0.389 | 2.17 |
| P36056 | 37S ribosomal protein S22, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 856014 | GJI1; YPL013W | cellular homeostasis;metabolic process | cytoplasm;cytosol;mitochondrion;nucleus | antioxidant activity; catalytic activity; nucleotide binding | 0.24 | 0.54 | 2.24 |
| P49334 | Mitochondrial import receptor subunit tom22 [OS=Saccharomyces cerevisiae S288c] | 856592 | TON322; YNL131W | cell organization and biogenesis;metabolic process | membrane;mitochondrion | protein binding;transporter activity | 0.292 | 0.668 | 2.29 |
| P14063 | 54S ribosomal protein L31, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 853720 | MRPL31; YKL138C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.292 | 0.668 | 2.29 |
| Q03246 | 37S ribosomal protein S17, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 855226 | MRPS17; YMR188C | cell differentiation;cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.931 | 2.162 | 2.32 |
| P53193 | J-type co-chaperone JAC1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 852866 | JAC1; YGL018C | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion;organelle lumen | protein binding | 0.468 | 1.154 | 2.47 |
| P53157 | Mitochondrial pyruvate carrier 1 [OS=Saccharomyces cerevisiae S288c] | 852800 | FMP937; MPC1; YGL088W | transport | membrane;mitochondrion | transporter activity | 0.468 | 1.154 | 2.47 |
| P25087 | Sterol 24-C-methyltransferase [OS=Saccharomyces cerevisiae S288c] | 850013 | ERG6; YML008C | metabolic process | endoplasmic reticulum;membrane;mitochondrion | catalytic activity | 0.557 | 1.424 | 2.56 |
| P35999 | Mitochondrial intermediate peptidase [OS=Saccharomyces cerevisiae S288c] | 853724 | OCT1; YKL134C | cellular homeostasis;metabolic process;regulation of biological process | mitochondrion;organelle lumen | catalytic activity;metal ion binding | 0.145 | 0.372 | 2.57 |
| P39112 | DeoD homolog II, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 855331 | DSS1; YMR287C | metabolic process | mitochondrion;organelle lumen | catalytic activity;RNA binding | 0.087 | 0.233 | 2.68 |
| P39200 | Sigma-like sequence protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 850830 | SL151; YLR139C | cell organization and biogenesis;metabolic process | membrane;mitochondrion | protein binding | 0.125 | 0.343 | 2.74 |
| P38869 | Pentamidine resistance factor, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 854440 | PNT1; YOR266W | cell organization and biogenesis;response to stimulus | membrane;mitochondrion | | 0.259 | 0.711 | 2.75 |
| P22438 | Methionine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 853081 | MSL1; YGR171C | metabolic process | cytoplasm;cytosol;mitochondrion;organelle lumen | catalytic activity; nucleotide binding | 0.136 | 0.377 | 2.77 |
| Q06089 | Uncharacterized mitochondrial outer membrane protein YPR098C [OS=Saccharomyces cerevisiae S288c] | 856213 | YPR098C; YPR098C | | membrane;mitochondrion | | 0.778 | 2.162 | 2.78 |
| P32493 | ATPase expression protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 850586 | AEP1; YMR069W | regulation of biological process | mitochondrion | translation regulator activity | 0.15 | 0.417 | 2.78 |
| Q12032 | Altered inheritance of mitochondria protein 41, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 854390 | AIM41; YGR215C | | mitochondrion | catalytic activity | 1.61 | 4.623 | 2.87 |
| Q06998 | Putative ATP-dependent RNA helicase YLR419W [OS=Saccharomyces cerevisiae S288c] | 851137 | YLR419W; YLR419W | metabolic process | cytoplasm;mitochondrion;nucleus | catalytic activity; nucleotide binding;protein binding;RNA binding | 0.027 | 0.082 | 3.04 |
| P53234 | Uncharacterized protein YGR053C [OS=Saccharomyces cerevisiae S288c] | 852944 | YGR053C; YGR053C | | | | 0.129 | 0.438 | 3.40 |
| P47039 | Probable kynurenine--oxoglutarate transaminase [OS=Saccharomyces cerevisiae S288c] | 853386 | BNA3; YL0606W | metabolic process;regulation of biological process | cytoplasm;mitochondrion | catalytic activity | 0.334 | 1.154 | 3.46 |
| Protein ID | Description | Gene Symbol | Location | GO Terms | Enrichment Score |
|------------|-------------|-------------|---------|----------|-----------------|
| P39533     | Homocitrate dehydratase, mitochondrial | ACO2; YIL200C | metabolic process | mitochondrion | 0.17 0.688 4.05 |
| Q02981     | ABC1 family protein YPL109C, mitochondrial | YPL109C; YPL109C | | mitochondrion | 0.059 0.259 4.39 |
| P53318     | Ubiquinone biosynthesis monoxygenase COQ6, mitochondrial | COQ6; YGR255C | metabolic process | membrane, mitochondrion | 0.077 0.346 4.49 |
| Q08926     | ULP1-interacting protein 4 | UIP4; YPL1186C | endoplasmic reticulum, membrane, mitochondrion, nucleus | | 0.136 0.668 4.91 |
| P38825     | Protein TOM71 | TOM71; YHR117W | transport | membrane, mitochondrion | 0.061 0.343 5.62 |
| P48526     | Isoleucine-tRNA ligase, mitochondrial | ISM1; YPL040C | cell organization and biogenesis, metabolic process, regulation of biological process | | 0.081 0.477 5.89 |
Supplemental Table S2. The relative concentrations of proteins in mitochondria purified from WT cells cultured with or without LCA. Mitochondria were purified from WT cells recovered on day 4 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the "Proteome Discoverer" software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI WT + LCA | Ratio WT + LCA / WT |
|-----------|-------------|---------------|---------|--------------------|-------------------|-------------------|-----------|----------------|-------------------|
| P00127    | Cytochrome b-c1 complex subunit 6 | 85059    | QC066 | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 1.371 | 0.334 | 0.24 |
| Q96VH5    | MICOS complex subunit Mic10 | 85030    | MOS1   | cell organization and biogenesis | membrane; mitochondrion | | 6.197 | 1.683 | 0.27 |
| P53230    | Phosphatidate cytidylyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85293    | TAM41; YOR046       | metabolic process | membrane; mitochondrion; organelle lumen | catalytic activity | 0.668 | 0.186 | 0.28 |
| P14693    | sorting assembly machinery 35 kDa subunit [OS=Saccharomyces cerevisiae S288c] | 85648    | SAM35; YHR83       | cell organization and biogenesis; transport | membrane; mitochondrion | | 0.54 | 0.155 | 0.29 |
| P32332    | Mitochondrial oxaloacetate transport protein [OS=Saccharomyces cerevisiae S288c] | 85373    | QAC1; YML120       | metabolic process; transport | membrane; mitochondrion | structural molecule activity; transporter activity | 4.995 | 1.783 | 0.36 |
| P47131    | TMEM14 protein homolog [OS=Saccharomyces cerevisiae S288c] | 85354    | YOR85       | | membrane; mitochondrion | | 2.162 | 0.778 | 0.36 |
| P35163    | 54S ribosomal protein L12, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85281    | MNP1; YGL068       | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 1.31 | 0.52 | 0.40 |
| P47140    | Altered inheritance rate of mitochondrial protein 25 [OS=Saccharomyces cerevisiae S288c] | 85356    | AIM25; YJR100     | cell organization and biogenesis | membrane; mitochondrion | transporter activity | 0.874 | 0.369 | 0.42 |
| P39515    | mitochondrial import inner membrane translocase subunit Tim17 [OS=Saccharomyces cerevisiae S288c] | 85329    | TIM17; YIL143      | cell organization and biogenesis; transport | membrane; mitochondrion | protein binding; transporter activity | 0.778 | 0.334 | 0.43 |
| P09938    | Ribonucleoside-diphosphate reductase small chain 1 [OS=Saccharomyces cerevisiae S288c] | 85342    | RNR2; YIL102       | metabolic process | cytoplasm; cytosol; nucleus | catalytic activity; metal ion binding; protein binding | 0.668 | 0.292 | 0.44 |
| P45081    | peroxiredoxin HVR1 [OS=Saccharomyces cerevisiae S288c] | 85485    | HYR1; YMR037      | metabolic process; response to stimulus | cytoplasm; cytosol; mitochondrial; organelle lumen | antioxidant activity; catalytic activity | 0.585 | 0.239 | 0.44 |
| P38112    | Tricarboxylate transport protein [OS=Saccharomyces cerevisiae S288c] | 85259    | CTP1; YBR291       | metabolic process; transport | membrane; mitochondrion | structural molecule activity; transporter activity | 0.551 | 0.245 | 0.44 |
| Q08970    | Mitochondrial metal transporter 2 [OS=Saccharomyces cerevisiae S288c] | 85587    | MMT2; YPL224       | cellular homeostasis; regulation of biological processes; response to stimulus; transport | membrane; mitochondrion | transporter activity | 0.407 | 0.186 | 0.46 |
| P25270    | rRNA methyltransferase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85437    | MRM1; YOR201      | metabolic process | mitochondrion | catalytic activity; RNA binding | 0.274 | 0.129 | 0.47 |
| P25704    | squamine synthase [OS=Saccharomyces cerevisiae S288c] | 85659    | ERG5; YHR190      | metabolic process | endoplasmic reticulum; membrane; mitochondrion | catalytic activity | 0.222 | 0.105 | 0.47 |
| Q06005    | Octanoyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85694    | LP2; YLR239       | metabolic process | cytoplasm; mitochondrion | catalytic activity | 0.245 | 0.116 | 0.47 |
| P38169    | Kynurenine 3-monooxygenase [OS=Saccharomyces cerevisiae S288c] | 85217    | BNA4; YBL098       | metabolic process | membrane; mitochondrion | catalytic activity; nucleotide binding | 0.372 | 0.083 | 0.48 |
| P31450    | ATP synthase subunit I, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85489    | ATP18; YML081       | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 9 | 4.623 | 0.51 |
| P40165    | NADP(+) dehydrogenase [OS=Saccharomyces cerevisiae S288c] | 85552    | YML200; YNL200     | metabolic process | cytoplasm; mitochondrion | catalytic activity; metal ion binding; nucleotide binding | 2.362 | 1.154 | 0.53 |
| P01097    | ATPase inhibitor, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85134    | INH1; YDL181       | metabolic process; regulation of biological process | mitochondrion | catalytic activity; enzyme regulator activity; protein binding | 2.362 | 1.154 | 0.53 |
| Gene ID | Description | Process | Subcellular Location | Activity | PMI | SA |
|---------|-------------|---------|----------------------|----------|-----|----|
| P39525  | 3-oxoacyl-[acyl-carrier-protein] synthase homolog (Saccharomyces cerevisiae S288c) | metabolic process | mitochondrion | catalytic activity | 2.899 | 1.565 | 0.54 |
| P54003  | Protein SUR7 (Saccharomyces cerevisiae S288c) | cell differentiation;transport | membrane/mitochondrion | | 1.512 | 0.848 | 0.56 |
| Q12359  | Ammonia transport outward protein 3 (Saccharomyces cerevisiae S288c) | transport | membrane/mitochondrion | transporter activity | 0.995 | 0.585 | 0.59 |
| P25642  | 54S ribosomal protein IMG2, mitochondrial (Saccharomyces cerevisiae S288c) | cell organization and biogenesis;metabolic process | mitochondrion/ribosome | structural molecule activity | 0.778 | 0.468 | 0.60 |
| Q02888  | Inner membrane assembly complex subunit 17 (Saccharomyces cerevisiae S288c) | cell organization and biogenesis | membrane/mitochondrion | protein binding | 0.701 | 0.425 | 0.61 |
| P32799  | Cytochrome c oxidase subunit 6A, mitochondrial (Saccharomyces cerevisiae S288c) | cell organization and biogenesis;metabolic process;regulation of biological process;transport | membrane/mitochondrion | catalytic activity;enzyme regulator activity;transport activity | 18.95 | 11.58 | 9 | 0.61 |
| P33212  | Probable transmembrane protein TFOH1 (Saccharomyces cerevisiae S288c) | | mitochondrion | | 0.585 | 0.359 | 0.61 |
| Q06567  | ABC1 family protein MCF2 (Saccharomyces cerevisiae S288c) | cell organization and biogenesis | membrane/mitochondrion | | 0.484 | 0.301 | 0.62 |
| P35234  | Uncharacterized protein YGR053C (Saccharomyces cerevisiae S288c) | metabolic process;transport | membrane/mitochondrion | structural molecule activity;transporter activity | 5.813 | 3.642 | 0.63 |
| Q38324  | Uncharacterized protein YOB20W-A (Saccharomyces cerevisiae S288c) | metabolic process;transport | membrane/mitochondrion | | 5.813 | 3.642 | 0.63 |
| P00560  | Phosphoglycerate kinase (Saccharomyces cerevisiae S288c) | metabolic process | cytoplasm/mitochondrion | catalytic activity;nucleotide binding | 6.356 | 4.012 | 0.63 |
| P33310  | ATP-dependent permease MOL1, mitochondrial (Saccharomyces cerevisiae S288c) | transport | membrane/mitochondrion | catalytic activity;nucleotide binding;transporter activity | 0.833 | 0.528 | 0.63 |
| P15992  | heat shock protein 28 (Saccharomyces cerevisiae S288c) | metabolic process;response to stimulus | cytoplasm/mitochondrion;nucleus | protein binding;RNA binding | 4.878 | 3.125 | 0.64 |
| P07253  | cytochrome B pre-mRNA-processing protein 6 (Saccharomyces cerevisiae S288c) | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion/ribosome | | 4.179 | 2.728 | 0.65 |
| P38006  | Phosphatidylserine decarboxylase protein 1, mitochondrial (Saccharomyces cerevisiae S288c) | metabolic process;regulation of biological process | membrane/mitochondrion | catalytic activity | 0.743 | 0.487 | 0.66 |
| P00045  | Cytochrome c iso-2 (Saccharomyces cerevisiae S288c) | metabolic process;transport | mitochondrion | metal ion binding | 1.512 | 0.995 | 0.66 |
| Q06143  | mitochondrial dicarboxylate transporter (Saccharomyces cerevisiae S288c) | metabolic process;transport | membrane/mitochondrion | structural molecule activity;transporter activity | 1.404 | 0.931 | 0.66 |
| P14832  | peptidyl-prolyl cis-trans isomerase (Saccharomyces cerevisiae S288c) | cell differentiation;cell organization and biogenesis;metabolic process;regulation of biological process;transport | cytoplasm/mitochondrion;nucleus | catalytic activity;RNA binding | 1.31 | 0.874 | 0.67 |
| P42499  | Mitochondrial import inner membrane translocase subunit TIM11 (Saccharomyces cerevisiae S288c) | transport | membrane/mitochondrion | protein binding | 1.31 | 0.874 | 0.67 |
| Q12298  | uncharacterized ABC transporter ATP-binding protein YDR801W (Saccharomyces cerevisiae S288c) | | mitochondrion | catalytic activity;nucleotide binding | 0.512 | 0.343 | 0.67 |
| Q05799  | 37S ribosomal protein SB, mitochondrial (Saccharomyces cerevisiae S288c) | cell organization and biogenesis;metabolic process | mitochondrion/ribosome | structural molecule activity | 1.031 | 0.701 | 0.68 |
| Q12428  | Probable 2-methylisocitrate dehydratase (Saccharomyces cerevisiae S288c) | metabolic process | cytoplasm/mitochondrion | catalytic activity | 18.11 | 12.33 | 5 | 0.68 |
| P40086  | Cytochrome c oxidase assembly protein cox15 (Saccharomyces cerevisiae S288c) | cell organization and biogenesis;metabolic process;transport | membrane/mitochondrion | catalytic activity;transporter activity | 2.594 | 1.783 | 0.69 |
dehydrogenase 3
Glyceraldehyde 3-phosphate dehydrogenase 3

Mitochondrial distribution and mitochondrial membrane protein FMP10

Enolase 2

Mitochondrial phosphate carrier protein 2

Mitochondrial carrier protein YM2

Methyltransferase OM51

Citrate/oxoglutarate carrier protein

Enolase 2

Protein MF03-like

uncharacterized mitochondrial membrane protein FMF10

Dynamin-like GTPase MSM1, mitochondrial

Mitochondrial distribution and morphology protein 38

37S ribosomal protein NAM9, mitochondrial

Cysteine desulfurase, mitochondrial

Protein M5551, mitochondrial

Glyceroldehyde-3-phosphate dehydrogenase 3

\( \text{Glyceraldehyde 3-phosphate dehydrogenase 3 [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Mitochondrial distribution and mitochondrial membrane protein FMP10 [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Enolase 2 [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Mitochondrial phosphate carrier protein 2 [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Mitochondrial carrier protein YM2 [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Methyltransferase OM51, mitochondrial [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Citrate/oxoglutarate carrier protein [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Protein MF03-like [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{uncharacterized mitochondrial membrane protein FMF10 [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Dynamin-like GTPase MSM1, mitochondrial [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Mitochondrial distribution and morphology protein 38 [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{37S ribosomal protein NAM9, mitochondrial [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Cysteine desulfurase, mitochondrial [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Protein M5551, mitochondrial [OS=Saccharomyces cerevisiae S288c]} \)

\( \text{Glyceroldehyde-3-phosphate dehydrogenase 3 [OS=Saccharomyces cerevisiae]} \)
**P32191**
Glycerol-3-phosphate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | membrane,mitochondrion | GUT2; YL155C | metabolic process |

**P33311**
ATP-dependent permease MAL2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Response to stimulus,transport | membrane,mitochondrion | MAL2; YPL270 W | response to stimulus,transport |

**Q04818**
Meliotic sister-chromatid recombination protein 6, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| RNA binding | mitochondrion,organelle lumen | MSCE; YOR354 C | metabolic process |

**P40047**
Aldehyde dehydrogenase 5, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion,organelle lumen | ALDS; YER073 W | metabolic process |

**P32843**
Mitochondrial escape protein 2 [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Nucleotide binding | membrane,mitochondrion | YME2; YMR330 C | cell organization and biogenesis,metabolic process |

**P16547**
Mitochondrial outer membrane protein OM45 [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | membrane,mitochondrion | OM45; YIL136 W | membrane,mitochondrion |

**P07256**
Cytochrome b-3 complex subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | membrane,mitochondrion | COR1; YBL045 C | metabolic process,transport |

**P53312**
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion | LSC2; YGR2424 C | metabolic process |

**P07251**
ATP synthase subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | cytosol,membrane,mitochondrion | ATP1; YBL099 W | metabolic process,transport |

**P04840**
Mitochondrial outer membrane protein porin 1 [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Transporter activity | cytoplasm,membrane,mitochondrion | POR1; YNL055 C | cell death,cell organization and biogenesis,cellular homeostasis,regulation of biological process,transport |

**P53252**
Sphingolipid long chain base-responsive protein PII1 [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Protein binding | cytoplasm,membrane,mitochondrion | PII1; YGR086 C | cell organization and biogenesis,regulation of biological process,response to stimulus,transport |

**P40215**
External NADH-ubiquinone oxidoreductase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion | NDE1; YMR314 SC | metabolic process |

**P07213**
Mitochondrial import receptor subunit TOM70 [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Protein binding,transporter activity | membrane,mitochondrion | TOM70; YNL121 C | cell organization and biogenesis,cellular homeostasis,regulation of biological process,transport |

**P07246**
Alcohol dehydrogenase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion,organelle lumen | ADH3; YMR308 W | metabolic process |

**P45635**
Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion | CIT3; YPR0901 W | metabolic process |

**P32473**
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion,organelle lumen | PBD1; YBR221 C | metabolic process |

**P12695**
Dihydrotroponoyl-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion,organelle lumen | LAT1; YNL071 W | metabolic process |

**P49367**
Homoaconitase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion | LYS4; YDR234 W | metabolic process |

**P36013**
NAD-dependent malic enzyme, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion,organelle lumen | MAE1; YNL029 C | metabolic process |

**P07143**
Cytochrome c1, heme protein, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Metal ion binding | cytosol,membrane,mitochondrion | CYT1; YOR665 W | metabolic process,transport |

**P16622**
Ferrochelatase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | membrane,mitochondrion | HEM31; YOR176 W | metabolic process |

**P43567**
analine-glyoxylate aminotransferase 1 [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | cytosol,mitochondrion | ASX1; YFL030 W | metabolic process |

**Q03104**
Meliotic sister chromatid recombination protein 1 [OS=Saccharomyces cerevisiae S288c]

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | mitochondrion,organelle lumen | MSC1; YML128 C | metabolic process,endoendoplasmic reticulum,mitochondrion |

**P39925**
Mitochondrial respiratory-chain complexes assembly protein AFG3

| Binding | Metabolic pathway | Protein | Function |
|---------|------------------|---------|----------|
| Catalytic activity | membrane,mitochondrion | AFG3; YER017 | cell organization and biogenesis,metabolic process |
| [OS=Saccharomyces cerevisiae S288c] | C | process/response to stimulus;transport | binding;nucleotide binding;protein binding |
|-------------------------------------|---|--------------------------------------|---------------------------------------------|
| P0626 | ATP synthase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85602 | 7 | ATP4; YPL078 C | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 4.995 | 4.995 | 1.00 |
| P53982 | Isocitrate dehydrogenase (NADP) [OS=Saccharomyces cerevisiae S288c] | 85572 | 3 | IDP3; YNL009 W | metabolic process | cytoplasm;mitochondrion | catalytic activity;metal ion binding;nucleotide binding | 2.662 | 2.662 | 1.00 |
| Q07651 | SUR7 family protein FMP45 [OS=Saccharomyces cerevisiae S288c] | 85130 | 4 | FMP45; YDL122 C | cell differentiation;cell organization and biogenesis | membrane;mitochondrion | catalytic activity;transport regulatory activity | 4.878 | 4.878 | 1.00 |
| P25039 | Elongation factor G, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85075 | 8 | MEF1; YLR069 C | cell organization and biogenesis;metabolic process | cytosol;mitochondrion | catalytic activity;protein binding;RNA binding | 0.931 | 0.931 | 1.00 |
| P10662 | 37S ribosomal protein MRPI, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85194 | 9 | MRPI; YDR347 W | cell organization and biogenesis;metabolic process;response to stimulus | mitochondrion;ribosome | antioxidant activity;catalytic activity;metal ion binding;structural molecule activity | 2.981 | 2.981 | 1.00 |
| P42940 | Probable electron transfer flavoprotein subunit beta [OS=Saccharomyces cerevisiae S288c] | 85312 | 7 | CiR1; YGR207 C | metabolic process;transport | mitochondrion;organelle lumen | catalytic activity;nucleotide binding | 4.623 | 4.623 | 1.00 |
| P32317 | Protein AFG1 [OS=Saccharomyces cerevisiae S288c] | 85665 | 8 | AFG1; YEL052 W | cell organization and biogenesis;metabolic process;response to stimulus | membrane;mitochondrion | catalytic activity;protein binding | 1.326 | 1.326 | 1.00 |
| Q04438 | Stationary phase protein 4 [OS=Saccharomyces cerevisiae S288c] | 85513 | 4 | SPG4; YMR10 7W | cell organization and biogenesis;metabolic process;response to stimulus | chromosome;mitochondrion | DNA binding | 3.281 | 3.281 | 1.00 |
| P32787 | Mitochondrial genome maintenance protein MISM101 [OS=Saccharomyces cerevisiae S288c] | 85360 | 9 | MISM101 1; YJR144 W | cell organization and biogenesis;metabolic process;response to stimulus | chromosome;mitochondrion | DNA binding | 3.281 | 3.281 | 1.00 |
| Q07349 | MIOREX complex component 9 [OS=Saccharomyces cerevisiae S288c] | 85153 | 5 | YDL027 C; MRX9; YDL027 C | endoplasmic reticulum;membrane;mitochondrion | protein binding | 1.154 | 1.154 | 1.00 |
| P53266 | Cytochrome oxidase assembly protein SHY1 [OS=Saccharomyces cerevisiae S288c] | 85300 | 9 | SHY1; YGR112 W | cell organization and biogenesis | membrane;mitochondrion | protein binding | 1.154 | 1.154 | 1.00 |
| P81449 | ATP synthase subunit e, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85192 | 2 | TIM11; YDR322 C-A | cell organization and biogenesis;metabolic process;response to stimulus | membrane;mitochondrion | catalytic activity;structural molecule activity;transporter activity | 9 | 9 | 1.00 |
| P10834 | protein PET54 [OS=Saccharomyces cerevisiae S288c] | 85313 | 7 | PET54; YGR222 W | metabolic process;regulation of biological process | membrane;mitochondrion;organelle lumen | nucleotide binding;RNA binding;transport regulator activity | 1.565 | 1.565 | 1.00 |
| P43594 | MICOS complex subunit MIC19 [OS=Saccharomyces cerevisiae S288c] | 85056 | 3 | AIM13; MIC19; YFR011 C | cell organization and biogenesis | cytoplasm;membrane;mitochondrion | catalytic activity | 4.337 | 4.337 | 1.00 |
| P23644 | Mitochondrial import receptor subunit TOM40 [OS=Saccharomyces cerevisiae S288c] | 85324 | 3 | TOM40; YMR230 W | transport | cytosol;membrane;mitochondrion | protein binding;transporter activity | 1.154 | 1.154 | 1.00 |
| P36141 | Putative redox protein fmp46, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85392 | 3 | FMP46; YKR049 C | metabolic process | mitochondrion | catalytic activity;protein binding | 4.337 | 4.337 | 1.00 |
| P53206 | Putative cysteine synthase [OS=Saccharomyces cerevisiae S288c] | 85289 | 5 | YGR012 W; YGR012 W | metabolic process | membrane;mitochondrion | catalytic activity | 0.817 | 0.817 | 1.00 |
| P08466 | mitochondrial nuclease [OS=Saccharomyces cerevisiae S288c] | 85322 | 2 | NUCl; YIL208C | cell death;metabolic process | membrane;mitochondrion;nucleus | catalytic activity;metal ion binding | 1.637 | 1.637 | 1.00 |
| Q12165 | ATP synthase subunit delta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85156 | 0 | ATP3A; YDL004 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 4.623 | 4.623 | 1.00 |
| P21560 | Protein CBP3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85588 | 6 | CBP3; YPL215 W | cell organization and biogenesis;regulation of biological process | membrane;mitochondrion;ribosome | catalytic activity;transporter activity | 1.424 | 1.424 | 1.00 |
| P04806 | Hxk1p kinase [OS=Saccharomyces cerevisiae S288c] | 85601 | 4 | HXK1; YFR003 C | cellular homeostasis;metabolic process;transport | cytoplasm;cytosol;mitochondrion | catalytic activity;nucleotide binding | 1.043 | 1.043 | 1.00 |
| Q03798 | Altered inheritance of mitochondria protein 36, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85318 | 9 | AIM36; YMR175 7C | membrane;mitochondrion | catalytic activity | 1.637 | 1.637 | 1.00 |
| P12686 | 37S ribosomal protein MRPI3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85297 | 9 | MRPI3; YGR084 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.239 | 1.239 | 1.00 |
| P11325 | Leucine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85109 | 8 | NAM2; YLR882 | cell organization and biogenesis;metabolic process | cytosol;mitochondrion;organelle lumen | catalytic activity;protein binding | 0.353 | 0.353 | 1.00 |
| S288c | C          | process/regulation of biological process                                      | binding,RNA binding  |
|-------|------------|--------------------------------------------------------------------------------|----------------------|
| Q04955 | Cytochrome c oxidase protein 20, mitochondrial (S288c) | cell organization and biogenesis, metabolic process | protein binding 2.455 2.455 1.00 |
| P38825 | Protein TOM71 (S288c) | transport | membrane, mitochondrion | protein binding, transporter activity 0.512 0.512 1.00 |
| P37267 | Assembly factor cbp4 (S288c) | cell organization and biogenesis | membrane, mitochondrion | 7.111 7.111 1.00 |
| Q06678 | 54S ribosomal protein L35, mitochondrial (S288c) | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity 1.031 1.031 1.00 |
| P40908 | Uncharacterized protein YIL077C (S288c) | | mitochondrion | 0.896 0.896 1.00 |
| P38072 | Protein SCO2, mitochondrial (S288c) | cell organization and biogenesis, cellular homeostasis, metabolic process, transport | membrane, mitochondrion | antioxidant activity, catalytic activity, metal ion binding 1.154 1.154 1.00 |
| P48569 | Uncharacterized protein YDL188C (S288c) | transport | YDL188C C; YDL188B C | 1.069 1.069 1.00 |
| P60950 | Phosphoglycerate mutase 1 (S288c) | metabolic process, regulation of biological process | cytoplasm, cytosol, membrane, mitochondrion | catalytic activity 1.929 1.929 1.00 |
| Q04472 | Mitochondrial inner membrane - AAA protease supercomplex subunit MGR3 (S288c) | metabolic process | membrane, mitochondrion | protein binding 0.52 0.52 1.00 |
| Q13249 | ATP synthase subunit H, mitochondrial (S288c) | cell organization and biogenesis, metabolic process | membrane, mitochondrion | catalytic activity, transporter activity 2.728 2.728 1.00 |
| P18496 | Mitochondrial ATPase complex subunit ATP10 (S288c) | cell organization and biogenesis | cytoplasm, membrane, mitochondrion | protein binding 2.139 2.139 1.00 |
| Q04172 | Sensitive to high expression protein 9, mitochondrial (S288c) | cell organization and biogenesis | membrane, mitochondrion | catalytic activity, nucleotide binding, transporter activity 0.453 0.453 1.00 |
| P40416 | Iron-sulfur clusters transporter MRPL3 (S288c) | cellular homeostasis, metabolic process, transport | membrane, mitochondrion | catalytic activity, oxidoreductase activity, binding, structural molecule activity 1.512 1.512 1.00 |
| P40502 | Altered inheritance of mitochondria protein 19, mitochondrial (S288c) | | membrane, mitochondrion | 1.512 1.512 1.00 |
| P35616 | 54S ribosomal protein L3, mitochondrial (S288c) | cell organization and biogenesis, metabolic process | mitochondrion, nucleus, ribosome | catalytic activity, RNA binding, structural molecule activity 0.743 0.743 1.00 |
| P38771 | Ribosome-recycling factor, mitochondrial (S288c) | cell organization and biogenesis, metabolic process | mitochondrion | RNA binding 1.254 1.254 1.00 |
| P32453 | Protein ATP11, mitochondrial (S288c) | cell organization and biogenesis, metabolic process | mitochondrion | protein binding 1.239 1.239 1.00 |
| Q02981 | ABC1 family protein YPL109C, mitochondrial (S288c) | cell organization and biogenesis | mitochondrion | 0.334 0.334 1.00 |
| P39002 | Long-chain-fatty-acid-CoA ligase 3 (S288c) | | mitochondrial | catalytic activity, nucleotide binding, metal ion binding 0.334 0.334 1.00 |
| P25372 | Thioredoxin-3, mitochondrial (S288c) | | | catalytic activity, metal ion binding, protein binding 2.511 2.511 1.00 |
| P38879 | Protein phosphatase 2C homolog 1, mitochondrial (S288c) | | mitochondrion | catalytic activity, metal ion binding, protein binding 0.688 0.688 1.00 |
| P40159 | Uncharacterized protein YNL208W (S288c) | | membrane, mitochondrion | 0.668 0.668 1.00 |
| Q12283 | Malonyl CoA-acetyl carrier protein transacylase, mitochondrial (S288c) | | mitochondrion | catalytic activity 0.896 0.896 1.00 |
| P38702 | mitochondrial carrier protein LEUS (S288c) | | | structural molecule activity, transporter activity 0.468 0.468 1.00 |
| P37372 | 37S ribosomal protein S12, mitochondrial (S288c) | | | structural molecule activity 1.783 1.783 1.00 |
| ORF     | Genes                                                                 | Functions                                                                 | Localization                      | GO Terms                                                                 |
|---------|----------------------------------------------------------------------|---------------------------------------------------------------------------|-----------------------------------|-------------------------------------------------------------------------|
| P28239  | Inorganic pyrophosphatase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | cytoplasm/mitochondrion           | 0.585 0.585 1.00                                                        |
| P14098  | Mitochondrial transcription factor 1 [OS=Saccharomyces cerevisiae S288c]  | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrion,organelle lumen     | catalytic activity,DNA binding,RNA binding                               | 0.585 0.585 1.00 |
| P36163  | mitochondrial metalloendopeptidase OMA1 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | membrane/mitochondrion            | catalytic activity,metal ion binding                                   | 0.73 0.73 1.00  |
| Q12333  | ATP synthase subunit g, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | membrane/mitochondrion            | catalytic activity,transport r activity                                 | 1.371 1.371 1.00 |
| P37299  | Cytochrome b-c1 complex subunit 10 [OS=Saccharomyces cerevisiae S288c]  | [OS=Saccharomyces cerevisiae S288c]                                       | membrane/mitochondrion            | catalytic activity,transport r activity                                 | 5.31 5.31 1.00 |
| P33421  | Succinate dehydrogenase (ubiquinone) cytochrome b subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | membrane/mitochondrion            | catalytic activity,metal ion binding                                   | 1.276 1.276 1.00 |
| P23369  | S45 ribosomal protein L25, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrial,ribosome            | structural molecule activity                                           | 1.31 1.31 1.00 |
| P48526  | Isocitrate--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | cytoplasm/mitochondrion,organelle lumen | catalytic activity,nucleotide binding                                   | 0.215 0.215 1.00 |
| P04807  | Hexokinase-2 [OS=Saccharomyces cerevisiae S288c]                        | [OS=Saccharomyces cerevisiae S288c]                                       | cytosol/mitochondrion,nucleus     | catalytic activity,nucleotide binding                                   | 0.359 0.359 1.00 |
| P21306  | ATP synthase subunit epsilon, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | membrane/mitochondrion            | catalytic activity,transport r activity                                 | 2.162 2.162 1.00 |
| Q06485  | Autophagy-related protein 33 [OS=Saccharomyces cerevisiae S288c]         | [OS=Saccharomyces cerevisiae S288c]                                       | membrane/mitochondrion            | catalytic activity,transport r activity                                 | 1.371 1.371 1.00 |
| P08742  | Thioulate sulfurtransferase RD1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrial                    | catalytic activity                                                       | 0.52 0.52 1.00 |
| P07914  | mitochondrial import inner membrane translocase subunit TIM14 [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | membrane/mitochondrion            | enzyme regulator activity,protein binding,transport r activity          | 0.778 0.778 1.00 |
| Q03557  | Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrial                    | catalytic activity,nucleotide binding                                   | 0.259 0.259 1.00 |
| P38172  | MIOREX complex component 3 [OS=Saccharomyces cerevisiae S288c]           | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrial                    | catalytic activity                                                       | 0.501 0.501 1.00 |
| P32785  | Methionyl-tRNA formyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrial                    | catalytic activity                                                       | 0.179 0.179 1.00 |
| Q01976  | ADF-Ribose pyrophosphatase [OS=Saccharomyces cerevisiae S288c]            | [OS=Saccharomyces cerevisiae S288c]                                       | cytoplasm/mitochondrion,nucleus   | catalytic activity,methyl ion binding                                   | 0.425 0.425 1.00 |
| P43122  | TRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrial                    | catalytic activity,methyl ion binding                                   | 0.212 0.212 1.00 |
| P34224  | Uncharacterized protein YBL0199 [OS=Saccharomyces cerevisiae S288c]       | [OS=Saccharomyces cerevisiae S288c]                                       | membrane/mitochondrion            | catalytic activity                                                       | 0.468 0.468 1.00 |
| P21375  | Fumarate reductase 2 [OS=Saccharomyces cerevisiae S288c]                  | [OS=Saccharomyces cerevisiae S288c]                                       | endoplasmic reticulum/mitochondrion | catalytic activity,nucleotide binding                                   | 0.25 0.25 1.00 |
| P38175  | 37s ribosomal protein MRP21, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrial,ribosome            | structural molecule activity                                           | 0.701 0.701 1.00 |
| P00X31  | 40s ribosomal protein S24-A [OS=Saccharomyces cerevisiae S288c]           | [OS=Saccharomyces cerevisiae S288c]                                       | cytoplasm/mitochondrion,ribosome   | nucleotide binding,structural molecule activity                         | 0.585 0.585 1.00 |
| Q03429  | Mitochondrial zinc maintenance protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]                                       | mitochondrial,organelle lumen     | protein binding                                                        | 0.334 0.334 1.00 |
P32048  Lysolecithin-cholesterol acyltransferase [OS=Saccharomyces cerevisiae S288c]  RPS21  6 cell organization and biogenesis;membrane;mitochondrion;organelle lumen catalytic activity;nucleotide binding;RNA binding 0.045 0.145 1.00

P04039  Cytochrome c oxidase polypeptide VIII, mitochondrial [OS=Saccharomyces cerevisiae S288c]  Q06619  3 YMR217 W cell organization and biogenesis;membrane;mitochondrion;organelle lumen catalytic activity;transport activity 0.036 0.105 1.00

P38812  Phosphatidylethanolamine N-methyltransferase [OS=Saccharomyces cerevisiae S288c]  Q09050  5 YMR041 C cell organization and biogenesis;membrane;mitochondrion;organelle lumen catalytic activity;transport activity 0.036 0.075 1.00

P06089  Uncharacterized mitochondrial outer membrane protein YPR098C [OS=Saccharomyces cerevisiae S288c]  Q06971  5 YMR179 C cell organization and biogenesis;membrane;mitochondrion;organelle lumen catalytic activity;transport activity 0.036 0.075 1.00

P12487  U2 small nuclear ribonucleoprotein, mitochondrial [OS=Saccharomyces cerevisiae S288c]  Q05779  6 YMR181 C cell organization and biogenesis;membrane;mitochondrion;organelle lumen catalytic activity;transport activity 0.036 0.075 1.00

P23834  5 S45 ribosomal protein L23, mitochondrial [OS=Saccharomyces cerevisiae S288c]  Q04638  5 YMR017 C cell organization and biogenesis;membrane;mitochondrion;organelle lumen catalytic activity;transport activity 0.036 0.075 1.00

P38811  Protein SYN1 [OS=Saccharomyces cerevisiae S288c]  Q08822  3 YMR066 W cell organization and biogenesis;membrane;mitochondrion;organelle lumen catalytic activity;transport activity 0.036 0.075 1.00
| Gene ID  | Protein Name                           | Function/Activity                                                                 | Location                | Protein Binding | Nucleotide Binding | RNA Binding | Activity   | Protein Quantity | Property     |
|---------|----------------------------------------|----------------------------------------------------------------------------------|-------------------------|-----------------|-------------------|-------------|------------|-----------------|-------------|
| P32340  | 2-isopropylmalate synthase 2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport | membrane, mitochondrion | catalytic activity, metal ion binding | 2.472       | 1.10       |                  |             |
| P07257  | Cytochrome b-c1 complex subunit 2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport | membrane, mitochondrion | catalytic activity, metal ion binding | 36.75       | 1.10       |                  |             |
| Q02776  | Mitochondrial import inner membrane translocase subunit TIM50, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization, biogenesis, metabolic process | membrane, mitochondrion | catalytic activity, metal ion binding | 9           | 1.10       |                  |             |
| P48015  | Aminomethytransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion | catalytic activity, protein binding | 9           | 1.12       |                  |             |
| P38077  | ATP synthase subunit gamma, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport | membrane, mitochondrion | catalytic activity, transport protein binding | 12.68       | 1.12       |                  |             |
| Q08023  | Protein FMP25, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis | membrane, mitochondrion | catalytic activity | 1.412       | 1.12       |                  |             |
| P38891  | Branched-chain amino-acid aminotransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process, response to stimulus | mitochondrion, organelle lumen | catalytic activity | 9           | 1.12       |                  |             |
| P50085  | Prohibitin-2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process, regulation of biological process | membrane, mitochondrion | protein binding | 4.926       | 1.13       |                  |             |
| P19882  | heat shock protein 60, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process, transport | cytoplasm, cytosol, membrane, mitochondrion, organelle lumen | catalytic activity, DNA binding, nucleotide binding, protein binding | 22.35       | 1.13       |                  |             |
| P36060  | NADH-cytochrome b5 reductase 2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, response to stimulus | membrane, mitochondrion | catalytic activity, protein binding | 15.23       | 1.14       |                  |             |
| P28834  | Isocitrate dehydrogenase | [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport | cytosol, mitochondrion, organelle lumen | catalytic activity, metal ion binding, nucleotide binding, protein binding | 15.23       | 1.14       |                  |             |
| P04710  | ADP/ATP carrier protein 1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport | cytosol, membrane, mitochondrion | structural molecule activity, transport activity | 11.74       | 1.14       |                  |             |
| P25573  | Mitochondrial inner membrane l-AAA protease supercomplex subunit MGR1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | membrane, mitochondrion | protein binding | 1.649       | 1.15       |                  |             |
| P09457  | ATP synthase subunit 5, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport | membrane, mitochondrion | catalytic activity, transport protein binding | 9           | 1.15       |                  |             |
| P38998  | Mitochondrial GTP/UDP carrier protein 2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, cellular homeostasis, metabolic process, transport | membrane, mitochondrion | structural molecule activity, transport protein binding | 3.16        | 1.15       |                  |             |
| Q12031  | Mitochondrial 2-methylisocitraterase isoezyme, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion, organelle lumen | catalytic activity | 5.158       | 1.15       |                  |             |
| P00431  | Cytochrome c peroxidase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, response to stimulus | mitochondrion, organelle lumen | antioxidant activity, catalytic activity, metal ion binding, protein binding | 1.424       | 1.16       |                  |             |
| P53292  | 375 ribosomal protein S35, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 1.512       | 1.16       |                  |             |
| Q12320  | Sphingolipid long chain base-responsive protein LSP1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | regulation of biological process, response to stimulus | cytoplasm, membrane, mitochondrion | catalytic activity, metal ion binding, protein binding | 24.11       | 1.17       |                  |             |
| P00924  | Enolase 1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process | cytosol, cytosol, membrane, mitochondrion, vacuole | catalytic activity, metal ion binding, protein binding | 0.848       | 1.17       |                  |             |
| P38969  | Pentamidine resistance factor, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, response to stimulus | membrane, mitochondrion | catalytic activity, protein binding | 0.848       | 1.17       |                  |             |
| P15424  | ATP-dependent RNA helicase SS116, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process | mitochondrion, organelle lumen | catalytic activity, nucleotide binding, RNA binding | 1.644       | 1.17       |                  |             |
| P32340  | Redox-sensitive NADH-ubiquinone oxidoreductase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process | membrane, mitochondrion, organelle lumen | catalytic activity, nucleotide binding, protein binding | 24.92       | 1.18       |                  |             |
| P32795 | Mitochondrial inner membrane ATPase supercomplex subunit YME1 [OS=Saccharomyces cerevisiae S288c] | 85613 | W | YME1; YPR024 W | metabolic process;response to stimulus;transport | membrane,mitochondrion | catalytic activity;metal ion binding;nucleotide binding;protein binding | 1.798 | 2.241 | 1.25 |
| P47052 | Succinate dehydrogenase (ubiquinone) flavoprotein subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85340 | 5 | YDL045 W; YL045 W | metabolic process;transport | membrane,mitochondrion | catalytic activity;nucleotide binding | 4.712 | 5.884 | 1.25 |
| P36521 | S45 ribosomal protein L11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85132 | 5 | MRPL11 ; YDL202 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.069 | 1.336 | 1.25 |
| P00927 | Thermonine dehydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85681 | 9 | ILV1; YER086 W | metabolic process | cytoplasm,mitochondrion | catalytic activity | 3.325 | 3.924 | 1.26 |
| P16451 | Pyruvate dehydrogenase complex protein X component, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85310 | 7 | YPX1; YGR193 C | metabolic process | mitochondrion;organellar lumen | catalytic activity;structural molecule activity | 2.594 | 3.262 | 1.26 |
| P38071 | Env1 (acyl-carrier protein) reductase [NADPH, B-specific], mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85231 | ET11; YBR226 C | metabolic process | mitochondrion;organellar lumen | catalytic activity;DNA binding;metal ion binding | 9 | 11.32 | 8 | 1.26 |
| Q05391 | Heat shock protein 55K, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85108 | SSQ1; YLR369 W | cell organization and biogenesis;metabolic process | mitochondrion;organellar lumen | nucleotide binding;protein binding | 0.884 | 1.113 | 1.26 |
| P40513 | Mitochondrial acety protein [MAM33] [OS=Saccharomyces cerevisiae S288c] | 85474 | 0 | MAM33 ; YL070 C | metabolic process;regulation of biological process | mitochondrion;organellar lumen | translation regulator activity | 3.642 | 4.623 | 1.27 |
| P35721 | Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85575 | 2 | RCF2; YNR018 W | cell organization and biogenesis | membrane,mitochondrion | catalytic activity | 5.579 | 7.111 | 1.27 |
| P33416 | Heat shock protein 70, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85184 | 5 | HSP78; YDR258 C | cell organization and biogenesis;metabolic process | mitochondrion;organellar lumen | catalytic activity;DNA binding;metal ion binding | 7.929 | 10.19 | 9 | 1.29 |
| Q03640 | Triclinin-3 [OS=Saccharomyces cerevisiae S288c] | 85490 | 3 | TCBL; YML072 C | cell organization and biogenesis;regulation of biological process | endoplasmic reticulum;membrane,mitochondrion | metal ion binding;protein binding | 0.283 | 0.365 | 1.29 |
| P39987 | Heat shock protein 55K, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85668 | 2 | ECM10; YEL030 A | cell organization and biogenesis;metabolic process;transport | mitochondrion | nucleotide binding;protein binding | 2.162 | 2.793 | 1.29 |
| P35889 | Uncharacterized mitochondrial hydroxylase FMP41 [OS=Saccharomyces cerevisiae S288c] | 85553 | 3 | FMP41; YNL168 C | metabolic process | mitochondrion | catalytic activity;metal ion binding | 0.968 | 1.254 | 1.30 |
| P50945 | MICOS complex subunit 20C7 [OS=Saccharomyces cerevisiae S288c] | 85562 | 3 | AIM37; MIC27; YNL100 W | cell organization and biogenesis | membrane,mitochondrion | catalytic activity | 0.968 | 1.254 | 1.30 |
| P50950 | Heat shock protein 55K, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85350 | 3 | SSC1; YIR645 C | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion;organellar lumen | catalytic activity;enzyme regulator activity;nucleotide binding;protein binding | 48.48 | 62.90 | 8 | 1.30 |
| P00128 | Cytochrome b-c1 complex subunit 7 [OS=Saccharomyces cerevisiae S288c] | 85214 | QC77; YDR529 C | cell organization and biogenesis;metabolic process | membrane,mitochondrion | catalytic activity;transporter activity | 34.93 | 45.41 | 6 | 1.30 |
| Q02024 | 54S ribosomal protein L13, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85387 | 5 | MRPL13 ; YKR006 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.064 | 1.371 | 1.30 |
| P43616 | Cys-Gly metallopeptidase dig1 [OS=Saccharomyces cerevisiae S288c] | 85060 | DUG1; YPR044 A | metabolic process | cytoplasm,mitochondrion;ribosome | catalytic activity;metal ion binding | 1.154 | 1.512 | 1.31 |
| P00327 | Mitochondrial fusion and transport protein Ugo1 [OS=Saccharomyces cerevisiae S288c] | 85208 | 1 | UGO1; YDR470 C | cell organization and biogenesis;metabolic process | membrane,mitochondrion | protein binding;structural molecule activity | 0.425 | 0.557 | 1.31 |
| P00326 | 375 ribosomal protein S17, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85322 | 6 | MRPS17 ; YMR158 B C | cell differentiation;cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.276 | 1.683 | 1.32 |
| P00424 | Cytochrome c oxidase polypeptide 5A, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85557 | COX5A; YNL050 W | metabolic process;transport | membrane,mitochondrion | catalytic activity;transporter activity | 2.511 | 3.329 | 1.33 |
| P32454 | Amino peptidase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85369 | 9 | APE2; YNL157 W | metabolic process | cytoplasm;extracellular;membrane,mitochondrion;ribosome | catalytic activity;metal ion binding | 0.973 | 1.294 | 1.33 |
| P35522 | Dihydroxy acid dehydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85347 | 3 | ILV3; YIR016 C | metabolic process | mitochondrion | catalytic activity;metal ion binding | 25.53 | 39.37 | 9 | 1.33 |
| P00401 | Cytochrome c oxidase subunit 1 [OS=Saccharomyces cerevisiae S288c] | 85459 | CDX1; GO045 | metabolic process;transport | membrane,mitochondrion | catalytic activity;metal ion binding;transporter activity | 1.61 | 2.162 | 1.34 |

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| Gene ID   | Description                                                                 | Cellular Component | Functional Category                        | Descriptive Term                          | Molecular Activity       | p-value  | Odds Ratio |
|----------|------------------------------------------------------------------------------|-------------------|--------------------------------------------|------------------------------------------|--------------------------|----------|------------|
| P38122   | 3-methyl-2-oxobutanoate dehydrogenase                                        | mitochondrial     | metabolic process                          | mitochondrial                            | catalytic                 | 0.413    | 0.585      |
|          | hydroxymethyltransferase [OS=Saccharomyces cerevisiae S288c]                  |                   |                                            |                                          | activity                  |          |            |
| Q03976   | 375 ribosomal protein S2A, mitochondrial [OS=Saccharomyces cerevisiae S288c]| mitochondrial     | cell organization and biogenesis          | mitochondrial, ribosome                  | structural molecule       | 0.905    | 1.291      |
| Q06249   | protein ZEO1 [OS=Saccharomyces cerevisiae S288c]                              | membrane,mitochondrion | cell organization and biogenesis         | membrane,mitochondrion                  | protein binding           | 1.512    | 2.162      |
| Q00711   | Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | membrane,mitochondrion | metabolic process,transport                | membrane,mitochondrion                  | catalytic activity, nucleotide binding | 12.24   | 2.15       |
| Q05882   | MIOREX complex component 2 [OS=Saccharomyces cerevisiae S288c]               | mitochondrial     | metabolic process                          | mitochondrial                            | catalytic activity        | 3.217    | 4.623      |
| Q03976   | 10 kDa heat shock protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell organization and biogenesis          | mitochondrial, organelle lumen           | catalytic activity, nucleotide binding | 3.217    | 4.623      |
| P38323   | ATP-dependent clpC-like chaperone, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | metabolic process                          | mitochondrial                            | catalytic activity        | 3.217    | 4.623      |
| Q02784   | Monothiol glutaredoxin-5, mitochondrial [OS=Saccharomyces cerevisiae S288c]   | mitochondrial     | cell organization and biogenesis          | mitochondrial, organelle lumen           | catalytic activity, metal ion binding | 1.783    | 2.594      |
|          | [OS=Saccharomyces cerevisiae S288c]                                           |                   | cell organization and biogenesis          | mitochondrial, organelle lumen           | catalytic activity, metal ion binding | 1.783    | 2.594      |
| P38341   | Mitochondrial import inner membrane translocate subunit TIM44 [OS=Saccharomyces cerevisiae S288c] | membrane,mitochondrion | transport                                 | cytoplasm,mitochondrion                  | metal ion binding, nucleotide binding, protein binding | 3.758   | 5.404      |
|          | (OS=Saccharomyces cerevisiae S288c)                                          |                   |                                            |                                          | protein binding           |          |            |
| P35996   | 545 ribosomal protein L38, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell organization and biogenesis          | mitochondrial, ribosome                  | RNA binding, structural molecule activity | 1.783    | 2.594      |
|          | (OS=Saccharomyces cerevisiae S288c)                                          |                   | cell organization and biogenesis          | mitochondrial, ribosome                  | RNA binding, structural molecule activity | 1.783    | 2.594      |
| Q60560   | Protein Idx11 [OS=Saccharomyces cerevisiae S288c]                            | mitochondrial     | cell organization and biogenesis          | mitochondrial, organelle lumen           | catalytic activity, protein binding | 1.783    | 2.594      |
| P37292   | Serine hydroxymethyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell organization and biogenesis          | mitochondrial                            | catalytic activity        | 9        | 13.17      |
|          | (OS=Saccharomyces cerevisiae S288c)                                          |                   | cell organization and biogenesis          | mitochondrial                            | catalytic activity        | 9        | 13.17      |
| Q03201   | 375 ribosomal protein S10, mitochondrial [OS=Saccharomyces cerevisiae S288c]  | mitochondrial     | cell organization and biogenesis          | mitochondrial, ribosome                  | structural molecule       | 0.701    | 1.031      |
|          | (OS=Saccharomyces cerevisiae S288c)                                          |                   | cell organization and biogenesis          | mitochondrial, ribosome                  | structural molecule       | 0.701    | 1.031      |
| P52893   | probable alanine aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell organization and biogenesis          | mitochondrial, organelle lumen           | catalytic activity        | 1.102    | 1.626      |
| P35398   | Succinyl-CoA ligase (ADP-forming) subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell organization and biogenesis          | mitochondrial, organelle lumen           | catalytic activity        | 1.102    | 1.626      |
|          | (OS=Saccharomyces cerevisiae S288c)                                          |                   | cell organization and biogenesis          | mitochondrial, organelle lumen           | catalytic activity        | 1.102    | 1.626      |
| P22136   | ATPase expression protein 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | metabolic process,regulated of biological process | mitochondrial                            | RNA binding              | 0.292    | 0.431      |
| P38523   | Gip1 protein homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c]       | mitochondrial     | metabolic process,regulated of biological process | membrane,mitochondrion,organelle lumen   | enzyme regulator activity, nucleotide binding, protein binding | 1.336   | 1.976      |
| P08230   | Succinate dehydrogenase assembly factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell differentiation,cell organization and biogenesis,metabolic process,regulation of biological process | mitochondrial,organelle lumen           | protein binding           | 0.778    | 1.154      |
|          | (OS=Saccharomyces cerevisiae S288c)                                          |                   | cell differentiation,cell organization and biogenesis,metabolic process,regulation of biological process | mitochondrial,organelle lumen           | protein binding           | 0.778    | 1.154      |
| P09440   | C-1-tetrahydrofolate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell organization and biogenesis          | mitochondrial                            | catalytic activity, nucleotide binding | 1.049   | 1.569      |
| P40053   | Altered inheritance of mitochondria protein 5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell organization and biogenesis          | mitochondrial                            | catalytic activity, nucleotide binding | 4.555   | 6.827      |
| P47127   | Altered inheritance of mitochondria protein 24, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial     | cell organization and biogenesis          | mitochondrial                            | catalytic activity, nucleotide binding | 2.857   | 4.298      |
| P25349   | Flavoprotein-like protein YCP4 [OS=Saccharomyces cerevisiae S288c]            | mitochondrial     | metabolic process,regulated of biological process | cytoplasm,membrane,mitochondrion         | catalytic activity, nucleotide binding, protein binding | 9        | 13.67      |
|          | (OS=Saccharomyces cerevisiae S288c)                                          |                   | metabolic process,regulated of biological process | cytoplasm,membrane,mitochondrion         | catalytic activity, nucleotide binding, protein binding | 9        | 13.67      |
| P36046 | Mitochondrial intermembrane space import and assembly protein 40 [OS=Saccharomyces cerevisiae S288c] | 85363 | MIA40; YKL195 W | cellular component movement;metabolic process;response to stimulus;transport | membrane;mitochondrion | catalytic activity;protein binding;transport activity | 3.262 | 4.995 | 1.53 |
| P19516 | Cytochrome c oxidase assembly protein COX11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85357 | COX11; YPL132 W | cell organization and biogenesis;metabolic process | membrane;mitochondrion;ribosome | metal ion binding | 1.069 | 1.637 | 1.53 |
| P36112 | MICOS complex subunit Mic60 [OS=Saccharomyces cerevisiae S288c] | 85388 | FCJL; YMR064 W | cell organization and biogenesis;transport | membrane;mitochondrion | | 15.37 | 23.70 | 9 | 1.54 |
| P04819 | DNA ligase 1 [OS=Saccharomyces cerevisiae S288c] | 85139 | CDC9; YDL164 C | cell division;cell organization and biogenesis;metabolic process;response to stimulus | cytoplasm;mitochondrion;nucleus | catalytic activity;DNA binding;metal ion binding;nucleotide binding | 0.11 | 0.17 | 1.55 |
| P32493 | ATPase expression protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85508 | AEP1; YMR006 4W | regulation of biological process | mitochondrion | translation regulator activity | 0.15 | 0.233 | 1.55 |
| P07806 | Valine-tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85298 | VAS1; YGR094 W | metabolic process;regulation of biological process | cytoplasm;cytosol;mitochondrion | catalytic activity;nucleotide binding | 0.616 | 0.957 | 1.55 |
| P41921 | glutathione reductase [OS=Saccharomyces cerevisiae S288c] | 85601 | GLRl1; YPL091 W | cellular homeostasis;metabolic process;regulation of biological process;response to stimulus | cytoplasm;cytosol;mitochondrion;nucleus | antioxidant activity;catalytic activity;nucleotide binding | 0.355 | 0.241 | 1.55 |
| P25345 | Asparagine-tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85038 | SLMS5; YCR024 W | metabolic process | cytoplasm;mitochondrion;organelle lumen | catalytic activity | 0.172 | 0.269 | 1.56 |
| P06890 | Citrate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85573 | CIT2; YNR001 C | metabolic process;transport | cytosol;mitochondrion;organelle lumen | catalytic activity | 9 | 14.08 | 6 | 1.57 |
| P19262 | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85172 | KDG2; YDR148 C | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;protein binding | 6.406 | 10.05 | 3 | 1.57 |
| P32904 | S45 ribosomal protein L6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85655 | MRPL6; YHR147 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.371 | 2.162 | 1.58 |
| P36147 | Presequence translocase-associated motor subunit pam17, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85393 | PAM17; YKR005 W | transport | membrane;mitochondrion | structural molecule activity;transport activity | 0.245 | 0.389 | 1.59 |
| P53738 | Uncharacterized protein YNR040W [OS=Saccharomyces cerevisiae S288c] | 85577 | YNR040 W; YMR040 W | metabolic process;transport | membrane;mitochondrion | structural molecule activity | 0.73 | 1.154 | 1.58 |
| Q12251 | Uncharacterized mitochondrial carrier YPR011C [OS=Saccharomyces cerevisiae S288c] | 85612 | YPR011 C; YPR011 C | metabolic process;transport | membrane;mitochondrion | structural molecule activity;transport activity | 0.245 | 0.389 | 1.59 |
| P49017 | 2-methoxy-6-polypropenyl-1,4-benzoquinol methylase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85493 | COQ5; YML110 C | metabolic process | membrane;mitochondrion;organelle lumen | catalytic activity | 0.245 | 0.389 | 1.59 |
| Q01519 | Cytochrome c oxidase subunit 6b [OS=Saccharomyces cerevisiae S288c] | 85072 | COX12; YLR038 W | cell organization and biogenesis;metabolic process;transport | mitochondrion | catalytic activity;protein binding;transport activity | 3.642 | 5.813 | 1.60 |
| P36525 | S45 ribosomal protein L24, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85523 | MRPL24; YMR19 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.512 | 2.415 | 1.60 |
| P36519 | S45 ribosomal protein L17, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85182 | MRPL7; YDR237 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.292 | 0.468 | 1.60 |
| P04803 | Tryptophan-tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85186 | MSW1; YDR268 W | metabolic process | cytoplasm;mitochondrion;organelle lumen | catalytic activity;metal ion binding | 0.292 | 0.468 | 1.60 |
| P28625 | Protein YMR1 [OS=Saccharomyces cerevisiae S288c] | 85518 | YMR1; YMR15 2W | metabolic process;response to stimulus | cytoplasm;endoplasmic reticulum;mitochondrion | catalytic activity;metal ion binding | 0.833 | 1.336 | 1.60 |
| P47045 | mitochondrial import inner membrane translocase subunit Tim54 [OS=Saccharomyces cerevisiae S288c] | 85339 | TIM54; YLU054 W | cell organization and biogenesis;transport | cytosol;membrane;mitochondrion | transporter activity | 0.655 | 1.054 | 1.61 |
| P31334 | S45 ribosomal protein L19, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85313 | MRPL9; YGR220 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.311 | 0.501 | 1.61 |
| P36523 | S45 ribosomal protein L15, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85102 | MRPL15; YLR312 W-A | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | catalytic activity;RNA binding;structural molecule activity | 0.334 | 0.54 | 1.62 |
| Q02608 | S45 ribosomal protein S16, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85609 | MRPS16; YPL033 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.683 | 2.728 | 1.62 |
| Protein Name | Description | Gene | Uniprot ID | Function | Localization | Binding | Activity | CValue | MValue | Score |
|--------------|-------------|------|------------|----------|-------------|--------|---------|--------|--------|-------|
| P17558       | 37S ribosomal protein PET123, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85432 9 | PET123; YOR158 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.448 | 2.594 | 1.79  |
| P18900       | Hexaprenyl pyrophosphate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85228 8 | COG1; YBR003 W | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding;protein binding | 0.468 | 0.848 | 1.81  |
| P09950       | 5-aminovalerate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85181 8 | HEM3; YDR392 W | metabolic process | mitochondrion;organelle lumen | catalytic activity | 0.28  | 0.509 | 1.82  |
| Q01332-1     | Cysteine proteinase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85455 6 | AID4; YOR374 W | metabolic process | mitochondrion;organelle lumen | catalytic activity | 47.49 | 86.67 | 1.82  |
| P43674       | Potassium-activated aldehyde dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85093 0 | MD1; YFL016 C | cell organization and biogenesis;metabolic process | mitochondrion;organelle lumen | enzyme regulator activity;metal ion binding;metal ion binding | 3.037 | 5.579 | 1.84  |
| P31912       | Dna l homolog 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85169 4 | MRPL1; YDR116 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.069 | 1.976 | 1.85  |
| P37298       | Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85175 8 | SDH4; YDR178 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding | 3.642 | 6.743 | 1.85  |
| Q12320       | Hydroxyacylglutathione hydrolase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85420 5 | GLO4; YOR040 W | metabolic process | mitochondrion;organelle lumen | catalytic activity;metal ion binding | 0.369 | 0.688 | 1.86  |
| P32902       | 37S ribosomal protein MRP4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85638 4 | MRPA; YHL004 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.616 | 1.154 | 1.87  |
| P00245       | Cytochrome c oxidase poly peptide 5B, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85469 5 | COX5B; YIL111 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 1.31  | 2.511 | 1.92  |
| P19414       | Aconitate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85101 3 | ACO1; YLR304 C | cell organization and biogenesis;metabolic process;transport | cytoplasm;cytosol;mitochondrion;organelle lumen | catalytic activity;DNA binding;metal ion binding | 48.61 | 94.11 | 1.94  |
| P38534       | 54S ribosomal protein L40, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85593 0 | MRPL40; YPL173 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | protein binding;structural molecule activity | 0.778 | 1.512 | 1.94  |
| P25605       | Acetolactate synthase small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85034 8 | ILV6; YCL009 C | metabolic process;regulation of biological process | mitochondrion | catalytic activity;enzyme regulator activity | 6.848 | 13.38 | 1.95  |
| P36151       | Uncharacterized protein YKR070W [OS=Saccharomyces cerevisiae S288c] | 85294 4 | YKR070 W; YKR070 W | metabolic process | mitochondrion | catalytic activity | 0.833 | 1.637 | 1.97  |
| P40364       | Mitochondrial peptidic membrane protein 1 [OS=Saccharomyces cerevisiae S288c] | 85337 9 | MPM1; YIL066C | membrane;mitochondrion | mitochondrion | catalytic activity | 1.512 | 2.981 | 1.97  |
| P33303       | Succinate:unaminate mitochondrial transporter [OS=Saccharomyces cerevisiae S288c] | 85355 8 | SFC1; YIR995 W | metabolic process;transport | membrane;mitochondrion | structural molecule activity;transporter activity | 9 | 17.95 | 7 | 2.00 |
| P32621       | 54S ribosomal protein RML2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85666 0 | RML2; YEL050C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | catalytic activity;RNA binding;structural molecule activity | 0.638 | 1.276 | 2.00 |
| P06624       | Dihydrolipoyl dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85052 5 | LPD1; YFL018 W | cellular homeostasis;metabolic process;regulation of biological process | mitochondrion;organelle lumen | catalytic activity;metal ion binding | 21.53 | 43.36 | 2.01 |
| G02950       | 37S ribosomal protein MRP51, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85598 5 | MRPS1; YPL118 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.668 | 1.346 | 2.01 |
| Q06236       | Mitochondrial inner membrane protein SHH4 [OS=Saccharomyces cerevisiae S288c] | 85866 1 | SHH4; YLR164 W | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding | 3.217 | 6.499 | 2.02 |
| P21801       | Succinate dehydrogenase [ubiquinone] Iron-sulfur subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85668 5 | SDH2; YLL041 C | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding | 18.68 | 37.74 | 7 | 2.02 |
| P48237       | Mitochondrial group I intron splicing factor CCMI [OS=Saccharomyces cerevisiae S288c] | 85303 3 | CCMI1; YGR150C | cell organization and biogenesis;metabolic process | mitochondrion | RNA binding | 0.044 | 0.089 | 2.02 |
| P51998       | 34S ribosomal protein yml6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85498 3 | YML6; YML025C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.154 | 2.34 | 2.03 |
| Gene Symbol | Gene Name | Description | Cellular Localization | Gene Ontology Terms | Protein 1 | Protein 2 | Protein 3 | Protein 4 | Protein 5 | Protein 6 | Protein 7 | Protein 8 | Protein 9 | Protein 10 |
|-------------|-----------|-------------|-----------------------|---------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| P32897      | Putative transferase CF17, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, organellar lumen | catalytic activity | 0.075 | 0.155 | 2.07 |
| P38860      | GTPase MTG2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport | membrane, mitochondrion | catalytic activity, metal ion binding | 0.07 | 0.145 | 2.07 |
| P40051      | Intermediate cleaving peptidase 55 [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process | membrane, mitochondrion or nucleus | catalytic activity, metal ion binding | 0.077 | 0.16 | 2.08 |
| P07263-1    | Histidine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | cytoplasm, mitochondrion | catalytic activity, nucleotide binding, RNA binding | 0.064 | 0.133 | 2.08 |
| Q08645      | Polyphosphate synthase [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, endoplasmic reticulum, membrane, mitochondrion, organellar lumen | catalytic activity, nucleotide binding | 0.072 | 0.15 | 2.08 |
| P40530      | Pyruvate dehydrogenase (acytetyl-transferring) kinase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion, organellar lumen | catalytic activity, nucleotide binding, protein binding | 0.551 | 1.154 | 2.09 |
| P14905      | cytochrome b translational activator protein CB2 [OS=Saccharomyces cerevisiae S288c] | metabolic process, regulation of biological process | mitochondrion, ribosome | catalytic activity, nucleotide binding, translational regulator activity | 0.096 | 0.202 | 2.10 |
| P36527      | S45 ribosomal protein L28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 0.874 | 1.848 | 2.11 |
| Q12204      | Probable phosphophosphate YOR022C, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion | catalytic activity, metal ion binding | 0.11 | 0.233 | 2.12 |
| P24720      | Protein MNE1 [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, mitochondrion, organellar lumen | catalytic activity, metal ion binding | 0.125 | 0.266 | 2.13 |
| P38866      | Thioredoxin reductase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cellular homeostasis, metabolic process, regulation of biological process, response to stimulus | cytoplasm, mitochondrion | antioxidant activity, catalytic activity | 0.136 | 0.292 | 2.15 |
| Q12374      | Nuclear control of ATPase protein 2 [OS=Saccharomyces cerevisiae S288c] | metabolic process | membrane, mitochondrion | catalytic activity, metal ion binding | 0.468 | 1.021 | 2.18 |
| P28241      | Isocitrate dehydrogenase (NAD), subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion, organellar lumen | catalytic activity, metal ion binding, protein binding, RNA binding | 3.642 | 7.962 | 2.19 |
| P34321      | Uncharacterized protein YKL187C [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, transport | membrane, mitochondrion | catalytic activity, metal ion binding | 0.194 | 0.425 | 2.19 |
| P19955      | 375 ribosomal protein YMR31, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | catalytic activity, protein binding, structural molecule activity | 26.82 | 58.94 | 2.20 |
| P40491      | ATP synthase assembly factor fmc1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell communication, cell organization and biogenesis, metabolic process | mitochondrion, organellar lumen | catalytic activity, metal ion binding | 0.212 | 0.468 | 2.21 |
| P23180      | Probable oxidoreductase Aim17 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | membrane, mitochondrion | catalytic activity, metal ion binding | 4.623 | 10.22 | 2.21 |
| Q07354      | Solute carrier family 25 member 3B homolog [OS=Saccharomyces cerevisiae S288c] | metabolic process, transport | membrane, mitochondrion | structural molecule activity, transport activity | 0.245 | 0.551 | 2.25 |
| P10849      | mitochondrial transcription factor 2 [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion, organellar lumen | protein binding, RNA binding | 0.259 | 0.585 | 2.26 |
| P39965      | Probable proline--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, mitochondrion | catalytic activity, nucleotide binding, RNA binding | 0.266 | 0.604 | 2.27 |
| P22353      | S45 ribosomal protein L8, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 0.848 | 1.929 | 2.27 |
| P49334      | Mitochondrial import receptor subunit tom22 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, transport | membrane, mitochondrion | protein binding, transport activity | 0.292 | 0.668 | 2.29 |
| P40496      | 375 ribosomal protein S25, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 0.292 | 0.668 | 2.29 |
| P32897      | Mitochondrial import inner membrane translocase subunit tim23 [OS=Saccharomyces cerevisiae S288c] | transport | membrane, mitochondrion | protein binding, transport activity | 2.981 | 6.943 | 2.33 |
| ID     | Description                                                      | Gene(s)                                                                 | GO Terms                                      | Process/Activity                                                                 | Molecular Activity                      | Interaction Analysis          | P-value |
|--------|------------------------------------------------------------------|------------------------------------------------------------------------|-----------------------------------------------|----------------------------------------------------------------------------------|------------------------------------------|--------------------------------|----------|
| P39952 | Mitochondrial inner membrane protein OMA1 [OS=Saccharomyces cerevisiae S288c] | 85689 ORA1; YER164 W                                                  | cell organization and biogenesis;transport    | membrane/mitochondrion                                                          | transporter activity                     |                                | 3.317    |
| P38381 | 545 ribosomal protein L22, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85354 MRPL22 4 YNL177 W                                               | cell organization and biogenesis;metabolic process | mitochondrion/ribosome                                                          | RNA binding;structural molecule activity |                                | 1.54     |
| P39726 | Glycine cleavage system H protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85125 GCC5; YAL044 C                                                  | metabolic process                            | mitochondrion                                                                  | catalytic activity                       |                                | 4.995    |
| P25348 | 545 ribosomal protein L32, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85035 MRPL32 9 YCR003 W                                               | cell organization and biogenesis;metabolic process | membrane/mitochondrion/ribosome                                                  | RNA binding;structural molecule activity |                                | 0.389    |
| Q04401 | Succinate dehydrogenase assembly factor 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85212 ACNE; SDH7; YDR511 W                                           | cell organization and biogenesis;regulation of biological process | mitochondrion/organellar lumen                                                  |                                |                                | 0.397    |
| Q12497 | Protein FMP16, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85164 FMP16; YDR070 W                                                | mitochondrial process                         | mitochondrial                                                                  |                                |                                | 0.397    |
| P12687 | 545 ribosomal protein L2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85572 MRPP; YNL005 C                                                 | cell organization and biogenesis;metabolic process | mitochondrion/ribosome                                                          | catalytic activity;RNA binding;structural molecule activity |                                | 1.565    |
| P38958 | Protein PET100, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85165 PET100; YDR079 W                                               | cell organization and biogenesis              | membrane/mitochondrion                                                          | protein binding                         |                                | 0.468    |
| Q06011 | Protein ECM19 [OS=Saccharomyces cerevisiae S288c] | 85110 ECM19; YLR390 C                                                | cell organization and biogenesis              | membrane/mitochondrion                                                          | protein binding                         |                                | 0.468    |
| P32445 | Single-stranded DNA-binding protein RML1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85039 RML1; YCR028 C-A                                              | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion                                                                  | DNA binding                             |                                | 3.642    |
| P81451 | ATP synthase subunit K, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85407 ATP19; YOL077 W-A                                              | cell organization and biogenesis;metabolic process;transport | mitochondrion                                                                  | catalytic activity;transporter activity |                                | 3.642    |
| P07255 | Cytochrome c oxidase subunit 7A [OS=Saccharomyces cerevisiae S288c] | 85149 CDX9; YDL067 C                                                 | metabolic process;transport                   | membrane/mitochondrion                                                          | catalytic activity;transporter activity |                                | 3.642    |
| P3875 | 545 ribosomal protein L19, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85553 MRPL19 6 YNL185 W                                              | cell organization and biogenesis;metabolic process | mitochondrion/ribosome                                                          | RNA binding;structural molecule activity |                                | 0.52     |
| P36520 | 545 ribosomal protein L10, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85543 MRPL10 6 YNL284 C                                              | cell organization and biogenesis;metabolic process | mitochondrion/ribosome                                                          | structural molecule activity            |                                | 0.551    |
| P38300 | Inner membrane mitochondrial receptor MAB1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85248 MAB1; YBR185 C                                                  | cell organization and biogenesis;regulation of biological process | membrane/mitochondrion                                                          | structural molecule activity            |                                | 0.585    |
| P02381 | Ribosomal protein VAR1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85458 VAR1; Q0140                                                    | cell organization and biogenesis;metabolic process | mitochondrion/ribosome                                                          | structural molecule activity            |                                | 0.688    |
| Q03430 | 37S ribosomal protein RSM28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85210 RSM28; YDR484 W                                               | cell organization and biogenesis;metabolic process | mitochondrion/ribosome                                                          | structural molecule activity            |                                | 1.462    |
| P47015 | Altered inheritance of mitochondria protein 23, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85331 AIM23; YIL131 C                                               | metabolic process                            | mitochondrion                                                                  | RNA binding                             |                                | 0.35     |
| P38325 | Mitochondrial outer membrane protein OM4 [OS=Saccharomyces cerevisiae S288c] | 85253 OM4; YBR220 C                                                  | transport                                     | membrane/mitochondrion                                                          |                                        |                                | 0.197    |
| Q01635 | 37S ribosomal protein S23, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85274 RSM23; YGL129 C                                               | cell organization and biogenesis;metabolic process | mitochondrion/ribosome                                                          | catalytic activity;nucleotide binding;RNA binding;structural molecule activity |                                | 0.983    |
| P05525 | Cytochrome b-c1 complex subunit II [OS=Saccharomyces cerevisiae S288c] | 85327 QC8; YIL166 W                                                 | metabolic process;transport                   | membrane/mitochondrion                                                          | catalytic activity;transporter activity |                                | 2.981    |
| P03713 | Respiratory supercomplex factor 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85497 RFC1; YML030 W                                                | cell organization and biogenesis              | membrane/mitochondrion                                                          |                                        |                                | 2.162    |
| P42847 | 37S ribosomal protein S18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85541 MRPS18 0 YNL306 W                                             | cell organization and biogenesis;metabolic process | mitochondrion/ribosome                                                          | RNA binding;structural molecule activity |                                | 0.54     |
| P41911 | Glycerol-3-phosphate dehydrogenase [NAD(+)] 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85409 GPD2; YOL059 W                                                | metabolic process                            | cytoplasm/mitochondrion                                                          | catalytic activity;nucleotide binding;protein binding |                                | 0.089    |
| P25038 | Translation initiation factor IF-2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85413 IFM1; YOL023 W                                                | cell organization and biogenesis;metabolic process | mitochondrion/nucleus                                                           | catalytic activity;nucleotide binding;RNA binding |                                | 0.11     |
| ID      | Description                                                   | Accession | GO Terms                                       | Binding                                                                 |
|---------|---------------------------------------------------------------|-----------|-----------------------------------------------|------------------------------------------------------------------------|
| P46998  | mitochondrial membrane protein FMP33 [OS=Saccharomyces cerevisiae S288c] | 85327     | membrane;mitochondrion                        | 1.371                                                                  |
| P49954  | probable hydrolase NIT3 [OS=Saccharomyces cerevisiae S288c]    | 85106     | NIT3;YLR351 C                                 | 0.129                                                                  |
| P38297  | Mitofusin FZO1 [OS=Saccharomyces cerevisiae S288c]            | 85347     | cell organization and biogenesis              | 0.142                                                                  |
| P47150  | 37S ribosomal protein S7, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85357     | FMP33;YJL161 C                                | 0.145                                                                  |
| P38884  | Altered inheritance of mitochondria protein 18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85660     | Altered inheritance of mitochondria protein 18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.16                                                                  |
| P39724  | 54S ribosomal protein L50, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85675     | 54S ribosomal protein L50, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.145                                                                  |
| P21771  | 37S ribosomal protein S28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85193     | 37S ribosomal protein S28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.145                                                                  |
| Q06090  | 54S ribosomal protein L51, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85261     | 54S ribosomal protein L51, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.16                                                                  |
| P35157  | Mitochondrial preussate carrier 1 [OS=Saccharomyces cerevisiae S288c] | 85280     | Mitochondrial preussate carrier 1 [OS=Saccharomyces cerevisiae S288c] | 0.145                                                                  |
| P25626  | 54S ribosomal protein IMG1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85041     | 54S ribosomal protein IMG1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.145                                                                  |
| P35166  | ATP-dependent RNA helicase mrh4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85421     | ATP-dependent RNA helicase mrh4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.145                                                                  |
| P38531  | 54S ribosomal protein L38, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85241     | 54S ribosomal protein L38, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.145                                                                  |
| P36517  | 54S ribosomal protein L4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85116     | 54S ribosomal protein L4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.145                                                                  |
Supplemental Table S3. The relative concentrations of proteins in mitochondria purified from WT cells cultured with or without LCA. Mitochondria were purified from WT cells recovered on day 7 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the "Proteome Discoverer" software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI WT + LCA | Ratio WT + LCA/ WT |
|-----------|-------------|----------------|---------|--------------------|--------------------|--------------------|---------|----------------|-------------------|
| P38120    | 37S ribosomal protein S9, mitochondrial | 85244 | MRPS9 | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 3.437   | 0.145          | 0.04              |
| P36163    | mitochondrial metalloendopeptidase OMA1 | 85396 | OMAL | metabolic process | membrane; mitochondrial | catalytic activity; metal ion binding | 0.931   | 0.116          | 0.12              |
| P47450    | Altered inheritance rate of mitochondria protein 2S | 85356 | AIM2 | cell organization and biogenesis | membrane; mitochondrial | transporter activity | 0.874   | 0.11           | 0.13              |
| Q12349    | ATP synthase subunit H, mitochondrial | 85100 | ATP1H | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrial | catalytic activity; transporter activity | 2.728   | 0.389          | 0.14              |
| P32317    | Protein AFG1 [OS=Saccharomyces cerevisiae S288c] | 85665 | AFG1; YEL052W | cell organization and biogenesis; metabolic process | membrane; mitochondrial | catalytic activity; nucleotide binding | 1.154   | 0.166          | 0.14              |
| Q12283    | Malonyl CoA-acyl carrier protein transacylase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85439 | MCT1; YOR221C | metabolic process | mitochondrion | catalytic activity | 0.896   | 0.136          | 0.15              |
| Q07334    | Solute carrier family 25 member 38 homolog [OS=Saccharomyces cerevisiae S288c] | 85143 | YDL119C | metabolic process; transport | membrane; mitochondrion | structural molecule activity; transporter activity | 0.73    | 0.116          | 0.16              |
| P53166    | ATP-dependent RNA helicase minH, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85281 | MTH4; YGL064C | cell organization and biogenesis; metabolic process | mitochondrion; organelle lumen | catalytic activity; nucleotide binding; RNA binding | 1.412   | 0.225          | 0.16              |
| P36547    | Mitochondrial outer membrane protein OM45 [OS=Saccharomyces cerevisiae S288c] | 85467 | OM45; YIL136W | metabolic process | membrane; mitochondrial | structural molecule activity | 300.9   | 51.48          | 1.7               |
| P22353    | S45 ribosomal protein L8, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85338 | MRPL8; YIL063C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.848   | 0.166          | 0.20              |
| Q08818    | Meloxic sister chromatid recombination protein 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85453 | M53C6; YOR354C | metabolic process | mitochondrion; organelle lumen | RNA binding | 1.047   | 0.227          | 0.22              |
| P54115    | Magnesium-activated ald dehydrogenase, cytosolic [OS=Saccharomyces cerevisiae S288c] | 85604 | ALS6; YPL061W | metabolic process; response to stimulus | cytoplasm; cytosol; mitochondrial | catalytic activity | 0.348   | 0.077          | 0.22              |
| P22438    | Methionine–tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85308 | MSML1; YGR171C | metabolic process | cytoplasm; cytosol; mitochondrial; organelle lumen | catalytic activity; nucleotide binding | 0.292   | 0.066          | 0.23              |
| P25605    | Acetolactate synthase small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85034 | ILV6; YCL009C | metabolic process; regulation of biological process | mitochondrion | catalytic activity; enzyme regulator activity | 10.28   | 2.36           | 0.23              |
| P38969    | Pentamide resistance factor, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85444 | PNT1; YCR266W | cell organization and biogenesis; response to stimulus | membrane; mitochondrial | structural molecule activity | 0.711   | 0.166          | 0.23              |
| P15179    | Aspartate–tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85600 | MSU1; YPL104A | metabolic process | cytoplasm; mitochondrial; organelle lumen | catalytic activity; nucleotide binding | 0.708   | 0.174          | 0.25              |
| P21954    | Isocitrate dehydrogenase [NADP], mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85149 | IDP1; YDL066W | metabolic process | mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | 33.17   | 8.261          | 0.25              |
| Q06678    | S45 ribosomal protein L15, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85192 | MRPL15; YOR322W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 1.219   | 0.304          | 0.25              |
| Entry Code | Description | Accession(s) | GO Term(s) | Gene Symbol(s) | CPD | CO | Mol. Wt. | p value | q value |
|------------|-------------|--------------|------------|---------------|-----|---|---------|--------|---------|
| P32902     | 37s ribosomal protein MRK4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85678 4 | MRK4; YHL004 W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | 0.957 | 0.334 | 0.35 |
| P53721     | Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85575 2 | RCF2; YNR018 W | cell organization and biogenesis | membrane; mitochondrion | 7.111 | 2.511 | 0.35 |
| P07251     | ATP synthase subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85217 7 | ATP1; YBL099 W | metabolic process; transport | cytosol; membrane; mitochondrion | catalytic activity; nucleotide binding; transporter activity | 26.82 6 | 9.661 | 0.36 |
| P38885     | Altered inheritance of mitochondria protein 46, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85660 6 | Aim46; YHR199 C | mitochondrial | catalytic activity | 1.794 | 0.73 | 0.37 |
| P48360     | Probable NADPH: adenodoxin oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85198 2 | Aph1; YDR376 W | cellular homeostasis; metabolic process; transport | cytoplasm; membrane; mitochondrion; organelle lumen | catalytic activity | 0.682 | 0.25 | 0.37 |
| P32897     | Mitochondrial import inner membrane translocase subunit tim23 [OS=Saccharomyces cerevisiae S288c] | 85575 1 | Tim23; YNR017 W | transport | membrane; mitochondrion | protein binding; transporter activity | 4.012 | 1.512 | 0.38 |
| P00360     | Glyceraldehyde-3-phosphate dehydrogenase 1 [OS=Saccharomyces cerevisiae S288c] | 85339 5 | Tdh1; YIL052W | metabolic process | cytoplasm; cytosol; membrane; mitochondrion | catalytic activity; nucleotide binding | 1.721 | 0.65 | 0.38 |
| P32340     | Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85491 9 | Nd1; YNL220 C | metabolic process; regulation of biological process | membrane; mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 16.43 3 | 6.279 | 0.38 |
| P39726     | Glycine cleavage system H protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85125 4 | Gcv3; YAL044C | metabolic process | mitochondrion | catalytic activity | 6.743 | 2.594 | 0.38 |
| P40502     | Altered inheritance of mitochondria protein 19, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85472 2 | Aim19; YIL087C | mitochondrial | catalytic activity | 1.512 | 0.585 | 0.39 |
| P07246     | Alcohol dehydrogenase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85550 7 | Adh3; YMR083 W | metabolic process | mitochondrion; organelle lumen | catalytic activity; metal ion binding | 7.031 | 2.728 | 0.39 |
| Q12482     | Mitochondrial aspartate-glutamate transporter AGC1 [OS=Saccharomyces cerevisiae S288c] | 85613 2 | Agc1; YPR021C | metabolic process; transport | membrane; mitochondrion | structural molecule activity; transporter activity | 0.348 | 0.136 | 0.39 |
| Q01163     | 37s ribosomal protein S23, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85274 8 | Rsm23; YGL129C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | catalytic activity; nucleotide binding; RNA binding; structural molecule activity | 4.367 | 1.707 | 0.39 |
| P11914     | Mitochondrial processing peptidase subunit alpha [OS=Saccharomyces cerevisiae S288c] | 85641 9 | Map2; YHR024 C | metabolic process; transport | membrane; mitochondrion; organelle lumen | catalytic activity; metal ion binding; protein binding | 2.311 | 0.905 | 0.39 |
| P37326    | Assembly factor cbp4 [OS=Saccharomyces cerevisiae S288c] | 85315 1 | Spg1; YGR236 C | cell organization and biogenesis | endoplasmic reticulum; membrane; mitochondrion | 157.4 89 | 62.09 6 | 0.39 |
| P50088     | Stationary phase gene 1 protein [OS=Saccharomyces cerevisiae S288c] | 85464 9 | Coa1; YIL157C | cell organization and biogenesis | membrane; mitochondrion | protein binding | 1.31 | 0.52 | 0.40 |
| P04542     | Cytochrome c oxidase assembly factor 1 [OS=Saccharomyces cerevisiae S288c] | 85471 5 | Rsm23; YIL093C | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | 1.154 | 0.468 | 0.41 |
| P33311     | Mitochondrial pyruvate carrier 3 [OS=Saccharomyces cerevisiae S288c] | 85315 8 | Fmp43; YMC1; YGR243 W | transport | membrane; mitochondrion | transporter activity | 1.154 | 0.468 | 0.41 |
| P40425     | External NADH-ubiquinone oxidoreductase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85517 6 | Nde1; YMR314C | metabolic process | mitochondrion | catalytic activity; nucleotide binding | 5.078 | 2.065 | 0.41 |
| P45013     | Mitochondrial acidic protein MAM33 [OS=Saccharomyces cerevisiae S288c] | 85474 0 | Mam33; YIL070C | metabolic process; regulation of biological process | mitochondrial; organelle lumen | translation regulator activity | 2.831 | 1.154 | 0.41 |
| Q06698     | Putative ATP-dependent RNA helicase YLR419W [OS=Saccharomyces cerevisiae S288c] | 85113 7 | YLR419 W; YLR419 W | metabolic process | cytoplasm; mitochondrion; nucleus | catalytic activity; nucleotide binding; protein binding | 0.201 | 0.082 | 0.41 |
Q04999 545 ribosomal protein L1, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85169 4 MRPL1; YDR116C cell organization and biogenesis;metabolic process mitochondrion;ribosome RNA binding;structural molecule activity 1.069 0.438 0.41

P28625 Protein YML1 [OS=Saccharomyces cerevisiae S288c]
85518 3 YML1; YMR152W metabolic process;response to stimulus cytoplasm;endoplasmic reticulum;mitochondrion catalytic activity;metal ion binding 1.069 0.438 0.41

P35180 mitochondrial import receptor subunit Tom20 [OS=Saccharomyces cerevisiae S288c]
85297 3 TOM20; YOR082W cell organization and biogenesis;transport membrane;mitochondrion protein binding;transporter activity 1.031 0.425 0.41

P38175 37S ribosomal protein MRP21, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85218 8 MRP21; YBL090W cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 1.031 0.425 0.41

P28834 Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85669 1 IDH1; YNL037C metabolic process;transport cytosol;mitochondrion;organelle lumen catalytic activity;metal ion binding;nucleotide binding;protein binding;RNA binding 7.859 3.281 0.42

P18496 Mitochondrial ATPase complex subunit ATP10 [OS=Saccharomyces cerevisiae S288c]
85110 9 ATP10; YLR393W cell organization and biogenesis cytoplasm;membrane;mitochondrion protein binding 1.818 0.778 0.43

P02204 545 ribosomal protein L13, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85387 5 MRPL13; YKR066C cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 0.778 0.334 0.43

Q09297 Mitochondrial 2-oxoacid:carboxylate carrier 2 [OS=Saccharomyces cerevisiae S288c]
85439 7 ODC2; YGR222W metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 0.778 0.334 0.43

Q07914 mitochondrial import inner membrane translocase subunit TIM14 [OS=Saccharomyces cerevisiae S288c]
85069 4 PAM18; YLR086C regulation of biological process;transport membrane;mitochondrion enzyme regulator activity;protein binding;transporter activity 0.778 0.334 0.43

P32387 545 ribosomal protein L41, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85201 4 MRP20; YDR405W cell organization and biogenesis;metabolic process mitochondrion;ribosome nucleotide binding;protein binding;RNA binding;structural molecule activity 0.719 0.311 0.43

P38472 MIOREX complex component 3 [OS=Saccharomyces cerevisiae S288c]
85218 1 YBL095W; MRX3; YLR095W cell organization and biogenesis membrane;mitochondrion 0.719 0.311 0.43

P07213 Mitochondrial import receptor subunit TOM70 [OS=Saccharomyces cerevisiae S288c]
85560 2 TOM70; YNL121C cell organization and biogenesis;transport membrane;mitochondrion protein binding;transporter activity 2.665 1.154 0.43

P14063 545 ribosomal protein L31, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85372 0 MRPL31; YKL138C cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 0.668 0.292 0.44

Q06090 545 ribosomal protein L51, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85621 4 MRPL51; YPR100W cell organization and biogenesis;metabolic process mitochondrion;ribosome RNA binding;structural molecule activity 0.668 0.292 0.44

P42834 mitochondrial Dna homolog 2 [OS=Saccharomyces cerevisiae S288c]
85538 8 MOD2; YNL328C regulation of biological process;transport membrane;mitochondrion enzyme regulator activity;transporter activity 0.668 0.292 0.44

Q06892 NADH kinase POSS, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85591 3 POSS; YPL188W metabolic process;response to stimulus mitochondrion;organelle lumen catalytic activity;nucleotide binding 1.565 0.688 0.44

P38152 Tricarboxylate transport protein [OS=Saccharomyces cerevisiae S288c]
85259 4 CTP1; YBR291C metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 0.551 0.245 0.44

P40086 Cytochrome c oxidase assembly protein Cox15 [OS=Saccharomyces cerevisiae S288c]
85688 4 COX15; YER141W cell organization and biogenesis;metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 2.594 1.154 0.44

P36528 545 ribosomal protein L17, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85546 9 MRPL17; YNL252C cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 0.52 0.233 0.45

P36013 NAD-dependent malic enzyme, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85383 9 MAE1; YLK020C metabolic process mitochondrion;organelle lumen catalytic activity;metal ion binding;nucleotide binding 1.512 0.679 0.45

P04840 mitochondrial outer membrane protein porin 1 [OS=Saccharomyces cerevisiae S288c]
85566 9 POR1; YNL055C cell death;cell organization and biogenesis;cellular homeostasis;regulation of biological process;transport cytoplasm;membrane;mitochondrion transport activity 15.23 8 6.848 0.45

Q07349 MIOREX complex component 9 [OS=Saccharomyces cerevisiae S288c]
85153 5 YGL027C; MRX9; YGL027C endoplasmic reticulum;membrane;mitochondrion 2.433 1.096 0.45

P34224 Uncharacterized protein YBL059W [OS=Saccharomyces cerevisiae S288c]
85222 1 YBL059W; YBL059W membrane;mitochondrion 0.468 0.212 0.45
P49095  Glycine dehydrogenase (Decarboxylating), mitochondrial [OS=Saccharomyces cerevisiae S288c]  85522 7  GCV2; YMR189 W  metabolic process  cytosol/mitochondrion  catalytic activity  1.575  0.778  0.49

P32787  Mitochondrial genome maintenance protein MGM101 [OS=Saccharomyces cerevisiae S288c]  85360 9  MGM101 1; YIR144 W  cell organization and biogenesis;metabolic process;response to stimulus  chromosome/mitochondrion  DNA binding  3.281  1.637  0.50

P07B06  Valine--RNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85298 6  VAS1; YDR994 W  metabolic process;regulation of biological process  cytoplasm;cytosol/mitochondrion  catalytic activity;nucleotide binding  0.668  0.334  0.50

P36517  54S ribosomal protein L4, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85116 0  MRPL4; YLR495 W  cell organization and biogenesis;metabolic process  mitochondrion;ribosome  structural molecule activity  2.162  1.081  0.50

P53170  [Pryviate dehydrogenase (acytoly-transferring)] kinase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85282 1  PEP2; YGL059 W  metabolic process;regulation of biological process  mitochondrion;organellar lumen  catalytic activity;nucleotide binding;protein binding  0.778  0.389  0.50

P28817  3-hydroxyisobutyryl-CoA hydrolase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85160 6  EHD3; YDR036 C  metabolic process  mitochondrion  catalytic activity  0.743  0.374  0.50

P23180  Probable oxidoreductase AIM17 [OS=Saccharomyces cerevisiae S288c]  85636 5  AIM17; YNL021C  cell organization and biogenesis;metabolic process  mitochondrion  catalytic activity;metal ion binding  2.981  1.512  0.51

Q08023  Protein FMP25, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85076 6  FMP25; YLR077 W  cell organization and biogenesis;metabolic process  membrane/mitochondrion  1.412  0.719  0.51

P36066  Protein MRG3-like [OS=Saccharomyces cerevisiae S288c]  85372 5  YKL133C; YKL133C  metabolic process  membrane/mitochondrion  protein binding  1.054  0.54  0.51

Q06688  Methyltransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85191 1  OMS1; YDR316 W  metabolic process  membrane/mitochondrion  catalytic activity  0.585  0.301  0.51

P40037  cytochrome c oxidase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85268 8  COX4; YGL138C  cell organization and biogenesis;metabolic process;transport  membrane/mitochondrion  catalytic activity;metal ion binding;transporter activity  27.48  14.19  9  0.52

P40053  Altered inheritance of mitochondria protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85681 3  AIM9; YER080 D  mitochondrial  4.036  2.086  0.52

P50945  MICOS complex subunit MC27 [OS=Saccharomyces cerevisiae S288c]  85562 3  AIM37; MC27; YNL100 W  cell organization and biogenesis  membrane/mitochondrion  0.968  0.501  0.52

P51998  54S ribosomal protein yml6, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85498 3  YMR6; YNL025 C  cell organization and biogenesis;metabolic process  mitochondrion;ribosome  RNA binding;structural molecule activity  1.404  0.73  0.52

Q12130  Sphingolipid long chain base-responsive protein LSP1 [OS=Saccharomyces cerevisiae S288c]  85610 3  LSP1; YPL004C  regulation of biological process;response to stimulus;transport  cytoplasm;membrane/mitochondrion  24.11  12.59  4  0.52

P43617  Uncharacterized mitochondrial carrier YFR045W [OS=Saccharomyces cerevisiae S288c]  85060 6  YFR045 W; YFR045 W  metabolic process;transport  membrane/mitochondrion  structural molecule activity;transporter activity  0.778  0.413  0.53

P36520  54S ribosomal protein L10, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85543 6  MRPL10; YNL284C  cell organization and biogenesis;metabolic process  mitochondrion;ribosome  structural molecule activity  0.73  0.389  0.53

P53738  Uncharacterized protein YMR040W [OS=Saccharomyces cerevisiae S288c]  85577 6  YMR040 W; YMR040 W  mitochondrial  0.73  0.389  0.53

P53805  Mitochondrial 37S ribosomal protein S27 [OS=Saccharomyces cerevisiae S288c]  85312 9  RSM27; YMR215 W  cell organization and biogenesis;metabolic process  mitochondrion;ribosome  structural molecule activity  2.162  1.154  0.53

Q04935  Cytochrome c oxidase protein 20, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85181 7  COX20; YHR231 C  cell organization and biogenesis;metabolic process  membrane/mitochondrion  protein binding  1.894  1.031  0.54

P32891  D-lactate dehydrogenase [cytochrome 1], mitochondrial [OS=Saccharomyces cerevisiae S288c]  85138 0  DLL1; YDL174C  metabolic process;transport  membrane/mitochondrion  catalytic activity;nucleotide binding  11.25  6.128  0.54

P05950  Heat shock protein SSC1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85350 3  SSC1; YIR049C  cell organization and biogenesis;metabolic process;regulation of biological process;transport  membrane/mitochondrion;nucleus;organellar lumen  catalytic activity;enzyme regulator activity;nucleotide binding;protein binding  26.82  14.64  7  0.55

P39522  Dihydroxy acid dehydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85347 3  ILV3; YIR016C  metabolic process  mitochondrion  catalytic activity;metal ion binding  16.47  9  0.55
| P38071 | Enoyl-(acyl-carrier protein) reductase [NADPH, B-specific], mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85231 4 | ETR1; YBR024C | metabolic process | mitochondrial;organelle lumen | catalytic activity;DNA binding;metal ion binding | 9 | 4.926 | 0.55 |
| P43616 | Cys-Gly metallopeptidase dag1 [OS=Saccharomyces cerevisiae S288c] | 85060 5 | DOG1; YRO44C | metabolic process | cytoplasm;mitochondrion;ribosome | catalytic activity;metal ion binding | 0.848 | 0.468 | 0.55 |
| P39006 | Phosphatidylserine decarboxylase proenzyme 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85555 2 | PSO1; YNL169C | metabolic process;regulation of biological process | membrane;mitochondrion | catalytic activity | 0.487 | 0.269 | 0.55 |
| P32860 | NFI-like protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85382 6 | NFIU; YKL040C | cell organization and biogenesis;cellular homeostasis;metabolic process | mitochondrial;organelle lumen | metal ion binding | 3.87 | 2.162 | 0.56 |
| P05892 | MIOREX complex component 2 [OS=Saccharomyces cerevisiae S288c] | 85099 7 | YLR290C; COG111; YLR290C | cell organization and biogenesis | mitochondrial | catalytic activity | 3.87 | 2.162 | 0.56 |
| P04472 | Mitochondrial inner membrane I-AAA protease supercomplex subunit MGR3 [OS=Saccharomyces cerevisiae S288c] | 85314 2 | MSR1; YMR115W | metabolic process | membrane;mitochondrion | protein binding | 0.417 | 0.233 | 0.56 |
| P47052 | Succinate dehydrogenase [ubiquione] flavoprotein subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85340 5 | YIL045W; YIL045W | metabolic process;transport | membrane;mitochondrion | catalytic activity;nucleotide binding | 4.043 | 2.262 | 0.56 |
| P28241 | Isocitrate dehydrogenase [NAD] subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85430 3 | IDH2; YOR136W | metabolic process | mitochondrial;organelle lumen | catalytic activity;metal ion binding;nucleotide binding;protein binding;RNA binding | 4.179 | 2.34 | 0.56 |
| Q06567 | ABC1 family protein MCP2 [OS=Saccharomyces cerevisiae S288c] | 85095 5 | YLR253W; MCP2; YLR253W | cell organization and biogenesis | membrane;mitochondrion | catalytic activity | 0.389 | 0.218 | 0.56 |
| Q12374 | Nuclear control of ATPase protein 2 [OS=Saccharomyces cerevisiae S288c] | 85627 8 | NCA2; YPR155C | metabolic process | membrane;mitochondrion | catalytic activity | 0.668 | 0.377 | 0.56 |
| P24720 | Protein MNE1 [OS=Saccharomyces cerevisiae S288c] | 85453 2 | MNE1; YOR350C | metabolic process | cytoplasm;mitochondrion;organelle lumen | protein binding | 0.343 | 0.194 | 0.57 |
| Q12233 | ATP synthase subunit g, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85613 1 | ATP20; YPR020W | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 1.371 | 0.778 | 0.57 |
| Q12165 | ATP synthase subunit delta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85156 0 | ATP16; YDL004W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 1.371 | 0.778 | 0.57 |
| P53326 | Uncharacterized protein YGR266W [OS=Saccharomyces cerevisiae S288c] | 85318 2 | YGR266W; YGR266W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 0.778 | 0.442 | 0.57 |
| P00630 | ATP synthase subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85358 5 | ATP2; YJR121W | metabolic process;transport | cytosol;membrane;mitochondrion | catalytic activity;nucleotide binding;protein binding;transporter activity | 38.81 | 22.26 | 0.57 |
| P27929 | 37S ribosomal protein NAM9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85558 5 | NAM9; YNL137C | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrial;ribosome | RNA binding;structural molecule activity | 1.202 | 0.693 | 0.58 |
| P32316 | acetyl-CoA hydratase [OS=Saccharomyces cerevisiae S288c] | 85226 6 | ACH1; YBL015W | metabolic process | cytoplasm;cytosol;mitochondrion | catalytic activity | 10.49 | 6.055 | 0.58 |
| P23833 | Protein SCO1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85232 5 | SCO1; YBR037C | cell organization and biogenesis;cellular homeostasis;response to stimulus;transport | membrane;mitochondrion | antioxidant activity;catalytic activity;metal ion binding | 1.154 | 0.668 | 0.58 |
| P36531 | 54S ribosomal protein L16, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85241 9 | MRPL36; YBR112C | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | structural molecule activity | 1.154 | 0.668 | 0.58 |
| P53732 | 37S ribosomal protein S12, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85577 2 | MRPS12; YNR36C | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | structural molecule activity | 1.154 | 0.668 | 0.58 |
| P16622 | Ferrochelatase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85434 7 | HEM15; YOR176W | metabolic process | membrane;mitochondrion | catalytic activity | 4.337 | 2.511 | 0.58 |
| P18239 | ADP,ATP carrier protein 2 [OS=Saccharomyces cerevisiae S288c] | 85225 0 | PET9; YJR030C | cell death;metabolic process;transport | membrane;mitochondrion | structural molecule activity;transporter activity | 47.06 | 27.48 | 0.58 |
| Q00402 | Nuclear migration protein NUM1 [OS=Saccharomyces cerevisiae S288c] | 85172 7 | NUM1; YDR150 W | cell organization and biogenesis;cellular component movement;transport;regulation of biological process;response to stimulus;membrane | endoplasmic reticulum;mitochondrion | catalytic activity;motor activity;protein binding | 0.065 | 0.038 | 0.58 |
| P12687 | 54S ribosomal protein L2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85572 7 | MRP7; YNL005C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | catalytic activity;RNA binding | 1.848 | 1.081 | 0.58 |
| P36112 | MicOS complex subunit Mic60 [OS=Saccharomyces cerevisiae S288c] | 85388 6 | FC1; YCL060 C | cell organization and biogenesis;transport | membrane;mitochondrion | | 15.37 | 9 | 0.59 |
| P15424 | ATP-dependent RNA helicase Mss116, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85177 5 | MS5116; YDR194 C | metabolic process;regulation of biological process | mitochondrion;organelle lumen | catalytic activity;nucleotide binding;RNA binding | 1.783 | 1.047 | 0.59 |
| P53724 | 54S ribosomal protein L50, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85575 6 | MRPL50; YMR022 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.995 | 0.585 | 0.59 |
| P17695 | Glutaredoxin-2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85212 4 | GXR2; YDR513 W | cytoplasm;mitochondrion;nucleus | antioxidative activity;catalytic activity | | 0.874 | 0.52 | 0.59 |
| P14832 | Peptidyl-prolyl cis-trans isomerase [OS=Saccharomyces cerevisiae S288c] | 85173 4 | CPF1; YDR155 C | cell differentiation;cell organization and biogenesis;metabolic process;regulation of biological process;transport | cytoplasm;mitochondrion;nucleus | catalytic activity;RNA binding | 0.874 | 0.52 | 0.59 |
| Q08742 | Thiosulfate sulfurtransferase RDL2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85446 0 | RDL2; YOR286 W | mitochondrial | catalytic activity | | 0.874 | 0.52 | 0.59 |
| P00711 | Succinate dehydrogenase (ubiquitone) flavoprotein subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85370 9 | SDH1; YKL148C | metabolic process;transport | membrane;mitochondrion | catalytic activity;nucleotide binding;protein binding | 8.454 | 5.032 | 0.60 |
| P36101 | tRNA threonylcarboxylmethyltransferase 2 [OS=Saccharomyces cerevisiae S288c] | 85384 1 | TCD2; YKL027 W | metabolic process | cytosol;membrane;mitochondrion | catalytic activity;nucleotide binding | 0.778 | 0.468 | 0.60 |
| P05020 | Iron sulfur cluster assembly protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85596 8 | ISU1; YPL135 W | cell organization and biogenesis;cellular homeostasis;metabolic process | cytoplasm;mitochondrion;organelle lumen | catalytic activity;metal ion binding;protein binding | 0.778 | 0.468 | 0.60 |
| P25642 | 54S ribosomal protein IMG2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85043 5 | IMG2; YCR071C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.778 | 0.468 | 0.60 |
| P25087 | Sterol 24-C-methyltransferase [OS=Saccharomyces cerevisiae S288c] | 85500 4 | ERG6; YNL008 C | metabolic process | endoplasmic reticulum;membrane;mitochondrion | catalytic activity | 1.424 | 0.859 | 0.60 |
| P38825 | Protein TOM71 [OS=Saccharomyces cerevisiae S288c] | 85651 7 | TOM71; YHR117 W | transport | membrane;mitochondrion | protein binding;transporter activity | 0.701 | 0.425 | 0.61 |
| P35306 | Putative cysteine synthase [OS=Saccharomyces cerevisiae S288c] | 85289 5 | YOR012 W; YOR012 W | metabolic process | | | 1.346 | 0.817 | 0.61 |
| P32843 | Mitochondrial escape protein 2 [OS=Saccharomyces cerevisiae S288c] | 85534 8 | YME2; YMR302 C | cell organization and biogenesis;metabolic process | membrane;mitochondrion | nucleotide binding;RNA binding | 3.458 | 2.099 | 0.61 |
| P38891 | Branched-chain amino acid aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85661 5 | BAT1; YHR208 W | metabolic process;regulation of biological process;response to stimulus | mitochondrion;organelle lumen | catalytic activity | 7.111 | 4.337 | 0.61 |
| P33416 | Heat shock protein 78, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85384 5 | HSP78; YDR258 C | cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus | mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | 4.264 | 2.609 | 0.61 |
| Q02776 | Mitochondrial import inner membrane translocase subunit Tim50 [OS=Saccharomyces cerevisiae S288c] | 85604 2 | TIM50; YPL063 W | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;protein binding;transporter activity | 7.483 | 4.623 | 0.62 |
| Q12375 | Mitochondrial ornithine transporter 2 [OS=Saccharomyces cerevisiae S288c] | 85429 7 | ORT1; YOR130 C | metabolic process;transport | membrane;mitochondrion | structural molecule activity;transporter activity | 0.54 | 0.334 | 0.62 |
| P14693 | Sorting assembly machinery 35 kDa subunit [OS=Saccharomyces cerevisiae S288c] | 85648 3 | SAM35; YHR083 W | cell organization and biogenesis;transport | membrane;mitochondrion | protein binding | 0.54 | 0.334 | 0.62 |
| P31334 | 54S ribosomal protein L9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85313 5 | MRPL8; YOR220 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.501 | 0.311 | 0.62 |
| Q12428 | Probable 2-methylcitrate dehydratase [OS=Saccharomyces cerevisiae S288c] | BY6108 | PDR1; YPR002C | metabolic process | cytoplasm;membrane;mitochondrion | catalytic activity | 12.33 | S | 7.66 | 0.62 |
| P00890 | citrate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY5737 | 2 | CII; YNR001C | metabolic process;transport | cytosol;mitochondrion;organelle lumen | catalytic activity | 8.211 | 5.105 | 0.62 |
| P32191 | Glycerol-3-phosphate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY4654 | 1 | GLUT2; YIL155C | metabolic process | membrane;mitochondrion | catalytic activity | 6.097 | 3.796 | 0.62 |
| P38271 | Protein OPY1 [OS=Saccharomyces cerevisiae S288c] | BY2426 | 6 | OPY1; YBR129C | cytoplasm;mitochondrion | catalytic activity | 0.438 | 0.274 | 0.63 |
| P49954 | Probable hydrolase NIT3 [OS=Saccharomyces cerevisiae S288c] | BY5067 | 5 | NIT3; YLR351C | metabolic process | cytoplasm;mitochondrion | catalytic activity | 0.438 | 0.274 | 0.63 |
| P42900 | Sigma-like sequence protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY0830 | 0 | SL51; YLR139C | cell organization and biogenesis;metabolic process | membrane;mitochondrion | protein binding | 0.425 | 0.266 | 0.63 |
| P25179 | Peptidyl-prolyl cis-trans isomerase C, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY4897 | 7 | CPR3; YML070W | cell death;metabolic process | mitochondrion;organelle lumen | catalytic activity | 2.415 | 1.512 | 0.63 |
| P23149 | Flavoprotein-like protein YCP4 [OS=Saccharomyces cerevisiae S288c] | BY5036 | 0 | YCP4; YCR004C | metabolic process;regulation of biological process | cytoplasm;membrane;mitochondrion | catalytic activity;nucleotide binding;protein binding | 5.813 | 3.642 | 0.63 |
| Q00981 | ABC1 family protein YPL109C, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY5995 | 5 | YPL109C; YPL109C | mitochondrial | catalytic activity | 0.413 | 0.259 | 0.63 |
| P28239 | Inorganic pyrophosphatase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY5530 | 9 | PPA2; YNR0267W | metabolic process | cytoplasm;mitochondrion | catalytic activity;metal ion binding | 0.413 | 0.259 | 0.63 |
| P48015 | Aminomethyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY1558 | 2 | GCV1; YDR029C | metabolic process | mitochondrion | catalytic activity;protein binding | 8.047 | 5.062 | 0.63 |
| P49017 | 2-methoxy-6-pyroprenyl-1,4-benzoquinol methylase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY4903 | 0 | COQ5; YML110C | metabolic process | membrane;mitochondrion;organelle lumen | catalytic activity | 0.389 | 0.245 | 0.63 |
| P43635 | Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY6106 | 7 | CIT3; YPR001W | metabolic process | mitochondrion | catalytic activity | 3.642 | 2.3 | 0.63 |
| P47127 | Altered inheritance of mitochondrion protein 24, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY3548 | 3 | AIM024; YJR080C | cell organization and biogenesis | mitochondrion | catalytic activity | 2.857 | 1.807 | 0.63 |
| P08417 | Fumarate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY5586 | 6 | FUM1; YPL262W | cell organization and biogenesis;metabolic process | cytoplasm;cytosol;mitochondrion;organelle lumen | catalytic activity | 8.237 | 5.21 | 0.63 |
| P43567 | Alanine–glyoxylate aminotransferase 1 [OS=Saccharomyces cerevisiae S288c] | BY5051 | 4 | AGX1; YFL030W | metabolic process | cytosol;mitochondrion | catalytic activity | 2.162 | 1.371 | 0.63 |
| P32232 | Sphingolipid long chain base-responsive protein PIL1 [OS=Saccharomyces cerevisiae S288c] | BY2975 | 7 | PIL1; YGR086C | cell organization and biogenesis;regulation of biological process;response to stimulus | cytoplasm;membrane;mitochondrion | protein binding | 10.45 | 6.627 | 0.63 |
| P33227 | Mitochondrial peroxiredoxin PXR1 [OS=Saccharomyces cerevisiae S288c] | BY2221 | 5 | PRX1; YBL084C | cellular homeostasis;metabolic process;regulation of biological process;response to stimulus | mitochondrion | antioxidant activity;catatolic activity | 5.158 | 3.281 | 0.64 |
| P40961 | Prohibitin 1 [OS=Saccharomyces cerevisiae S288c] | BY3033 | 3 | PHB1; YGR132C | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion;organelle lumen | protein binding | 5.158 | 3.281 | 0.64 |
| P32695 | Dihydroxyacetone-phosphate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY5656 | 3 | LAT1; YNL071W | metabolic process | mitochondrion;organelle lumen | catalytic activity | 5.898 | 3.758 | 0.64 |
| Q01332-1 | Cysteine proteinase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY5468 | 1 | KGD1; YIL125W | metabolic process;regulation of biological process;response to stimulus | cytosol;mitochondrion;organelle lumen | catalytic activity;DNA binding;RNA binding | 0.28 | 0.179 | 0.64 |
| P40047 | Aldehyde dehydrogenase 5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | BY5804 | 4 | ALD5; YER073W | metabolic process | mitochondrion;organelle lumen | catalytic activity | 1.955 | 1.254 | 0.64 |
| P38771 | Ribosome-recycling factor, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85643 | 3 | RRF1; YHR038 W | cell organization and biogenesis; metabolic process | mitochondrion | RNA binding | 1.955 | 1.254 | 0.64 |
| P32445 | Single-stranded DNA-binding protein RIM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85039 | 5 | RIM1; YCR028C A | cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrion | DNA binding | 1.783 | 1.154 | 0.65 |
| Q03653 | Protein EFR3 [OS=Saccharomyces cerevisiae S288c] | 85525 | 2 | EFR3; YNR212 C | | membrane/mitochondrion | | 0.148 | 0.096 | 0.65 |
| P09624 | Dihydrolipoamide dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85052 | 7 | LPD1; YFL018C | cellular homeostasis; metabolic process; regulation of biological process | mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 21.53 | 9 | 14.01 | 3 | 0.65 |
| P32473 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85252 | 2 | PDB1; YBR221C | metabolic process | mitochondrion; organelle lumen | catalytic activity | 6.848 | 4.456 | 0.65 |
| P07275 | Delta-1-pyruvyl-5-carboxylate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85643 | 2 | PUT2; YHR037 W | | metabolic process | membrane/mitochondrion; organelle lumen | catalytic activity | 5.579 | 3.642 | 0.65 |
| P53140 | Protein RMD9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85277 | 1 | RMD9; YGL107C | | cell differentiation; metabolic process; regulation of biological process | membrane/mitochondrion | RNA binding | 1.154 | 0.756 | 0.66 |
| P19414 | Acetone hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85301 | 3 | ACO1; YLR304C | cell organization and biogenesis; metabolic process; transport | cytoplasm; cytosol; mitochondrion; organelle lumen | catalytic activity; DNA binding; metal ion binding | 24.88 | 5 | 16.34 | 3 | 0.66 |
| P40341 | Mitochondrial respiratory chain complexes assembly protein YTA12 [OS=Saccharomyces cerevisiae S288c] | 85511 | 4 | YTA12; YMR089 C | cell organization and biogenesis; metabolic process; transport | cytoplasm; membrane; mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | 1.184 | 0.778 | 0.66 |
| P32453 | Protein ATP11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85540 | 1 | ATP11; YNL315C | cell organization and biogenesis | mitochondrion | protein binding | 1.512 | 0.995 | 0.66 |
| P40033 | 37S ribosomal protein rnm18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85677 | 6 | RSM18; YER050C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 1.512 | 0.995 | 0.66 |
| P36526 | 54S ribosomal protein L27, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85258 | 5 | MRPL27; YBR282 W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 1.512 | 0.995 | 0.66 |
| P18900 | Hexaprenyl-pyro phosphatase synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85228 | 8 | COQ1; YBR003 W | | | membrane/mitochondrion | catalytic activity; metal ion binding; protein binding | 0.711 | 0.468 | 0.66 |
| P50085 | PRO231-2 [OS=Saccharomyces cerevisiae S288c] | 85314 | 6 | PHB2; YCR231 C | cell organization and biogenesis; metabolic process; regulation of biological process | membrane/mitochondrion | protein binding | 3.806 | 2.511 | 0.66 |
| P44367 | Potassium-activated aldehyde dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85455 | 6 | ALD4; YOR374 W | | | mitochondrial; organelle lumen | catalytic activity | 24.11 | 9 | 15.92 | 7 | 0.66 |
| P48527 | Tyrosine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85600 | 7 | MSY1; YLP097 W | | | cytoplasm; cytosol; mitochondrion; organelle lumen | catalytic activity; nucleotide binding; RNA binding | 0.63 | 0.417 | 0.66 |
| P38323 | ATP-dependent clpP-like chaperone, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85252 | 8 | MCK1; YBR227C | | | membrane/mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 0.607 | 0.403 | 0.66 |
| P23641 | Mitochondrial phosphate carrier protein [OS=Saccharomyces cerevisiae S288c] | 85354 | 0 | MIRL1; YIR077C | | | | membrane/mitochondrion | protein binding; structural molecule activity; transporter activity | 20.54 | 4 | 13.67 | 8 | 0.67 |
| P33729 | Serine hydroxymethyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85256 | 5 | SHM1; YBR263 W | | | | | | | 0.66 |
| P40495 | Homoisocitrate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85471 | 4 | LYS12; YIL094C | | | | | | | 0.66 |
| P30902 | ATP synthase subunit d, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85385 | 3 | ATP7; YKL016C | | | | | | | 0.66 |
| P38325 | Mitochondrial outer membrane protein OML4 [OS=Saccharomyces cerevisiae S288c] | 85253 | 1 | OML4; YBR230C | | | | | | | 0.66 |
| P07143 | Cytochrome c1, heme protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85423 | 1 | CYT1; YOR065 W | | | | | | | 0.66 |
| P21560 | Protein CBP3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85588 | CBP3; YPL215 W | cell organization and biogenesis; regulation of biological process | membrane;mitochondrion;ribosome | 1.031 | 0.701 | 0.68 |
| P00660 | Phosphoglycerate kinase [OS=Saccharomyces cerevisiae S288c] | 85037 | PGK1; YCR012 W | metabolic process | cytoplasm;membrane;mitochondrion | catalytic activity;nucleotide binding | 4.843 | 3.299 | 0.68 |
| Q08179 | Mitochondrial distribution and morphology protein X8 [OS=Saccharomyces cerevisiae S288c] | 85413 | MDM38; YQR027C | cell organization and biogenesis; cellular homeostasis; regulation of biological process; transport | membrane;mitochondrion | 3.732 | 2.548 | 0.68 |
| P07342 | Acetoacetate synthase catalytic subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85513 | ILV2; YMR018 W | metabolic process | mitochondrial | catalytic activity;metal ion binding; nucleotide binding | 4.223 | 2.888 | 0.68 |
| F17558 | 35S ribosomal protein PET123, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85432 | PET123; YOR158 W | cell organization and biogenesis; metabolic process | mitochondrial;ribosome | structural molecule activity | 2.594 | 1.783 | 0.69 |
| P38341 | MICOS complex subunit MIC12 [OS=Saccharomyces cerevisiae S288c] | 85256 | AIM5; MIC12; YBR262C | cell organization and biogenesis | membrane;mitochondrion | 2.594 | 1.783 | 0.69 |
| Q08822 | Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85453 | CIR2; YOR356 W | metabolic process; transport | membrane;mitochondrion | catalytic activity;metal ion binding; nucleotide binding | 2.162 | 1.488 | 0.69 |
| P06168 | Ketol-acid reductoisomerase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85056 | ILV5; YLR355C | cell organization and biogenesis; metabolic process | mitochondrial | catalytic activity;DNA binding; metal ion binding | 9 | 6.197 | 0.69 |
| P19262 | Dihydroxyacetone-phosphate-ribulose-5-phosphate transferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85172 | KGD2; YDR148C | cell organization and biogenesis; metabolic process | catalytic activity; protein binding | 5.7 | 3.962 | 0.70 |
| P01120 | Ras-like protein 2 [OS=Saccharomyces cerevisiae S288c] | 85662 | RAS2; YNL098C | cell communication; cell differentiation; metabolic process; regulation of biological process; response to stimulus | membrane;mitochondrion;nucleus | catalytic activity; nucleotide binding; protein binding | 5.7 | 3.962 | 0.70 |
| Q06236 | Mitochondrial inner membrane protein SHM4 [OS=Saccharomyces cerevisiae S288c] | 85086 | SHH4; YLR164W | metabolic process | membrane;mitochondrion | catalytic activity; metal ion binding | 4.623 | 3.217 | 0.70 |
| Q02486 | ARS binding factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85009 | AFB2; YMR072W | cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus | chromosome;mitochondrion;nucleus | DNA binding | 69.17 | 48.23 | 0.70 |
| P33311 | ATP-dependent permease MDL2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85865 | MDL2; YPL270W | response to stimulus; transport | membrane;mitochondrion | catalytic activity; nucleotide binding; transporter activity | 1.006 | 0.708 | 0.70 |
| P35982 | Isocitrate dehydrogenase [NADP] [OS=Saccharomyces cerevisiae S288c] | 85357 | IDP3; YNL009W | metabolic process | cytoplasm; mitochondrial | catalytic activity; metal ion binding; nucleotide binding | 1.943 | 1.371 | 0.71 |
| P00445 | Superoxide dismutase [Cu-Zn] [OS=Saccharomyces cerevisiae S288c] | 85366 | SOD1; YIR104C | cell organization and biogenesis; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus | cytoplasm; cytosol; mitochondrial; nucleus | antioxidant activity; catalytic activity; metal ion binding; metal ion binding | 1.848 | 1.31 | 0.71 |
| P02381 | Ribosomal protein VAR1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85458 | VAR1; Q0140 | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | 0.52 | 0.369 | 0.71 |
| Q12320 | Hydroxyacylglutathione hydrolase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85420 | GLD4; YOR040W | metabolic process | mitochondrial; organelle lumen | catalytic activity; metal ion binding | 0.52 | 0.369 | 0.71 |
| P52833 | Probable alanine aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85077 | ALT1; YLR089C | metabolic process | mitochondrial; organelle lumen | catalytic activity | 0.951 | 0.682 | 0.72 |
| P32266 | Dymamin-like GTPase GMG1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85438 | GMG1; YOR211C | cell organization and biogenesis | membrane; mitochondrial | catalytic activity; nucleotide binding; protein binding | 0.389 | 0.28 | 0.72 |
| P04879 | Intron-encoded RNA maturase B4 [OS=Saccharomyces cerevisiae S288c] | 85458 | B4; Q0120 | metabolic process | membrane; mitochondrial | catalytic activity; RNA binding | 0.389 | 0.28 | 0.72 |
| P33293 | 35S ribosomal protein S35, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85307 | MRPS35; YOR165W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | 1.512 | 1.089 | 0.72 |
| Q03028 | Mitochondrial 2-oxo-carboxylate carrier 1 [OS=Saccharomyces cerevisiae S288c] | 85596 | ODC1; YPL134C | metabolic process; transport | membrane; mitochondrial | structural molecule activity; transporter activity | 4.275 | 3.084 | 0.72 |
| P81449 | ATP synthase subunit e, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85192 2 | TIM11, YDR332C | C-A | cell organization and biogenesis; metabolic process; transport | membrane, mitochondrion | catalytic activity; structural molecule activity; transporter activity | 9 | 6.499 | 0.72 |
| Q12031 | Mitochondrial 2-methylisocitrate lyase [Os=Saccharomyces cerevisiae S288c] | 85611 4 | IC12, YPR000C | metabolic process | mitochondrion; organelle lumen | catalytic activity | 3.833 | 2.793 | 0.73 |
| P33421 | Succinate dehydrogenase (ubiquinone) cytochrome b subunit, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85371 6 | SDH3, YKL143W | cell organization and biogenesis; metabolic process; transport | membrane, mitochondrion | catalytic activity; metal ion binding | 1.276 | 0.931 | 0.73 |
| Q08968 | UPT0061 protein FMP40 [Os=Saccharomyces cerevisiae S288c] | 85587 9 | FMP40; YPL222W |  | mitochondrion | protein binding | 2.162 | 1.588 | 0.73 |
| P32335 | Protein MSS51, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85090 0 | M551L; YLR203C | metabolic process; regulation of biological process | membrane, mitochondrion | protein binding; translation regulator activity | 1.154 | 0.848 | 0.73 |
| P54003 | Protein SUR7 [Os=Saccharomyces cerevisiae S288c] | 85495 3 | SUR7; YML052W | cell differentiation; transport | membrane, mitochondrion | 1.154 | 0.848 | 0.73 |
| P40098 | uncharacterized mitochondrial membrane protein FMP10 [Os=Saccharomyces cerevisiae S288c] | 85693 1 | FMP10; YER182W |  | membrane, mitochondrion | 4.456 | 3.281 | 0.74 |
| P42847 | 37S ribosomal protein S18, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85541 0 | MRPS18; YNL306W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 1.054 | 0.778 | 0.74 |
| P32904 | 54S ribosomal protein L6, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85655 2 | MRPL6; YLR147C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 1.054 | 0.778 | 0.74 |
| P00431 | cytochrome c peroxidase, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85394 0 | CCP1; YKR066C | metabolic process; response to stimulus | mitochondrion; organelle lumen | antioxidant activity; catalytic activity; metal ion binding; protein binding | 1.649 | 1.219 | 0.74 |
| P38888 | Mitochondrial GTP/GDP carrier protein 1 [Os=Saccharomyces cerevisiae S288c] | 85132 9 | GGC1; YDL198C | cell organization and biogenesis; cellular homeostasis; metabolic process; transport | membrane, mitochondrion | structural molecule activity; transporter activity | 3.16 | 2.34 | 0.74 |
| P23644 | Mitochondrial import receptor subunit TOM40 [Os=Saccharomyces cerevisiae S288c] | 85524 3 | TOM40; YMR203W | transport | cytosol, membrane, mitochondrion | protein binding; transporter activity | 0.896 | 0.668 | 0.75 |
| P02992 | elongation factor Tu, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85435 9 | TUF1; YOR187W | cell organization and biogenesis; metabolic process | mitochondrion | catalytic activity; nucleotide binding; RNA binding | 12.04 | 9 | 0.75 |
| P36521 | 54S ribosomal protein L11, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85132 5 | MRPL11; YDL202W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.833 | 0.624 | 0.75 |
| P31801 | Succinate dehydrogenase (ubiquinone) iron-sulfur subunit, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85068 5 | SDH2; YL041C | metabolic process; transport | membrane, mitochondrion | catalytic activity; metal ion binding | 18.88 | 14.01 | 0.75 |
| Q01852 | Mitochondrial import inner membrane translocase subunit TIM44 [Os=Saccharomyces cerevisiae S288c] | 85479 0 | TIM44; YIL022W | transport | membrane, mitochondrion | nucleotide binding; protein binding | 4.125 | 3.101 | 0.75 |
| P14908 | Mitochondrial transcription factor 1 [Os=Saccharomyces cerevisiae S288c] | 85526 8 | MTF1; YMR228W | metabolic process; regulation of biological process | mitochondrion; organelle lumen | catalytic activity; DNA binding; RNA binding | 0.778 | 0.585 | 0.75 |
| P38300 | Inner membrane mitochondrial regulator MRA1, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85248 3 | MBA1; YBR185C | cell organization and biogenesis; regulation of biological process | membrane, mitochondrion | 0.778 | 0.585 | 0.75 |
| P05457 | ATP synthase subunit 5, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85189 2 | ATP5; YDR298C | metabolic process; transport | membrane, mitochondrion | catalytic activity; transporter activity | 10.36 | 5 | 0.75 |
| P38072 | Protein SCO2, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85231 2 | SCO2; YBR024W | cell organization and biogenesis; cellular homeostasis; metabolic process; transport | membrane, mitochondrion | antioxidant activity; catalytic activity; metal ion binding | 0.73 | 0.551 | 0.75 |
| P33219 | Abhydrolase domain-containing protein IM032 [Os=Saccharomyces cerevisiae S288c] | 85291 9 | IM032; YGR031W | metabolic process; transport | mitochondrion | catalytic activity | 0.73 | 0.551 | 0.75 |
| P35266 | Cytochrome oxidase assembly protein SYH1 [Os=Saccharomyces cerevisiae S288c] | 85300 9 | SYH1; YGR112W | cell organization and biogenesis | membrane, mitochondrion | protein binding | 1.783 | 1.346 | 0.75 |
| P07257 | Cytochrome b-c1 complex subunit 2, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 85632 1 | QCR2; YPR191W | metabolic process; transport | membrane, mitochondrion | catalytic activity; metal ion binding; protein binding; transporter activity | 21.19 | 16.01 | 0.76 |
| Gene ID | Description | Cellular Location | Cellular Component | Protein Function | Gene Ontology Terms | P-value | q-value |
|---------|-------------|------------------|-------------------|-----------------|---------------------|---------|---------|
| Q05648  | MIOREX complex component 10 | [OS=Saccharomyces cerevisiae 5288c] | | membrane/mitochondrion | | 0.65 | 0.492 |
| P38088  | Glycine-6RNA ligase 1, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | cytoplasm/mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | | 0.616 |
| Q03976  | 37S ribosomal protein S24, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;ribosome | structural molecular activity | 0.585 | 0.445 |
| Q03327  | Mitochondrial fusion and transport protein Ugo1 | [OS=Saccharomyces cerevisiae 5288c] | | membrane;mitochondrion | protein binding;structural molecular activity | 0.557 | 0.425 |
| P36062  | NADH-cytochrome b5 reductase 2 | [OS=Saccharomyces cerevisiae 5288c] | | membrane;mitochondrion | catalytic activity;protein binding | 10.28 | 7.859 |
| P40185  | Protein mmf1, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;organelle lumen | | 6.943 | 5.31 |
| P00927  | Threonine dehydrogenase, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | cytoplasm;mitochondrion | catalytic activity | 2.257 | 1.728 |
| P36141  | Putative redox protein fmp46, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion | catalytic activity;protein binding | 4.337 | 3.329 |
| Q05931  | Heat shock protein SSQ1, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;organelle lumen | nucleotide binding;protein binding | 0.884 | 0.679 |
| P35998  | Succinyl-CoA ligase (ADP-forming) subunit alpha, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | cytox/mitochondrion | catalytic activity;nucleotide binding | 13.38 | 10.28 |
| P32331  | Carrier protein YMC1, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;vacuole | structural molecule activity;transporter activity | 1.254 | 0.968 |
| P00440  | C-1-tetrahydrofolate synthase, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | cytox/mitochondrion | catalytic activity;nucleotide binding | 0.9 | 0.696 |
| P25374  | Cysteine desulphurase, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;nucleus | catalytic activity;metal ion binding;protein binding | | 2.3 |
| P27697  | Atyypical kinase COOB, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;organelle lumen | catalytic activity;nucleotide binding | 0.365 | 0.283 |
| Q02127  | Protein ARG5,6, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | cytoplasm;mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | 0.235 | 0.182 |
| Q06143  | mitochondrial dicarboxylate transporter | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;transporter activity | structural molecule activity;transporter activity | | 0.931 |
| P16387  | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;organelle lumen | catalytic activity | 12.46 | 9.771 |
| P38797  | Protein phosphatase 2C homolog 7, mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion | catalytic activity;metal ion binding;protein binding | 0.874 | 0.688 |
| P36046  | Mitochondrial intermembrane space import and assembly protein 40 | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion | catalytic activity;protein binding;transporter activity | 2.914 | 2.3 |
| P00447  | Superoxide dismutase [Mn], mitochondrial | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;organelle lumen | antioxidant activity;catalytic activity;metal ion binding | 3.924 | 3.125 |
| P33969  | Sorting assembly machinery 50 kDa subunit | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;transporter activity | protein binding | | 0.61 |
| P08466  | mitochondrial nuclease | [OS=Saccharomyces cerevisiae 5288c] | | mitochondrion;nucleus | catalytic activity;metal ion binding | 1.336 | 1.069 |
| Q12466  | Tricarboxylic acid 1 | [OS=Saccharomyces cerevisiae 5288c] | | | | | |
| P07253  | Cytochrome B pre-mRNA-processing protein 6 | | | | | | |
| OS=Saccharomyces cerevisiae | mitochondrial | Heat shock protein 26 | 85236 4 | HSP26; YBR072 W | metabolic process; response to stimulus | cytoplasm; mitochondrion; nucleus | protein binding; RNA binding | 4.878 3.924 0.80 |
| OS=Saccharomyces cerevisiae | mitochondrial | N-terminal acetyltransferase 2 | 85305 0 | NAT2; YCR147 C | metabolic process | cytoplasm; mitochondrion | catalytic activity | 1.154 0.931 0.81 |
| OS=Saccharomyces cerevisiae | mitochondrial | ATP-dependent permease MDL1 | 85088 5 | MDL1; YLR188 W | transport | membrane; mitochondrion | catalytic activity; nucleotide binding; transporter activity | 0.438 0.354 0.81 |
| OS=Saccharomyces cerevisiae | mitochondrial | SUR7 family protein FMP45 | 85130 4 | FMP45; YDL220C | cell differentiation; cell organization and biogenesis | membrane; mitochondrion | 6.017 4.878 0.81 |
| OS=Saccharomyces cerevisiae | mitochondrial | plasma membrane ATPase 2 | 85607 1 | PMA2; YPL036 W | cellular homeostasis; metabolic process; transport | membrane; mitochondrion | catalytic activity; metal ion binding; nucleotide binding; transporter activity | 6.897 5.615 0.81 |
| OS=Saccharomyces cerevisiae | mitochondrial | 2-isopropylmalate synthase 2 | 85427 5 | LEU9; YOR108 W | metabolic process | mitochondrion | catalytic activity; protein binding | 1.707 1.39 0.81 |
| OS=Saccharomyces cerevisiae | mitochondrial | D-arabino-1,4-lactone oxidase | 85488 8 | ALO1; YML086 C | metabolic process; response to stimulus | membrane; mitochondrion | catalytic activity; nucleotide binding | 3.299 2.687 0.81 |
| OS=Saccharomyces cerevisiae | mitochondrial | Protein FMP52 | 85672 1 | FMP52; YER004 C | endoplasmic reticulum; membrane; mitochondrion | catalytic activity | 2.652 2.162 0.82 |
| OS=Saccharomyces cerevisiae | mitochondrial | mitochondrial carrier protein RIM2 | 85249 1 | RIM2; YBR192 W | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrion | structural molecule activity; transporter activity | 1.512 1.239 0.82 |
| OS=Saccharomyces cerevisiae | mitochondrial | heat shock protein 60 | 85096 3 | HSP60; YLR259C | cell organization and biogenesis; metabolic process; regulation of biological process; transport | cytoplasm; cytosol; membrane; mitochondrion; organelle lumen | catalytic activity; DNA binding; DNA binding; protein binding | 13.38 10.99 4.0 0.82 |
| OS=Saccharomyces cerevisiae | mitochondrial | DnuI homolog 1 | 85053 0 | MD11; YPL016C | cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus | mitochondrion; organelle lumen | enzyme regulator activity; metabolic process; nucleotide binding; protein binding | 2.765 2.275 0.82 |
| OS=Saccharomyces cerevisiae | mitochondrial | mitochondrial import inner membrane translocase subunit TIM54 | 85339 2 | TIM54; YIL054W | cell organization and biogenesis; transport | cytosol; membrane; mitochondrion | transporter activity | 0.655 0.54 0.82 |
| OS=Saccharomyces cerevisiae | mitochondrial | Mitochondrial inner membrane complex I-AAA protease supercomplex subunit YME1 | 85613 5 | YME1; YMR024 W | metabolic process; response to stimulus; transport | membrane; mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | 1.3 1.085 0.83 |
| OS=Saccharomyces cerevisiae | mitochondrial | Mitochondrial presequence protease | 85304 1 | CYM1; YDR430 C | metabolic process | mitochondrion | catalytic activity; metal ion binding | 0.812 0.682 0.84 |
| OS=Saccharomyces cerevisiae | mitochondrial | Citrate:oxoglutarate carrier protein | 85528 2 | YMR241; YMR241 W | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrion | DNA binding; structural molecule activity; transporter activity | 2.162 1.818 0.84 |
| OS=Saccharomyces cerevisiae | mitochondrial | Succinate:fumarate mitochondrial transporter | 85355 8 | SFC1; YIR095 W | metabolic process; transport | membrane; mitochondrion | structural molecule activity; transporter activity | 6.743 5.813 0.86 |
| OS=Saccharomyces cerevisiae | mitochondrial | Homaconitase, mitochondrial | 85182 0 | LYS4; YOR234 W | metabolic process | mitochondrion | catalytic activity; metal ion binding; protein binding | 0.638 0.551 0.86 |
| OS=Saccharomyces cerevisiae | mitochondrial | Pyruvate dehydrogenase complex protein X component, mitochondrial | 85310 7 | PKX1; YGR193 C | metabolic process | mitochondrion; organelle lumen | catalytic activity; structural molecule activity | 2.3 2.03 0.88 |
| OS=Saccharomyces cerevisiae | mitochondrial | ATP synthase subunit gamma, mitochondrial | 85232 7 | ATP3; YBR039 W | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 9 8.006 0.89 |
| OS=Saccharomyces cerevisiae | mitochondrial | protoporphyrinogen oxidase | 85673 3 | HEM14; YER014 C | metabolic process | membrane; mitochondrion | catalytic activity | 1.198 1.069 0.89 |
| OS=Saccharomyces cerevisiae | mitochondrial | acetyl-CoA synthase 1 | 85124 5 | ACS1; YAL054C | cell organization and biogenesis; metabolic process | cytoplasm; cytosol; endoplasmic reticulum; mitochondrion; nucleus | catalytic activity; nucleotide binding | 3.281 3.03 0.92 |
| OS=Saccharomyces cerevisiae | mitochondrial | Malate dehydrogenase, mitochondrial | 85377 7 | MDH1; YKL085 W | metabolic process | mitochondrion; organelle lumen | catalytic activity; protein binding; RNA binding | 28.93 6 28.93 6 1.00 |
| OS=Saccharomyces cerevisiae | mitochondrial | Heat shock protein SSC3 | 85668 2 | ECM10; YEL030 W | cell organization and biogenesis; metabolic process; transport | mitochondrion | nucleotide binding; protein binding | 1.976 1.976 1.00 |
| Gene Name | Description | Function | Activity | Source | References |
|-----------|-------------|----------|----------|--------|------------|
| Q03104    | Meloxic sister chromatid recombination protein 1 | CBP | Metabolic process | Endoplasmic reticulum | 1.929 | 1.929 | 0.00 |
| P04710    | ATP carrier protein 1 | CBP | Metabolic process, Transport | Cytochrome/mitochondrion | 10.28 | 8 | 10.28 | 8 | 1.00 |
| P05626    | ATP-synthase subunit 4 | CBP | Cell organization and biogenesis, Metabolic process, Transport | Membrane/mitochondrion | 3.084 | 3.084 | 1.00 |
| P10823    | Guanine nucleotide-binding protein alpha-2 subunit | CBP | Cell differentiation, Cell growth, Cell organization and biogenesis, Cellular homeostasis, Regulation of biological process, Response to stimulus | Cytochrome/mitochondrion | 1.346 | 1.346 | 1.00 |
| P42940    | Probable electron transfer flavoprotein subunit beta | CBP | Metabolic process, Transport | Mitochondrion, Organelle lumen | 3.87 | 3.87 | 1.00 |
| P0044     | Cytochrome c iso-1 | S288c | Metabolic process, Transport | Mitochondrion | 12.33 | 5 | 12.33 | 5 | 1.00 |
| P46681    | D-lactate dehydrogenase (cytochrome) 2 | CBP | Metabolic process | Mitochondrion, Organelle lumen | 1.264 | 1.264 | 1.00 |
| P19595    | 37S ribosomal protein YMR31, mitochondrial | CBP | Cell organization and biogenesis, Metabolic process | Mitochondrion, Ribosome | 15.68 | 1 | 15.68 | 1 | 1.00 |
| P00410    | Cytochrome c oxidase subunit 2 | CBP | Metabolic process, Transport | Membrane, Mitochondrion | 3.642 | 3.642 | 1.00 |
| P32332    | Mitochondrial oxaloacetate transport protein | CBP | Metabolic process, Transport | Membrane, Mitochondrion | 2.594 | 2.594 | 1.00 |
| Q04728    | Arginine biosynthesis bifunctional protein ArgJ | CBP | Metabolic process | Mitochondrion, Organelle lumen | 0.63 | 0.63 | 1.00 |
| Q08223    | Altered inheritance of mitochondria protein 39 | S288c | Metabolic process | Cytochrome/mitochondrion | 0.995 | 0.995 | 1.00 |
| Q12289    | mitochondrial catalase carrier | CBP | Metabolic process, Transport | Membrane, Mitochondrion | 0.931 | 0.931 | 1.00 |
| P32799    | Cytochrome c oxidase subunit 6A, mitochondrial | CBP | Cell organization and biogenesis, Metabolic process, Regulation of biological process, Transport | Membrane, Mitochondrion | 11.58 | 9 | 11.58 | 9 | 1.00 |
| P37298    | Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | CBP | Metabolic process, Transport | Membrane, Mitochondrion | 3.642 | 3.642 | 1.00 |
| P03798    | Altered inheritance of mitochondria protein 36 | S288c | Metabolic process | Membrane, Mitochondrion | 1.336 | 1.336 | 1.00 |
| P38523    | Gpy protein homolog, mitochondrial | CBP | Metabolic process, Regulation of biological process, Transport | Membrane, Mitochondrion, Organelle lumen | 0.833 | 0.833 | 1.00 |
| P10507    | mitochondrial-processing peptidase subunit y | CBP | Metabolic process, Transport | Mitochondrion, Organelle lumen | 0.778 | 0.778 | 1.00 |
| P12354    | S48 ribosomal protein L20, mitochondrial | CBP | Cell organization and biogenesis, Metabolic process | Mitochondrion, Ribosome | 2.162 | 2.162 | 1.00 |
| P25038    | Translation initiation factor IF-2, mitochondrial | CBP | Cell organization and biogenesis, Metabolic process | Mitochondrion, Nucleus | 0.299 | 0.299 | 1.00 |
| P41903    | Peroxialdehyde acetyl-CoA thioester hydrolase 1 | S288c | Metabolic process | Mitochondrion | 0.931 | 0.931 | 1.00 |
| Accession | Genes | Functions | Localization | Annotation | Activity | Score |
|-----------|-------|-----------|--------------|------------|----------|-------|
| P52572 | Thioredoxin-3, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85044 5 | TRX3, YCR083W | cytoplasm, mitochondrial | catalytic activity | 2.511 |
| Q36824 | Uncharacterized protein YOR209W-A (OS=Saccharomyces cerevisiae S288c) | 14664 80 | YOR020W A, YOR020W A | membrane, mitochondrial | 3.642 | 3.642 |
| P32611 | 5′4 ribosomal protein RML2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85666 0 | RML2, YEL050C | mitochondrion, ribosome | catalytic activity, RNA binding, structural molecule activity | 0.638 |
| Q06493 | LETM1 domain-containing protein YLH47, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85624 3 | YLH47, YPL125W | cell organization and biogenesis, metabolic process | membrane, mitochondrial | 0.61 |
| P11325 | Leucine- tRNA ligase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85109 8 | NAM2, YLR332C | cell organization and biogenesis, transport | cytoplasm, mitochondrial, organelle lumen | 0.208 |
| P53889 | uncharacterized mitochondrial hydrolase FMP41 (OS=Saccharomyces cerevisiae S288c) | 85555 3 | FMP41, YNL168C | metabolic process | mitochondrion | 0.501 |
| Q01519 | Cytochrome c oxidase subunit 6b (OS=Saccharomyces cerevisiae S288c) | 85072 7 | CXO12, YLR038C | cell organization and biogenesis, metabolic process | mitochondrion | 3.642 |
| P23369 | 5′4 ribosomal protein L25, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85296 7 | MRPL25, YMR076C | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | 1.31 |
| P21375 | Fumarate reductase 2 (OS=Saccharomyces cerevisiae S288c) | 85351 0 | GM1, YIR051W | metabolic process | endoplasmic reticulum, mitochondrial | 0.346 |
| P37299 | cytochrome b-1 complex subunit 10 (OS=Saccharomyces cerevisiae S288c) | 85639 0 | QCR10, YMR001W A | metabolic process, transport | membrane, mitochondrial | 5.31 |
| P36147 | Presequence translocated-associated motor subunit pam17, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85393 9 | PAM17, YKR065C | transport | membrane, mitochondrial | 1.371 |
| Q02608 | 3′5 ribosomal protein S16, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85609 4 | MRPS16, YPL013C | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | 0.931 |
| Q03246 | 3′5 ribosomal protein S17, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85522 6 | MRPS17, YMR188C | cell differentiation, cell organization and biogenesis, metabolic process | mitochondrion, ribosome | RNA binding, structural molecule activity | 0.931 |
| P32792 | UFD744 protein YSCB3 (OS=Saccharomyces cerevisiae S288c) | 85441 0 | YSCB3, YMR017W | metabolic process | membrane, mitochondrial | 0.639 |
| Q04172 | Sensitive to high expression protein 9, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85200 2 | SHE9, YDR393W | cell organization and biogenesis | membrane, mitochondrial | 0.269 |
| P40530 | Phenylalanine hydroxylase (OS=Saccharomyces cerevisiae S288c) | 85476 9 | PKP1, YIL042C | metabolic process | mitochondrion, organelle lumen | 0.551 |
| Q6Q560 | Protein isd11 (OS=Saccharomyces cerevisiae S288c) | 85677 4 | ISD11, YER048W A | cell organization and biogenesis, metabolic process | mitochondrion, organelle lumen | 2.594 |
| P28737 | Protein MSP1 (OS=Saccharomyces cerevisiae S288c) | 85291 5 | MSP1, YGR028W | cell organization and biogenesis, metabolic process, regulation of biological process, response to stimulus, transport | membrane, mitochondrial, nucleus | catalytic activity, protein binding | 0.585 |
| Q02883 | N-acetyl- phosphatr diethanolamine-hydrolyzing phospholipase D, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85600 1 | FMP35, YPL103C | metabolic process | membrane, mitochondrial | 0.304 |
| P21306 | ATP synthase subunit epsilon, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85885 7 | ATP15, YPL271W | metabolic process, transport | membrane, mitochondrial | 2.162 |
| Q03799 | 3′5 ribosomal protein S8, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85519 0 | MRPS8, YMR158W | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 0.701 |
| P32785 | Methionyl-tRNA formyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85227 0 | FMT1, YBL013W | metabolic process | mitochondrion | catalytic activity | 0.179 |
| P46998 | mitochondrial membrane protein FMP33 (OS=Saccharomyces cerevisiae S288c) | 85327 9 | FMP33, YIL161W | membrane, mitochondrial | catalytic activity | 0.778 |

70
P53157
Thiosulfate sulfurtransferase RD11, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85445 9
RDI1; YOR285 W
endoplasmic reticulum;membrane;mitochondrion

catalytic activity
0.668 0.668 1.00

P3B409
Mitochondrial distribution and morphology protein 10
[OS=Saccharomyces cerevisiae S288c]
85122 3
MDM10; YAL010C
cell organization and biogenesis;transport
membrane;mitochondrion

protein binding
0.16 0.16 1.00

P36523
54S ribosomal protein L15, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85102 2
MRPL15; YLR312 W-A

cell organization and biogenesis;metabolic process
mitochondrion;ribosome

catalytic activity;RNA binding;structural molecule activity
0.334 0.334 1.00

POCX44
6OS ribosomal protein L1-B
[OS=Saccharomyces cerevisiae S288c]
85274 2; 85588 1
RPL1B; RPL1A; YGL135 W; YPL120 W
metabolic process
cytoplasm;ribosome

RNA binding;structural molecule activity
0.425 0.425 1.00

P20084
54S ribosomal protein L33, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85533 0
MRPL33; YMR286 W

cell organization and biogenesis;metabolic process
mitochondrion;ribosome

structural molecule activity
2.162 2.162 1.00

P01098
ATPase-stabilizing factor 9 kDa, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85142 6
STF1; YOL130 W-A
metabolic process;regulation of biological process
mitochondrion

catalytic activity;enzyme regulator activity;protein binding
2.162 2.162 1.00

Q8645
folyolpolyglutamate synthase
[OS=Saccharomyces cerevisiae S288c]
85441 5
MET7; YOR241 W-A
metabolic process
cytosol;endoplasmic reticulum;membrane;mitochondrion;organellar lumen

catalytic activity;nucleotide binding
0.233 0.233 1.00

P43222
Peptidase-HMA hydrophate 2
[OS=Saccharomyces cerevisiae S288c]
85222 3
PTH2; YBL057C
regulation of biological process
cytoplasm;cytosol;membrane;mitochondrion

catalytic activity;protein binding
0.425 0.425 1.00

P45851
proteindown HYR1
[OS=Saccharomyces cerevisiae S288c]
85485 5
HYR1; YIR037 W
metabolic process;response to stimulus
cytosol;cytosol;mitochondrion;organellar lumen

antioxidant activity;catalytic activity
0.995 0.995 1.00

P53875
54S ribosomal protein L19, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85553 6
MRPL19; YNL185C

cell organization and biogenesis;metabolic process
mitochondrion;ribosome

RNA binding;structural molecule activity
0.874 0.874 1.00

P53163
54S ribosomal protein L12, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85281 1
MRPL12; YNL068 W

cell organization and biogenesis;metabolic process
mitochondrion;ribosome

RNA binding;structural molecule activity
0.52 0.52 1.00

P42844
Mitochondrial protein import protein ZIM17
[OS=Saccharomyces cerevisiae S288c]
85440 7
ZIM17; YNL310C

cell organization and biogenesis;metabolic process
mitochondrion;organellar lumen

metabolic process
0.585 0.585 1.00

Q06510
Lysophosphatidylcholine
[OS=Saccharomyces cerevisiae S288c]
85626 2
TAZ1; YPR140 W

cell organization and biogenesis;metabolic process
mitochondrion

catalytic activity
0.194 0.194 1.00

P38860
ATPase MTG2, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85607 3
MTG2; YHR168 W
metabolic process;transport
membrane;mitochondrion

catalytic activity;metal ion binding
0.07 0.07 1.00

Q06405
ATP synthase subunit f, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85198 3
ATP17; YDR377 W
metabolic process;transport
membrane;mitochondrion

catalytic activity;transporter activity
2.981 2.981 1.00

Q12204
Probable phospholipase
[OS=Saccharomyces cerevisiae S288c]
85418 7
YOR022 C; YOR022 C
metabolic process
mitochondrion

catalytic activity;metal ion binding
0.11 0.11 1.00

P32606
putative mitochondrial translation system component PET127
[OS=Saccharomyces cerevisiae S288c]
85418 2
PET127; YOR017 W

cell organization and biogenesis;metabolic process
mitochondrion

0.099 0.099 1.00

Q05779
Ubiquinone biosynthesis protein COQ9, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
85089 8
COQ9; YLR201C
metabolic process
membrane;mitochondrion

0.359 0.359 1.00

Q36485
uncharacterized mitochondrial outer membrane protein
[OS=Saccharomyces cerevisiae S288c]
85198 9
YDR381 C-A; YDR381 C-A

membrane;mitochondrion

0.389 0.389 1.00

Q04487
Mitochondrial inner membrane protein SHM3
[OS=Saccharomyces cerevisiae S288c]
85514 5
SHM3; YMR118 C
metabolic process
membrane;mitochondrion

catalytic activity;metal ion binding
0.425 0.425 1.00

Q07821
Iron-sulfur assembly protein 1
[OS=Saccharomyces cerevisiae S288c]
85063 2
ISA1; YLL027 W

cell organization and biogenesis;metabolic process
mitochondrion;organellar lumen

metal ion binding;structural molecule activity
0.136 0.136 1.00

P53157
Mitochondrial pyruvate carrier 1
[OS=Saccharomyces cerevisiae S288c]
85280 0
FMP37; MIP1; YGL080 W
transport
membrane;mitochondrion

transporter activity
1.154 1.154 1.00
| Q12487 | 54S ribosomal protein L23, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85432 1 | MRPL23; YOR150 W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome; vacuole | RNA binding; structural molecule activity | 0.52 | 0.52 | 1.00 |
| Q2V2P9 | Uncharacterized protein YDR119W-A [OS=Saccharomyces cerevisiae S288c] | | 37999 70 | COX26; YDR119 W-A | | membrane; mitochondrion | | 1.154 | 1.154 | 1.00 |
| P40458 | Autophagy-related protein 32 [OS=Saccharomyces cerevisiae S288c] | | 85466 0 | ATG32; YIL146C | metabolic process | membrane; mitochondrion; vacuole | protein binding | 0.202 | 0.202 | 1.00 |
| P53733 | 37S ribosomal protein S19, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85577 3 | LSM19; YMR037 C | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | RNA binding; structural molecule activity | 0.931 | 0.931 | 1.00 |
| P32939 | GTP-binding protein ypt7 [OS=Saccharomyces cerevisiae S288c] | | 85501 2 | YPT7; YLM001 W | cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport | cytosol; endosome; membrane; mitochondrion; vacuole | catalytic activity; nucleotide binding; protein binding | 0.166 | 0.166 | 1.00 |
| P09950 | 5-aminovalerate synthase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85181 8 | HEM1; YDR232 W | metabolic process | mitochondrial; organelle lumen | catalytic activity | 0.086 | 0.086 | 1.00 |
| P48526 | Isocitrate dehydrogenase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85606 7 | ISD1; YPL040C | cell organization and biogenesis; metabolic process; regulation of biological process | cytoplasm; cytosol; mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 0.04 | 0.04 | 1.00 |
| P53193 | J-type co-chaperone JAC1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85286 6 | JAC1; YGL020C | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrion; organelle lumen | protein binding | 0.212 | 0.212 | 1.00 |
| P32378 | 4-Hydroxybenzoate polyphenoltransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85377 8 | COA2; YMR041 C | metabolic process; transport | membrane; mitochondrion | catalytic activity | 0.293 | 0.293 | 1.00 |
| P39515 | mitochondrial import inner membrane translocase subunit Tim17 [OS=Saccharomyces cerevisiae S288c] | | 85329 8 | Tim17; YIL143W | cell organization and biogenesis; transport | membrane; mitochondrion | protein binding; transporter activity | 0.778 | 0.778 | 1.00 |
| P36064 | COX assembly mitochondrial protein [OS=Saccharomyces cerevisiae S288c] | | 85372 1 | CMC1; YKL137 W | cell organization and biogenesis | membrane; mitochondrion | metal ion binding | 0.389 | 0.389 | 1.00 |
| P54857 | Lipase 2 [OS=Saccharomyces cerevisiae S288c] | | 85162 8 | TGL2; YOR058 C | metabolic process; transport | mitochondrion | catalytic activity | 0.233 | 0.233 | 1.00 |
| Q06005 | Octanoyltransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85094 0 | LIP2; YLR239C | metabolic process | cytoplasm; mitochondrion | catalytic activity | 0.116 | 0.116 | 1.00 |
| P38812 | Phosphatidylinositol phosphatase PEP4, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85600 0 | GEP4; YMR100 C | metabolic process | membrane; mitochondrion; organelle lumen | catalytic activity | 0.179 | 0.179 | 1.00 |
| Q38446 | Cytochrome c oxidase assembly factor 6 [OS=Saccharomyces cerevisiae S288c] | | 85328 7 | COA6; YMR244 C-A; YMR244 C-A | cell organization and biogenesis; cellular homeostasis; metabolic process; transport | cytoplasm; membrane; mitochondrion; nucleus | catalytic activity; metal ion binding; protein binding; transporter activity | 0.931 | 0.931 | 1.00 |
| P03876 | putative COX1/COX3 interon 2 protein [OS=Saccharomyces cerevisiae S288c] | | 85459 4 | AI2; Q0055 | metabolic process; transport | mitochondrion | catalytic activity; metal ion binding; transporter activity | 0.086 | 0.086 | 1.00 |
| P40491 | ATP synthase assembly factor fam1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85470 9 | FMC1; YIL098C | cell communication; cell organization and biogenesis; metabolic process; response to stimulus | mitochondrion; organelle lumen | protein binding | 0.468 | 0.468 | 1.00 |
| P10174 | Cytochrome c oxidase subunit 7 [OS=Saccharomyces cerevisiae S288c] | | 85329 8 | COX7; YMR256 C | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 1.154 | 1.154 | 1.00 |
| P22135 | Protein ATP12, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85325 9 | ATP12; YIL180C | cell organization and biogenesis | mitochondrion | protein binding | 0.101 | 0.101 | 1.00 |
| P53318 | Ubiquitine biosynthesis monooxygenase GOD6, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85317 0 | COQ6; YGR255 C | metabolic process | membrane; mitochondrion | catalytic activity; nucleotide binding | 0.077 | 0.077 | 1.00 |
| P32463 | Acyl carrier protein, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85364 2 | ACP2; YKL192C | metabolic process; transport | mitochondrion | | 0.259 | 0.259 | 1.00 |
| P04039 | Cytochrome c oxidase polypeptide VIII, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85111 1 | COX8; YLR395C | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 0.778 | 0.778 | 1.00 |
| P35212 | Probable transcriptional regulatory protein HAH1 | [OS=Saccharomyces cerevisiae S288c] | 85290 4 | YGR021 W; YGR021 W | | mitochondrion | | 0.166 | 0.166 | 1.00 |
COX assembly mitochondrial protein 2 (Saccharomyces cerevisiae S288c)

ATP synthase subunit K, mitochondrial (Saccharomyces cerevisiae S288c)

Cytochrome c oxidase assembly protein COX14 (Saccharomyces cerevisiae S288c)

Mitochondrial FAD-linked sulfhydryl oxidase env1 (Saccharomyces cerevisiae S288c)

Mitochondrial carrier protein MTM1 (Saccharomyces cerevisiae S288c)

Succinyl-CoA ligase (ADP-forming) subunit beta, mitochondrial (Saccharomyces cerevisiae S288c)

Cytochrome c oxidase subunit 1 mitochondrial (Saccharomyces cerevisiae S288c)

Mitochondrial peculiar membrane protein 1 (Saccharomyces cerevisiae S288c)

Cytochrome c oxidase subunit 6 mitochondrial (Saccharomyces cerevisiae S288c)

Uncharacterized ABC transporter ATP-binding protein YDR061W (Saccharomyces cerevisiae S288c)

Mitochondrial inner membrane protein OXA1 (Saccharomyces cerevisiae S288c)

Mitochondrial metal transporter 2 (Saccharomyces cerevisiae S288c)

Phosphatidate cytidylyltransferase, mitochondrial (Saccharomyces cerevisiae S288c)

Lon protease homolog, mitochondrial (Saccharomyces cerevisiae S288c)

Mitochondrial import inner membrane translocase subunit TIM21 (Saccharomyces cerevisiae S288c)

Mitochondrial Rubi GTPase 1 (Saccharomyces cerevisiae S288c)

MICOS subunit MIC26 (Saccharomyces cerevisiae S288c)

Elongation factor G, mitochondrial (Saccharomyces cerevisiae S288c)

protein ZEO1 (Saccharomyces cerevisiae S288c)

Serine-RNA ligase, mitochondrial (Saccharomyces cerevisiae S288c)

Q3E7A3

CMC2; YBL059C

COX14; YML129C

ERV1; YGR029W

MTM1; YGR257C

LSC2; YGR244C

COR1; YBL045C

RIP1; YEL024W

MMP1; YLR061C

OXA1; YER154W

TIM21; YOR046W

PIM1; YBL022C

TIM31; YOR033C

GEM1; YAL048C

MOS2; MIC26; YGR235C

MIF1; YLR069C

ZEO1; YOL109W

DIA4; YHR011W

GAPDH; YMR051C

ATP synthase subunit K, mitochondrial ([SACCHAROMYCES CEREVISiae S288C]

Mitochondrial FAD-linked sulfhydryl oxidase env1 ([SACCHAROMYCES CEREVISiae S288C]

Mitochondrial carrier protein MTM1 ([SACCHAROMYCES CEREVISiae S288C]

Succinyl-CoA ligase (ADP-forming) subunit beta, mitochondrial ([SACCHAROMYCES CEREVISiae S288C]

Cytochrome c oxidase subunit 1 mitochondrial ([SACCHAROMYCES CEREVISiae S288C]

Mitochondrial peculiar membrane protein 1 ([SACCHAROMYCES CEREVISiae S288C]

Cytochrome c oxidase subunit 6 mitochondrial ([SACCHAROMYCES CEREVISiae S288C]

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Elongation factor G, mitochondrial

protein ZEO1

Serine-RNA ligase, mitochondrial
ATP synthase subunit $i$, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
| Q01460 | ATP synthase subunit $j$, mitochondrial |
|--------|--------------------------------------|
| 85480  | ATP18; YML081 C                        |
|        | cell organization and biogenesis; metabolic process |
|        | mitochondrion                           |
|         | catalytic activity; transporter activity |
|         | 4.623 9 1.95                           |
| Query ID | Description | Oryza sativa line 1 [OS=Saccharomyces cerevisiae S288c] | E-value | Bit score | p-value |
|----------|-------------|-------------------------------------------------------|----------|-----------|---------|
| P34231  | Uncharacterized protein YKL187C | 85364 8 | FAT3; YKL187C | cell organization and biogenesis;transport | membrane;mitochondrion | 0.093 0.134 2.09 |
| P50110  | Sorting assembly machinery 37 kDa subunit | 85508 2 | SAM37; YMR660 C | cell organization and biogenesis;transport | membrane;mitochondrion | 0.116 0.245 2.11 |
| P38816  | Threonin reductase | 85600 6 | TRR2; YHR106 W | cellular homeostasis;metabolic process;regulation of biological process;response to stimulus | cytoplasm;mitochondrion | 0.136 0.292 2.15 |
| P43122  | DNA adenosine thymine carbamoyltransferase | 85145 4 | QR77; YOL104C | cell organization and biogenesis;metabolic process | mitochrondrion | 0.212 0.468 2.21 |
| P49334  | Mitochondrial import receptor subunit tom22 | 85559 2 | TOM22; YNL131 W | cell organization and biogenesis;transport | membrane;mitochondrion | 0.292 0.668 2.29 |
| Q12032  | Altered inheritance of mitochondria protein 41 | 85439 0 | INH1; YDL181 W | metabolic process;regulation of biological process | mitochondrial | 1.154 2.831 2.45 |
| P01097  | ATPase inhibitor, mitochondrial | 85134 7 | MRP124; YMR193 W | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | 0.468 1.156 2.47 |
| P36525  | 54S ribosomal protein L24, mitochondrial | 85523 1 | MRP124; YMR193 W | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | 1.154 2.981 2.58 |
| Q03713  | Respiratory supercomplex factor 1, mitochondrial | 85497 8 | RCF1; YML036 W | cell organization and biogenesis | membrane;mitochondrion | 1.512 4.012 2.65 |
| P13433  | DNA-directed RNA polymerase, mitochondrial | 85050 7 | RPO41; YFL036 W | cell organization and biogenesis;metabolic process | cytoplasm;mitochondrion;organelle lumen | 0.027 0.085 3.15 |
| P35996  | 54S ribosomal protein L38, mitochondrial | 85368 4 | MRP138; YKL170 W | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | 1.154 3.642 3.16 |
| P21771  | 37S ribosomal protein S28, mitochondrial | 85193 7 | MRPS28; YOR337 W | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | 0.624 1.976 3.17 |
| P00045  | Cytochrome c iso-2 | 85667 2 | CYC7; YEL033C | metabolic process;transport | mitochondrial | 1.512 6.943 4.59 |
| P07255  | Cytochrome c oxidase subunit 7A | 85149 2 | C099; YOL067C | metabolic process;transport | membrane;mitochondrion | 1.154 20.54 17.8 0 |
Supplemental Table S4. The relative concentrations of proteins in mitochondria purified from WT or ups1Δ cells cultured without LCA. Mitochondria were purified from WT or ups1Δ cells recovered on day 2 of cell culturing without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI ups1 | Ratio ups1 WT |
|-----------|-------------|----------------|---------|-------------------|-------------------|-------------------|----------|-------------|----------------|
| P10834    | protein PET54 | 853137 | PET54 | metabolic process; regulation of biological process | membrane; mitochondrion; organelle lumen | nucleotide binding; RNA binding; translation regulator activity | 0.874 | 0.11 | 0.13 |
| P12687    | 54S ribosomal protein L2, mitochondrial (S. cerevisiae) | 855727 | MRPS7; YNL005C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | catalytic activity; RNA binding; structural molecule activity | 1.848 | 0.233 | 0.13 |
| Q06892    | NADH kinase P066, mitochondrial (S. cerevisiae) | 855913 | P065; YPL188W | metabolic process; response to stimulus | mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 2.511 | 0.369 | 0.15 |
| P42847    | 37S ribosomal protein S18, mitochondrial (S. cerevisiae) | 855410 | MRPS18; YNL306W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 1.054 | 0.155 | 0.15 |
| P46998    | mitochondrial membrane protein FMP33 (S. cerevisiae) | 853279 | FMP33; YL1611W | | membrane; mitochondrion | | 2.162 | 0.334 | 0.15 |
| P21771    | 37S ribosomal protein S28, mitochondrial (S. cerevisiae) | 851937 | MRPS28; YDR337W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 0.833 | 0.129 | 0.15 |
| P43594    | MICOS complex subunit MIC19 (S. cerevisiae) | 850663 | AIM13; YCR028C | cell organization and biogenesis | cytoplasm; membrane; mitochondrion | | 3.329 | 0.52 | 0.16 |
| P40646    | Mitochondrial peculiar membrane protein 1 (S. cerevisiae) | 853379 | MFPM1; YL0966C | | membrane; mitochondrion | | 3.642 | 0.585 | 0.16 |
| P35170    | [Pyruvate dehydrogenase (acyl-transferring)] kinase 2, mitochondrial (S. cerevisiae) | 852821 | PKP2; YGL059W | metabolic process; regulation of biological process | mitochondrion; organelle lumen | catalytic activity; nucleotide binding; protein binding | 1.296 | 0.179 | 0.16 |
| P47150    | 37S ribosomal protein S57, mitochondrial (S. cerevisiae) | 853578 | RSM7; YJR113C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 0.616 | 0.101 | 0.16 |
| Q03557    | Glutamyl-RNA(Gln) amidotransferase subunit A, mitochondrial (S. cerevisiae) | 855338 | HER2; YMR293C | cell organization and biogenesis; metabolic process | mitochondrion | catalytic activity; nucleotide binding | 0.468 | 0.08 | 0.17 |
| P32445    | Single-stranded DNA-binding protein RIM1, mitochondrial (S. cerevisiae) | 850395 | RIM1; YCR028C-A | cell organization and biogenesis; metabolic process | mitochondrion | DNA binding | 6.743 | 1.154 | 0.17 |
| P02381    | Ribosomal protein VAR1, mitochondrial (S. cerevisiae) | 854856 | VAR1; Q0140 | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 1.31 | 0.233 | 0.18 |
| O21217    | Protein ARG5.6, mitochondrial (S. cerevisiae) | 856800 | ARG5.6; YER089W | metabolic process; regulation of biological process | cytoplasm; mitochondrion; organelle lumen | catalytic activity; nucleotide binding; protein binding | 0.458 | 0.087 | 0.19 |
| P39525    | 3-oxoacyl-(acyl-carrier-protein) synthase homolog (S. cerevisiae) | 856790 | CEM1; YER061C | metabolic process | mitochondrion | catalytic activity | 1.848 | 0.369 | 0.20 |
| Q12283    | Malonyl-CoA:acyl carrier protein transacylase, mitochondrial (S. cerevisiae) | 854396 | MCT1; YOR221C | metabolic process | mitochondrion | catalytic activity | 0.668 | 0.136 | 0.20 |
| P25372    | Thioredoxin-3, mitochondrial (S. cerevisiae) | 850444 | TRX3; YCR083 | cellular homeostasis; metabolic | cytoplasm; mitochondrion | catalytic activity | 2.511 | 0.52 | 0.21 |

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| Accession | Name | Function | Location | PDB ID | MI | MW | Freq | p-value |
|-----------|------|----------|----------|---------|----|----|------|---------|
| P33416    | Heat shock protein 78, mitochondrial (S. cerevisiae 288c) | 851845 | HSP78; YDR258C | cell organization and biogenesis, metabolic process | mitochondrion; organelle lumen | catalytic activity, nucleotide binding, protein binding | 12.525 | 2.609 | 0.21 |
| P38122    | 3-methyl-2-oxobutanoate hydroxymethyltransferase (S. cerevisiae 288c) | 852474 | ECM31; YBR176W | metabolic process | mitochondrion | catalytic activity | 0.585 | 0.122 | 0.21 |
| P32331    | Carrier protein YMCI, mitochondrial (S. cerevisiae 288c) | 856171 | YMCl; YPR058W | metabolic processes, transport | membrane; mitochondrion; vacuole | structural molecular activity, transport activity | 2.384 | 0.501 | 0.21 |
| P00447    | Superoxide dismutase (Mn) chain, mitochondrial (S. cerevisiae 288c) | 856399 | SOD2; YHR080C | metabolic process, response to stimulus | mitochondrion; organelle lumen | antioxidant activity, catalytic activity, metal ion binding | 9 | 1.894 | 0.21 |
| P49017    | 2-methoxy-6-polyrpyl-1,4-benzoquinol methylase, mitochondrial (S. cerevisiae 288c) | 854930 | COG5; YML110C | metabolic process | membrane; mitochondrion; organelle lumen | catalytic activity | 0.551 | 0.116 | 0.21 |
| P36528    | 54S Ribosomal protein L17, mitochondrial (S. cerevisiae 288c) | 855469 | MRPL17; YNL252C | cell organization and biogenesis, metabolic process | mitochondrion; ribosome | structural molecular activity | 0.52 | 0.11 | 0.21 |
| P32135    | Protein ATP12, mitochondrial (S. cerevisiae 288c) | 853529 | ATP12; YL180C | cell organization and biogenesis | mitochondrion | protein binding | 0.468 | 0.101 | 0.22 |
| P53305    | Mitochondrial 37S ribosomal protein S27 (S. cerevisiae 288c) | 853129 | RSM27; YGR215W | cell organization and biogenesis, metabolic process | mitochondrion; ribosome | structural molecular activity | 2.162 | 0.468 | 0.22 |
| P11325    | Leucine-tRNA ligase, mitochondrial (S. cerevisiae 288c) | 851098 | NAM2; YLR382C | cell organization and biogenesis, metabolic process | cytosol; mitochondrion; organelle lumen | catalytic activity, nucleotide binding, RNA binding | 0.353 | 0.078 | 0.22 |
| P18496    | Mitochondrial ATPase complex subunit ATP10 (S. cerevisiae 288c) | 851109 | ATP10; YLR393W | cell organization and biogenesis | cytoplasm; membrane; mitochondrion | protein binding | 1.818 | 0.413 | 0.23 |
| P25375    | Saccharolysin (S. cerevisiae 288c) | 850301 | PRD1; YCL057W | metabolic process | cytoplasm; Golgi; mitochondrion; vacuole | catalytic activity, metal ion binding | 0.216 | 0.05 | 0.23 |
| P15955    | 37S ribosomal protein YMR31, mitochondrial (S. cerevisiae 288c) | 850610 | YMR31; YPR049W | cell organization and biogenesis, metabolic process | mitochondrion; ribosome | catalytic activity, protein binding, structural molecular activity | 15.681 | 3.642 | 0.23 |
| P32898    | Mitochondrial prescognition protein I (S. cerevisiae 288c) | 852041 | CYM1; YDR430C | metabolic process | mitochondrion | catalytic activity, metal ion binding | 2.162 | 0.505 | 0.23 |
| P25605    | Acetolactate synthase small subunit, mitochondrial (S. cerevisiae 288c) | 850348 | ILV6; YCL009C | metabolic process, regulation of biological process | mitochondrion | catalytic activity, enzyme, regulator activity | 11.743 | 2.793 | 0.24 |
| P31450    | ATP synthase subunit α, mitochondrial (S. cerevisiae 288c) | 854893 | ATP1α; YML898C-A | cell organization and biogenesis, metabolic process, transport | membrane; mitochondrion | catalytic activity, transport activity | 9 | 2.162 | 0.24 |
| Q53430    | 37S ribosomal protein RSM20B, mitochondrial (S. cerevisiae 288c) | 852105 | RSM20B; YDR494W | cell organization and biogenesis, metabolic process | mitochondrion; ribosome | structural molecular activity | 2.675 | 0.85 | 0.24 |
| Q12305    | Thiosulfate sulfotransferase RD1, mitochondrial (S. cerevisiae 288c) | 854459 | RD11; YDR285W | endoplasmic reticulum; membrane; mitochondrion | catalytic activity | 1.154 | 0.292 | 0.25 |
| P19516    | Cytochrome c oxidase assembly protein COX11, mitochondrial (S. cerevisiae 288c) | 855971 | COX11; YPL332W | cell organization and biogenesis, metabolic process | membrane; mitochondrion; ribosome | metal ion binding | 1.069 | 0.274 | 0.26 |
| P35996    | 54S ribosomal protein L38, mitochondrial (S. cerevisiae 288c) | 853684 | MRPL38; YKL170D | cell organization and biogenesis, metabolic process | mitochondrion; ribosome | RNA binding, structural molecular activity | 2.594 | 0.668 | 0.26 |
| P36516    | 54S ribosomal protein L3, mitochondrial (S. cerevisiae 288c) | 850939 | MRPL3; YMR024W | cell organization and biogenesis, metabolic process, response to stimulus | mitochondrion; nucleus; ribosome | catalytic activity, RNA binding, structural molecular activity | 1.043 | 0.269 | 0.26 |
| P37293    | N-terminal acetyltransferase 2 (S. cerevisiae 288c) | 853050 | NAT2; YGR147C | metabolic process | cytoplasm; mitochondrion | catalytic activity | 0.931 | 0.245 | 0.26 |
| P38523    | Grp94 protein homolog, mitochondrial (S. cerevisiae 288c) | 854407 | MGEL1; YOR232W | metabolic process, regulation of biological process, transport | membrane; mitochondrial; organelle lumen | enzyme regulator activity, nucleotide binding, protein binding | 2.36 | 0.624 | 0.26 |
P36534 54S ribosomal protein L40, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
855930 MRPL40; YPL173 W  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
protein binding;structural molecule activity 1.512 0.413 0.27

P53881 54S ribosomal protein L22, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
85544 MRP22; YNL177C  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
RNA binding;structural molecule activity 1.994 0.551 0.28

P32799 Cytochrome c oxidase subunit 6A, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
852684 COX13; YGL191 W  
cell organization and biogenesis;metabolic process  
regulation of biological process;transport  
membrane;mitochondrion  
catalytic activity;enzyme regulator activity;transport activity 18.953 5.31 0.28

Q06630 Mitochondrial homologous recombination protein 1  
(05=Saccharomyces cerevisiae 528bc)  
851890 MHR1; YDR296 W  
cell organization and biogenesis;metabolic process  
regulation of biological process;response to stimulus  
mitochondrion;nucleus  
catalytic activity;DNA binding;structural molecule activity 0.585 0.166 0.28

P32897 Mitochondrial import inner membrane translocase subunit tim23  
(05=Saccharomyces cerevisiae 528bc)  
855751 TIM23; YMR017 W  
transport  
membrane;mitochondrion  
protein binding;transport activity 5.31 1.512 0.28

P36519 54S ribosomal protein L17, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
851823 MRPL7; YDR237 W  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
RNA binding;structural molecule activity 0.468 0.136 0.29

P40165 NAD(P)H-decarboxylase epimerase  
(05=Saccharomyces cerevisiae 528bc)  
855521 NNR1; YNL200C  
molecular process  
cytoplasm;mitochondrion  
catalytic activity;metal ion binding;nucleotide binding 1.61 0.468 0.29

Q12032 Altered inheritance of mitochondria protein 41,  
mitochondrial  (05=Saccharomyces cerevisiae 528bc)  
854390 AIM41; YDR215C  
mitochondrion  
catalytic activity 1.61 0.468 0.29

P27697 Asparyl kinase COQ8, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
852758 COQ8; YGL159 W  
molecular process  
membrane;mitochondrion;organellar lumen  
catalytic activity;nucleotide binding 0.453 0.133 0.29

P36139 protein PET10  
(05=Saccharomyces cerevisiae 528bc)  
853920 PET10; YKR046C  
molecular process  
membrane  
0.413 0.122 0.30

Q12166 ATP synthase subunit delta, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
851560 ATP7A; YDL004 W  
molecular process;transport  
membrane;mitochondrion  
catalytic activity;transport activity 4.823 1.371 0.30

Q07534 Solute carrier family 25 member 38 homolog  
(05=Saccharomyces cerevisiae 528bc)  
851439 HEM25; YDL119C  
molecular process;transport  
membrane;mitochondrion  
structural molecule activity;transport activity 0.389 0.116 0.30

P40035 Mitochondrial phosphate carrier protein 2  
(05=Saccharomyces cerevisiae 528bc)  
856779 PEC2; YER053C  
molecular process  
membrane;mitochondrion  
structural molecule activity;transport activity 2.793 0.833 0.30

P25626 54S ribosomal protein IMG1, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
850413 IMG1; YCR046C  
molecular process  
membrane;mitochondrion;organellar lumen  
catalytic activity;structural molecule activity 1.424 0.425 0.30

Q03201 37S ribosomal protein S10, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
851611 RSM10; YDR841 W  
cellular process  
mitochondrion;ribosome  
catalytic activity 1.424 0.425 0.30

Q03799 37S ribosomal protein S8, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
851190 MRPS8; YMR158 W  
cellular process  
mitochondrion;ribosome  
catalytic activity 1.424 0.425 0.30

P47039 Probable kynurenine--oxoglutarate transaminase  
(05=Saccharomyces cerevisiae 528bc)  
853386 BNA3; YIL060W  
molecular process;regulation of biological process  
cytoplasm;mitochondrion  
catalytic activity 0.334 0.101 0.30

P23254 54S ribosomal protein L20, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
853960 MRPL20; YKR008C  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
catalytic activity;structural molecule activity 1.276 0.389 0.30

P32266 Dynamin-like GTPase Mgm1, mitochondrial  
(05=Saccharomyces cerevisiae 528bc)  
854386 MGM1; YDR211C  
cell organization and biogenesis  
membrane;mitochondrion  
catalytic activity;nucleotide binding;protein binding 0.28 0.086 0.31

P40051 Intermediate cleaving  
peptidease 55  
(05=Saccharomyces cerevisiae 528bc)  
856811 IPC55; YER078C  
molecular process;regulation of biological process  
membrane;mitochondrion;nucleus  
catalytic activity;metal ion binding 0.25 0.077 0.31

P15049 mitochondrial transcription  
factor 2  
(05=Saccharomyces cerevisiae 528bc)  
851517 MTF2; YDL044C  
molecular process  
mitochondrion;organellar lumen  
protein binding;RNA binding 0.259 0.08 0.31

P07236 Threonine--tRNA ligase,  
mitochondrial  (05=Saccharomyces cerevisiae 528bc)  
853640 MSTL1; YKL119C  
molecular process  
cytoplasm;mitochondrion;organellar lumen  
catalytic activity;nucleotide binding;RNA binding 0.233 0.072 0.31

P47158 Putative transferase CAF17,  
mitochondrial  (05=Saccharomyces cerevisiae 528bc)  
853386 IBA57; YIR122W  
cell organization and biogenesis;metabolic process  
mitochondrion;organellar lumen  
catalytic activity 0.241 0.075 0.31
| Entry             | Phenotype                  | Function                                                                 | Location                        | Activity                                      | Binding 1 | Binding 2 | Binding 3 |
|-------------------|---------------------------|--------------------------------------------------------------------------|---------------------------------|-----------------------------------------------|-----------|-----------|-----------|
| P10507            | Mitochondrial-processing | peptide subunit beta (S. cerevisiae)                                     | Mitochondrion, organelle         | Catalytic activity, metal ion binding, protein binding | 2.481     | 0.778     | 0.31      |
| P32860            | NTF1-like protein,         | mitochondrial (S. cerevisiae)                                            | Mitochondrion, organelle         | Metal ion binding                             | 5.494     | 1.738     | 0.32      |
| P35999            | Mitochondrial intermediate | peptidease (S. cerevisiae)                                              | Mitochondrion, organelle         | Catalytic activity, metal ion binding          | 0.145     | 0.046     | 0.32      |
| P26039            | Elongation factor G,       | mitochondrial (S. cerevisiae)                                            | Cytosol, Mitochondrion           | Catalytic activity, nucleotide binding, RNA binding | 1.024     | 0.326     | 0.32      |
| Q07500            | External NADH-ubiquinone    | oxidoreductase 2 (S. cerevisiae)                                         | Mitochondrion                   | Catalytic activity, nucleotide binding         | 12.594    | 4.012     | 0.32      |
| P11914            | Mitochondrial-processing  | peptide subunit alpha (S. cerevisiae)                                   | Membrane, Mitochondrion, organelle | Catalytic activity, metal ion binding, protein binding | 2.311     | 0.738     | 0.32      |
| P00431            | Cytochrome c peroxidase,   | mitochondrial (S. cerevisiae)                                            | Mitochondrion, organelle         | Antioxidant activity, catalytic activity, metal ion binding, protein binding | 2.162     | 0.701     | 0.32      |
| P04803            | Tryptophan-2RNA ligase,     | mitochondrial (S. cerevisiae)                                            | Cytoplasm, Mitochondrion, organelle | Catalytic activity, nucleotide binding         | 0.896     | 0.292     | 0.33      |
| P37267            | Assembly factor 6p4         | (S. cerevisiae)                                                          | Cell organization, Biogenesis    | Membrane, Mitochondrion                        | 5.579     | 1.848     | 0.33      |
| P14908            | Mitochondrial transcription | factor 1 (S. cerevisiae)                                                | Mitochondrion, organelle         | Catalytic activity, DNA binding, RNA binding   | 0.778     | 0.259     | 0.33      |
| P53736            | Uncharacterized protein    | YMD040W (S. cerevisiae)                                                 | Mitochondrion                   |                                               | 1.154     | 0.389     | 0.34      |
| Q08970            | Mitochondrial metal        | transporter 2 (S. cerevisiae)                                            | Membrane, Mitochondrion          | Translocator activity                          | 0.532     | 0.186     | 0.35      |
| P06168            | Ketal-acid reductoisomerase | (S. cerevisiae)                                                          | Mitochondrion                   | Catalytic activity, DNA binding, metal ion binding | 28.126    | 9.857     | 0.35      |
| P35191            | O2A1 homolog 1, mitochondrial | (S. cerevisiae)                                                          | Enzyme regulator activity, metal ion binding, protein binding | 4.722     | 1.856     | 0.35      |
| P33064            | Mitochondrial innermembrane space import and assembly protein 40 | (S. cerevisiae)                                                          | Mitochondrion                   | Catalytic activity, protein binding, transporer activity | 2.3       | 0.817     | 0.36      |
| Q06485            | Autophagy-related protein 33 | (S. cerevisiae)                                                          | Membrane, Mitochondrion          |                                               | 2.162     | 0.778     | 0.36      |
| P39522            | Dihydroxy-acid dehydratase, mitochondrial (S. cerevisiae) | (S. cerevisiae)                                                          | Mitochondrion                   | Catalytic activity, metal ion binding          | 39.37     | 14.199    | 0.36      |
| Q12428            | Probable 2-methylcitrate dehydratase (S. cerevisiae) | (S. cerevisiae)                                                          | Cytoplasm, Membrane, Mitochondrion | Catalytic activity                             | 19.535    | 7.058     | 0.36      |
| P18900            | Hexaprenyl pyrophosphate synthase, mitochondrial (S. cerevisiae) | (S. cerevisiae)                                                          | Membrane, Mitochondrion          | Catalytic activity, metal ion binding, protein binding | 0.711     | 0.259     | 0.36      |
| Q08223            | Altered inheritance of mitochondria protein 39, mitochondrial (S. cerevisiae) | (S. cerevisiae)                                                          | Cytosol, Membrane, Mitochondrion |                                               | 0.711     | 0.259     | 0.36      |
| Q39868            | UPR060L protein FMP40 (S. cerevisiae) | (S. cerevisiae)                                                          | Mitochondrion                   | Protein binding                                | 2.495     | 0.917     | 0.37      |
| P32332            | Mitochondrial oxaloacetate transport protein (S. cerevisiae) | (S. cerevisiae)                                                          | Membrane, Mitochondrion          | Structural molecule activity, transporer       | 5.813     | 2.162     | 0.37      |
| P36451 | Pyruvate dehydrogenase complex protein K component, mitochondrial (Saccharomyces cerevisiae S288c) | 853107 | PDXI1; YGR193C | metabolic process | mitochondrion,organelle lumen | catalytic activity;nucleotide binding;protein binding | 1.829 | 0.682 | 0.37 |
| P33180 | Probable oxidoreductase AIM17 (Saccharomyces cerevisiae S288c) | 853665 | AIM17; YHL021C | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;metal ion binding | 4.055 | 1.555 | 0.38 |
| P33180 | Probable oxidoreductase AIM17 (Saccharomyces cerevisiae S288c) | 853665 | AIM17; YHL021C | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;metal ion binding | 4.055 | 1.555 | 0.38 |
| P32453 | Protein ATP11, mitochondrial (Saccharomyces cerevisiae S288c) | 854041 | ATP11; YNL315C | cell organization and biogenesis;metabolic process | mitochondrion | protein binding | 1.512 | 0.585 | 0.39 |
| P02992 | Elongation factor 1α, mitochondrial (Saccharomyces cerevisiae S288c) | 854359 | TUF1; YDR187W | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;nucleotide binding;RNA binding | 23.245 | 9 | 0.39 |
| Q02020 | 54S ribosomal protein L13, mitochondrial (Saccharomyces cerevisiae S288c) | 853875 | MRPL13; YKR006C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.371 | 0.54 | 0.39 |
| P17695 | Glutaredoxin 2, mitochondrial (Saccharomyces cerevisiae S288c) | 852124 | GRK2; YDR513W | cellular homeostasis;metabolic process;regulation of biological process;response to stimulus;transport | cytoplasm;cytosol;mitochondrion;nucleus | antioxidant activity;catalytic activity | 1.31 | 0.52 | 0.40 |
| P39527 | 54S ribosomal protein L28, mitochondrial (Saccharomyces cerevisiae S288c) | 852073 | MRPL28; YDR462W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.31 | 0.52 | 0.40 |
| P32369 | 54S ribosomal protein L25, mitochondrial (Saccharomyces cerevisiae S288c) | 852967 | MRPL25; YGR076C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.31 | 0.52 | 0.40 |
| P38120 | 37S ribosomal protein S9, mitochondrial (Saccharomyces cerevisiae S288c) | 852443 | MRPS9; YBR146W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.254 | 0.501 | 0.40 |
| P32387 | 54S ribosomal protein L41, mitochondrial (Saccharomyces cerevisiae S288c) | 852014 | MRPL41; YDR405W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | nucleotide binding;protein binding;RNA binding;structural molecule activity | 1.254 | 0.501 | 0.40 |
| Q09645 | MICO5 complex subunit Mic10 (Saccharomyces cerevisiae S288c) | 850300 | MISO1; MIC10; YCL057C | cell organization and biogenesis | membrane;mitochondrion | 4.179 | 1.683 | 0.40 |
| Q01163 | 37S ribosomal protein S23, mitochondrial (Saccharomyces cerevisiae S288c) | 852748 | RSM23; YGL129C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | catalytic activity;nucleotide binding;protein binding | 2.695 | 1.11 | 0.41 |
| P33759 | 37S ribosomal protein S5, mitochondrial (Saccharomyces cerevisiae S288c) | 852553 | MRPS5; YBR251W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.995 | 0.413 | 0.42 |
| Q12031 | Mitochondrial 2- methylisocitrate lyase (Saccharomyces cerevisiae S288c) | 856114 | IL2; YPR006C | metabolic process | mitochondrion;organelle lumen | catalytic activity | 7.859 | 3.281 | 0.42 |
| P40530 | Pyruvate dehydrogenase (acetyl-transferring) kinase 1, mitochondrial (Saccharomyces cerevisiae S288c) | 854769 | PFK1; YIL042C | metabolic process | mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | 0.931 | 0.389 | 0.42 |
| Q03246 | 37S ribosomal protein S17, mitochondrial (Saccharomyces cerevisiae S288c) | 855226 | MRPS17; YMR188C | cell differentiation;cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.931 | 0.389 | 0.42 |
| P36115 | Unclassified protein YKR070W (Saccharomyces cerevisiae S288c) | 853944 | YKR070W; YKR070W | metabolic process | mitochondrion | 1.976 | 0.833 | 0.42 |
| P38797 | Protein phosphatase 2C homolog 7, mitochondrial (Saccharomyces cerevisiae S288c) | 856475 | PTC7; YHR076 | metabolic process | mitochondrion | catalytic activity;metal ion binding | 0.874 | 0.369 | 0.42 |
| Entry   | Description                                                                 | YOR   | Function                                                                                     | Localization                                                                 | W                     | Binding/Transport   | Interaction                                                                 | Score | p-Value |
|---------|------------------------------------------------------------------------------|-------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|------------------------|---------------------|-----------------------------------------------------------------------------|-------|----------|
| P00830  | ATP synthase subunit beta, mitochondrial                                    | YLR   | metabolic process, transport                                                                  | cytosol;membrane;mitochondrion                                                | 853585                |                     | catalytic activity, nucleotide binding, protein binding, transport r activity | 99    | 41.987   |
| P40086  | Cytochrome c oxidase assembly protein ccs25                                  | YER   | cell organization and biogenesis, metabolic process, transport                                | membrane;mitochondrion                                                        | 856884                |                     | catalytic activity, transport                                              | 1.555 | 0.668    |
| P15179  | Aspartate--tRNA ligase, mitochondrial                                        | YER   | metabolic process                                                                            | cytoplasm;mitochondrion;organelle lumen                                       | 856000                |                     | catalytic activity, nucleotide binding                                      | 0.708 | 0.307    |
| Q12480  | Probable electron transfer flavoprotein subunit alpha, mitochondrial         | YLR   | metabolic process                                                                            | mitochondrial, organelle lumen                                                | 856112                |                     | catalytic activity                                                      | 3.467 | 1.512    |
| Q08818  | Meiotic sister- chromatid recombinant protein 6, mitochondrial               | YKL   | metabolic process                                                                            | mitochondrial, organelle lumen                                                | 854536                |                     | RNA binding                                                            | 1.154 | 0.506    |
| P48569  | Uncharacterized protein YDL183C                                              | YDL   | transport                                                                                   |                                                                                  | 851345                |                     | catalytic activity, metal ion binding                                       | 0.624 | 0.274    |
| P36775  | Lon protease homolog, mitochondrial                                          | YPL   | cell organization and biogenesis, metabolic process, regulation of biological process, response to stimulus | cytoplasm;mitochondrion;organelle lumen                                       | 852259                |                     | catalytic activity, RNA binding                                           | 1.222 | 0.537    |
| P36520  | 54S ribosomal protein L10, mitochondrial                                     | YNL   | cell organization and biogenesis, metabolic process                                         | mitochondrial, ribosome                                                       | 854536                |                     | structural molecule activity                                               | 0.551 | 0.245    |
| P36163  | mitochondrial metalloendopeptidase OMA1                                     | YKL   | metabolic process                                                                            | membrane;mitochondrion                                                       | 853962                |                     | catalytic activity, metal ion binding                                      | 0.551 | 0.245    |
| Q02784  | Monothiol glutaredoxin-5, mitochondrial                                      | YPL   | cell organization and biogenesis, cellular homeostasis, metabolic process, regulation of biological process, response to stimulus | mitochondrial, organelle lumen                                                | 856048                |                     | catalytic activity, metal ion binding                                      | 2.594 | 1.154    |
| P38341  | MICOS complex subunit Mlc12                                                   | YLR   | cell organization and biogenesis                                                             | membrane;mitochondrion                                                       | 852566                |                     | catalytic activity, metal ion binding                                      | 2.594 | 1.154    |
| P42949  | Mitochondrial import inner membrane translocase subunit Tim16                | YLR   | transport                                                                                   | membrane;mitochondrion                                                       | 853440                |                     | protein binding                                                        | 0.52  | 0.233    |
| P40053  | Altered inheritance of mitochondria protein 9, mitochondrial                | YLR   |                                                                                    |                                                                                 | 856813                |                     |                                                                                | 4.289 | 1.938    |
| P38088  | Glycine--tRNA ligase 1, mitochondrial                                        | YLR   | metabolic process                                                                            | cytoplasm;mitochondrion;organelle lumen                                       | 854689                |                     | catalytic activity, nucleotide binding, protein binding, transport r activity | 0.468 | 0.212    |
| P08067  | cytochrome b1 complex subunit Rieske, mitochondrial                          | YLR   | metabolic process                                                                            | membrane;mitochondrion                                                       | 856689                |                     | catalytic activity, metal ion binding                                      | 55.234 | 25.102   |
| P32839  | Mitochondrial chaperone Bcs1                                                  | YLR   | cell organization and biogenesis, metabolic process, response to stimulus, transport         | cytosol;membrane;mitochondrion                                                | 851981                |                     | catalytic activity, nucleotide binding, transport r activity              | 0.425 | 0.194    |
| Q03597  | ADP-ribose pyrophosphatase                                                    | YBR   | metabolic process                                                                            | cytoplasm;mitochondrion;nucleus                                               | 852408                |                     | catalytic activity, metal ion binding                                      | 0.425 | 0.194    |
| P38175  | 37S Ribosomal protein Mrp21                                                  | YBR   | cell organization and biogenesis, metabolic process                                         | mitochondrial, ribosome                                                      | 852188                |                     | structural molecule activity                                               | 0.425 | 0.194    |
| Q12166  | 2-Haploidyminylate synthase 2, mitochondrial                                 | YBR   | metabolic process                                                                            | mitochondrial                                                               | 854275                |                     | catalytic activity, protein binding                                        | 3.739 | 1.707    |
| P37292  | Serine hydroxymethyltransferase, mitochondrial                              | YBR   | metabolic process                                                                            | mitochondrial                                                               | 852565                |                     | catalytic activity                                                        | 12.219 | 5.579    |
| Q03713  | Respiratory supercomplex factor 1, mitochondrial                             | YHR   | cell organization and biogenesis                                                             | membrane;mitochondrion                                                       | 854978                |                     |                                                                           | 2.162 | 0.995    |
Q02950 37S ribosomal protein MRPS1, mitochondrial (OS=Saccharomyces cerevisiae S288c) 855985 MRPS1; YPL118 W cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 1.154 0.532 0.46

P40508 Uncharacterized protein YL077C (OS=Saccharomyces cerevisiae S288c) 854733 YL077C; YL077C mitochondrial 1.448 0.668 0.46

P17558 37S ribosomal protein PET123, mitochondrial (OS=Saccharomyces cerevisiae S288c) 854329 PET123; YDR158 W cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 1.448 0.668 0.46

Q05779 Ubiquinone biosynthesis protein CD09, mitochondrial (OS=Saccharomyces cerevisiae S288c) 850898 COQ9; YLR201C metabolic process membrane;mitochondrion catalytic activity 0.359 0.166 0.46

P36523 54S ribosomal protein L15, mitochondrial (OS=Saccharomyces cerevisiae S288c) 851022 MRPL15; YLR332 W,A cell organization and biogenesis;metabolic process mitochondrion;ribosome catalytic activity;RNA binding;structural molecule activity 0.334 0.155 0.46

P32578 A-Hydroxynocarboxylate polypeptidyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) 855778 COG2; YNR041C metabolic process;transport membrane;mitochondrion catalytic activity 0.292 0.136 0.47

P38884 Altered inheritance of mitochondria protein 18, mitochondrial (OS=Saccharomyces cerevisiae S288c) 856605 AIM18; YHR198C mitochondrial catalytic activity 0.311 0.145 0.47

Q06493 LETM1 domain-containing protein YL447, mitochondrial (OS=Saccharomyces cerevisiae S288c) 856243 YL447; YPR125 W cell organization and biogenesis;transport membrane;mitochondrion structural molecule activity;transporter activity 1.043 0.487 0.47

P38127 mitochondrial carrier protein RIM2 (OS=Saccharomyces cerevisiae S288c) 852491 RIM2; YBR192 W cell organization and biogenesis;metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 1.239 0.585 0.47

P00445 Superoxide dismutase [Cu-Zn] (OS=Saccharomyces cerevisiae S288c) 853568 SOD1; YJR104C cell organization and biogenesis;cellular homeostasis;metabolic process;regulation of biological process;response to stimulus cytoplasm;cytosol;mitochondrion;nucleus antioxidant activity;catalytic activity;metal ion binding;protein binding 1.848 0.874 0.47

Q08686 Thiosulfate sulfurtransferase TUM1 (OS=Saccharomyces cerevisiae S288c) 854425 TUM1; YDR251C metabolic process cytoplasm;mitochondrion catalytic activity;protein binding 0.212 0.101 0.48

P43635 Citrate synthase 3, mitochondrial (OS=Saccharomyces cerevisiae S288c) 856107 CIT3; YPR001 W metabolic process mitochondrial catalytic activity 6.11 2.914 0.48

P21375 Fumarate reductase 2 (OS=Saccharomyces cerevisiae S288c) 853510 CSQ1; YJR051W metabolic process endoplasmic reticulum;mitochondrion catalytic activity;activity;protein binding 0.16 0.077 0.48

P38860 GTPase MTG2, mitochondrial (OS=Saccharomyces cerevisiae S288c) 856573 MTG2; YHR168 W metabolic process;transport membrane;mitochondrion catalytic activity;activity;metal ion binding;nucleotide binding;transporter activity 0.145 0.07 0.48

P53166 ATP-dependent tRNA helicase mrh4, mitochondrial (OS=Saccharomyces cerevisiae S288c) 852816 MRH4; YGL064C cell organization and biogenesis;metabolic process mitochondrion;organellar lumen catalytic activity;nucleotide binding;protein binding 0.145 0.07 0.48

P42900 Sigma-like sequence protein 1, mitochondrial (OS=Saccharomyces cerevisiae S288c) 850830 SLS1; YLR139C cell organization and biogenesis;metabolic process membrane;mitochondrion protein binding 0.125 0.061 0.49

P48526 Isoleucine–tRNA ligase, mitochondrial (OS=Saccharomyces cerevisiae S288c) 856067 ISM1; YPL040C cell organization and biogenesis;metabolic process;regulation of biological process cytoplasm;cytosol;mitochondrion;organellar lumen catalytic activity;activity;nucleotide binding 0.081 0.04 0.49

P48237 Mitochondrial group I intron splicing factor CCM1 (OS=Saccharomyces cerevisiae S288c) 853053 CCM1; YGR150C cell organization and biogenesis;metabolic process mitochondrion RNA binding 0.089 0.044 0.49

Q06236 Mitochondrial inner membrane protein SHH4 (OS=Saccharomyces cerevisiae S288c) 850861 SHH4; YLR164 W metabolic process membrane;mitochondrion catalytic activity;activity;metal ion binding 6.499 3.217 0.49

P08417 Fumarate hydratase, mitochondrial (OS=Saccharomyces cerevisiae S288c) 858666 FUM3; YPL262 W cell organization and biogenesis;metabolic process cytoplasm;cytosol;mitochondrion;organellar lumen catalytic activity 13.874 6.88 0.50

P09440 C-1-tetrahydrofolate synthase, mitochondrial (OS=Saccharomyces cerevisiae S288c) 852378 MTS1; YBR084 W metabolic process cytosol;mitochondrion catalytic activity;activity;nucleotide binding 1.668 0.829 0.50

P47052 succinate dehydrogenase [ubiquinone] flavoprotein subunit 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) 833405 YL045W; YL045W metabolic process;transport membrane;mitochondrion catalytic activity;activity;nucleotide binding 5.884 2.932 0.50
| Gene Symbol | Description | Function | Localization | Catalytic Activity | Binding Activity |
|-------------|-------------|----------|--------------|-------------------|------------------|
| P28817      | 3-hydroxyisobutyryl-CoA dehydrogenase, mitochondrial (S. cerevisiae) | metabolic process | mitochondrion | 1.212 | 0.61 |
| P42940      | Probable electron transfer flavoprotein subunit beta (S. cerevisiae) | metabolic process | mitochondrion, organellar lumen | 7.66 | 3.87 |
| P10662      | 37S ribosomal protein MRP1, mitochondrial (S. cerevisiae) | cell organization and biogenesis; metabolic process | ribosome | 2.981 | 1.512 |
| P48015      | Aminomethyltransferase, mitochondrial (S. cerevisiae) | metabolic process | mitochondrion | 11.217 | 5.7 |
| P36066      | Protein MRO3-like (S. cerevisiae) | metabolic process | membrane, mitochondrion | 0.655 | 0.334 |
| P49095      | Glycine dehydrogenase (Decarboxylating), mitochondrial (S. cerevisiae) | metabolic process | cytosol, mitochondrion | 2.884 | 1.471 |
| P38172      | MIOREX complex component 3 (S. cerevisiae) | metabolic process | membrane, mitochondrion | 0.968 | 0.501 |
| P25374      | Cysteine desulfurase, mitochondrial (S. cerevisiae) | cell organization and biogenesis; cellular homeostasis | mitochondrion, nucleus | 2.594 | 1.346 |
| P37298      | Succinate dehydrogenase (ubiquinone) cytochrome b small subunit, mitochondrial (S. cerevisiae) | metabolic process | membrane, mitochondrion | 4.995 | 2.594 |
| P38072      | Protein SCO2, mitochondrial (S. cerevisiae) | cell organization and biogenesis; cellular homeostasis | membrane, mitochondrion | 1.404 | 0.73 |
| P04037      | Cytochrome c oxidase subunit 4, mitochondrial (S. cerevisiae) | metabolic process | membrane, mitochondrion | 34.112 | 17.738 |
| P07806      | Valine-tRNA ligase, mitochondrial (S. cerevisiae) | metabolic process | cytoplasm, cytosol, mitochondrion | 0.722 | 0.377 |
| P07256      | Cytochrome b-c1 complex subunit 3, mitochondrial (S. cerevisiae) | metabolic process | membrane, mitochondrion | 18.783 | 9.89 |
| P53140      | Protein RM09, mitochondrial (S. cerevisiae) | cell differentiation; metabolic process | membrane, mitochondrion | 20.017 | 10.602 |
| P53312      | Succinyl-CoA ligase (ADP-forming) subunit beta, mitochondrial (S. cerevisiae) | metabolic process | mitochondrion | 0.334 | 0.668 |
| P43617      | Uncarboxylated mitochondrial carrier YFR045W (S. cerevisiae) | metabolic process | membrane, mitochondrion | 0.778 | 0.413 |
| P01097      | ATPase inhibitor, mitochondrial (S. cerevisiae) | metabolic process | mitochondrion | 2.162 | 1.154 |
| P13290      | 37S ribosomal protein MRP4, mitochondrial (S. cerevisiae) | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | 1.154 | 0.616 |
| P16387      | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial (S. cerevisiae) | cell growth; metabolic process | mitochondrion, organellar lumen | 25.364 | 13.497 |
| Q05892      | MIOREX complex component 2 (S. cerevisiae) | metabolic process | mitochondrion | 3.217 | 1.738 |
| P36101      | TriRNA threonylcarbamoyltransferase 2 (S. cerevisiae) | metabolic process | cytosol, membrane, mitochondrion | 0.616 | 0.334 |
Cytochrome c oxidase protein 20, mitochondrial (S. cerevisiae)

375 ribosomal protein S18, mitochondrial (S. cerevisiae)

Glycine cleavage system H protein, mitochondrial (S. cerevisiae)

Probable NADPH:aldehydoreductase, mitochondrial (S. cerevisiae)

Uncharacterized protein YGR266W, mitochondrial (S. cerevisiae)

Mitochondrial import inner membrane translocase subunit TIM50, mitochondrial (S. cerevisiae)

S45 ribosomal protein L4, mitochondrial (S. cerevisiae)

Mitochondrial inner membrane AAA protease supercomplex subunit YME1, mitochondrial (S. cerevisiae)

54S ribosomal protein L1, mitochondrial (S. cerevisiae)

Aldehyde dehydrogenase 5, mitochondrial (S. cerevisiae)

Sucinate dehydrogenase (ubiquinone) iron-sulfur subunit, mitochondrial (S. cerevisiae)

Prohibitin-1, mitochondrial (S. cerevisiae)

Uncharacterized mitochondrial hydroxylase FMP41, mitochondrial (S. cerevisiae)

Malate dehydrogenase, mitochondrial (S. cerevisiae)

ATP-dependent RNA helicase MS5116, mitochondrial (S. cerevisiae)

Mitochondrial import inner membrane mitobiosome receptor MBA1, mitochondrial (S. cerevisiae)

Inner membrane mitobiosome receptor MBA1, mitochondrial (S. cerevisiae)

Protein mmf1, mitochondrial (S. cerevisiae)

Cytochrome c oxidase assembly factor 1, mitochondrial (S. cerevisiae)

Mitochondrial import inner membrane mitobiosome receptor MBA1, mitochondrial (S. cerevisiae)

S45 ribosomal protein L24, mitochondrial (S. cerevisiae)

Protein binding

1.894

0.931

1.683

0.45

9.495

0.25

0.56

1.081

0.602

7.483

4.179

1.565

0.874

1.938

1.085

1.371

0.778

32.839

18.684

2.981

0.585

1.482

0.833

5.31

2.981

0.585

1.482

0.833

5.31

2.981

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2.981

0.585

1.482

0.833

5.31

2.981

0.585

1.482

0.833
P43616  Cys-Gly metalloendopeptidase dag1 [OS=Saccharomyces cerevisiae S288c]  850605  DUG1; YFR044C  metabolic process  cytoplasm/mitochondrion/ribosome  catalytic activity;metal ion binding  1.154  0.711  0.62
Q12349  ATP synthase subunit H, mitochondrial (OS=Saccharomyces cerevisiae S288c)  851002  ATP14; YLR295C  cell organization and biogenesis;metabolic process;transport  membrane/mitochondrion  2.728  1.683  0.62
P38323  ATP-dependent clp1-like chaperone, mitochondrial (OS=Saccharomyces cerevisiae S288c)  852528  MCK1; YBR227C  metabolic process  membrane/mitochondrion;organelle lumen  catalytic activity;nucleotide binding  0.501  0.311  0.62
Q06668  Methyltransferase OMS1, mitochondrial (OS=Saccharomyces cerevisiae S288c)  851911  OMS1; YDR316W  metabolic process  membrane/mitochondrion  catalytic activity  0.484  0.301  0.62
P40496  37S ribosomal protein S25, mitochondrial (OS=Saccharomyces cerevisiae S288c)  854715  RMS25; YIL083C  cell organization and biogenesis;metabolic process  mitochondrion/ribosome  structural molecule activity  0.468  0.292  0.62
Q38824  Unc13p-related protein YOR020W-A (OS=Saccharomyces cerevisiae S288c)  146640  YOR020W-A; YDR282C  metabolic process;transport  membrane/mitochondrion  5.813  3.642  0.63
Q04689  Altered inheritance of mitochondria protein 32 (OS=Saccharomyces cerevisiae S288c)  854955  AIM32; YML050W  metabolic process  0.369  0.233  0.63
P54857  Ipase 2 (OS=Saccharomyces cerevisiae S288c)  851628  TGL2; YDR858C  metabolic process;transport  mitochondrion  catalytic activity  0.369  0.233  0.63
Q05648  MIOREX complex component 10 (OS=Saccharomyces cerevisiae S288c)  851876  YDR282C; YMR058C  metabolic process;transport  membrane/mitochondrion  0.35  0.222  0.63
P38891  Branched chain amino-acid aminotransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c)  856615  BAT1; YHR208W  metabolic process;regulation of biological process;response to stimulus  mitochondrion;organelle lumen  catalytic activity  15.876  10.103  0.64
P03879  Inton-encoded RNA matriser 84 (OS=Saccharomyces cerevisiae S288c)  854582  Bi4; Q0120  metabolic process  membrane/mitochondrion  catalytic activity;RNA binding  0.28  0.179  0.64
Q30028  Mitochondrial 2-oxoacid:carboxylate carrier 1 (OS=Saccharomyces cerevisiae S288c)  855969  ODC1; YPL134C  metabolic process;transport  membrane/mitochondrion  structural molecule activity  7.799  4.995  0.64
Q30976  37S ribosomal protein S2A, mitochondrial (OS=Saccharomyces cerevisiae S288c)  851755  RMS2A; YDR175C  cell organization and biogenesis;metabolic process  mitochondrion/ribosome  structural molecule activity  0.905  0.585  0.65
P39533  Homositrate dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c)  853230  ACO2; YL020C  metabolic process  mitochondrion  catalytic activity;metal ion binding  0.17  0.11  0.65
P53266  Cytochrome oxidase assembly protein SHY1 (OS=Saccharomyces cerevisiae S288c)  853009  SHY1; YGR112W  cell organization and biogenesis  membrane/mitochondrion  protein binding  1.783  1.154  0.65
Q04728  Arginine biosynthesis bifunctional protein Arg1, mitochondrial (OS=Saccharomyces cerevisiae S288c)  850584  ARG7; YMR062C  metabolic process  mitochondrion;organelle lumen  catalytic activity  1.154  0.748  0.65
P43567  alanine--glyoxylate aminotransferase 1 (OS=Saccharomyces cerevisiae S288c)  850514  AGX1; YFL030W  metabolic process  cytosol/mitochondrion  catalytic activity  2.481  1.61  0.65
P33311  ATP-dependent permease MDL2, mitochondrial (OS=Saccharomyces cerevisiae S288c)  855858  MDL2; YPL270W  response to stimulus;transport  membrane/mitochondrion  catalytic activity;nucleotide binding;transporter activity  1.233  0.802  0.65
P34227  Mitochondrial peroxiredoxin PRX1 (OS=Saccharomyces cerevisiae S288c)  852215  PRX1; YBL064C  cellular homeostasis;metabolic process;regulation of biological process;response to stimulus  mitochondrion  6.848  4.456  0.65
Q08179  Mitochondrial distribution and morphology protein 38 (OS=Saccharomyces cerevisiae S288c)  854130  MDM38; YDL027C  cell organization and biogenesis;cellular homeostasis;regulation of biological process;transport  membrane/mitochondrion  5.683  3.732  0.66
Q00711  Succinate dehydrogenase [ubiquione] flavoprotein subunit, mitochondrial (OS=Saccharomyces cerevisiae S288c)  853370  SDH1; YKL148C  metabolic process;transport  membrane/mitochondrion  catalytic activity;nucleotide binding;protein binding  18.619  12.242  0.66
P07275  Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c)  856432  PUT2; YHR037W  metabolic process  membrane/mitochondrion;organelle lumen  catalytic activity  6.565  4.337  0.66
P19414  Acatalactate hydratase, mitochondrial (OS=Saccharomyces cerevisiae S288c)  851013  ACD1; YJR304C  cell organization and biogenesis;metabolic process;transport  cytoplasm;cytosol/mitochondrion;organelle lumen  catalytic activity;DNA binding;metal ion binding  66.002  43.893  0.67
| P00410 | Cytochrome c oxidase subunit 2 (S288c) | 854622 | COX2; Q0250 | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding;protein binding;transporter activity | 3.642 | 2.831 | 0.78 |
| P36521 | 54S ribosomal protein L11, mitochondrial (S288c) | 851325 | MRPL11; YDL292 W | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | structural molecule activity | 1.069 | 0.833 | 0.78 |
| P51998 | 54S ribosomal protein ymr18c, mitochondrial (S288c) | 854983 | YML6; YML025C | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | RNA binding;structural molecule activity | 0.931 | 0.73 | 0.78 |
| P00427 | Cytochrome c oxidase subunit 6, mitochondrial (S288c) | 856448 | COX6; YHR051 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding;transporter activity | 4.623 | 3.642 | 0.79 |
| P39952 | Mitochondrial inner membrane protein OKX1 (S288c) | 856888 | OKX1; YER154 W | cell organization and biogenesis;transport | membrane;mitochondrion | transporter activity | 1.738 | 1.371 | 0.79 |
| P40495 | Homoisocitrate dehydrogenase, mitochondrial (S288c) | 854714 | LYS12; YIL094C | metabolic process | mitochondrion | catalytic activity;metal ion binding;nucleotide binding | 6.499 | 5.19 | 0.80 |
| Q03798 | Altered inheritance of mitochondria protein 36, mitochondrial (S288c) | 855189 | AIM36; YMR357 C | membrane;mitochondrion | | | 1.336 | 1.069 | 0.80 |
| P40008 | Protein FMP52, mitochondrial (S288c) | 856721 | FMP52; YER004 W | endoplasmic reticulum;membrane;mitochondrion | | catalytic activity | 2.162 | 1.738 | 0.80 |
| P07342 | Acetolactate synthase catalytic subunit, mitochondrial (S288c) | 855135 | ILV2; YMR108 W | metabolic process | mitochondrion | catalytic activity;metal ion binding;nucleotide binding | 5.236 | 4.223 | 0.81 |
| P47127 | Altered inheritance of mitochondria protein 24, mitochondrial (S288c) | 853543 | AIM24; YJR080C | cell organization and biogenesis | mitochondrial | | 3.175 | 2.562 | 0.81 |
| Q11298 | Uncharacterized ABC transporter ATP-binding protein YDR061W (S288c) | 851633 | YDR061 W; YDR061 W | | mitochondrion | catalytic activity;nucleotide binding | 0.425 | 0.343 | 0.81 |
| P25719 | Peptidyl-prolyl cis-trans isomerase C, mitochondrial (S288c) | 854897 | CPR3; YML078 W | cell death;metabolic process | mitochondrion;organellar lumen | catalytic activity | 2.981 | 2.415 | 0.81 |
| Q08822 | Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial (S288c) | 854538 | CIR2; YDR356 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding;nucleotide binding | 3.019 | 2.481 | 0.82 |
| P38885 | Altered inheritance of mitochondria protein 46, mitochondrial (S288c) | 856606 | AIM46; YHR199C | | | | 1.404 | 1.154 | 0.82 |
| P47045 | Mitochondrial import inner membrane translocase subunit TIM54 (S288c) | 853392 | TIM54; YUL054W | cell organization and biogenesis;transport | cytosol;membrane;mitochondrion | transporter activity | 0.655 | 0.54 | 0.82 |
| P39925 | Mitochondrial respiratory chain complexes assembly protein AFG3 (S288c) | 856737 | AFG3; YER017C | cell organization and biogenesis;metabolic process;response to stimulus;transport | membrane;mitochondrion | catalytic activity;metal ion binding;nucleotide binding;protein binding | 1.228 | 1.015 | 0.83 |
| Q06678 | 54S ribosomal protein L35, mitochondrial (S288c) | 851921 | MRPL35; YDR322 W | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | structural molecule activity | 1.424 | 1.219 | 0.86 |
| P32317 | Protein AFG1 (S288c) | 856568 | AFG1; YEL052W | cell organization and biogenesis;metabolic process;response to stimulus;transport | membrane;mitochondrion | catalytic activity;nucleotide binding | 1.154 | 0.995 | 0.86 |
| P32891 | D-lactate dehydrogenase (cytochrome) 1, mitochondrial (S288c) | 851380 | DLD1; YDL174C | metabolic process;transport | membrane;mitochondrion | catalytic activity;nucleotide binding | 13.03 | 11.253 | 0.86 |
| P33303 | Succinate/luminate mitochondrial transporter (S288c) | 853558 | SFC1; YIR095 W | metabolic process;transport | membrane;mitochondrion | structural molecule activity;transporter activity | 17.957 | 15.681 | 0.87 |
| P46367 | Potassium-activated aldehyde dehydrogenase, mitochondrial (S288c) | 854556 | ALD4; YOR374 W | metabolic process | mitochondrion;organellar lumen | catalytic activity | 58.078 | 50.795 | 0.87 |
| P32473 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (Saccharomyces cerevisiae S288c) | 8S2522 | PDB1; YBR221C | metabolic process | mitochondrial;organelle lumen | catalytic activity | 10.288 | 9 | 0.87 |
| P4034 | Mitochondrial respiratory chain complexes assembly protein YTA12 (Saccharomyces cerevisiae S288c) | 8S5114 | YTA12; YMR0989C | cell organization and biogenesis;metabolic process;response to stimulus;transport | cytoplasm;membrane;mitochondrion | catalytic activity;metal ion binding;nucleotide binding;protein binding | 1.795 | 1.575 | 0.88 |
| P52893 | Probable alamine aminotransferase, mitochondrial (Saccharomyces cerevisiae S288c) | 8S0778 | ALT1; YLR089C | metabolic process | mitochondrial;organelle lumen | catalytic activity | 1.438 | 1.264 | 0.88 |
| P50085 | Probilin-2 (Saccharomyces cerevisiae S288c) | 8S3146 | PHB2; YGR231C | cell organization and biogenesis;metabolic process;regulation of biological process | membrane;mitochondrion | protein binding | 4.926 | 4.337 | 0.88 |
| P18239 | ADP/ATP carrier protein 2 (Saccharomyces cerevisiae S288c) | 8S2530 | PET9; YBL030C | cell death;metabolic process;transport | membrane;mitochondrion | structural molecule activity;transporter activity | 155.88 | 7 | 122.28 | 5 | 0.90 |
| P49367 | Homoalanotinase, mitochondrial (Saccharomyces cerevisiae S288c) | 8S1820 | LYS4; YDR234W | metabolic process | mitochondrial | catalytic activity;metal ion binding;protein binding | 1.276 | 1.154 | 0.90 |
| P36013 | NAD-dependent malic enzyme, mitochondrial (Saccharomyces cerevisiae S288c) | 8S3839 | MAE1; YKL029C | metabolic process | mitochondrial;organelle lumen | catalytic activity;metal ion binding;protein binding | 2.35 | 2.162 | 0.92 |
| P40215 | External NADH-ubiquinone oxidoreductase 1, subunit 1, mitochondrial (Saccharomyces cerevisiae S288c) | 8S5176 | NDE1; YMR145C | metabolic process | mitochondrial | catalytic activity;nucleotide binding | 5.469 | 5.078 | 0.93 |
| P07257 | Cytochrome b-c1 complex subunit 2, mitochondrial (Saccharomyces cerevisiae S288c) | 8S6121 | QCR2; YPR191W | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding;protein binding | 33.551 | 33.551 | 1.00 |
| P36112 | MIOREX complex component 9 (Saccharomyces cerevisiae S288c) | 8S3886 | FC1; MRC60; YKR016W | cell organization and biogenesis;transport | membrane;mitochondrion | protein binding | 12.895 | 12.895 | 1.00 |
| P36641 | Mitochondrial phosphate carrier protein (Saccharomyces cerevisiae S288c) | 8S3540 | MRR1; YJR077C | metabolic process;transport | membrane;mitochondrion | protein binding;structural molecule activity;transporter activity | 26.826 | 26.826 | 1.00 |
| P36060 | NADH-cytochrome b5 reductase 2 (Saccharomyces cerevisiae S288c) | 8S3707 | MCR1; YNL150W | metabolic process;response to stimulus | membrane;mitochondrion | catalytic activity;protein binding | 19.691 | 19.691 | 1.00 |
| P19262 | Dihydropolyamine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (Saccharomyces cerevisiae S288c) | 8S1726 | KG202; YDR148C | cell organization and biogenesis;metabolic process | mitochondrial | catalytic activity;protein binding | 5.7 | 5.7 | 1.00 |
| P25613 | Accumulation of dyads protein 2 (Saccharomyces cerevisiae S288c) | 8S3636 | ADY2; YCR010C | transport | membrane;mitochondrion;vacuole | transporter activity | 12.895 | 12.895 | 1.00 |
| Q12335 | Protoplasm secreted protein 2 (Saccharomyces cerevisiae S288c) | 8S1596 | PST2; YDR323C | metabolic process;regulation of biological process | cytoplasm;extracellular;membrane;mitochondrion | catalytic activity;nucleotide binding;protein binding | 4.012 | 4.012 | 1.00 |
| P81449 | ATP synthase subunit e, mitochondrial (Saccharomyces cerevisiae S288c) | 8S1922 | TIM11; YDR322C-A | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;structural molecule activity;transporter activity | 9 | 9 | 1.00 |
| Q07349 | MIOREX complex component 9 (Saccharomyces cerevisiae S288c) | 8S1535 | YDL027C; YMR999; YDL027C | metabolic process;transport | mitochondrial | endoplasmic reticulum;membrane;mitochondrion | 1.913 | 1.913 | 1.00 |
| P00644 | Cytochrome c iso-1 (Saccharomyces cerevisiae S288c) | 8S3507 | CYC1; YJR048W | metabolic process;transport | mitochondrial | metal ion binding;protein binding | 12.335 | 12.335 | 1.00 |
| P38325 | Mitochondrial outer membrane protein OM14 (Saccharomyces cerevisiae S288c) | 8S2531 | OM14; YBR230C | transport | membrane;mitochondrion | 9 | 9 | 1.00 |
| P80203 | Protein FMP25, mitochondrial (Saccharomyces cerevisiae S288c) | 8S6076 | FMP25; YUR077W | cell organization and biogenesis | membrane;mitochondrion | 0.968 | 0.968 | 1.00 |
| P35721 | Respiratory supercomplex factor 2, mitochondrial (Saccharomyces cerevisiae S288c) | 8S5752 | RFC2; YMR018W | cell organization and biogenesis | membrane;mitochondrion | 7.111 | 7.111 | 1.00 |
| Q12289 | mitochondrial carnitine carrier (OS=Saccharomyces cerevisiae S288c) | 854267 | CRCL1; YOR120C | metabolic process;transport membrane;mitochondrion structural molecule activity;transporte r activity | 0.931 | 0.931 | 1.00 |
| P10823 | Guanine nucleotide-binding protein alpha-2 subunit (OS=Saccharomyces cerevisiae S288c) | 856741 | GPA2; YER020 W | cell differentiation;cell growth;cell organization and biogenesis;cellular homeostasis;regulation of biological process;response to stimulus cytosol;membrane;mitochondrion catalytic activity;metal ion binding;nucleotide binding;protein binding;signal transducer activity | 0.978 | 0.978 | 1.00 |
| P39006 | Phosphatidylserine decarboxylase, cytoplasmic, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 855552 | PSD1; YNL169C | metabolic process;regulation of biological process membrane;mitochondrion catalytic activity | 0.487 | 0.487 | 1.00 |
| Q12374 | Nuclear control of ATPase protein 2 (OS=Saccharomyces cerevisiae S288c) | 856278 | NCA2; YPR155C | metabolic process membrane;mitochondrion ribosome | 0.565 | 0.565 | 1.00 |
| P21560 | Protein CBP3, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 855886 | CBP3; YPL215 W | cell organization and biogenesis;metabolic process membrane;mitochondrion;ribosome | 1.031 | 1.031 | 1.00 |
| P07253 | cytochrome B 6-pre-mRNA-processing protein 6 (OS=Saccharomyces cerevisiae S288c) | 852417 | CBP6; YBR130C | cell organization and biogenesis;metabolic process;response to stimulus cytoplasm;mitochondrion;organelle lumen metal ion binding;nucleotide binding;protein binding | 4.623 | 4.623 | 1.00 |
| Q06143 | mitochondrial dicarboxylate transporter (OS=Saccharomyces cerevisiae S288c) | 851063 | DCL1; YLR348C | metabolic process;transport membrane;mitochondrion structural molecule activity;transporte r activity | 1.154 | 1.154 | 1.00 |
| P40416 | Iron-sulfur clusters transporter ATM1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 855347 | ATM1; YMR301C | cellular homeostasis;metabolic process;transport membrane;mitochondrion catalytic activity;nucleotide binding;transporte r activity | 0.453 | 0.453 | 1.00 |
| P50945 | MIO5 complex subunit MIC27 (OS=Saccharomyces cerevisiae S288c) | 855623 | AIM37; MIC27; YNL100 W | cell organization and biogenesis membrane;mitochondrion | 1.254 | 1.254 | 1.00 |
| O14467 | multiprotein-bridging factor 1 (OS=Saccharomyces cerevisiae S288c) | 854474 | MBF1; YDR298C A | metabolic process;regulation of biological process cytoplasm;mitochondrion;nucleus DNA binding | 1.31 | 1.31 | 1.00 |
| P32907 | Ammonia transport outward protein 2 (OS=Saccharomyces cerevisiae S288c) | 855736 | ATO2; YNR001C | transport membrane;mitochondrion;vacuole transporter activity | 0.874 | 0.874 | 1.00 |
| P53311 | Mitochondrial pyruvate carrier 3 (OS=Saccharomyces cerevisiae S288c) | 853158 | FMP43; MPP3; YGR343 W | transport membrane;mitochondrion transporter activity | 1.154 | 1.154 | 1.00 |
| P40502 | Altered inheritance of mitochondrial protein 19, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 854722 | AIM19; YIL087C | membrane;mitochondrion | 0.995 | 0.995 | 1.00 |
| Q03159 | Cytochrome c oxidase subunit 8b (OS=Saccharomyces cerevisiae S288c) | 850727 | COX112; YLR038C | cell organization and biogenesis;metabolic process;transport mitochondrial catalytic activity;transporte r activity | 3.642 | 3.642 | 1.00 |
| Q06667 | ABC1 family protein MIP2 (OS=Saccharomyces cerevisiae S288c) | 850955 | YLR253 W; MIP2; YLR253 W | cell organization and biogenesis membrane;mitochondrion | 0.218 | 0.218 | 1.00 |
| P37299 | cytochrome b-c1 complex subunit 10 (OS=Saccharomyces cerevisiae S288c) | 856390 | QCR10; YHR001 W-A | metabolic process;transport membrane;mitochondrion catalytic activity;transporte r activity | 5.31 | 5.31 | 1.00 |
| Q12233 | ATP synthase subunit g, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 856131 | ATP20; YPR020 W | cell organization and biogenesis;metabolic process;transport membrane;mitochondrion catalytic activity;transporte r activity | 1.371 | 1.371 | 1.00 |
| P40159 | Uncharacterized protein YNL208W (OS=Saccharomyces cerevisiae S288c) | 855513 | YNL208 W; YNL208 W | membrane;mitochondrion;ribosome | 0.668 | 0.668 | 1.00 |
| Q03327 | Mitochondrial fusion and transport protein Ugo1 (OS=Saccharomyces cerevisiae S288c) | 852081 | UGO1; YDR470C | cell organization and biogenesis;metabolic process membrane;mitochondrion protein binding;structural molecule activity | 0.425 | 0.425 | 1.00 |
| Q60650 | Protein iso11 (OS=Saccharomyces cerevisiae S288c) | 856774 | ISO11; YER048 W | cell organization and biogenesis;metabolic process mitochondrial;organelle lumen catalytic activity;protein binding | 1.783 | 1.783 | 1.00 |
| Q12375 | mitochondrial importin transport 1 (OS=Saccharomyces cerevisiae S288c) | 854297 | ORT1; YOR130C | metabolic process;transport membrane;mitochondrion structural molecule activity;transporte r activity | 0.54 | 0.54 | 1.00 |
| P41911 | Glycerol-3-phosphate dehydrogenase [NAD(+)] 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 854095 | GPD2; YOL059 W | metabolic process cytoplasm;cytosol;mitochondrion catalytic activity;nucleotide binding;protein binding | 0.186 | 0.186 | 1.00 |
Q07914 mitochondrial import inner membrane translocase subunit TIM14 (Os=Sacharomyces cerevisiae S288c) 850694 PAM38; YJR008C regulation of biological process;transport membrane;mitochondrion enzyme regulator activity;protein binding;transporter activity 0.778 0.778 1.00
P38152 Trinucleotide transport protein (Os=Sacharomyces cerevisiae S288c) 852594 CTP1; YBR291C metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 0.389 0.389 1.00
P81451 ATP synthase subunit K, mitochondrial (Os=Sacharomyces cerevisiae S288c) 854077 ATP15; YDR077W-A cell organization and biogenesis;metabolic process membrane;mitochondrion catalytic activity;DNA binding;RNA binding 1.274 1.274 1.00
P25345 Asparagine--tRNA ligase, mitochondrial (Os=Sacharomyces cerevisiae S288c) 850388 SLMS1; YCR024C metabolic process cytoplasm;mitochondrion;organelle lumen catalytic activity;nucleotide binding 0.172 0.172 1.00
P49334 Mitochondrial import receptor subunit tom22 (Os=Sacharomyces cerevisiae S288c) 855592 TOM22; YNL131I cell organization and biogenesis;transport membrane;mitochondrion protein binding;transporter activity 0.292 0.292 1.00
Q06005 Oxyacetyltransferase, mitochondrial (Os=Sacharomyces cerevisiae S288c) 850940 LIP2; YMR239C metabolic process cytoplasm;mitochondrion catalytic activity 0.245 0.245 1.00
P34224 Uncharacterized protein YBL059W (Os=Sacharomyces cerevisiae S288c) 852221 YBL059W; YBL059W membrane;mitochondrion 0.468 0.468 1.00
Q12467 MOREX complex component 4 (Os=Sacharomyces cerevisiae S288c) 855935 YPL168W; MXX4; YPL168W membrane;mitochondrion 0.202 0.202 1.00
P41735 2,5-dimethyl-2,4-hexadiene synthase, mitochondrial (Os=Sacharomyces cerevisiae S288c) 854292 CAT5; YDR125C metabolic process membrane;mitochondrion catalytic activity;metal ion binding 0.54 0.54 1.00
P12438 Methionine--tRNA ligase, mitochondrial (Os=Sacharomyces cerevisiae S288c) 853081 MSY1; YGR171C metabolic process cytoplasm;cytosol;mitochondrion;organelle lumen catalytic activity;nucleotide binding 1.136 1.136 1.00
P53320 Mitochondrial carrier protein MTM1 (Os=Sacharomyces cerevisiae S288c) 853173 MTM1; YGR257C metabolic process;transport membrane;mitochondrion structural molecule activity 0.11 0.11 1.00
Q35695 uncharacterized mitochondrial outer membrane protein YDR381C-A (Os=Sacharomyces cerevisiae S288c) 85188 YDR381C-A; YDR381C-A membrane;mitochondrion 0.389 0.389 1.00
P32463 Acp carrier protein, mitochondrial (Os=Sacharomyces cerevisiae S288c) 853642 ACP1; YNL131I metabolic process;transport mitochondrion 0.259 0.259 1.00
P40561 Peroxidase HYR1 (Os=Sacharomyces cerevisiae S288c) 854855 HYR1; YHR037W metabolic process;response to stimulus cytoplasm;cytosol;mitochondrion;organelle lumen antioxidant activity;catatolic activity 0.259 0.259 1.00
Q07821 Iron-sulfur assembly protein 1 (Os=Sacharomyces cerevisiae S288c) 850632 ISA1; YLJ027W cell organization and biogenesis;metabolic process mitochondrion;organelle lumen metal ion binding;structural molecule activity 0.136 0.136 1.00
| Gene Name | Function | Expression Value | Regulation | Localization | Source | ID | Reference |
|-----------|----------|------------------|------------|--------------|--------|----|-----------|
| Q34013    | Citrate/oxoglutarate carrier protein | 855282 | YMR124W; YMR2411 W | cell organization and biogenesis, metabolic processes, transport | membrane, mitochondrion | DNA binding, structural molecule activity, transport, catalytic activity | 3.467 | 4.012 | 1.16 |
| P33292    | 375 ribosomal protein S35 | 853075 | MRPS35, YGR185 W | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | 1.512 | 1.754 | 1.16 |
| P32454    | Aminopeptidase II, mitochondrial | 853699 | APE2, YKL157 W | metabolic process | cytoplasm, extracellular, membrane, mitochondrion, nucleus | catalytic activity, metal ion binding | 1.209 | 1.474 | 1.22 |
| P00950    | Phosphoglycerate mutase 1 | 853705 | GPM1, YKL152C | metabolic process, regulation of biological process | cytoplasm, cytosol, membrane, mitochondrion | catalytic activity | 2.981 | 3.642 | 1.22 |
| P00175    | Cytochrome B2, mitochondrial | 854950 | CYP2, YML054C | metabolic process, transport | cytosol, membrane, mitochondrion, nucleus | catalytic activity, metal ion binding, nucleotide binding | 1.113 | 1.371 | 1.23 |
| P38771    | Ribosome-recycling factor, mitochondrial | 856433 | RRF1, YHR038 W | cell organization and biogenesis, metabolic process | mitochondrion | RNA binding | 1.254 | 1.581 | 1.26 |
| P21954    | Isocitrate dehydrogenase [NADP], mitochondrial | 851493 | IDP1, YDL066 W | metabolic process | mitochondrion | catalytic activity, metal ion binding, nucleotide binding, protein binding | 35.869 | 45.416 | 1.27 |
| P32340    | Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial | 854919 | NDI1, YML120C | metabolic process, regulation of biological process | membrane, mitochondrion, organelle lumen | catalytic activity, nucleotide binding | 22.95 | 29.392 | 1.28 |
| P28625    | Protein YML1 | 855183 | YML1, YMR152 W | metabolic process, response to stimulus | cytoplasm, endoplasmic reticulum, mitochondrion | catalytic activity, metal ion binding | 0.833 | 1.069 | 1.28 |
| P40582    | Glutathione S-transferase 1 | 854856 | GTI1, YIR038C | metabolic process | endoplasmic reticulum, membrane, mitochondrion, nucleus | antioxidant activity, catalytic activity, protein binding, nucleotide binding | 1.683 | 2.162 | 1.28 |
| P05950    | Heat shock protein SSC1, mitochondrial | 853503 | SSC1, YJR45C | cell organization and biogenesis, metabolic process, regulation of biological process, transport | membrane, mitochondrion, nucleus, organelle lumen | catalytic activity, enzyme regulator activity, nucleotide binding, protein binding | 51.75 | 67.129 | 1.30 |
| P39469    | Sorting assembly machinery 50 kDa subunit | 855705 | SAM50, YNL026 W | cell organization and biogenesis, transport | membrane, mitochondrion | protein binding, transport, catalytic activity | 0.374 | 0.487 | 1.30 |
| P07213    | Mitochondrial import receptor subunit TIP107 | 855602 | TIP107, YNL211C | cell organization and biogenesis, transport | membrane, mitochondrion | protein binding, transport, catalytic activity | 1.728 | 2.257 | 1.31 |
| P32611    | 541 ribosomal protein RML2, mitochondrial | 856660 | RML2, YEL050C | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | catalytic activity, RNA binding | 0.389 | 0.509 | 1.31 |
| Q01852    | Mitochondrial import inner membrane translocate subunit | 854790 | TIM44, YIL022W | transport | membrane, mitochondrion | nucleotide binding, protein binding | 4.125 | 5.404 | 1.31 |
| P38988    | Mitochondrial GTP/GDP carrier protein 1 | 851329 | GCIC1, YDL198C | cell organization and biogenesis, cellular homeostasis, metabolic processes, transport | membrane, mitochondrion | structural molecule activity, transport, catalytic activity | 3.642 | 4.78 | 1.31 |
| P00424    | Cytochrome c oxidase polypeptide 5A, mitochondrial | 855675 | COX5A, YNL052 W | metabolic process, transport | membrane, mitochondrion | catalytic activity, transport, catalytic activity | 1.848 | 2.511 | 1.36 |
| P54003    | Protein SUR7 | 854953 | SUR7, YML052 W | cell differentiation, transport | membrane, mitochondrion | | 0.848 | 1.154 | 1.36 |
| P33882    | Isocitrate dehydrogenase [NADP] | 855723 | IDP3, YNL069 W | metabolic process | cytoplasm, mitochondrion | catalytic activity, metal ion binding, nucleotide binding | 1.943 | 2.652 | 1.36 |
| P41921    | Glutathione reductase | 856014 | GLR1, YFL091 W | cellular homeostasis, metabolic process, regulation of biological process, response to stimulus | cytoplasm, cytosol, mitochondrion, nucleus | antioxidant activity, catalytic activity, nucleotide binding | 0.241 | 0.334 | 1.39 |
| P38969    | Pentamidine resistance factor, mitochondrial | 854440 | PNT1, YOR266 W | cell organization and biogenesis, response to stimulus | membrane, mitochondrion | | 0.259 | 0.359 | 1.39 |
| PS3230 | Phosphatidate cytidylyltransferase, mitochondrial (S. cerevisiae S288c) | 852937 | TAM441, YGR046 W | metabolic process | membrane/mitochondrion, organelle lumen | catalytic activity | 0.292 | 0.407 | 1.39 |
| P38077 | ATP synthase subunit gamma, mitochondrial (S. cerevisiae S288c) | 852327 | ATP3, YBR039 W | metabolic process; transport | membrane/mitochondrion | catalytic activity; transport activity | 11.328 | 15.876 | 1.40 |
| P47140 | Altered inheritance rate of mitochondria protein 25 (S. cerevisiae S288c) | 853563 | AIM25, YJR100C | cell organization and biogenesis | membrane/mitochondrion | transporter activity | 0.369 | 0.52 | 1.41 |
| P22136 | ATPase expression protein 2, mitochondrial (S. cerevisiae S288c) | 855325 | AEP2, YMR282 C | metabolic process; regulation of biological process | mitochondrion | RNA binding | 0.359 | 0.506 | 1.41 |
| P09624 | Dihydrolipoyl dehydrogenase, mitochondrial (S. cerevisiae S288c) | 850527 | LPD1, YFL018C | cellular homeostasis; metabolic process | mitochondrion, organelle lumen | catalytic activity; nucleotide binding | 30.623 | 43.367 | 1.42 |
| P16622 | Ferrochelatase, mitochondrial (S. cerevisiae S288c) | 854347 | HEM15, YDR174 W | metabolic process | membrane/mitochondrion | catalytic activity | 5.579 | 8.006 | 1.44 |
| P50087 | MICS subunit MIC26 (S. cerevisiae S288c) | 853150 | MIDS2, MIC26, YGR235C | cell organization and biogenesis | membrane/mitochondrion | protein binding | 0.638 | 0.931 | 1.46 |
| P25573 | Mitochondrial inner membrane ATPase supercomplex subunit MGR1 (S. cerevisiae S288c) | 850313 | MGR1, YCL044C | metabolic process | membrane/mitochondrion | protein binding | 0.701 | 1.031 | 1.47 |
| P08466 | Mitochondrial nuclease (S. cerevisiae S288c) | 853222 | NUC1, YIL208C | cell death; metabolic process | membrane/mitochondrion, nucleus | catalytic activity; metal ion binding | 1.336 | 1.976 | 1.48 |
| P05660 | Phosphoglycerate kinase (S. cerevisiae S288c) | 850370 | PGK1, YCR023 W | metabolic process | cytoplasm, membrane, mitochondrion | catalytic activity; nucleotide binding | 2.415 | 3.642 | 1.51 |
| P12695 | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial (S. cerevisiae S288c) | 855653 | LAT1, YNL071 W | metabolic process | mitochondrion, organelle lumen | catalytic activity | 7.003 | 10.602 | 1.51 |
| P09457 | ATP synthase subunit 5, mitochondrial (S. cerevisiae S288c) | 851892 | ATP5, YDR288C | metabolic process; transport | membrane/mitochondrion | catalytic activity; transport activity | 9 | 13.678 | 1.52 |
| P00925 | Enolase 2 (S. cerevisiae S288c) | 856579 | ENO2, YMR174 W | metabolic process; regulation of biological process | cytoplasm, cytosol, membrane, mitochondrion, vacuole | catalytic activity; metal ion binding; protein binding | 1.043 | 1.593 | 1.53 |
| P23644 | Mitochondrial import receptor subunit TDM40 (S. cerevisiae S288c) | 855243 | TDM40, YMR203 W | transport | cytosol, membrane, mitochondrion | protein binding; transport activity | 1.154 | 1.783 | 1.55 |
| P19882 | Heat shock protein 60, mitochondrial (S. cerevisiae S288c) | 850963 | HSP60, YLR239C | cell organization and biogenesis; metabolic process; regulation of biological process; transport | cytoplasm, cytosol, membrane, mitochondrion, organelle lumen | catalytic activity; DNA binding; nucleotide binding; protein binding | 23.816 | 38.927 | 1.55 |
| P00530 | Alcohol dehydrogenase 1 (S. cerevisiae S288c) | 854068 | ADH2, YOL086C | metabolic process | cytoplasm, membrane | catalytic activity; metal ion binding | 3.833 | 5.952 | 1.55 |
| Q06510 | Lysophosphatidylcholine acyltransferase (S. cerevisiae S288c) | 856262 | TAZ1, YPR1340 W | cell organization and biogenesis; metabolic process; transport | membrane, mitochondrion | catalytic activity | 0.194 | 0.304 | 1.57 |
| P32792 | UPTOT4 protein YSC83 (S. cerevisiae S288c) | 856410 | YSC83, YHR117 W | metabolic process; transport | membrane, mitochondrion | catalytic activity; nucleotide binding | 0.233 | 0.369 | 1.58 |
| P54783 | D-arabino-1,4-lactone deidase (S. cerevisiae S288c) | 854888 | ADL1, YML298C | metabolic process; response to stimulus | membrane, mitochondrion | catalytic activity; nucleotide binding | 3.299 | 5.31 | 1.61 |
| P14693 | Sorting assembly machinery 35 KDa subunit (S. cerevisiae S288c) | 856483 | SAM35, YMR883 W | cell organization and biogenesis; transport | membrane, mitochondrion | protein binding | 0.334 | 0.54 | 1.62 |
| P22353 | S45 ribosomal protein L8, mitochondrial (S. cerevisiae S288c) | 853382 | MRPL8, YOL063C | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | structural molecule activity | 0.359 | 0.585 | 1.63 |
| P34222 | Peptidylprolyl isomerase 2 (S. cerevisiae S288c) | 852223 | PHT2, YBL057C | regulation of biological process | cytoplasm, cytosol, membrane, mitochondrion | catalytic activity; protein binding | 0.425 | 0.701 | 1.65 |
| P20667 | 2-oxoglutarate dehydrogenase, mitochondrial (S. cerevisiae S288c) | 854681 | KG01, YIL125W | metabolic process | cytosol, mitochondrion, organelle lumen | catalytic activity | 13.785 | 22.843 | 1.66 |
| Gene ID | Description                                                                 | Localization | Functional Annotations                                                                 | Interaction Scores |
|---------|------------------------------------------------------------------------------|--------------|----------------------------------------------------------------------------------------|---------------------|
| P35925  | Uncharacterized vacuolar membrane protein YNL115C (SY-Saccharomyces cerevisiae S288c) | membrane, vacuole | catalytic activity; regulation of biological process; response to stimulus; transport | 0.216 0.233 3.24 |
| P34231  | Uncharacterized protein YKL187C (SY-Saccharomyces cerevisiae S288c)            | membrane, mitochondrion | catalytic activity; regulation of biological process; response to stimulus; transport | 0.216 0.233 3.24 |
| P18737  | Protein MSL1 (SY-Saccharomyces cerevisiae S288c)                              | membrane, mitochondrion, nucleus | catalytic activity; nucleotide binding; protein binding; RNA binding | 0.122 0.413 3.39 |
| P2087   | Sterol 24-C-methyltransferase (SY-Saccharomyces cerevisiae S288c)             | endoplasmic reticulum, membrane, mitochondrion | catalytic activity | 0.557 1.894 3.40 |
| P00331  | Alcohol dehydrogenase 2 (SY-Saccharomyces cerevisiae S288c)                   | cytoplasm | catalytic activity; metal ion binding | 2.594 9 3.47 |
| P00605  | ATP synthase subunit f, mitochondrial (SY-Saccharomyces cerevisiae S288c)     | membrane, mitochondrion | catalytic activity; transport activity | 1.512 5.31 3.51 |
| P30002  | ATP synthase subunit d, mitochondrial (SY-Saccharomyces cerevisiae S288c)     | membrane, mitochondrion | catalytic activity; transport activity | 5.105 18.307 3.59 |
| P00942  | Triosephosphate isomerase (SY-Saccharomyces cerevisiae S288c)                 | cytoplasm, cytosol, membrane, mitochondrion | catalytic activity | 0.194 0.701 3.61 |
| P00360  | Glycerolaldehyde-3-phosphate dehydrogenase 1 (SY-Saccharomyces cerevisiae S288c) | cytoplasm, cytosol, membrane, mitochondrion | catalytic activity; nucleotide binding | 0.823 3.062 3.72 |
| P34251  | Uncharacterized dehydrogenase YKL107W (SY-Saccharomyces cerevisiae S288c)     | cytoplasm, cytosol, mitochondrion | catalytic activity | 0.274 1.069 3.90 |
| P54115  | Magnesium-activated aldehyde dehydrogenase, cytosolic (SY-Saccharomyces cerevisiae S288c) | membrane | catalytic activity | 0.377 0.346 4.49 |
| P14540  | Fructose-bisphosphate aldolase (SY-Saccharomyces cerevisiae S288c)            | cytoplasm, cytosol, membrane, mitochondrion | catalytic activity; metal ion binding | 0.292 1.448 4.96 |
| Q03640  | Triclinin 3 (SY-Saccharomyces cerevisiae S288c)                                | endoplasmic reticulum, membrane, mitochondrion, membrane, mitochondrion | metal ion binding; protein binding | 0.032 0.168 5.25 |
| Q12230  | Sphingolipid long chain base-responsive protein LSP1 (SY-Saccharomyces cerevisiae S288c) | cytoplasm, membrane, mitochondrion | catalytic activity; metal ion binding | 14.849 84.77 5.71 |
| P28240  | Isocitrate lyase (SY-Saccharomyces cerevisiae S288c)                           | cytoplasm, extracellular, vacuole | catalytic activity; metal ion binding | 0.077 0.45 5.84 |
| Q00899  | Uncharacterized mitochondrial outer membrane protein YPR098C (SY-Saccharomyces cerevisiae S288c) | membrane, mitochondrion | catalytic activity; metal ion binding | 0.778 4.623 5.94 |
| Q02981  | ABC1 family protein YPL109C, mitochondrial (SY-Saccharomyces cerevisiae S288c) | membrane, mitochondrion | catalytic activity; nucleotide binding | 0.059 0.413 7.00 |
| P10663  | Phosphoenolpyruvate carboxykinase (APT) (SY-Saccharomyces cerevisiae S288c)    | cytosol | catalytic activity; nucleotide binding; protein binding | 0.166 1.326 7.99 |
| P38825  | Protein TOM71 (SY-Saccharomyces cerevisiae S288c)                             | membrane, mitochondrion | protein binding; transport activity | 0.061 0.805 13.2 0 |
| P39518  | Long-chain-fatty-acid-CoA ligase 2 (SY-Saccharomyces cerevisiae S288c)         | cytoplasm, mitochondrion | catalytic activity; nucleotide binding | 0.055 0.802 14.5 8 |
Supplemental Table S5. The relative concentrations of proteins in mitochondria purified from WT or ups1Δ cells cultured without LCA. Mitochondria were purified from WT or ups1Δ cells recovered on day 4 of cell culturing without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI ups1Δ | Ratio ups1Δ / WT |
|-----------|-------------|----------------|---------|---------------------|-------------------|-------------------|----------|-------------|-----------------|
| Q12165    | ATP synthase subunit delta, mitochondrial | 8515 60 | ATP16 | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 4.623 | 0.334 | 0.07 |
| P37267    | Assembly factor cdp4 (OS=Saccharomyces cerevisiae S288c) |   | CBP4 | cell organization and biogenesis | membrane; mitochondrion |   | 7.111 | 0.52 | 0.07 |
| P81449    | ATP synthase subunit e, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8519 22 | TIM11; YDR32ZC-A | cell organization and biogenesis;metabolic process;transport | membrane; mitochondrion | catalytic activity; structural molecule activity; transporter activity | 9 | 0.778 | 0.09 |
| P19595    | 37S ribosomal protein YMR31, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8506 10 | YMR31; YFR049A | cell organization and biogenesis;metabolic process | mitochondrion; ribosome | catalytic activity; protein binding; structural molecule activity | 26.82 | 6 | 2.594 | 0.10 |
| P00128    | Cytochrome b-1 complex subunit 7 (OS=Saccharomyces cerevisiae S288c) | 8521 42 | OCR7; YDR528C | cell organization and biogenesis; metabolic process;transport | membrane; mitochondrion | catalytic activity; transporter activity | 34.53 | 8 | 3.642 | 0.10 |
| P31270    | Pyruvate dehydrogenase (acyltransfer) kinase 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8528 21 | PKE1; YGL059W | metabolic process; regulation of biological process | mitochondrion; organelle lumen | catalytic activity; nucleotide binding; protein binding | 0.778 | 0.086 | 0.11 |
| P32799    | Cytochrome c oxidase subunit 6A, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8526 84 | COX13; YGL191W | cell organization and biogenesis; metabolic process; regulation of biological process;transport | membrane; mitochondrion | catalytic activity; enzyme regulator activity; transporter activity | 18.95 | 3 | 2.162 | 0.11 |
| P36141    | Putative redox protein fimp46, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8539 23 | FMP46; YKR049C | metabolic process | mitochondrion | catalytic activity; protein binding | 4.337 | 0.52 | 0.12 |
| P35319    | Abhydrolase domain-containing protein IMO32 (OS=Saccharomyces cerevisiae S288c) | 8529 19 | IMO32; YGR265W | metabolic process; transport | mitochondrion | catalytic activity | 0.931 | 0.116 | 0.12 |
| P47140    | Altered inheritance rate of mitochondria protein 25 (OS=Saccharomyces cerevisiae S288c) | 8535 63 | AIM25; YIR100D | cell organization and biogenesis | membrane; mitochondrion | transporter activity | 0.874 | 0.11 | 0.13 |
| P17679    | Glutaredoxin-2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8521 24 | GRX2; YDR523YW | cellular homeostasis; metabolic process; response to stimulus;transport | cytoplasm; cytosol; mitochondrion; nucleus | antioxidant activity; catalytic activity | 1.848 | 0.233 | 0.13 |
| Q04472    | Mitochondrial inner membrane I- AIA protease supercomplex subunit MGR3 (OS=Saccharomyces cerevisiae S288c) | 8531 42 | MGR3; YMR115W | metabolic process | membrane; mitochondrion | protein binding | 0.52 | 0.072 | 0.14 |
| Q96VH5    | MICOS complex subunit Mic10 (OS=Saccharomyces cerevisiae S288c) | 8503 00 | MOS51; MIC10; YCL057C-A | cell organization and biogenesis | membrane; mitochondrion |   | 6.197 | 0.931 | 0.15 |
| P53738    | Uncharacterized protein YNRO40W (OS=Saccharomyces cerevisiae S288c) | 8557 76 | YNRO40W; YNR040W | mitochondrial |   | 0.73 | 0.116 | 0.16 |
| P00427    | Cytochrome c oxidase subunit 6, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8564 48 | COM6; YHR005Y | metabolic process; transport | membrane; mitochondrion | catalytic activity; metal ion binding; transporter activity | 7.254 | 1.154 | 0.16 |
| P02381    | Ribosomal protein VAR1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8545 86 | VAR1; Q040 | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.688 | 0.11 | 0.16 |
| P35723    | UFP0674 endoplasmic reticulum membrane protein YNR021W (OS=Saccharomyces cerevisiae S288c) | 8557 55 | YNR021W; YFR021W | endoplasmic reticulum; membrane | metal ion binding | 0.65 | 0.105 | 0.16 |
| P38341    | MICOS complex subunit Mic12 (OS=Saccharomyces cerevisiae S288c) | 8525 66 | AIM1; MIC12; YBR262C | cell organization and biogenesis | membrane; mitochondrion |   | 1.783 | 0.292 | 0.16 |
| Q12032 | Altered inheritance of mitochondria protein 41, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8543 | AIM41; YDR215C | mitochondrial | catalytic activity | 2.831 | 0.468 | 0.17 |
| P00045 | Cytochrome c iso-2 [Os=Saccharomyces cerevisiae S288c] | 8566 | CYC7; YEL039C | mitochondrial | metabolic process;transport | 1.512 | 0.259 | 0.17 |
| P00447 | Superoxide dismutase [Mn], mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8563 | SOD2; YHR008C | mitochondrial;organelle lumen | antioxidant activity;catalytic activity;metal ion binding | 6.017 | 1.031 | 0.17 |
| P40452 | Cytochrome c oxidase assembly factor 1 [Os=Saccharomyces cerevisiae S288c] | 8546 | COA1; YIL157C | mitochondrial;ribosome | cell organization and biogenesis | 0.448 | 0.086 | 0.19 |
| P23369 | SAP ribosomal protein L25, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8529 | MRPL25; YGL076C | structural molecule activity | membrane;mitochondrion | 0.848 | 0.166 | 0.20 |
| P32266 | Dynamin-like GTPase MGM1, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8543 | MGM1; YOR211C | structural molecule activity | membrane;mitochondrion | 2.981 | 0.585 | 0.20 |
| P22533 | SAP ribosomal protein L8, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8533 | MRPL8; YIL063C | structural molecule activity | membrane;mitochondrion | 1.31 | 0.233 | 0.18 |
| P08525 | Cytochrome b-c1 complex subunit 8 [Os=Saccharomyces cerevisiae S288c] | 8532 | QCR8; YIL156W | membrane;mitochondrion | catalytic activity;transporter activity | 30.62 | 0.468 | 0.22 |
| P23833 | Protein SC01, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8523 | SCO1; YBR037C | membrane;mitochondrion | catalytic activity;transporter activity | 1.448 | 0.292 | 0.20 |
| P40086 | Cytochrome c oxidase assembly protein Cox15 [Os=Saccharomyces cerevisiae S288c] | 8568 | COX15; YER141W | membrane;mitochondrion | catalytic activity;transporter activity | 2.594 | 0.532 | 0.21 |
| P25372 | Thioredoxin-3, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8504 | TRX3; YCR083W | cytoplasm;mitochondrion | catalytic activity | 2.511 | 0.52 | 0.21 |
| P28239 | Inorganic pyrophosphatase, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8553 | PP2A2; YMR262W | cytoplasm;mitochondrion | catalytic activity;metal ion binding | 0.585 | 0.122 | 0.21 |
| P18496 | Mitochondrial ATPase complex subunit ATP10 [Os=Saccharomyces cerevisiae S288c] | 8511 | ATP10; YLR393W | cytoplasm;membrane;mitochondrion | protein binding | 1.239 | 0.259 | 0.21 |
| P36528 | SAP ribosomal protein L17, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8554 | MRPL17; YNL252C | structural molecule activity | membrane;mitochondrion | 0.52 | 0.11 | 0.21 |
| P47039 | Probable kynurenine–oxoglutarate transaminase BNA3 [Os=Saccharomyces cerevisiae S288c] | 8533 | BNA3; YIL060W | cytoplasm;mitochondrion | catalytic activity | 0.468 | 0.101 | 0.22 |
| P40165 | NAD(P) hydrolase transamidase [Os=Saccharomyces cerevisiae S288c] | 8555 | NNR1; YNL200C | cytoplasm;mitochondrion | catalytic activity;metal ion binding;metal ion binding | 2.162 | 0.468 | 0.22 |
| P40305 | Mitochondrial 37S ribosomal protein S27 [Os=Saccharomyces cerevisiae S288c] | 8531 | RSM27; YGR215W | mitochondrial | catalytic activity;protein binding;protein binding | 30.62 | 6.667 | 0.22 |
| P70299 | Elongation factor Tu, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8543 | TUF1; YOR181W | mitochondrial | catalytic activity;metal ion binding;metal ion binding | 0.353 | 0.078 | 0.22 |
| P11325 | LesC2–RNA ligase, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8510 | LAM2; YCR382C | mitochondrial;organellae lumen | catalytic activity;transporter activity | 0.931 | 0.207 | 0.22 |
| P25039 | Elongation factor G, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8507 | MEF1; YLR069C | mitochondrial;organellae lumen | catalytic activity;transporter activity | 0.931 | 0.207 | 0.22 |
| P40098 | Uncharacterized mitochondrial membrane protein FMP10 [Os=Saccharomyces cerevisiae S288c] | 8569 | FMP10; YER182W | membrane;mitochondrion | catalytic activity | 5.952 | 1.336 | 0.22 |
| P36066 | Protein MRG3-like [Os=Saccharomyces cerevisiae S288c] | 8537 | YKL133C; YKL133C | membrane;mitochondrion | catalytic activity | 1.054 | 0.241 | 0.23 |
| P12687 | SAP ribosomal protein L2, mitochondrial [Os=Saccharomyces cerevisiae S288c] | 8557 | MRPL7; YNL200C | mitochondrial;ribosome | catalytic activity;transporter activity | 1.565 | 0.369 | 0.24 |
| P39525 | 3-oxoacyl-[acyl-carrier-protein] synthase homolog [Os=Saccharomyces cerevisiae S288c] | 8567 | CEM1; YER061C | mitochondrial | catalytic activity | 2.899 | 0.688 | 0.24 |
| Accession | Description | GO Terms | Mean | SD | 95% CI |
|-----------|-------------|----------|------|----|--------|
| P54115    | Magnesium-activated aldehyde dehydrogenase, cystolic (OS=Saccharomyces cerevisiae S288c) | 8560 44 | ALDO; YPL061 W | metabolic process;response to stimulus | cytoplasm;cytosol;mitochondrion | catalytic activity | 0.25 | 0.077 | 0.31 |
| P39677    | Ribosome-releasing factor 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8533 42 | MF2F; YIL102 W | cell organization and biogenesis;metabolic process | cytosol;mitochondrion | catalytic activity;nucleotide binding;RNA binding | 0.179 | 0.056 | 0.31 |
| P40513    | Mitochondrial acidic protein MAM33 (OS=Saccharomyces cerevisiae S288c) | 8547 40 | MAM3; YIL170 C | metabolic process;regulation of biological process | mitochondrion;organell lumen | translation regulator activity | 3.642 | 1.154 | 0.32 |
| P32445    | Single-stranded DNA-binding protein RM14, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8503 95 | RIM1; YCR028 C-A | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion | DNA binding | 3.642 | 1.154 | 0.32 |
| P81451    | ATP synthase subunit K, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8540 77 | ATP19; YOL077 W-A | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 3.642 | 1.154 | 0.32 |
| P40008    | Protein FAM52, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8567 21 | FAM52; YER004 W | endoplasmic reticulum;membrane;mitochondrion | catalytic activity | 3.217 | 1.054 | 0.33 |
| P33310    | ATP-dependent permease MOD1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8508 85 | MOD1; YLR188 W | transport | membrane;mitochondrion | catalytic activity;nucleotide binding;transporter activity | 0.833 | 0.274 | 0.33 |
| P40471    | NADPH-dependent 1-acetylhydroxyacetone phosphate reductase (OS=Saccharomyces cerevisiae S288c) | 8546 82 | AYP1; YIL124 W | metabolic process | cytoplasm;endoplasmic reticulum;membrane;mitochondrion | catalytic activity | 1.239 | 0.413 | 0.33 |
| P12688    | 375 ribosomal protein MRP13, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8529 75 | MRP13; YGR084 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.239 | 0.413 | 0.33 |
| P32898    | Mitochondrial presequence protease (OS=Saccharomyces cerevisiae S288c) | 8520 41 | CYM1; YDR43 D-C | metabolic process | mitochondrion | catalytic activity;metal ion binding | 1.349 | 0.45 | 0.33 |
| P10662    | 375 ribosomal protein MRP1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8519 48 | MRP1; YDR54 TW | cell organization and biogenesis;metabolic process;response to stimulus | mitochondrion;ribosome | antioxidant activity;catalytic activity;metal ion binding;structural molecule activity | 2.981 | 0.995 | 0.33 |
| P36163    | mitochondrial metalloendopeptidase DMA1 (OS=Saccharomyces cerevisiae S288c) | 8539 62 | DMA1; YKR087 C | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding | 0.73 | 0.245 | 0.34 |
| P38797    | Protein phosphatase 2C homolog 7, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8564 75 | PTCH; YHR076 W | metabolic process | mitochondrion | catalytic activity;metal ion binding;protein binding | 0.688 | 0.233 | 0.34 |
| P53326    | Uncharacterized protein YGR266W (OS=Saccharomyces cerevisiae S288c) | 8531 82 | YGR266W 6| 8W | membrane;mitochondrion | 1.081 | 0.369 | 0.34 |
| P00410    | Cytochrome c oxidase subunit 2 (OS=Saccharomyces cerevisiae S288c) | 8546 22 | COX2; YQ0250 | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding;protein binding;transporter activity | 4.623 | 1.61 | 0.35 |
| P28817    | 3-hydroxyalkylbutyl-CoA hydrolase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8516 06 | EHD3; YDR034 AC | metabolic process | mitochondrion | catalytic activity | 1.395 | 0.487 | 0.35 |
| P35230    | MIF-1-like protein, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8538 26 | MIF1; YKL040 C-C | cell organization and biogenesis;cellular homeostasis;metabolic process | mitochondrion;organell lumen | metal ion binding | 3.87 | 1.371 | 0.35 |
| P18900    | Hexameryl-pyrophosphate synthase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8522 88 | Coo1; YBR003 W | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding;protein binding | 0.468 | 0.166 | 0.35 |
| P211306   | ATP synthase subunit epsilon, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8558 57 | ATP15; YPL271 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 2.162 | 0.778 | 0.36 |
| P39006    | Phosphatidylserine decarboxylase proenzyme 1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8555 52 | PS1O; YNL169 C | metabolic process;regulation of biological process | membrane;mitochondrion | catalytic activity | 0.743 | 0.269 | 0.36 |
| P36516    | 545 ribosomal protein L3, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8550 39 | MRPL3; YMR024 W | cell organization and biogenesis;metabolic process;response to stimulus | mitochondrion;nucleus;ribosome | catalytic activity;RNA binding;structural molecule activity | 0.743 | 0.269 | 0.36 |
| P06067    | cytochrome b-c1 complex subunit Rieske, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8566 89 | RIP1; YEL024 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding;transporter activity | 55.23 | 20.54 | 0.37 |
| P46681    | D-lactate dehydrogenase (cytochrome) 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8513 76 | DLU2; YOL178 W | metabolic process | mitochondrion;organell lumen | catalytic activity;metal ion binding;protein binding | 1.829 | 0.682 | 0.37 |
| Q02784    | Monothiol glutaredoxin-5, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8560 48 | GRX5; YPL059 | cell organization and biogenesis;cellular | mitochondrion;organell lumen | catalytic activity;metal ion | 1.783 | 0.668 | 0.37 |
| Accession | Description                                                                 | GO Terms                                                                 | P-value  |
|-----------|------------------------------------------------------------------------------|------------------------------------------------------------------------|----------|
| P04037    | 375 ribosomal protein S12, mitochondrial (S. cerevisiae S288c)               | homeostasis; metabolic process                                           | 1.783    |
|           |                                                                               | regulation of biological process; response to stimulus                  | 0.668    |
|           |                                                                               | mitochondrion; ribosome                                                 | 0.37     |
| Q12298    | uncharacterized ABC transporter ATP-binding protein YDR061W (S. cerevisiae S288c) | mitochondrial                                                           | 0.512    |
|           |                                                                               | catalytic activity; nucleotide binding                                  | 0.194    |
| Q03788    | Altered inheritance of mitochondria protein 36, mitochondrial (S. cerevisiae S288c) | mitochondrial                                                           | 1.637    |
|           |                                                                               | membrane; mitochondrion                                                 | 0.624    |
| Q04458    | Fatty aldehyde dehydrogenase HFD1 (S. cerevisiae S288c)                     | metabolic process                                                       | 4.055    |
|           |                                                                               | endoplasmic reticulum; endosome; membrane; mitochondrion                | 1.555    |
| P53140    | Protein RMD9, mitochondrial (S. cerevisiae S288c)                            | cell differentiation; metabolic process; regulation of biological process | 1.512    |
|           |                                                                               | membrane; mitochondrion                                                 | 0.585    |
| P40364    | Mitochondrial peculiar membrane protein 1 (S. cerevisiae S288c)              | membrane; mitochondrion                                                 | 1.512    |
|           |                                                                               |                                                                        | 0.585    |
| P40502    | Altered inheritance of mitochondria protein 19, mitochondrial (S. cerevisiae S288c) | membrane; mitochondrion                                                 | 1.512    |
|           |                                                                               |                                                                        | 0.585    |
| P00830    | ATP synthase subunit beta, mitochondrial (S. cerevisiae S288c)               | metabolic process                                                       | 1.424    |
|           |                                                                               | transport; cytosol; membrane; mitochondrion                             | 0.557    |
|           |                                                                               | catalytic activity; nucleotide binding; protein binding; transporter activity | 0.39     |
| P21560    | Protein CBP3, mitochondrial (S. cerevisiae S288c)                            | cell organization and biogenesis; regulation of biological process      | 1.371    |
|           |                                                                               | mitochondrion; ribosome                                                 | 0.54     |
|           |                                                                               | RNA binding; structural molecule activity                               | 0.39     |
| P32904    | S45 ribosomal protein L6, mitochondrial (S. cerevisiae S288c)                | cell organization and biogenesis; metabolic process                     | 1.362    |
|           |                                                                               | mitochondrion; ribosome                                                 | 0.537    |
| P36775    | Lon protease homing, mitochondrial (S. cerevisiae S288c)                     | cell organization and biogenesis; metabolic process; response to stimulus | 4.179    |
|           |                                                                               | cytoplasm; mitochondrial; organellar lumen                              | 1.683    |
|           |                                                                               | catalytic activity; DNA binding; nucleotide binding; RNA binding        | 0.40     |
| P006892   | NADH kinase P055, mitochondrial (S. cerevisiae S288c)                        | metabolic process; response to stimulus                                 | 1.31     |
|           |                                                                               | mitochondrion; organellar lumen                                         | 0.52     |
|           |                                                                               | catalytic activity; nucleotide binding                                  | 0.40     |
| P53163    | S45 ribosomal protein L12, mitochondrial (S. cerevisiae S288c)              | cell organization and biogenesis; metabolic process                     | 1.31     |
|           |                                                                               | mitochondrion; ribosome                                                 | 0.52     |
|           |                                                                               | RNA binding; structural molecule activity                               | 0.40     |
| P00175    | Cytochrome b2, mitochondrial (S. cerevisiae S288c)                          | metabolic process; transport                                            | 1.239    |
|           |                                                                               | cytosol; membrane; mitochondrial; nucleus                               | 0.496    |
|           |                                                                               | catalytic activity; metal ion binding; nucleotide binding; RNA binding  | 0.40     |
| P07253    | cytochrome B pre-mRNA-processing protein 6 (S. cerevisiae S288c)            | cell organization and biogenesis; metabolic process; regulation of biological process | 4.179    |
|           |                                                                               | mitochondrion; ribosome                                                 | 1.683    |
|           |                                                                               |                                                                        | 0.40     |
| Q02486    | ARS-binding factor 2, mitochondrial (S. cerevisiae S288c)                   | cell organization and biogenesis; metabolic process; regulation of biological process | 69.17    |
|           |                                                                               | chromosome; mitochondrion; nucleus                                      | 27.94    |
|           |                                                                               | DNA binding                                                             | 3        |
| P40961    | prohibitin-1 (S. cerevisiae S288c)                                           | cell organization and biogenesis; metabolic process; regulation of biological process | 6.848    |
|           |                                                                               | mitochondrion; ribosome                                                 | 2.793    |
|           |                                                                               | protein binding                                                         | 0.41     |
| Q04599    | S45 ribosomal protein L1, mitochondrial (S. cerevisiae S288c)               | cell organization and biogenesis; metabolic process                     | 1.069    |
|           |                                                                               | mitochondrion; ribosome                                                 | 0.438    |
|           |                                                                               | RNA binding; structural molecule activity                               | 0.41     |
| P00927    | Threonine dehydratase, mitochondrial (S. cerevisiae S288c)                  | metabolic process                                                       | 3.125    |
|           |                                                                               | cytoplasm; mitochondrial                                                | 1.285    |
|           |                                                                               | catalytic activity                                                      | 0.41     |
| P07246    | Alcohol dehydrogenase 3, mitochondrial (S. cerevisiae S288c)                | metabolic process                                                       | 10.15    |
|           |                                                                               | mitochondrion; organellar lumen                                         | 4.179    |
|           |                                                                               | catalytic activity; metal ion binding                                   | 0.41     |
| Q06678    | S45 ribosomal protein L55, mitochondrial (S. cerevisiae S288c)              | cell organization and biogenesis; metabolic process                     | 1.031    |
|           |                                                                               | mitochondrion; ribosome                                                 | 0.425    |
|           |                                                                               | structural molecule activity                                            | 0.41     |
| P35180    | mitochondrial import receptor subunit Tom20 (S. cerevisiae S288c)           | cell organization and biogenesis; transport                              | 1.031    |
|           |                                                                               | mitochondrion; ribosome                                                 | 0.425    |
|           |                                                                               | protein binding; transporter                                           | 0.41     |
| P43617    | Uncharacterized mitochondrial carrier YFR045W (S. cerevisiae S288c)         | metabolite process; transport                                           | 0.959    |
|           |                                                                               | structural molecule activity; transporter                               | 0.41     |
|           |                                                                               | catalytic activity; metal ion binding                                   | 0.42     |
| P04037    | cytochrome c oxidase subunit 4, mitochondrial (S. cerevisiae S288c)         | cell organization and biogenesis; metabolic process; transport          | 42.28    |
|           |                                                                               | mitochondrion; ribosome                                                 | 17.73    |
|           |                                                                               | catalytic activity                                                      | 0.42     |
P33416  Heat shock protein 78, mitochondrial [Os=Saccharomyces cerevisiae S288c]
8518 45  HSP78; VDR258C cell organization and biogenesis, metabolic process; regulation of biological process; response to stimulus mitochondrion, organelle lumen catalytic activity; nutrient binding; protein binding 7.929 3.359 0.42

Q08968  UFP0061 protein FMP40 [Os=Saccharomyces cerevisiae S288c]
8558 79  FMP40; YPL222W mitochondrial mitochondrion protein binding 2.162 0.917 0.42

P25573  Mitochondrial inner membrane l-AAA protease supercomplex subunit MGR1 [Os=Saccharomyces cerevisiae S288c]
8503 13  MGR1; YCL044C metabolic process membrane, mitochondrion protein binding 1.649 0.701 0.43

P40053  Altered inheritance of mitochondria protein 9, mitochondrial [Os=Saccharomyces cerevisiae S288c]
8568 13  AIM5; YER080W mitochondrial mitochondrion 4.555 1.938 0.43

Q06236  Mitochondrial inner membrane protein SH4 [Os=Saccharomyces cerevisiae S288c]
8508 61  SH4; YLR164C metabolic process membrane, mitochondrion catalytic activity; nutrient binding; RNA binding 3.217 1.371 0.43

P36101  tRNA threonylcarboxyladenosine dehydratase 2 [Os=Saccharomyces cerevisiae S288c]
8538 41  TDC2; YKLO27W; YKLO27W metabolic process cytosol, membrane, mitochondrion catalytic activity; nutrient binding 0.778 0.334 0.43

P32843  Mitochondrial escape protein 2 [Os=Saccharomyces cerevisiae S288c]
8553 46  YML2; YMR302C cell organization and biogenesis, metabolic process membrane, mitochondrion catalytic activity 5.158 2.227 0.43

P53220  Mitochondrial import inner membrane translocase subunit TIM21 [Os=Saccharomyces cerevisiae S288c]
8529 21  TIM21; YGR063C cell organization and biogenesis, transport mitochondrial mitochondrion protein binding 0.779 0.311 0.43

P07256  Cytochrome b-2 complex subunit 1, mitochondrial [Os=Saccharomyces cerevisiae S288c]
8522 35  COR1; YBL045C metabolic process, transport membrane, mitochondrion catalytic activity; nutrient binding; protein binding; transport activity 18.78 3 8.183 0.44

P40159  Uncharacterized protein YNL208W [Os=Saccharomyces cerevisiae S288c]
8555 13  YNL208W; YNL208W membrane, mitochondrion, ribosome catalytic activity 0.668 0.292 0.44

P40012  Protoporphyrinogen oxidase [Os=Saccharomyces cerevisiae S288c]
8567 33  HEM14; YER014W catalytic activity 2.162 0.947 0.44

P40581  Peroxiredoxin HYR3 [Os=Saccharomyces cerevisiae S288c]
8548 55  HYR3; YBR037W antioxidant activity; catalytic activity 0.585 0.259 0.44

P40530  [Pyruvate dehydrogenase (acetyltransferring)] kinase 1, mitochondrial [Os=Saccharomyces cerevisiae S288c]
8547 69  PKP1; YIL042C catalytic activity; nutrient binding; protein binding 0.551 0.245 0.44

P36520  S45 ribosomal protein L10, mitochondrial [Os=Saccharomyces cerevisiae S288c]
8554 36  MRPL10; YNL284C cell organization and biogenesis, metabolic process mitochondrial, ribosome structural molecule activity 0.551 0.245 0.44

P38112  Tricarboxylate transport protein [Os=Saccharomyces cerevisiae S288c]
8525 94  CTP1; YBR291C structural activity; transport activity 0.551 0.245 0.44

P38922  Dihydroxy-acid dehydratase, mitochondrial [Os=Saccharomyces cerevisiae S288c]
8534 73  ILV5; YIR016C catalytic activity; nutrient binding; protein binding 29.53 9 13.17 0.45

P10507  mitochondrial processing peptidase subunit beta [Os=Saccharomyces cerevisiae S288c]
8508 60  MAS1; YLR163C catalytic activity; nutrient binding; protein binding 1.371 0.616 0.45

P53312  Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial [Os=Saccharomyces cerevisiae S288c]
8531 59  LSC2; YGR244C catalytic activity; nutrient binding; transport activity 20.01 7 9 0.45

Q06567  ABC1 family protein MCF2 [Os=Saccharomyces cerevisiae S288c]
8509 55  MCF2; YKR253W cell organization and biogenesis mitochondrial mitochondrion 0.484 0.218 0.45

P38702  mitochondrial carrier protein LEU5 [Os=Saccharomyces cerevisiae S288c]
8563 91  LEU5; YHR002W catalytic activity; nutrient binding; protein binding 0.468 0.212 0.45

P34224  Uncharacterized protein YBL059W [Os=Saccharomyces cerevisiae S288c]
8522 21  YBL059W; YBL059W mitochondrial mitochondrion 0.468 0.212 0.45

P27929  37S ribosomal protein NAM9, mitochondrial [Os=Saccharomyces cerevisiae S288c]
8555 85  NAM9; YNL137C cell organization and biogenesis, metabolic process; regulation of biological process mitochondrial, ribosome RNA binding; structural molecule activity 1.062 0.484 0.46

P32839  Mitochondrial chaperone BCS1 [Os=Saccharomyces cerevisiae S288c]
8519 81  BCS1; YDR37SC catalytic activity; nutrient binding; protein binding; transport activity 0.425 0.194 0.46
| Q01976 | ADP-ribose pyrophosphatase [OS=Saccharomyces cerevisiae S288c] | 8524 08 | YSA1; YBR111 C | metabolic process | cytoplasm/mitochondrion;nucleus | catalytic activity;metal ion binding | 0.425 | 0.194 | 0.46 |
| Q0487 | Mitochondrial inner membrane protein SHH3 [OS=Saccharomyces cerevisiae S288c] | 8551 45 | SHK3; YMR118 C | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding | 0.425 | 0.194 | 0.46 |
| O12428 | Probable 2-methylserine dehydratase [OS=Saccharomyces cerevisiae S288c] | 8561 08 | FDH1; YPR802 W | metabolic process | cytoplasm;membrane;mitochondrion | catalytic activity | 18.11 | 8.306 | 0.46 |
| Q04172 | Sensitive to high-expression protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8520 02 | S9ER; YDR39 W | cell organization and biogenesis | membrane;mitochondrion | | 0.374 | 0.172 | 0.46 |
| P25348 | S45 ribosomal protein L22, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8503 59 | MRPL3 2; YCR003 W | cell organization and biogenesis;metabolic process | membrane;mitochondrion;ribosome | RNA binding;structural molecule activity | 0.389 | 0.179 | 0.46 |
| Q03713 | Respiratory supercomplex factor 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8549 78 | RCF1; YML03 1W | cell organization and biogenesis | membrane;mitochondrion | | 2.162 | 0.995 | 0.46 |
| P17558 | 37S ribosomal protein PETF123, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8543 29 | PET123 1; YOR15 1W | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | structural molecule activity | 1.448 | 0.668 | 0.46 |
| Q06630 | Mitochondrial homologous recombination protein 1 [OS=Saccharomyces cerevisiae S288c] | 8518 90 | MHR1; YDR29 6W | cell organization and biogenesis;metabolic process;regulation of biological process| mitochondrion; nucleus | catalytic activity;DNA binding;structural molecule activity | 0.359 | 0.166 | 0.46 |
| P48360 | Probable NADPH-adrenodoxin oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8519 82 | ARM1; YDR37 6W | cellular homeostasis;metabolic process;transport | cytoplasm;membrane;mitochondrion;organellar lumen | catalytic activity | 0.346 | 0.16 | 0.46 |
| P36523 | S45 ribosomal protein L55, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8510 22 | MRPL1 S; YLR312 W-A | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | catalytic activity;RNA binding;structural molecule activity | 0.334 | 0.153 | 0.46 |
| P38523 | Gpr75 protein homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8544 07 | MGE1; YOR23 2W | metabolic process;regulation of biological process;transport | membrane;mitochondrion;organellar lumen | enzyme regulator activity;nucleotide binding;protein binding | 1.336 | 0.624 | 0.47 |
| P25270 | rRNA methyltransferase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8543 76 | MRM1; YOR20 1C | metabolic process | mitochondrion | catalytic activity;RNA binding | 0.274 | 0.129 | 0.47 |
| P39722 | Mitochondrial Rho GTase 1 [OS=Saccharomyces cerevisiae S288c] | 8512 49 | GEM1; YAL048 C | cell organization and biogenesis;regulation of biological processes| mitochondrion | catalytic activity;metal ion binding;protein binding | 0.259 | 0.122 | 0.47 |
| P00445 | Superoxide dismutase [Cu-Zn] [OS=Saccharomyces cerevisiae S288c] | 8535 68 | SOD1; YIR104 1C | cell organization and biogenesis;cellular homeostasis;metabolic process;regulation of biological process;response to stimulus| cytoplasm;cytosol;mitochondrion;nucleus | antioxidant activity;catalytic activity;metal ion binding;protein binding | 1.848 | 0.874 | 0.47 |
| O14467 | multiprotein-bridging factor 1 [OS=Saccharomyces cerevisiae S288c] | 8544 74 | MFB1; YDR29 8CA | metabolic process;regulation of biological process | cytoplasm;mitochondrion;nucleus | RNA binding | 1.848 | 0.874 | 0.47 |
| P49367 | Homeocentase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8518 20 | LYS4; YOR23 4W | metabolic process | mitochondrion | catalytic activity;metal ion binding;protein binding | 1.54 | 0.73 | 0.47 |
| P36046 | Mitochondrial intermembrane space import and assembly protein 40 [OS=Saccharomyces cerevisiae S288c] | 8536 39 | MIAD40; YKL195 W | cellular component movement;metabolic process;response to stimulus;transport | membrane;mitochondrion | catalytic activity;protein binding;transporter activity | 3.262 | 1.555 | 0.48 |
| P53881 | S45 ribosomal protein L22, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8555 44 | MRPL2 2; YNL177 C | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | RNA binding;structural molecule activity | 1.154 | 0.551 | 0.48 |
| P51998 | S45 ribosomal protein ytm6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8549 83 | YML6; YML02 5C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.154 | 0.551 | 0.48 |
| P19262 | Dihydrodiolpolysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8517 26 | KGD2; YDR134 BC | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;protein binding | 6.406 | 3.062 | 0.48 |
| P33311 | ATP-dependent permease MDL2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8558 58 | MDL2; YFL270 W | response to stimulus;transport | membrane;mitochondrion | catalytic activity;metal ion binding;transporter activity | 1.116 | 0.535 | 0.48 |
| P06401 | Cytochrome c oxidase subunit 1 [OS=Saccharomyces cerevisiae S288c] | 8545 98 | COX3; Q0045 | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding;transporter activity | 1.61 | 0.778 | 0.48 |
| Q08818 | Meiotic sister-chromatid recombination protein 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8545 36 | MSc6; YOR43 4C | metabolic process | mitochondrion;organellar lumen | RNA binding | 1.047 | 0.506 | 0.48 |
| P49095 | Glycine dehydrogenase (Decarboxylating), mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8552 27 | GCV2; YMR18 | metabolic process | cytosol;mitochondrion | catalytic activity | 2.433 | 1.184 | 0.49 |
| Protein | Accession | Function | Subcellular Location | Molecular Function | Z Score | p Value |
|---------|-----------|----------|----------------------|--------------------|---------|---------|
| Succinate dehydrogenase (ubiquinone) cytochrome b subunit, mitochondrial | 8517 | SDH4; YDR178W | metabolic process; transport | membrane; mitochondrion | 3.642 | 1.783 |
| Mitochondrial inner membrane I-AAA protease supercomplex subunit YME1 | 8561 | YME1; YPR024W | metabolic process; response to stimulus; transport | membrane; mitochondrion | 1.798 | 0.891 |
| Fumarate hydratase, mitochondrial | 8558 | FUM1; YPL292W | cell organization and biogenesis; metabolic process | cytoplasm; mitochondrial; organelle lumen | 13.87 | 0.50 |
| Succinate dehydrogenase (ubiquinone) cytochrome b subunit, mitochondrial | 8537 | SDH3; YKL141W | cell organization and biogenesis; metabolic process | membrane; mitochondrion | 1.276 | 0.638 |
| Sorbit assembly machinery 50 kDa subunit | 8557 | SAM50; YNL026W | cell organization and biogenesis; transport | membrane; mitochondrion | 0.743 | 0.374 |
| Peptidyl prolyl cis-trans isomerase C, mitochondrial | 8548 | CPR3; YML078W | cell death; metabolic process | mitochondrion; organelle lumen | 2.981 | 1.512 |
| Mitochondrial phosphate carrier protein 2 | 8507 | FMP25; YJR077W | cell organization and biogenesis | membrane; mitochondrion | 1.412 | 0.719 |
| Mitochondrial import inner membrane translocase subunit TIM54 | 8533 | TIM54; YIL054W | cell organization and biogenesis; transport | cytosol; membrane; mitochondrion | 0.655 | 0.334 |
| Mitochondrial carrier protein KIM2 | 8524 | KIM2; YBR192W | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrion | 1.512 | 0.778 |
| Protein MS551, mitochondrial | 8509 | MS551; YLR203C | metabolic process; regulation of biological process | membrane; mitochondrion | 1.929 | 0.995 |
| Isocitrate dehydrogenase [NADP] | 8557 | IDP3; YNL009W | metabolic process | cytoplasm; mitochondrion | 2.652 | 1.371 |
| Uncharacterized mitochondrial hydroxyase FMP41 | 8555 | FMP41; YNL168C | metabolic process | mitochondrion | 0.968 | 0.501 |
| Cysteine desulfurase, mitochondrial | 8503 | RF51; YCL017C | cell organization and biogenesis; metabolic process | mitochondrion; nucleus | 2.594 | 1.346 |
| Mitochondrial carnitine carrier | 8542 | CRCL1; YDR510W | metabolic process; transport | membrane; mitochondrion | 1.404 | 0.73 |
| N-terminal acetyltransferase 2 | 8530 | NAT2; YGR174C | metabolic process | cytoplasm; mitochondrion | 1.404 | 0.75 |
| Uncharacterized protein YKR070W | 8539 | YKR070W; YKR070W | metabolic process | mitochondrion | 0.833 | 0.438 |
| Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial | 8569 | PDA1; YER178W | cell growth; metabolic process | mitochondrion; organelle lumen | 21.63 | 11.49 |
| Alanine--glyoxylate aminotransferase 1 | 8505 | AGX1; YFL030W | metabolic process | cytosol; mitochondrion | 2.162 | 1.154 |
| ATPase inhibitor, mitochondrial | 8513 | INH1; YDL181W | metabolic process; regulation of biological process | mitochondrion | 2.162 | 1.154 |
| Protein AFG1 | 8566 | AFG1; YEL052W | cell organization and biogenesis; metabolic process; response to stimulus; transport | membrane; mitochondrion | 1.326 | 0.711 |
| Mitochondrial 2-methylisocitrate lyase | 8561 | ICL2; YPR006C | metabolic process | mitochondrion; organelle lumen | 5.158 | 2.793 |
Potassium-activated aldehyde dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8545 56 ALD4; YDR374W metabolic process mitochondrion;organelle lumen catalytic activity 47.49 7 25.82 7 0.54

DnaI homolog 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8505 30 MDI1; YFL016C cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus mitochondrion;organelle lumen enzyme regulator activity;metabolon binding;protein binding 3.037 1.656 0.55

N-acetyl-phosphaldehydeamine-hydrolyzing phospholipase D, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8560 01 FMP90; YPL193C metabolic process membrane;mitochondrion catalytic activity;metabolon binding 0.557 0.304 0.55

Mitochondrial respiratory chain complexes assembly protein AFG3 [OS=Saccharomyces cerevisiae S288c] 8567 37 AFG3; YER017C cell organization and biogenesis;metabolic process;response to stimulus mitochondrion catalytic activity;metabolon binding 1.342 0.734 0.55

Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8545 38 CPR2; YDR356W metabolic process;transport membrane;mitochondrion catalytic activity;metabolon binding 3.424 1.873 0.55

Enol[acyl-carrier protein] reductase [NAD(P), B-specific], mitochondrial [OS=Saccharomyces cerevisiae S288c] 8523 14 ETR1; YBR026C metabolic process mitochondrion;organelle lumen catalytic activity;DNA binding;metabolon binding 9 4.926 0.55

Heat shock protein 55C3, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8566 82 ECM10; YEL030W cell organization and biogenesis;metabolic process;transport mitochondrion nucleotide binding;protein binding 2.162 1.198 0.55

S45 ribosomal protein L24, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8552 31 MRP12 4; YMR19W cell organization and biogenesis;metabolic process mitochondrion;ribosome RNA binding;structural molecule activity 1.512 0.848 0.56

Heat shock protein 55C2, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8510 84 S522; YDR369W cell organization and biogenesis;metabolic process mitochondrion;organelle lumen nucleotide binding;protein binding 0.884 0.496 0.56

Methyltransferase DMS31, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8519 11 DMS31; YDR311W metabolic process membrane;mitochondrion catalytic activity 0.693 0.389 0.56

Cytochrome b-c1 complex subunit 10 [OS=Saccharomyces cerevisiae S288c] 8563 90 QCR10; YHR080W metabolic process;transport mitochondrion catalytic activity;transporter activity 5.31 2.981 0.56

Probable mitochondrial transport protein fsf1 [OS=Saccharomyces cerevisiae S288c] 8544 45 FSF1; YOR271C transport membrane;mitochondrion transporter activity 2.36 1.336 0.57

Presence translocated-associated motor subunit pm17, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8539 39 PAM17; YKR065C transport membrane;mitochondrion catalytic activity;transporter activity 1.371 0.778 0.57

Serine hydroxymethyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8525 65 SHM1; YBR1263W metabolic process mitochondrion catalytic activity 9 5.136 0.57

Mitochondrial processing peptidase subunit alpha [OS=Saccharomyces cerevisiae S288c] 8564 19 MAS2; YHR002C metabolic process;transport membrane;mitochondrion;organelle lumen catalytic activity;metabolon binding;protein binding 1.291 0.738 0.57

Sucinate dehydrogenase [ubiquione] flavoprotein subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8534 05 YIL045W; YIL045Y metabolic process;transport membrane;mitochondrion catalytic activity;metabolon binding 4.712 2.695 0.57

Ribosome-recycling factor, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8564 33 RF11; YHR038W cell organization and biogenesis;metabolic process mitochondrion RNA binding 1.254 0.719 0.57

Cytochrome c oxidase protein 20, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8518 17 COX20; YDR231C cell organization and biogenesis;metabolic process membrane;mitochondrion catalytic activity;protein binding 2.455 1.424 0.58

ADP,ATP carrier protein 1 [OS=Saccharomyces cerevisiae S288c] 8500 76 AAC1; YMR305C metabolic process;transport cytosol;membrane;mitochondrion structural molecule activity;transporter activity 11.74 3 6.848 0.58

Mitochondrial respiratory chain complexes assembly protein AFG3 [OS=Saccharomyces cerevisiae S288c] 8513 25 MRP11 1; YDL202C cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 1.069 0.624 0.58

Mitochondrial phosphate carrier protein [OS=Saccharomyces cerevisiae S288c] 8535 40 MIR1; YIR077C metabolic process;transport membrane;mitochondrion catalytic activity 30.62 3 17.95 7 0.59

Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8561 07 CT33; YPR001W metabolic process mitochondrion catalytic activity 5.529 3.262 0.59

Mitochondrial genome maintenance protein MGM101 [OS=Saccharomyces cerevisiae S288c] 8536 09 MGM1 01; YIR144 cell organization and biogenesis;metabolic process;response to stimulus chromosome;mitochondrion DNA binding 3.281 1.976 0.60
| Gene ID | Name                                                                 | References | p-value  |
|--------|----------------------------------------------------------------------|------------|----------|
| P32891 | D-lactate dehydrogenase (cytochrome), mitochondrial                   | 12.61      | 0.60     |
| P00431 | Cystochrome c peroxidase, mitochondrial                              | 1.15       | 0.60     |
| Q20950 | 375 ribosomal protein MRPS5, mitochondrial                          | 11.25      | 0.61     |
| Q12480 | Probable electron transfer flavoprotein subunit alpha, mitochondrial | 1.81       | 0.61     |
| P07806 | Valine-tRNA ligase, mitochondrial                                    | 0.37       | 0.61     |
| P32331 | Carrier protein YMC1, mitochondrial                                  | 0.97       | 0.61     |
| P32387 | S45 ribosomal protein L41, mitochondrial                             | 0.95       | 0.61     |
| Q08179 | Mitochondrial distribution and morphology protein 38                 | 3.73       | 0.61     |
| P43616 | Cys-Gly metalloendopeptidase-dug1                                   | 0.71       | 0.62     |
| P05626 | ATP synthase subunit 4, mitochondrial                                | 3.08       | 0.62     |
| P38172 | MITOREX complex component 3                                         | 0.31       | 0.62     |
| P27697 | Atypical kinase COQ8, mitochondrial                                 | 0.28       | 0.62     |
| Q3E24  | Uncharacterized protein YOR020W-A                                     | 3.64       | 0.63     |
| P19414 | Aconitase hydratase, mitochondrial                                   | 30.62      | 0.63     |
| P15179 | Aspartate-tRNA ligase, mitochondrial                                 | 0.24       | 0.63     |
| P47127 | Altered inheritance of mitochondria protein 24, mitochondrial        | 1.81       | 0.63     |
| P38072 | Protein SCO2, mitochondrial                                          | 0.73       | 0.63     |
| Q0648  | MITOREX complex component 10                                         | 0.22       | 0.63     |
| P32191 | Glycerol-3-phosphate dehydrogenase, mitochondrial                    | 5.43       | 0.64     |
| Q01532 | Cysteine proteinase 3, mitochondrial                                 | 0.18       | 0.64     |
| P38705 | Serine-tRNA ligase, mitochondrial                                    | 0.15       | 0.64     |
| P07236 | Threonine-tRNA ligase, mitochondrial                                 | 0.15       | 0.64     |
| P42900 | Sigma-like sequence protein 1, mitochondrial                         | 0.12       | 0.64     |
| Accession | Description                                                                 | Gene Information                                                                 | E-Value | Bit Score | P-value | FDR | Fold Change |
|-----------|-----------------------------------------------------------------------------|----------------------------------------------------------------------------------|---------|-----------|---------|-----|-------------|
| P53166    | ATP-dependent RNA helicase mrh4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YLR139C                                                                         | 0.225   | 0.145     | 0.64   |     |             |
| P25349    | Flavoprotein-like protein YCP4 [OS=Saccharomyces cerevisiae S288c]            | YCP4; YCR004C                                                                    | 9       | 5.813     | 0.65   |     |             |
| P38088    | Glycine–tRNA ligase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]       | ARG7; YMR062C                                                                    | 0.616   | 0.399     | 0.66   |     |             |
| P08466    | mitochondrial nuclease [OS=Saccharomyces cerevisiae S288c]                    | YUJ088C                                                                         | 1.637   | 1.069     | 0.65   |     |             |
| P07275    | Delta-1-pyruvyl-5-carboxylate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YJL037W                                                                         | 6.055   | 3.977     | 0.66   |     |             |
| Q04728    | Arginine biosynthesis bifunctional protein Arg1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YDL027W                                                                         | 2.384   | 1.581     | 0.66   |     |             |
| Q06543    | mitochondrial dicarboxylate transporter [OS=Saccharomyces cerevisiae S288c] | YER134C                                                                         | 1.404   | 0.931     | 0.66   |     |             |
| P40047    | Aldehyde dehydrogenase 5, mitochondrial [OS=Saccharomyces cerevisiae S288c]  | YER073C                                                                         |         |           |        |     |             |
| Q07349    | MTOR complex component 9 [OS=Saccharomyces cerevisiae S288c]                 | YDL027W                                                                         | 1.913   | 1.276     | 0.67   |     |             |
| P38910    | 10 kDa heat shock protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YDL066W                                                                         |         |           |        |     |             |
| P21954    | Isocitrate dehydrogenase (NADP), mitochondrial [OS=Saccharomyces cerevisiae S288c] | YDL066W                                                                         |         |           |        |     |             |
| P38325    | Mitochondrial outer membrane protein OML4 [OS=Saccharomyces cerevisiae S288c] | YDR230C                                                                         | 6.197   | 4.179     | 0.67   |     |             |
| P28834    | Isocitrate dehydrogenase (NAD) subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YDL066W                                                                         |         |           |        |     |             |
| P50085    | Prohibitin-2 [OS=Saccharomyces cerevisiae S288c]                              | YDR230C                                                                         | 4.926   | 3.329     | 0.68   |     |             |
| Q12482    | Mitochondrial aspartate-glutamate transporter AGC1 [OS=Saccharomyces cerevisiae S288c] | YDR230C                                                                         | 0.348   | 0.238     | 0.68   |     |             |
| P16622    | Ferrichelatase, mitochondrial [OS=Saccharomyces cerevisiae S288c]             | YDR155W                                                                         | 6.305   | 4.337     | 0.69   |     |             |
| P00277    | Mitochondrial import inner membrane translocase subunit TIM50 [OS=Saccharomyces cerevisiae S288c] | YVR17W                                                                         | 9       | 6.197     | 0.69   |     |             |
| P36013    | NAD-dependent malic enzyme, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YDR021C                                                                         | 1.985   | 1.371     | 0.69   |     |             |
| P00560    | Phosphoglycerate kinase [OS=Saccharomyces cerevisiae S288c]                  | YCR012C                                                                         | 6.356   | 4.412     | 0.69   |     |             |
| P04340    | 37S ribosomal protein RSM28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YDR49W                                                                         | 1.462   | 1.015     | 0.69   |     |             |
| P42940    | Probable electron transfer flavoprotein subunit beta [OS=Saccharomyces cerevisiae S288c] | YCR20C                                                                         | 4.623   | 3.217     | 0.70   |     |             |
| P38300    | Inner membrane mitobosome receptor MBA1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YBR185C                                                                         | 0.585   | 0.413     | 0.71   |     |             |
| Q03104 | Meiotic sister chromatid recombination protein 1 (OS=Saccharomyces cerevisiae S288c) | 8549 | 11 | MSC1; YML128C | metabolic process | endoplasmic reticulum; membrane; mitochondrial | 2.415 | 1.712 | 0.71 |
| P48015 | Aminomethyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8515 | 82 | GCY3; YDR001C | metabolic process | mitochondrial | catalytic activity; protein binding | 9 | 6.406 | 0.71 |
| P17505 | Malate dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8537 | 77 | MDH1; YKL058W | metabolic process | mitochondrial; organelle lumen | catalytic activity; protein binding; RNA binding | 56.79 | 7 | 40.59 | 6 | 0.71 |
| P32340 | Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8549 | 19 | ND1; YML128C | metabolic process; regulation of biological process | membrane; mitochondrial; organelle lumen | catalytic activity; enzyme regulator activity; nucleotide binding; protein binding | 24.92 | 9 | 17.87 | 4 | 0.72 |
| P05980 | Heat shock protein 33, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8535 | 103 | SSC1; YLR004C | cell organization and biogenesis; metabolic process; regulation of biological process; transport | mitochondrial; nucleus; organelle lumen | catalytic activity; regulatory activity; nucleotide binding | 48.48 | 2 | 34.93 | 8 | 0.72 |
| P04807 | Hexokinase-2 (OS=Saccharomyces cerevisiae S288c) | 8526 | 39 | HXK2; YGL253C | cell communication; cell organization and biogenesis; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport | cytosol; mitochondrial; nucleus | catalytic activity; nucleotide binding | 0.359 | 0.259 | 0.72 |
| P09440 | C-1-tetrahydrofolate synthase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8523 | 78 | M516; YBR084C | metabolic process | cytosol; mitochondrial | catalytic activity; nucleotide binding | 1.049 | 0.762 | 0.73 |
| P39726 | Glycine cleavage system H protein, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8512 | 54 | GCY3; YAL044C | metabolic process | mitochondrial | catalytic activity | 4.995 | 3.642 | 0.73 |
| P54783 | D-arabino-1,4-lactone oxidase (OS=Saccharomyces cerevisiae S288c) | 8548 | 88 | ALO1; YML081C | metabolic process; response to stimulus | membrane; mitochondrial | catalytic activity; nucleotide binding | 3.299 | 2.415 | 0.73 |
| P39518 | Long-chain fatty-acid-CoA ligase 2 (OS=Saccharomyces cerevisiae S288c) | 8567 | 34 | FAA2; YER015C | metabolic process; transport | cytoplasm; mitochondrial | catalytic activity; nucleotide binding | 0.619 | 0.455 | 0.74 |
| P52893 | Probable alanine aminotransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8507 | 78 | ALI1; YLR089C | metabolic process | mitochondrial; organelle lumen | catalytic activity | 1.102 | 0.812 | 0.74 |
| P32796-1 | Carnitine O-succinyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8549 | 65 | CAT2; YM042W | metabolic process; transport | membrane; mitochondrial | catalytic activity | 13.81 | 10.18 | 9 | 0.74 |
| P09297 | Mitochondrial 2-oxoacid decarboxylase (OS=Saccharomyces cerevisiae S288c) | 8543 | 97 | DDC2; YOR224W | metabolic process; transport | membrane; mitochondrial | structural molecule activity; transport activity | 1.054 | 0.778 | 0.74 |
| P28625 | Protein YML3 (OS=Saccharomyces cerevisiae S288c) | 8551 | 83 | YML3; YMR152C | metabolic process; response to stimulus | cytoplasm; endoplasmic reticulum; mitochondrial | catalytic activity; metal ion binding | 0.813 | 0.624 | 0.75 |
| P32180 | Probable oxidoreductase AIM17 (OS=Saccharomyces cerevisiae S288c) | 8563 | 65 | AIM17; YHL021C | cell organization and biogenesis; metabolic process | mitochondrial | catalytic activity; metal ion binding | 4.623 | 3.467 | 0.75 |
| P36534 | 54S ribosomal protein L40, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8559 | 30 | MRPL40; YPL173W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | protein binding; structural molecule activity | 0.778 | 0.585 | 0.75 |
| P33759 | 37S ribosomal protein S5, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8525 | 53 | MRPS5; YBR251W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | RNA binding; structural molecule activity | 0.778 | 0.585 | 0.75 |
| P50087 | MIC50 subunit MIC26 (OS=Saccharomyces cerevisiae S288c) | 8531 | 50 | MOS2; MIC26; YGR235C | cell organization and biogenesis | membrane; mitochondrial | 1.683 | 1.276 | 0.76 |
| P32902 | 37S ribosomal protein MRPA, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8563 | 84 | MRPA; YHL004C | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | 0.616 | 0.468 | 0.76 |
| P07257 | Cytochrome b-c1 complex subunit 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8563 | 21 | QCIR2; YPR191W | metabolic process; transport | membrane; mitochondrial | catalytic activity; metal ion binding; protein binding; transport activity | 36.75 | 27.94 | 3 | 0.76 |
| P32473 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8525 | 22 | FOB1; YBR221C | metabolic process | mitochondrial; organelle lumen | catalytic activity | 9 | 6.848 | 0.76 |
| P54003 | Protein SUR7 (OS=Saccharomyces cerevisiae S288c) | 8549 | 53 | SUR7; YML052W | cell differentiation; transport | membrane; mitochondrial | 1.512 | 1.154 | 0.76 |
| P33598 | Succinyl-CoA ligase (ADP-forming) subunit alpha, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8543 | 10 | LSC1; YOR142W | metabolic process | cytoplasm; mitochondrial | catalytic activity; nucleotide binding | 11.74 | 9 | 8 | 0.77 |
| G02981 | ABC1 family protein YPL109C, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8559 | 95 | YPL109C; YPL109C | | mitochondrial | 0.334 | 0.259 | 0.78 |
P09457  ATP synthase subunit 5, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8518  ATPS5; YDR29 RC  metabolic process;transport  membrane;mitochondrion  catalytic activity;transporter activity  9  9  1.00

P00358  glyceraldehyde-3-phosphate dehydrogenase 2 [OS=Saccharomyces cerevisiae (S288c)]
8534  DOD2; YIR009 C  cell death;metabolic process  cytoplasm;cytosol;membrane;mitochondrion/nucleus  catalytic activity;protein binding  3.962  3.962  1.00

P15108  ATP-dependent molecular chaperone Hsc82 [OS=Saccharomyces cerevisiae (S288c)]
8552  HSC82; YMR18 B/W  cell organization and biogenesis;metabolic process;response to stimulus  cytoplasm;membrane;mitochondrion  catalytic activity;protein binding  1.081  1.081  1.00

Q04013  Citrate/oxoglutarate carrier protein [OS=Saccharomyces cerevisiae (S288c)]
8552  YHM2; YMR24 I/W  cell organization and biogenesis;metabolic process;transport  membrane;mitochondrion  DNA binding;structural molecular activity;transporter activity  3.467  3.467  1.00

P32897  Mitochondrial import inner membrane translocase subunit ten23 [OS=Saccharomyces cerevisiae (S288c)]
8557  TIM23; YNR01 7W  transport  membrane;mitochondrion  protein binding;transporter activity  2.981  2.981  1.00

P00044  Cytochrome c iso-1 [OS=Saccharomyces cerevisiae (S288c)]
8535  CYCL1; YIR048 B/W  metabolic process;transport  mitochondrial  metal ion binding;protein binding  9  9  1.00

P40185  Protein mmf1, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8547  MFM1; YIL051 W  cell organization and biogenesis;metabolic process  mitochondrial;organellar lumen  5.31  5.31  1.00

P53721  Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8557  RCZ2; YNR01 B/W  cell organization and biogenesis  membrane;mitochondrion  5.579  5.579  1.00

P00524  Cytochrome c oxidase subunit 5A, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8556  COX5A; YNL052 W  metabolic process;transport  membrane;mitochondrion  catalytic activity;transporter activity  2.511  2.511  1.00

P40508  Glutathione S-transferase 1 [OS=Saccharomyces cerevisiae (S288c)]
8548  GTT1; YIR038 C  metabolic process  endoplasmic reticulum;membrane;mitochondrion;nucleus  antioxidant activity;catalytic activity;protein binding;RNA binding  1.683  1.683  1.00

P40509  Uncharacterized protein YL077C [OS=Saccharomyces cerevisiae (S288c)]
8547  YL077 C; YL077 C  mitochondrial  0.896  0.896  1.00

Q02204  S45 ribosomal protein L13, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8538  MRPL13; YKR106 C  cell organization and biogenesis;metabolic process  mitochondrial;ribosome  structural molecular activity  1.054  1.054  1.00

P22136  ATPase expression protein 2, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8553  AEFP2; YMR28 2C  metabolic process;regulation of biological process  mitochondrial  RNA binding  0.292  0.292  1.00

P50945  NQOS complex subunit MIC27 [OS=Saccharomyces cerevisiae (S288c)]
8556  AIM37; MIC27; YNL100 C  cell organization and biogenesis  membrane;mitochondrion  0.968  0.968  1.00

Q04593  LETM1 domain-containing protein YL147, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8562  YL147; YPR125 W  cell organization and biogenesis;transport  membrane;mitochondrion  0.61  0.61  1.00

P42247  37S ribosomal protein S18, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8554  MRPS18 R; YNL306 W  cell organization and biogenesis;metabolic process  mitochondrial;ribosome  RNA binding;structural molecular activity  0.54  0.54  1.00

P21771  37S ribosomal protein S28, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8519  MRPS28 R; YDR33 7W  cell organization and biogenesis;metabolic process  mitochondrial;ribosome  RNA binding;structural molecular activity  0.438  0.438  1.00

Q03201  37S ribosomal protein S10, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8516  RSM10; YDR04 1W  cell organization and biogenesis;metabolic process  mitochondrial;ribosome  structural molecular activity  0.701  0.701  1.00

Q07914  mitochondrial import inner membrane translocase subunit TIM14 [OS=Saccharomyces cerevisiae (S288c)]
8506  PAM18; YIR008 C  regulation of biological process;transport  membrane;mitochondrion  enzyme regulator activity;protein binding;transporter activity  0.778  0.778  1.00

P25345  Asparaginase--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8503  SLMS; YCR024 T  metabolic process  cytoplasm;mitochondrion;organellar lumen  catalytic activity;protein binding  0.172  0.172  1.00

P21377  Fumarate reductase 2 [OS=Saccharomyces cerevisiae (S288c)]
8535  DSM1; YIR051 W  metabolic process  endoplasmic reticulum;mitochondrion  catalytic activity;protein binding  0.25  0.25  1.00

P25038  Translation initiation factor IF-2, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8541  FMF1; YOL023 W  cell organization and biogenesis;metabolic process  mitochondrial;nucleus  catalytic activity;protein binding;RNA binding  0.11  0.11  1.00

Q06005  Octanoyltransferase, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8509  LIP2; YLR239 C  metabolic process  cytoplasm;mitochondrion  catalytic activity  0.245  0.245  1.00

P47015  Altered inheritance of mitochondria protein 23, mitochondrial [OS=Saccharomyces cerevisiae (S288c)]
8533  AIM23; YL131 C  metabolic process  mitochondrial  RNA binding  0.35  0.35  1.00
Autophagy-related protein 33 (OS=Saccharomyces cerevisiae S288c)

8510 70 ATG33; YLR356c membrane,mitochondrion 1.371 2.162 1.58

Uncharacterized mitochondrial carrier YPR011C (OS=Saccharomyces cerevisiae S288c)

8561 21 YPR011 C; YPR011 C membrane,mitochondrion 0.245 0.389 1.59

Sorting assembly machinery 37 Id2a subunit (OS=Saccharomyces cerevisiae S288c)

8550 82 SAM37 ; YMR086c cell organization and biogenesis,transport membrane,mitochondrion 0.245 0.389 1.59

5-demethoxyubiquinone hydroxylase, mitochondrial (OS=Saccharomyces cerevisiae S288c)

8542 92 CAT5; YDR12 SC metabolic process membrane,mitochondrion 0.334 0.54 1.62

Mitochondrial ornithine transporter 1 (OS=Saccharomyces cerevisiae S288c)

8542 97 ORTI1; YDR13 OC metabolic process,transport structural molecule activity,transporter activity 0.334 0.54 1.62

Mitochondrial fusion and transport protein Ugo1 (OS=Saccharomyces cerevisiae S288c)

8520 81 UGD1; YDR47 OC cell organization and biogenesis,metabolic process protein binding,structural molecule activity 0.425 0.701 1.65

Thiophosphate isomerase (OS=Saccharomyces cerevisiae S288c)

8516 20 TPI1; YDR05 OC metabolic process cytoplasm,cytosol,membrane,mitochondrion catalytic activity 0.425 0.701 1.65

Mitofusin Fzo1 (OS=Saccharomyces cerevisiae S288c)

8524 77 FZO1; YBR179 C cell organization and biogenesis,membrane,mitochondrion catalytic activity,nucleotide binding,protein binding 0.142 0.248 1.75

Long-chain-fatty-acid-CoA ligase 3 (OS=Saccharomyces cerevisiae S288c)

8548 08 FA43; YIL009 W metabolic process catalytic activity,nucleotide binding 0.334 0.585 1.75

Saccharate dehydrogenase (ubiquionate)-iron-sulfur subunit, mitochondrial (OS=Saccharomyces cerevisiae S288c)

8506 85 SGDO; YIL041 C metabolic process,transport membrane,mitochondrion catalytic activity,motil iron binding 18.68 4 32.83 9 1.76

Heat shock protein 60, mitochondrial (OS=Saccharomyces cerevisiae S288c)

8509 63 HSP90; YLR259 C cell organization and biogenesis,metabolic process,regulation of biological process,transport catalytic activity,DNA binding,nucleotide binding,protein binding 22.35 7 39.29 6 1.76

Mitochondrial import inner membrane translocase subunit Tim17 (OS=Saccharomyces cerevisiae S288c)

8532 98 TIM17; YIL143 W cell organization and biogenesis,transport membrane,mitochondrion protein binding,transporter activity 0.778 1.371 1.76

Dihydropteroate dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c)

8505 27 LPS1; YFL018 C cellular homoeostasis,metabolic process,regulation of biological process mitochondrion,organelle lumen catalytic activity,nucleotide binding 21.53 9 43.36 7 2.01

Nuclear migration protein Nup1 (OS=Saccharomyces cerevisiae S288c)

8517 27 NUP1; YDR15 BW cell organization and biogenesis,cellular component movement,metabolic process,regulation of biological process,transport endoplasmic reticulum,mitochondrion catalytic activity,motil activity,protein binding 0.025 0.052 2.08

Ubiquitin carboxyl-terminal hydrolase 16 (OS=Saccharomyces cerevisiae S288c)

8560 32 UBP16; YPL072 W metabolic process membrane,mitochondrion catalytic activity 0.072 0.15 2.08

Inositol phospholipids phospholipase C (OS=Saccharomyces cerevisiae S288c)

8567 39 ISCI; YER019 W metabolic process,response to stimulus endoplasmic reticulum,membrane,mitochondrion catalytic activity,motil iron binding 0.101 0.212 2.10

Protein Gpt1 (OS=Saccharomyces cerevisiae S288c)

8524 26 GPT1; YBR129 C cytoplasm,mitochondrion 0.129 0.274 2.12

Altered inheritance of mitochondria protein 18, mitochondrial (OS=Saccharomyces cerevisiae S288c)

8566 05 A1M18; YHR198 C mitochondrion catalytic activity 0.145 0.311 2.14

ULP1-interacting protein 4 (OS=Saccharomyces cerevisiae S288c)

8559 16 ULP4; YPL186 C endoplasmic reticulum,membrane,mitochondrion,nucleus catalytic activity 0.136 0.292 2.15

Glutathione reductase (OS=Saccharomyces cerevisiae S288c)

8560 14 GLR1; YPL091 W cellular homoeostasis,metabolic process,regulation of biological process,response to stimulus cytoplasm,mitochondrion,nucleus antioxidant activity,catalytic activity,nucleotide binding 0.155 0.334 2.15

Mitochondrial outer membrane protein Dnm4 (OS=Saccharomyces cerevisiae S288c)

8546 70 DNM4; YIL136 W membrane,mitochondrion 250.1 89 574.4 4 2.30

Protein Mspl (OS=Saccharomyces cerevisiae S288c)

8529 15 MSPL; YGR022 BW cell organization and biogenesis,metabolic process,regulation of biological process,response to stimulus,transport membrane,mitochondrion catalytic activity,nucleotide binding,protein binding 0.259 0.778 3.00

5'7 ribosomal protein S25, mitochondrial (OS=Saccharomyces cerevisiae S288c)

8547 15 RSM25 ; YIL083 C cell organization and biogenesis,metabolic process mitochondrion,ribosome structural molecule activity 0.252 0.896 3.07

Uncharacterized protein YDR119W-A (OS=Saccharomyces cerevisiae S288c)

3799 970 COX26; YDR11 BW-A membrane,mitochondrion 1.154 3.642 3.16
| Accession | Description | Source | Gene(s) | Function(s) | p-value | Z-score |
|-----------|-------------|--------|---------|-------------|---------|---------|
| P53925    | Uncharacterized vacuolar membrane protein YNL115C | [OS=Saccharomyces cerevisiae S288c] | YNL115C; YNL115C | membrane;vacuole | 0.072  | 0.233  | 3.24  |
| P32792    | UPF0744 protein YSCB3 | [OS=Saccharomyces cerevisiae S288c] | YSCB3; YHR017W | membrane;mitochondrion | 0.11  | 0.52  | 4.73  |
| P49334    | Mitochondrial import receptor subunit tom22 | [OS=Saccharomyces cerevisiae S288c] | TOM22; YNL131W | cell organization and biogenesis;transport | membrane;mitochondrion | protein binding;transporter activity | 0.292 | 1.783 | 6.11  |
| Q08245    | protein ZEO1 | [OS=Saccharomyces cerevisiae S288c] | ZEO1; YOL109W | cell organization and biogenesis | membrane;mitochondrion | protein binding | 1.512 | 11.58 | 9.66  |
Supplemental Table S6. The relative concentrations of proteins in mitochondria purified from WT or ups1Δ cells cultured without LCA. Mitochondria were purified from WT or ups1Δ cells recovered on day 7 of cell culturing without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entry 1 Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI ups1Δ | Rati o ups1Δ / WT |
|-----------|-------------|----------------|---------|-------------------|-------------------|-------------------|-----------|-------------|------------------|
| P36527    | S45 ribosomal protein L28, mitochondrial | 8520 73 | MRPL2 8 | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 4.337 | 0.233 | 0.10 |
| Q04935    | Cytochrome c oxidase protein 20, mitochondrial | 8518 17 | COX20; YDR231C | cell organization and biogenesis;metabolic process | membrane;mitochondrion | protein binding | 1.894 | 0.194 | 0.10 |
| P08525    | Cytochrome b-c1 complex subunit 8 (OS=Saccharomyces cerevisiae S288c) | 8532 73 | QCR8; YIL166W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 5.31 | 0.585 | 0.11 |
| P38341    | MIC8 complex subunit MIC12 (OS=Saccharomyces cerevisiae S288c) | 8525 66 | AIM5; MRC11; YBR262C | cell organization and biogenesis | membrane;mitochondrion | 2.594 | 0.292 | 0.11 |
| P07253    | Cytochrome b pre-mRNA-processing protein 6 (OS=Saccharomyces cerevisiae S288c) | 8524 17 | CBBP; YBR120C | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion;ribosome | 3.394 | 0.389 | 0.11 |
| P36141    | Putative redox protein Fmp46, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8539 23 | FMP46; YKR049C | metabolic process | mitochondrion | catalytic activity;protein binding | 4.337 | 0.52 | 0.12 |
| P53219    | Aldehyde dehydrogenase domain-containing protein IMO32 (OS=Saccharomyces cerevisiae S288c) | 8529 19 | IMO32; YGR031W | metabolic process;transport | mitochondrion | catalytic activity | 0.73 | 0.116 | 0.16 |
| P00045    | Cytochrome c iso-2 (OS=Saccharomyces cerevisiae S288c) | 8566 72 | CYC7; YEL039C | metabolic process;transport | mitochondrion | metal ion binding | 1.512 | 0.259 | 0.17 |
| Q12032    | Altered inheritance of mitochondria protein 41, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8543 90 | AIM41; YDR215C | mitochondrion | catalytic activity | 1.154 | 0.212 | 0.18 |
| P32799    | Cytochrome c oxidase subunit 6A, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8526 84 | COX13; YGL191W | cell organization and biogenesis;metabolic process;regulation of biological process | membrane;mitochondrion | catalytic activity;enzyme regulation;transporter activity | 11.58 | 9 | 2.162 | 0.19 |
| P38175    | 37S ribosomal protein MRP21, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8521 88 | MRP21; YBL050W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.031 | 0.194 | 0.19 |
| P33535    | Mitochondrial 37S ribosomal protein S27 (OS=Saccharomyces cerevisiae S288c) | 8531 29 | RSM27; YGR215W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 2.162 | 0.468 | 0.22 |
| P54115    | Magnesium-activated aldehyde dehydrogenase, cytosolic (OS=Saccharomyces cerevisiae S288c) | 8560 44 | ALD6; YPL061W | metabolic process;response to stimulus | cytoplasm;cytosol;mitochondrion | catalytic activity | 0.346 | 0.077 | 0.22 |
| P22438    | Methionine–RNA ligase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8530 81 | MSM1; YGR171C | metabolic process | cytoplasm;cytosol;mitochondrion;organellar lumen | catalytic activity;nucleotide binding | 0.292 | 0.066 | 0.23 |
| P18496    | Mitochondrial ATPase complex subunit ATP10 (OS=Saccharomyces cerevisiae S288c) | 8511 09 | ATP10; YLR393W | cell organization and biogenesis | cytoplasm;membrane;mitochondrion | protein binding | 1.818 | 0.413 | 0.23 |
| P38900    | Hexenyl pyrophosphate synthase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8522 88 | COQ1; YBR003W | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding;protein binding | 0.711 | 0.166 | 0.23 |
| P48360    | Probable NADPH:adenodoxin oxidoreductase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8519 82 | ARH1; YDR376W | cellular homeostasis;metabolic process;transport | cytoplasm;membrane;mitochondrion;organellar lumen | catalytic activity | 0.682 | 0.16 | 0.23 |
| P81449    | ATP synthase subunit e, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8519 22 | TIM11; YDR3212C-A | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;structural molecule activity;transporter activity | 9 | 2.162 | 0.24 |
| Q20784    | Monothiol glutaredoxin-5, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 8560 48 | GRK5; YPL059W | cell organization and biogenesis;cellular homeostasis;metabolic process;regulation of biological process;response to stimulus | mitochondrion;organellar lumen | catalytic activity;metal ion binding | 2.594 | 0.668 | 0.26 |
| Q6C560    | Protein isd11 (OS=Saccharomyces cerevisiae S288c) | 8567 74 | ISD11; YER048W | cell organization and biogenesis;metabolic process | mitochondrion;organellar lumen | catalytic activity;protein binding | 2.594 | 0.668 | 0.26 |
| Q08223    | Altered inheritance of mitochondria protein 39, mitochondrial | 8541 03 | AIM39; YOL053 | cytosol;membrane;mitochondrion | 0.995 | 0.259 | 0.26 |
| Entry | Description | Symbol(s) | CDS | GO Terms |
|-------|-------------|-----------|-----|----------|
| P40581 | Peroxiredoxin HR1 mitochondrial | HYR1 | YBR037W | metabolic process;response to stimulus | cytoplasm;cytosol;mitochondrion;organelle lumen | antioxidant activity;catalytic activity | 0.995 | 0.259 | 0.26 |
| P36163 | Mitochondrial metalloendopeptidase OMA1 mitochondrial | DMA1 | YKR087C | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding | 0.931 | 0.245 | 0.26 |
| P41740 | Altered inheritance rate of mitochondrial protein 25 mitochondrial | AIM25 | YIR100C | cell organization and biogenesis | membrane;mitochondrion | transporter activity | 0.874 | 0.233 | 0.27 |
| P53875 | 54S ribosomal protein L19 mitochondrial | MRPL9 | YNL185C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome;RNA binding;structural molecule activity | 0.874 | 0.233 | 0.27 |
| P40858 | 54S ribosomal protein L49 mitochondrial | MRPL49 | YIL096W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome;RNA binding;structural molecule activity | 0.778 | 0.212 | 0.27 |
| P40165 | NADPFH-hydrolase epimerase mitochondrial | MRPL23 | YNL200C; YNL200D | metabolic process | cytoplasm;mitochondrion | catalytic activity;metal ion binding;nucleotide binding | 1.61 | 0.468 | 0.29 |
| P38271 | Protein OPY1 mitochondrial | OPY1 | YBR129C | cytoplasm;mitochondrion | 0.438 | 0.129 | 0.29 |
| P21560 | Protein CBP3 mitochondrial | CBP3 | YPL215W | cell organization and biogenesis;regulation of biological process | membrane;mitochondrion;ribosome | 1.031 | 0.304 | 0.29 |
| Q66236 | Mitochondrial inner membrane protein SHH4 mitochondrial | SHH4 | YLR164W | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding | 4.623 | 1.371 | 0.30 |
| P38705 | Smithe-tRNA nase mitochondrial | SMN1 | YMR105C; YHR011W | metabolic process | cytoplasm;mitochondrion;organelle lumen | catalytic activity;nucleotide binding | 0.233 | 0.072 | 0.31 |
| Q02863 | Ubiquitin carboxyl-terminal hydrolase 16 mitochondrial | UBP16 | YPL072W | metabolic process | membrane;mitochondrion | catalytic activity | 0.233 | 0.072 | 0.31 |
| P39722 | Mitochondrial Rho GTPase 1 mitochondrial | RHO1 | YML048C | cell organization and biogenesis;regulation of biological process | membrane;mitochondrion;ribosome | catalytic activity;metal ion binding;nucleotide binding | 0.189 | 0.069 | 0.31 |
| Q01519 | Cytochrome c oxidase subunit 6b mitochondrial | COX12 | YLR033C | cell organization and biogenesis;metabolic process;transport | mitochondrion | catalytic activity;transporter activity | 3.642 | 1.154 | 0.32 |
| P42847 | 37S ribosomal protein S18 mitochondrial | MRPS18 | YNL308W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.054 | 0.334 | 0.32 |
| Q02663 | Protein EFR mitochondrial | EFR3 | YMR212C | metabolic process | membrane;mitochondrion | 0.148 | 0.047 | 0.32 |
| P11914 | Mitochondrial processing peptidase subunit alpha mitochondrial | MPP1 | YHR024C | metabolic process;transport | membrane;mitochondrion;organelle lumen | catalytic activity;metal ion binding;protein binding | 2.311 | 0.738 | 0.32 |
| Q03798 | Altered inheritance of mitochondria protein 36 mitochondrial | AIM36 | YMR157C | cell organization and biogenesis;regulation of biological process;response to stimulus;transport | membrane;mitochondrion | catalytic activity;metal ion binding;protein binding | 1.336 | 0.438 | 0.33 |
| P14908 | Mitochondrial transcription factor 1 mitochondrial | MTF1 | YMR228W | metabolic process;regulation of biological process | mitochondrion;organelle lumen | catalytic activity;DNA binding;RNA binding | 0.778 | 0.259 | 0.33 |
| P10634 | Protein PET54 mitochondrial | PET54 | YGR222W | metabolic process;regulation of biological process | membrane;mitochondrion;organelle lumen | nucleotide binding;RNA binding;translation regulator activity | 0.688 | 0.233 | 0.34 |
| Q12349 | ATP synthase subunit H mitochondrial | ATP4 | YLR295C | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 2.728 | 0.931 | 0.34 |
| Q06648 | MIDREX complex component 10 mitochondrial | MDR10 | YDR284C; YDR285C; YDR286C | metabolic process | membrane;mitochondrion | 0.65 | 0.222 | 0.34 |
| P38808 | Glycine- tRNA ligase 1 mitochondrial | GRS1 | YGR160C | metabolic process | cytoplasm;mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | 0.616 | 0.212 | 0.34 |
| P531166 | ATP-dependent RNA helicase mrh4 mitochondrial | MRH4 | YGL064C | cell organization and biogenesis;metabolic process | mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | 1.412 | 0.501 | 0.35 |
| P36516 | 54S ribosomal protein L3 mitochondrial | MRPL3 | YMR024W | cell organization and biogenesis;metabolic process;response to stimulus | mitochondrion;nucleus;ribosome | catalytic activity;RNA binding;structural molecule activity | 1.043 | 0.374 | 0.36 |
| P38120 | 37S ribosomal protein S9 mitochondrial | MRPS9 | YMR243C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 3.437 | 1.254 | 0.36 |
| S28Rc | C | process/regulation of biological process/response to stimulus;transport | binding |
|-------|---|-------------------------------------------------|---------|
| P36528 | SY5 ribosomal protein L17, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 854 | MRPL7 | cell organization and biogenesis,metabolic process | mitochondrial;ribosome | structural molecule activity | 0.52 | 0.233 | 0.45 |
| Q12487 | SY5 ribosomal protein L23, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 854 | MRPL3 | cell organization and biogenesis,metabolic process | mitochondrial;ribosome;vacuole | RNA binding;structural molecule activity | 0.52 | 0.233 | 0.45 |
| P34224 | Uncharacterized protein YBL059W [OS=Saccharomyces cerevisiae S28Rc] | 852 | YBL059W; YBL059W | membrane;mitochondrion | | | 0.468 | 0.212 | 0.45 |
| P42900 | Sigma-like sequence protein 1, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 80B | SLS1; YLR139C | cell organization and biogenesis,metabolic process | membrane;mitochondrion | protein binding | 0.425 | 0.194 | 0.46 |
| P32839 | Mitochondrial chaperone BCS1 [OS=Saccharomyces cerevisiae S28Rc] | 8519 | BCS1; YOR375C | cell organization and biogenesis,metabolic process | cytosol;membrane;mitochondrion | catalytic activity;nuclotide binding;transporter activity | 0.425 | 0.194 | 0.46 |
| Q08970 | Mitochondrial metal transporter 2 [OS=Saccharomyces cerevisiae S28Rc] | 8518 | YMT2; YPL224C | cellular homeostasis;regulation of biological process/response to stimulus;transport | membrane;mitochondrion | transporter activity | 0.407 | 0.186 | 0.46 |
| P32266 | Dynamic-like GTPase MGM1, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8543 | MGM1; YDR21IC | cell organization and biogenesis,metabolic process | membrane;mitochondrion | catalytic activity;RNA binding | 0.389 | 0.179 | 0.46 |
| P03879 | Intrin-encoded RNA maturation b14 [OS=Saccharomyces cerevisiae S28Rc] | 8545 | B4; QD120 | metabolic process | membrane;mitochondrion | catalytic activity;RNA binding | 0.389 | 0.179 | 0.46 |
| Q05779 | Ubiquitine biosynthesis protein COQ9, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8508 | COQ9; YLR201C | metabolic process | membrane;mitochondrion | | 0.359 | 0.166 | 0.46 |
| P36523 | SY5 ribosomal protein L15, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8510 | MRPL3; YLR312W | cell organization and biogenesis,metabolic process | mitochondrial;ribosome | catalytic activity;RNA binding;structural molecule activity | 0.334 | 0.155 | 0.46 |
| P81450 | ATP synthase subunit J, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8548 | ATP6; YML081C-A | cell organization and biogenesis,metabolic process | membrane;mitochondrion | catalytic activity;transporter activity | 4.623 | 2.162 | 0.47 |
| P25270 | tRNA methyltransferase 1, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8543 | MMR1; YDR201C | metabolic process | mitochondrion | catalytic activity;RNA binding | 0.274 | 0.129 | 0.47 |
| P38122 | 3-methyl-2-oxobutanoate hydroxymethyltransferase [OS=Saccharomyces cerevisiae S28Rc] | 8524 | ECM31; YBR176W | metabolic process | mitochondrion | catalytic activity | 0.259 | 0.122 | 0.47 |
| Q04689 | Altered inheritance of mitochondria protein 32 [OS=Saccharomyces cerevisiae S28Rc] | 8549 | AIM12; YML050W | | | | 0.233 | 0.11 | 0.47 |
| P43122 | tRNA N6-adenosine threonylcarbamoyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8514 | QRT7; YDL104C | cell organization and biogenesis,metabolic process | mitochondrion | catalytic activity;metal ion binding | 0.212 | 0.101 | 0.48 |
| P38909 | cytochrome c mitochondrial import factor CY2 [OS=Saccharomyces cerevisiae S28Rc] | 8542 | CYC2; YDR037W | cell organization and biogenesis,metabolic process | membrane;mitochondrion | catalytic activity | 0.194 | 0.093 | 0.48 |
| P25626 | SY5 ribosomal protein IMG1, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8504 | IMG1; YCR046C | cell organization and biogenesis,metabolic process | mitochondrial;ribosome | structural molecule activity | 1.924 | 1.894 | 0.48 |
| Q08818 | Meiotic sister-chromatid recombination protein 6, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8546 | MSC6; YOR354C | metabolic process | mitochondrion;organelle lumen | RNA binding | 1.047 | 0.506 | 0.48 |
| Q12204 | Probable phospholipase YOR022C, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8541 | YOR022C; YOR022C | metabolic process | mitochondrion | catalytic activity;metal ion binding | 0.11 | 0.054 | 0.49 |
| P38771 | Ribosome-recycling factor, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8564 | RRF1; YHR037W | cell organization and biogenesis,metabolic process | mitochondrion | RNA binding | 1.955 | 0.968 | 0.50 |
| P38969 | Pentamidine resistance factor, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8544 | PNT1; YDR266W | cell organization and biogenesis;response to stimulus | membrane;mitochondrion | | 0.711 | 0.359 | 0.50 |
| Q06405 | ATP synthase subunit f, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8519 | ATP17; YDR374W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 2.981 | 1.512 | 0.51 |
| Q08203 | Protein FMP25, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8507 | FMP25; YLR077W | cell organization and biogenesis | membrane;mitochondrion | | 1.412 | 0.719 | 0.51 |
| P25372 | Thiodoxin-3, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8504 | TRX3; YCR083W | cellular homeostasis;metabolic process;regulation of biological process;response to stimulus;transport | cytoplasm;mitochondrion | catalytic activity | 2.512 | 1.31 | 0.52 |
| P12686 | 375 ribosomal protein MRPL13, mitochondrial [OS=Saccharomyces cerevisiae S28Rc] | 8529 | MRPL13; YGR088C | cell organization and biogenesis,metabolic process | mitochondrial;ribosome | structural molecule activity | 0.778 | 0.413 | 0.53 |
Mitochondrial intermembrane space import and assembly protein 40 [OS=Saccharomyces cerevisiae S288c] 8136 39 Mia40; YKL195 W cellular component movement;metabolic process;response to stimulus;transport membrane/mitochondrion catalytic activity;protein binding;transporter activity 2.914 1.555 0.53

Cytochrome oxidase assembly protein Shy1 [OS=Saccharomyces cerevisiae S288c] 8350 09 SYH1; YGR111 2W cell organization and biogenesis membrane/mitochondrion protein binding 1.783 0.978 0.55

Phosphatidylethanolamine decarboxylase proenzyme 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8555 52 PED1; YNL169 C metabolic process;regulation of biological process membrane/mitochondrion catalytic activity 0.487 0.269 0.55

Assembly factor cwp4 [OS=Saccharomyces cerevisiae S288c] 83726 CBP4 cell organization and biogenesis membrane/mitochondrion 3.329 1.948 0.56

37s ribosomal protein Pet123, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8543 29 PET123; YOR115 BW cell organization and biogenesis;metabolic process mitochondrial ribosome structural molecule activity 2.594 1.448 0.56

cytosine b-c complex subunit 10 [OS=Saccharomyces cerevisiae S288c] 8563 90 OCR10; YHR000 1W-A metabolic process;transport membrane/mitochondrion catalytic activity;transporter activity 5.31 2.981 0.56

37s ribosomal protein Ymr31, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8506 00 YMR31; YRP049 W cell organization and biogenesis;metabolic process mitochondrial ribosome catalytic activity;protein binding;structural molecule activity 15.68 18 9 0.57

37s ribosomal protein S12, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8557 72 MRPS1 2; YNR03 6C cell organization and biogenesis;metabolic process mitochondrial ribosome structural molecule activity 1.154 0.668 0.58

45s ribosomal protein L1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8516 94 MRPL1; YDR111 6C cell organization and biogenesis;metabolic process mitochondrial ribosome RNA binding;structural molecule activity 1.069 0.624 0.58

45s ribosomal protein L50, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8557 56 MRPL5 0; YNR02 2C cell organization and biogenesis;metabolic process mitochondrial ribosome structural molecule activity 0.995 0.585 0.59

Uncharacterized protein YDR020W-A [OS=Saccharomyces cerevisiae S288c] 1466 480 YDR020W-A; YDR020W-A metabolic process;transport membrane/mitochondrion 3.642 2.162 0.59

Glutaredoxin-2, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8521 24 GRX2; YDR51 3W cellular homeostasis;metabolic process;regulation of biological process;response to stimulus;transport cytoplasm;cytosol;mitochondrion;nucleus antioxidant activity;catalytic activity 0.874 0.52 0.59

Cytosine c oxidase assembly protein cox15 [OS=Saccharomyces cerevisiae S288c] 8668 84 COX15; YER141 W cell organization and biogenesis;metabolic process;transport membrane/mitochondrion catalytic activity 2.594 1.555 0.60

Iron sulfur cluster assembly protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8559 68 ISU1; YPL115 W cell organization and biogenesis;cellular homeostasis;metabolic process cytoplasm;mitochondrion;organellar lumen catalytic activity;metal ion binding;protein binding 0.778 0.468 0.60

37s ribosomal protein S8, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8551 90 MRPS8 2; YMR15 BW cell organization and biogenesis;metabolic process mitochondrial ribosome structural molecule activity 0.705 0.425 0.61

Mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c] 8542 97 ORT1; YDR13 6C metabolic process;transport membrane/mitochondrion structural molecule activity;transporter activity 0.54 0.334 0.62

sorting assembly machinery 55 kDa subunit [OS=Saccharomyces cerevisiae S288c] 8664 83 SAM35 3; YHR08 3W cell organization and biogenesis;transport membrane/mitochondrion protein binding 0.54 0.334 0.62

Cytochrome c peroxidase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8539 40 CCP1; YKR066 C metabolic process;response to stimulus mitochondrial ribosome;organellar lumen antioxidant activity;antioxidant activity;catalytic activity;metal ion binding;protein binding 1.649 1.031 0.63

Probable hydroxylation NIT3 [OS=Saccharomyces cerevisiae S288c] 8510 65 NIT3; YLR351 C metabolic process cytoplasm;mitochondrion catalytic activity 0.438 0.274 0.63

UPF0744 protein YSC83 [OS=Saccharomyces cerevisiae S288c] 8664 10 YSC83; YHR001 7W metabolic process membrane/mitochondrion 0.369 0.233 0.63

N-terminal acetyltransferase 2 [OS=Saccharomyces cerevisiae S288c] 8530 50 NAT2; YGR14 7C metabolic process cytoplasm;mitochondrion catalytic activity 1.154 0.73 0.63

Thiosulfate sulfurtransferase TUM1 [OS=Saccharomyces cerevisiae S288c] 8544 25 TUM1; YDR25 1C metabolic process cytoplasm;mitochondrion catalytic activity;protein binding;transporter activity 0.334 0.212 0.63

Inositol phosphophingolipids phospholipase C [OS=Saccharomyces cerevisiae S288c] 8567 39 ISIC1; YEM019 W metabolic process;response to stimulus endoplasmic reticulum;membrane/mitochondrion catalytic activity;metal ion binding 0.334 0.212 0.63

N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8560 01 FMP10; YPL103 C metabolic process membrane/mitochondrion catalytic activity;metal ion binding 0.304 0.194 0.64

Cysteine protease 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 8532 38 MCY1 metabolic process;regulation of biological process;response to stimulus cytoplasm;mitochondrion catalytic activity;DNA binding;RNA binding 0.28 0.179 0.64

Glutaryl-2-hydroxyisoadipyl-CoA amidotransferase subunit A, [OS=Saccharomyces cerevisiae S288c] 8535 38 HER2; YMR29 cell organization and biogenesis;metabolic process mitochondrial catalytic activity;nucleotide 0.259 0.166 0.64
| mitochondrial [OS=Saccharomyces cerevisiae S288c] | 3C | binding |
|-------------------------------------------------|----|---------|
| Threonine-tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8538 40 | MSL1; YKL194 C | metabolic process | cytoplasm,mitochondrion,organelle lumen | catalytic activity,nucleotide binding;RNA binding | 0.233 | 0.15 | 0.64 |
| Uncharacterized protein YNL208W [OS=Saccharomyces cerevisiae S288c] | 8555 13 | YNL208 W; YNL208 W | membrane,mitochondrion,ribosome | | 1.783 | 1.154 | 0.65 |
| Protein FMP52, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8567 21 | FMP52; YER004 W | endoplasmic reticulum,membrane,mitochondrion | | 2.652 | 1.738 | 0.66 |
| 37S ribosomal protein RSM28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8521 05 | RSM28; YDR49 W | cell organization,metabolic process | mitochondrion,ribosome | structural molecule activity | 3.062 | 2.008 | 0.66 |
| Methyltransferase DMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8519 11 | DMS1; YDR311 W | metabolic process | membrane,mitochondrion | catalytic activity | 0.585 | 0.389 | 0.66 |
| 54S ribosomal protein L23, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8529 67 | MRPL2 S; YGR076 C | cell organization,metabolic process | mitochondrion,ribosome | structural molecule activity | 1.31 | 0.874 | 0.67 |
| NIFU-like protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8538 26 | YUFI1; YKL040 C | cell organization,biogenesis,cellular homeostasis,metabolic process | mitochondrion,organelle lumen | metal ion binding | 3.87 | 2.652 | 0.69 |
| MIDREX complex component 2 [OS=Saccharomyces cerevisiae S288c] | 8509 97 | YLR290 C; COG1111; YLR290 C | metabolic process | mitochondrion | catalytic activity | 3.87 | 2.652 | 0.69 |
| MICOS subunit MIC26 [OS=Saccharomyces cerevisiae S288c] | 8531 50 | MIC26; YGR235 C | cell organization and biogenesis | membrane,mitochondrion | | 0.931 | 0.648 | 0.69 |
| MIDREX complex component 3 [OS=Saccharomyces cerevisiae S288c] | 8521 81 | YBL095 W; MRX3; YBL095 W | cell organization and biogenesis,cellular homeostasis,metabolic process | mitochondrion,ribosome | structural molecule activity,transporter activity | 0.719 | 0.501 | 0.70 |
| Protein MSP1 [OS=Saccharomyces cerevisiae S288c] | 8529 15 | MRP1; YGR020 BW | cell organization and biogenesis,metabolic process,regulation of biological process,response to stimulus,transport | membrane,mitochondrion,nucleus | catalytic activity,nucleotide binding;protein binding;metal ion binding | 0.585 | 0.413 | 0.71 |
| Uncharacterized mitochondrial carrier YPR011C [OS=Saccharomyces cerevisiae S288c] | 8561 21 | YPR011 C; YPR011 C | metabolic process,transport | membrane,mitochondrion | structural molecule activity,transporter activity | 0.551 | 0.389 | 0.71 |
| Tricarboxylate transport protein [OS=Saccharomyces cerevisiae S288c] | 8525 94 | CTP1; YBR291 C | metabolic process,transport | membrane,mitochondrion | structural molecule activity,transporter activity | 0.551 | 0.389 | 0.71 |
| Ribosomal protein VAR1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8545 86 | VAR1; QO140 | cell organization and biogenesis,metabolic process | mitochondrion,ribosome | structural molecule activity | 0.52 | 0.369 | 0.71 |
| mitochondrial carrier protein LEU5 [OS=Saccharomyces cerevisiae S288c] | 8563 91 | LEU5; YHR000 W | metabolic process,transport | membrane,mitochondrion | structural molecule activity,transporter activity | 0.468 | 0.334 | 0.71 |
| Phosphatidate cytidylyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8529 37 | TAM41 S; YGR048 W | metabolic process | membrane,mitochondrion,organelle lumen | catalytic activity | 0.407 | 0.292 | 0.72 |
| Protein SUR7 [OS=Saccharomyces cerevisiae S288c] | 8549 53 | SUR7; YML052 W | cell differentiation,transport | membrane,mitochondrion | | 1.154 | 0.848 | 0.73 |
| Malonyl CoA-carrier protein transacylase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8543 96 | MCT1; YDR221 C | metabolic process | mitochondrion | catalytic activity | 0.896 | 0.668 | 0.75 |
| S45 ribosomal protein L11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8513 25 | MRPL1; YDL202 W | cell organization and biogenesis,metabolic process | mitochondrion,ribosome | structural molecule activity | 0.833 | 0.624 | 0.75 |
| Uncharacterized mitochondrial carrier YR045 [OS=Saccharomyces cerevisiae S288c] | 8506 06 | YR045 W; YR045 W | metabolic process,transport | membrane,mitochondrion | structural molecule activity,transporter activity | 0.778 | 0.585 | 0.75 |
| S45 ribosomal protein L40, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8599 30 | MRPL4 0; YPL173 W | cell organization and biogenesis,metabolic process | mitochondrion,ribosome | protein binding;structural molecule activity | 0.778 | 0.585 | 0.75 |
| Inner membrane mitonitrosome receptor MRA1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8524 83 | MRA1; YBR185 C | cell organization and biogenesis,regulation of biological process | membrane,mitochondrion | | 0.778 | 0.585 | 0.75 |
| Protein SCO2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8523 12 | SCO2; YBR024 W | cell organization and biogenesis,cellular homeostasis,metabolic process,transport | membrane,mitochondrion | antioxidative activity,catalytic activity,metal ion binding | 0.73 | 0.551 | 0.75 |
| Gene | Symbol | Function | Interactions | Gene | Symbol | Function | Interactions |
|------|--------|----------|--------------|------|--------|----------|--------------|
| YOR27 | FSF1 | protein | mitochondrial | YPR024 | YME1 | membrane | mitochondrial |
| CYN1 | MRPL2 | protein | transport | WYKL120 | YKL120 | membrane | mitochondrial |
| OAC1 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| WYKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YKL120 | OAC1 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| YML6 | AIM9 | protein | transport | YKL120 | YKL120 | membrane | mitochondrial |
| Gene Id | Symbol | Description | Function | Localization | Annotations |
|---------|--------|-------------|----------|--------------|-------------|
| P15424 |        | ATP-dependent RNA helicase | MS5116, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | catalytic activity; nucleotide binding; RNA binding |
| P47052 |        | Succinate dehydrogenase (ubiquitous) | YL045 W; YL045 W | metabolic process, transport | membrane/mitochondrion |
| P25605 |        | Acetolactate synthase small subunit, mitochondrial | ILV6; YCL099 C | metabolic process, regulation of biological process | mitochrondrion |
| P35398 |        | Succinyl-CoA ligase (ADP-forming) subunit alpha, mitochondrial | LSC1; YOR14 2W | metabolic process | cytoxol/mitochondrion |
| P33311 |        | ATP-dependent permease MDL2, mitochondrial | MDL2; YPL270 W | response to stimulus, transport | membrane/mitochondrion |
| P31540 |        | Protein RMD9, mitochondrial | RMD9; YGL107 C | cell differentiation, metabolic process, regulation of biological process | membrane/mitochondrion |
| P32843 |        | Mitochondrial escape protein 2 | YME2; YMR30 2C | cell organization and biogenesis, metabolic process | membrane/mitochondrion |
| P00927 |        | Threonine dehydratase, mitochondrial | ILV1; YER086 W | metabolic process | cytoplasm/mitochondrion |
| P07143 |        | Cytochrome c, heme protein, mitochondrial | CYT1; YDR06 5W | metabolic process, transport | cytoxol/mitochondrion, mitochondrial |
| P38071 |        | Enoyl-acyl-carrier protein reductase (NADPH, B-specific), mitochondrial | ETR1; YBR026 C | metabolic process | mitochrondrion,organelle lumen |
| P45367 |        | Alanine–glyoxylate aminotransferase 1 | AGX1; YPL030 W | metabolic process | cytoxol/mitochondrion |
| P07806 |        | Valine–tRNA ligase, mitochondrial | VAS1; YGR09 4W | metabolic process, regulation of biological process | cytoplasm, cytoxol/mitochondrion |
| P25374 |        | Cysteine desulphurase, mitochondrial | NFS1; YCL017 C | cell organization and biogenesis, cellular homeostasis, metabolic process | mitochrondrion, nucleus |
| P32787 |        | Mitochondrial genome maintenance protein MIM101 | MGM1 01; YLR144 W | cell organization and biogenesis, metabolic process, response to stimulus | chromosome/mitochondrion |
| P40098 |        | Uncharacterized mitochondrial membrane protein | FMP10; YER182 W | metabolic process | membrane/mitochondrion |
| P32897 |        | Mitochondrial import inner membrane translocase subunit tim23 | TIM23; YNR01 7W | transport | membrane/mitochondrion |
| Q06892 |        | NADH kinase P055, mitochondrial | P055; YLP118 W | metabolic process, response to stimulus | mitochrondrion,organelle lumen |
| P32317 |        | Protein AFG1 | AFG1; YEL052 W | cell organization and biogenesis, metabolic process, response to stimulus, transport | membrane/mitochondrion |
| P46681 |        | D-lactate dehydrogenase (cytochrome), mitochondrial | DLD2; YDI178 W | metabolic process | mitochrondrion,organelle lumen |
| P00410 |        | Cytochrome c oxidase subunit 2 | COX2; Q0250 | metabolic process, transport | membrane/mitochondrion |
| P35721 |        | Respiratory supercomplex factor 2, mitochondrial | CRC2; YMR01 8W | cell organization and biogenesis | membrane/mitochondrion |
| P40513 |        | Mitochondrial acidic protein MAN3 | MAM3 3; YUL070 C | metabolic process, regulation of biological process | mitochrondrion,organelle lumen |
| P12687 |        | S4S ribosomal protein L2, mitochondrial | MRP7; YNL005ir C | cell organization and biogenesis, metabolic process | mitochrondrion,ribosome |
| P40364 |        | Mitochondrial peculiar membrane protein 1 | MPM1; YLR066 C | cell organization and biogenesis | membrane/mitochondrion |
| Q00567 |        | ABC1 family protein MCP2 | YLR253 W; YLR253 W | cell organization and biogenesis | membrane/mitochondrion |
| Gene Symbol | Normalized Signal Intensity | Exp1 | Exp2 | Exp3 | Exp4 | Exp5 | Exp6 | Exp7 | Exp8 | Exp9 | Exp10 | Exp11 | Exp12 |
|-------------|---------------------------|------|------|------|------|------|------|------|------|------|-------|-------|-------|
|             |                           | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00   | 1.00   | 1.00   |

**Table 1: Normalized Signal Intensities for Gene Expression**

- **Exp1:** Sample 1
- **Exp2:** Sample 2
- **Exp3:** Sample 3
- **Exp4:** Sample 4
- **Exp5:** Sample 5
- **Exp6:** Sample 6
- **Exp7:** Sample 7
- **Exp8:** Sample 8
- **Exp9:** Sample 9
- **Exp10:** Sample 10
- **Exp11:** Sample 11
- **Exp12:** Sample 12

**Notes:**
- Normalized signal intensities are used to compare gene expression levels across different samples.
- Each experiment (Exp1 to Exp12) represents a different condition or sample.
- The values range from 1.00 to 1.00, indicating consistent expression levels across all samples.
Glycerol-3-phosphate dehydrogenase (NAD)(+) 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

P43519 | 545 ribosomal protein L7, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8518 | 23 | MRPL7; YDR23 7W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | RNA binding; structural molecule activity | 0.468 | 0.468 | 1.00

P33421 | Succinate dehydrogenase (ubiquinone) cytochrome b subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8537 | 16 | SDH3; YKL141 W | cell organization and biogenesis; metabolic process | membrane; mitochondrial | catalytic activity; metal ion binding | 1.276 | 1.276 | 1.00

P33759 | 375 ribosomal protein S5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8525 | 53 | MRPS5 ; YBR251 W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | RNA binding; structural molecule activity | 0.413 | 0.413 | 1.00

P36526 | 545 ribosomal protein L27, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8525 | 85 | MRPL2 7; YBR282 W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | 1.512 | 1.512 | 1.00

O95297 | Mitochondrial 2-oxocarboxylate transporter carrier 2 [OS=Saccharomyces cerevisiae S288c] | 8543 | 97 | ODC2; YDR22 2W | metabolic process; transport | membrane; mitochondrial | structural molecule activity; transporter activity | 0.778 | 0.778 | 1.00

O12298 | Uncharacterized ABC transport protein YDR061W [OS=Saccharomyces cerevisiae S288c] | 8516 | 33 | YDR06 1W; YDR06 1W | metabolic process | mitochondrial | catalytic activity; nucleotide binding | 0.266 | 0.266 | 1.00

P21306 | ATP synthase subunit epsilon, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8558 | 57 | ATPF15; YPL271 W | metabolic process; transport | membrane; mitochondrial | catalytic activity; transporter activity | 2.162 | 2.162 | 1.00

P18409 | Mitochondrial distribution and morphology protein 10 [OS=Saccharomyces cerevisiae S288c] | 8512 | 23 | MDM1 0; YAL010 C | cell organization and biogenesis; transport | membrane; mitochondrial | protein binding | 0.16 | 0.16 | 1.00

P25345 | Asparagine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8503 | 85 | SLARS; YCR003 C | metabolic process | cytoplasm; mitochondrial; organelle lumen | catalytic activity; nucleotide binding | 0.172 | 0.172 | 1.00

P25348 | 545 ribosomal protein L32, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8503 | 59 | MRPL3 2; YCR003 C | cell organization and biogenesis; metabolic process | membrane; mitochondrial; ribosome | RNA binding; structural molecule activity | 0.389 | 0.389 | 1.00

P34222 | Peptidyl-tRNA hydrolase 2 [OS=Saccharomyces cerevisiae S288c] | 8522 | 23 | PTH2; YPL057 C | regulation of biological process | cytoplasm; cytosol; membrane; mitochondrion | catalytic activity; protein binding | 0.425 | 0.425 | 1.00

Q06630 | Mitochondrial homologous recombination protein 1 [OS=Saccharomyces cerevisiae S288c] | 8518 | 90 | MRH1; YDR29 6W | cell organization and biogenesis; metabolic process; regulation of biological processes; response to stimulus | mitochondrial; nucleus | catalytic activity; DNA binding; structural molecule activity | 0.359 | 0.359 | 1.00

Q06510 | Lysophosphatidylcholine acyltransferase [OS=Saccharomyces cerevisiae S288c] | 8562 | 62 | TA21; YMR140 W | cell organization and biogenesis; metabolic process | membrane; mitochondrial | catalytic activity | 0.194 | 0.194 | 1.00

P38860 | GTPase MTG2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8565 | 73 | MTG2; YHR16 8W | metabolic process; transport | membrane; mitochondrial | catalytic activity; metal ion binding; structural molecule activity | 0.07 | 0.07 | 1.00

Q07914 | Mitochondrial import inner membrane translocase subunit TIM14 [OS=Saccharomyces cerevisiae S288c] | 8506 | 94 | PAM18 ; YLR008 C | regulation of biological process; transport | membrane; mitochondrial | enzyme regulator activity; protein binding; transporter activity | 0.778 | 0.778 | 1.00

P47150 | 375 ribosomal protein S7, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8355 | 78 | RSM7; YJR113 C | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | RNA binding; structural molecule activity | 0.334 | 0.334 | 1.00

P32606 | Putative mitochondrial translation system component PE127 [OS=Saccharomyces cerevisiae S288c] | 8541 | 82 | PE127 ; YDR01 7W | cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrial | 0.099 | 0.099 | 1.00

Q05467 | Uncharacterized protein YLR283W, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8509 | 88 | YLR283 W; YLR283 W | metabolic process; response to stimulus | endoplasmic reticulum; membrane; mitochondrial | 0.11 | 0.11 | 1.00

P38770 | 6-phosphogluconate dehydrogenase, decarboxylating 1 [OS=Saccharomyces cerevisiae S288c] | 8569 | 89 | GND1; YHR18 3W | metabolic process; response to stimulus | cytoplasm; mitochondrial | catalytic activity | 0.15 | 0.15 | 1.00

P07821 | Iron-sulfur assembly protein 1 [OS=Saccharomyces cerevisiae S288c] | 8506 | 32 | ISA1; YLI027 W | cell organization and biogenesis; metabolic process | mitochondrial; organelle lumen | metal ion binding; structural molecule activity | 0.136 | 0.136 | 1.00

P10849 | Mitochondrial transcription factor 2 [OS=Saccharomyces cerevisiae S288c] | 8515 | 17 | MTF2; YDR044 C | metabolic process | mitochondrial; organelle lumen | protein binding; RNA binding | 0.08 | 0.08 | 1.00

P39112 | Eukaryotic elongase II, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8553 | 31 | DSS6; YMR28 7C | metabolic process | mitochondrial; organelle lumen | catalytic activity; RNA binding | 0.087 | 0.087 | 1.00

P09955 | 5-aminoimidazole synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8513 | 18 | HEM1; YDR23 2W | metabolic process | mitochondrial; organelle lumen | catalytic activity | 0.086 | 0.086 | 1.00

P07263-1 | Histidine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8661 | 45 | HTI1; YPR033 C | cell organization and biogenesis; metabolic process | cytoplasm; mitochondrial | catalytic activity; nucleotide binding; RNA binding | 0.064 | 0.064 | 1.00
P33310  ATP-dependent permease MDL1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8508  85  MDL1; YLR188W  transport  membrane/mitochondrion  catalytic activity; nucleotide binding; transporter activity  0.438  0.528  1.21
Q06493  LETM1 domain-containing protein YLH47, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8562  43  YLH47; YPR125W  cell organization and biogenesis; transport  membrane/mitochondrion  0.61  0.743  1.22
P10662  37S ribosomal protein MRPL1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8519  48  MRPL1; YDR34T  cell organization and biogenesis; metabolic process; response to stimulus  mitochondrion/ribosome  antioxidant activity; catalytic activity; metal ion binding; structural molecular activity  1.239  1.512  1.22
P11325  Leucine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8510  98  NAM2; YLR382C  cell organization and biogenesis; metabolic process; regulation of biological process  cytosol/mitochondrion; organelle lumen  catalytic activity; nucleotide binding; RNA binding  0.208  0.254  1.22
P08466  mitochondrial nuclelease [OS=Saccharomyces cerevisiae S288c]  8532  22  NUC1; YL028C  cell death; metabolic process  membrane/mitochondrion; nucleus  catalytic activity; metal ion binding  1.336  1.637  1.23
Q07651  SUR7 family protein FMP45 [OS=Saccharomyces cerevisiae S288c]  8513  04  FMP45; YDL222C  cell differentiation; cell organization and biogenesis  membrane/mitochondrion  6.017  7.377  1.23
P33982  Isocitrate dehydrogenase [NADP] [OS=Saccharomyces cerevisiae S288c]  8557  27  IDP3; YNL009W  metabolic process  cytoplasm/mitochondrion  catalytic activity; metal ion binding; nucleotide binding  1.943  2.398  1.23
Q04458  Fatty aldehyde dehydrogenase HD1 [OS=Saccharomyces cerevisiae S288c]  8551  37  HD1; YMR110C  metabolic process  endoplasmic reticulum; endosome; membrane; mitochon drion  catalytic activity  3.642  4.505  1.24
Q06143  mitochondrial dicarboxylate transporter [OS=Saccharomyces cerevisiae S288c]  8510  63  DIC1; YLR348C  metabolic process; transport  membrane/mitochondrion  structural molecular activity; transport activity  0.931  1.154  1.24
P32331  Carrier protein YMC1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8561  71  YMC1; YPR058W  metabolic process; transport  membrane/mitochondrion; vacuole  structural molecular activity; transport activity  1.254  1.581  1.26
P40185  Protein mmf1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8547  60  MMF1; YIL051C  cell organization and biogenesis; metabolic process  mitochondrion; organelle lumen  6.943  9  1.30
P36112  MIC10 complex subunit Mic60 [OS=Saccharomyces cerevisiae S288c]  8538  86  FCZ1; MIC60; YKR016W  cell organization and biogenesis; transport  membrane/mitochondrion  15.37  9  19.96  2  1.30
P21375  Fumarate reductase 2 [OS=Saccharomyces cerevisiae S288c]  8535  30  OSM3; YLR051C  metabolic process  endoplasmic reticulum; mitochondrion  catalytic activity; nucleotide binding  0.346  0.45  1.30
P04710  ADP,ATP carrier protein 1 [OS=Saccharomyces cerevisiae S288c]  8550  78  AAC1; YMR005W  metabolic process; transport  cytosol;membrane;mitochondrion  structural molecular activity; transport activity  10.28  8  13.38  4  1.30
P38825  Protein TOM71 [OS=Saccharomyces cerevisiae S288c]  8565  17  TOM71; YHR117W  transport  membrane/mitochondrion  protein binding; transporter activity  0.701  0.954  1.30
Q01852  Mitochondrial import inner membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c]  8547  90  TIM44; YIL022W  transport  membrane/mitochondrion  nucleotide binding; protein binding  4.125  5.404  1.31
P36525  54S ribosomal protein L24, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8552  31  MRPL24; YMR193W  cell organization and biogenesis; metabolic process  mitochondrion/ribosome  RNA binding; structural molecular activity  1.154  1.512  1.31
P00128  Cytochrome b-c1 complex subunit 7 [OS=Saccharomyces cerevisiae S288c]  8531  42  QCR7; YDR529C  cell organization and biogenesis; metabolic process  membrane/mitochondrion  catalytic activity; protein binding; transporter activity  11.91  5  15.68  1  1.32
Q02776  Mitochondrial import inner membrane translocase subunit TIM50 [OS=Saccharomyces cerevisiae S288c]  8560  42  TIM50; YPL063W  cell organization and biogenesis; metabolic process; transport  membrane/mitochondrion  catalytic activity; protein binding; transporter activity  7.483  9.857  1.32
P21801  Succinate dehydrogenase (ubiquitone) iron-sulfur subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8506  85  SDH2; YLR041C  metabolic process; transport  membrane/mitochondrion  catalytic activity; metal ion binding  18.68  4  24.80  9  1.33
P53220  Mitochondrial import inner membrane translocase subunit TIM21 [OS=Saccharomyces cerevisiae S288c]  8529  21  TIM21; YGR032C  cell organization and biogenesis; transport  membrane/mitochondrion  protein binding  0.719  0.968  1.35
Q01574  acetyl-CoA synthetase 1 [OS=Saccharomyces cerevisiae S288c]  8532  45  ACS1; YAL034C  cell organization and biogenesis; metabolic process  cytosol;cytoplasm;endoplasmic reticulum; mitochondrion; nucleus  catalytic activity; nucleotide binding  3.281  4.456  1.36
P00445  Superoxide dismutase [Cu-Zn] [OS=Saccharomyces cerevisiae S288c]  8535  68  SOD1; YIR104C  cell organization and biogenesis; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus  cytosol;cytoplasm;mitochondrion; nucleus  antioxidant activity; catalytic activity; metal ion binding; protein binding  1.848  2.511  1.36
P44635  Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c]  8561  07  CTS3; YPR001W  metabolic process  mitochondrion  catalytic activity  3.642  4.995  1.37
P38169  Kynurenine 3-monooxygenase [OS=Saccharomyces cerevisiae S288c]  8521  79  BNA4; YBL098  metabolic process  membrane/mitochondrion  catalytic activity; nucleotide  0.269  0.374  1.39
| Gene ID | Symbol | Description | Localization | Cellular Activity | Gene Ontology Terms |
|--------|--------|-------------|--------------|------------------|---------------------|
| P40047 | ALS5   | Aldolase    | cytoplasm     | catalytic activity | metabolism;protein binding |
| P54783 | DAB21  | D-arabino-1,4-lactone oxidase | cytoplasm | catalytic activity | metabolism;protein binding |
| P38884 | AIN18  | Altered inheritance of mitochondria | membrane | catalytic activity | metabolism;protein binding |
| P40341 | YTA12  | Mitochondrial respiratory chain complexes assembly protein | cytoplasm, membrane | catalytic activity | metabolism;protein binding |
| P41735 | CAT5   | S-demethoxyaldehyde dehydrogenase, mitochondrial | membrane | catalytic activity | metabolism;protein binding |
| P07246 | ADH43  | Alcohol dehydrogenase 3, mitochondrial | cytoplasm, membrane | catalytic activity | metabolism;protein binding |
| P16622 | HMO1   | Ferrocyanochrome, mitochondrial | cytoplasm, membrane | catalytic activity | metabolism;protein binding |
| P00925 | YMR24  | Enoylase 2 | cytoplasm | catalytic activity | metabolism;protein binding |
| P32454 | YHR03  | Aminopeptidase 2, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| Q03201 | ALD5   | 375 ribosomal protein S10, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| P40515 | FIS1   | Mitochondria fission 1 protein | cytoplasm | catalytic activity | metabolism;protein binding |
| P35922 | ILV3   | Dihydroxy-acid dehydratase, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| Q08822 | YIR17  | Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| P40530 | NCA2   | (Pyruvate dehydrogenase (acyltransferase) kinase 1, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| Q02486 | ABF2   | AFS-binding factor 2, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| Q12374 | NCA2   | Nuclear control of ATPase protein 2 | cytoplasm | catalytic activity | metabolism;protein binding |
| P49095 | GCV2   | Glycine dehydrogenase (D-Glycine oxidase), mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| P07257 | PUT2   | Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| P39515 | YMR10  | Mitochondrial import outer membrane translocase subunit Tim17 | cytoplasm | catalytic activity | metabolism;protein binding |
| P16451 | PDX1   | Pynuvate dehydrogenase complex protein X component, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| Q12289 | YDR19  | Mitochondrial carnitine carrier | cytoplasm | catalytic activity | metabolism;protein binding |
| Q12480 | YMR08  | Probable electron transfer flavoprotein subunit alpha, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| P37292 | SMH1   | Serine hydroxymethyltransferase, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |
| Q04013 | YMR24  | Citrate/oxoglutarate carrier protein | cytoplasm | catalytic activity | metabolism;protein binding |
| Q03976 | YMR08  | 375 ribosomal protein S24, mitochondrial | cytoplasm | catalytic activity | metabolism;protein binding |

**Possible vocab:**
- **Localization:** cytoplasm, membrane, organelle lumen, chromosome, nucleus
- **Cellular Activity:** catalytic activity, metabolic process, binding process, structural activity
- **Gene Ontology Terms:** biogenesis;metabolic process, cell organization and biogenesis, membrane;mitochondrion, cytosol;mitochondrion, chromosome;mitochondrion, nucleus, cytoplasm;extracellular;membrane;mitochondrion;ribosome, membrane;mitochondrion, nuclear;membrane, membrane;mitochondrion;organelle lumen, mitochondrial import inner membrane translocase subunit Tim17;mitochondrion, organelle lumen;cytosol, mitochondrial

**Note:** The table includes a variety of genes and their functions, along with their localization and cellular activities. The gene ontology terms provide additional context to the functions described.
| Gene ID | Description | Molecular Location | Biological Process | Cellular Component | Molecular Function | Localization | RNA Binding | Protein Binding | Metabolic Network | Protein Information |
|---------|-------------|-------------------|--------------------|-------------------|-----------------|----------------|-------------|---------------|------------------|-------------------|
| P05626 | ATP synthase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | ATP60 27 | ATP4; YPL078 C | cell organization and biogenesis; metabolic process | membrane/mitochondrion | catalytic activity, transporter activity | 3.084 | 5.813 | 1.88 |
| Q06089 | Uncharacterized mitochondrial outer membrane protein YPR088C [OS=Saccharomyces cerevisiae S288c] | E562 13 | YPR088 BC | metabolic process | membrane/mitochondrion | | 4.623 | 9 | 1.95 |
| P25087 | Sterol 24-C-methyltransferase [OS=Saccharomyces cerevisiae S288c] | E550 03 | ERS6; YML00 BC | metabolic process | endoplasmic reticulum; membrane; mitochondrion | catalytic activity | 1.424 | 2.775 | 1.95 |
| P32473 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E525 22 | PDB1; YBR221 C | metabolic process | mitochondrial; organelle lumen | catalytic activity | 6.848 | 13.38 | 4 | 1.95 |
| Q00711 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E537 09 | SDH1; YKL148 C | metabolic process, transport | membrane/mitochondrion | catalytic activity; nucleotide binding; protein binding | 8.454 | 16.53 | 5 | 1.96 |
| P07213 | Mitochondrial import receptor subunit TOM70 [OS=Saccharomyces cerevisiae S288c] | E556 02 | TOM70; YNL121 C | cell organization and biogenesis; transport | membrane/mitochondrion | protein binding; transporter activity | 2.665 | 5.236 | 1.96 |
| P23644 | Mitochondrial import receptor subunit TOM40 [OS=Saccharomyces cerevisiae S288c] | E552 43 | TOM40; YMR20 BW | transport | cytosol; membrane/mitochondrion | protein binding; transporter activity | 0.896 | 1.783 | 1.99 |
| P07342 | Acetolactate synthase catalytic subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E551 35 | ILV2; YMR10 BW | metabolic process | mitochondrion | catalytic activity; metal ion binding; nucleotide binding | 4.223 | 8.427 | 2.00 |
| Q02950 | 375 ribosomal protein MRP51, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E559 85 | MRP51; YPL118 W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.668 | 1.346 | 2.01 |
| P38910 | 10 kDa heat shock protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E541 85 | HSP10; YDR02 OC | cell organization and biogenesis; metabolic process; response to stimulus; transport | cytoplasm; mitochondrion; organelle lumen | metal ion binding; nucleotide binding; protein binding | 3.217 | 6.499 | 2.02 |
| P46526 | Isoleucine–tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E560 67 | I5M6; YPL140 C | cell organization and biogenesis; metabolic process; regulation of biological process | cytoplasm; cytosol; mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 0.04 | 0.081 | 2.03 |
| P21954 | Isoctrate dehydrogenase [NADP], mitochondrial [OS=Saccharomyces cerevisiae S288c] | E514 93 | IDP1; YDL066 W | metabolic process | mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | 3.145 | 6.712 | 9 | 2.03 |
| P32445 | Single-stranded DNA-binding protein RIM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E503 95 | RIM1; YCR028 C A | cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrion | DNA binding | 1.783 | 3.642 | 2.04 |
| Q00402 | Nuclear migration protein NUM1 [OS=Saccharomyces cerevisiae S288c] | E517 27 | NUM1; YDR15 OW | cell organization and biogenesis; cellular component movement; metabolic process; regulation of biological process | endoplasmic reticulum; mitochondrion | catalytic activity; motor activity; protein binding | 0.065 | 0.134 | 2.06 |
| P10507 | Mitochondrial-processing peptidase subunit beta [OS=Saccharomyces cerevisiae S288c] | E508 60 | MAS1; YLR163 C | metabolic process, transport | mitochondrion; organelle lumen | catalytic activity; metal ion binding; protein binding | 0.778 | 1.61 | 2.07 |
| P43603 | LAS seventeen-binding protein 3 [OS=Saccharomyces cerevisiae S288c] | E505 80 | L8B3; YHR024 C A | cell organization and biogenesis; regulation of biological process | cytoplasm; mitochondrion | protein binding | 0.089 | 0.186 | 2.09 |
| Q08179 | Mitochondrial distribution and morphology protein 38 [OS=Saccharomyces cerevisiae S288c] | E541 30 | IMD3; YDL027 C | cell organization and biogenesis; cellular homeostasis; regulation of biological process; transport | membrane; mitochondrion | | 3.732 | 7.913 | 2.12 |
| P39965 | Probable proline–tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E568 20 | AIM10; YER087 W | metabolic process | cytoplasm; mitochondrion | catalytic activity; nucleotide binding; RNA binding | 0.125 | 0.266 | 2.13 |
| P21771 | 375 ribosomal protein S28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E509 37 | MRPS2; YDR33 7W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 0.624 | 1.336 | 2.14 |
| P32841 | Isoctrate dehydrogenase [NAD] subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E543 03 | IDH2; YOR13 6W | metabolic process | mitochondrion; organelle lumen | catalytic activity; metal ion binding; nucleotide binding; protein binding; RNA binding | 4.179 | 9 | 2.15 |
| P53212 | Probable transcriptional regulatory protein HAM1 [OS=Saccharomyces cerevisiae S288c] | E529 04 | YGR02 1W; YGR02 1W | | mitochondrion | | 0.166 | 0.359 | 2.16 |
| P43079 | Probable kynurenine–oxoglutarate transaminase BNA3 [OS=Saccharomyces cerevisiae S288c] | E533 86 | BNA3; YIL060 W | metabolic process; regulation of biological process | cytoplasm; mitochondrion | catalytic activity | 0.312 | 0.468 | 2.21 |
| P09440 | C-1-tetrahydrolipstatine synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | E523 78 | MIH1; YBR084 W | metabolic process | cytosol; mitochondrion | catalytic activity; nucleotide binding | 0.9 | 1.988 | 2.21 |
P49334
Mitochondrial import receptor subunit tom22 [Saccharomyces cerevisiae S288c]
8555 92 TOM22; YNL131 W cell organization and biogenesis;transport membrane/mitochondrion protein binding;transporter activity 0.292 0.668 2.29

P33416
Heat shock protein 70, mitochondrial [Saccharomyces cerevisiae S288c]
8518 45 HSP70; YDR25 BC cell organization and biogenesis;metabolic process;response to stimulus mitochondrion;organelle lumen catalytic activity;nucleotide binding;protein binding 4.264 9.784 2.29

P36775
Lyn protease homolog, mitochondrial [Saccharomyces cerevisiae S288c]
8522 59 PIM1; YBL022 C cell organization and biogenesis;metabolic process;response to stimulus cytoplasm/mitochondrion;organelle lumen catalytic activity;DNA binding;nucleotide binding;RNA binding 0.685 1.59 2.32

P23301
Eukaryotic translation initiation factor 5A-1 [Saccharomyces cerevisiae S288c]
8566 77 HPP2; YEL034 W metabolic process;regulation of biological process cytoplasm/mitochondrion;ribosome protein binding;RNA binding 0.334 0.778 2.33

P25349
Flavoprotein-like protein YCP4 [Saccharomyces cerevisiae S288c]
8003 60 YCP4; YCR004 C metabolic process;regulation of biological process cytoplasm/mitochondrion;mitochondrion catalytic activity;nucleotide binding;protein binding 5.813 13.67 2.35

P00830
ATP synthase subunit beta, mitochondrial [Saccharomyces cerevisiae S288c]
8535 85 ATP2; YIR121 W metabolic process;transport cytosol;membrane/mitochondrion catalytic activity;nucleotide binding;protein binding;transporter activity 38.81 91.61 2.36

P52893
Probable alanine aminotransferase, mitochondrial [Saccharomyces cerevisiae S288c]
8578 78 ALT1; YJR089 C metabolic process mitochondrion;organelle lumen catalytic activity 0.951 2.282 2.40

Q03028
Mitochondrial 2-oxoglutarate carrier 1 [Saccharomyces cerevisiae S288c]
8559 69 OGD1; YPL134 C metabolic process;transport membrane/mitochondrion structural molecule activity;transporter activity 4.275 10.36 2.42

P36013
NAD-dependent malic enzyme, mitochondrial [Saccharomyces cerevisiae S288c]
8538 39 MAE1; YKL029 C metabolic process mitochondrion;organelle lumen catalytic activity;metal ion binding;protein binding 1.512 3.732 2.47

P37298
Succinate dehydrogenase [ubiquione] cytochrome b small subunit, mitochondrial [Saccharomyces cerevisiae S288c]
8527 58 SDH4; YDR17 BW metabolic process;transport membrane/mitochondrion catalytic activity;metal ion binding 3.462 9 2.47

P07256
Cytochrome b-c1 complex subunit 1, mitochondrial [Saccharomyces cerevisiae S288c]
8322 35 COR1; YBL045 C metabolic process membrane/mitochondrion catalytic activity;nucleotide binding;protein binding;transporter activity 9.89 24.55 2.48

P38891
Branched-chain-amino-acid aminotransferase, mitochondrial [Saccharomyces cerevisiae S288c]
8566 15 BAT1; YHR20 BW metabolic process;regulation of biological process;response to stimulus mitochondrion;organelle lumen catalytic activity 7.111 17.73 2.49

P28834
Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial [Saccharomyces cerevisiae S288c]
8556 91 IDH1; YNL037 C metabolic process;transport cytosol/mitochondrion;organelle lumen catalytic activity;metal ion binding;protein binding;RNA binding 7.859 19.69 2.51

P39952
Mitochondrial inner membrane protein Oxa1p [Saccharomyces cerevisiae S288c]
8568 98 OXA1; YER154 W cell organization and biogenesis;transport membrane/mitochondrion transporter activity 1.054 2.652 2.52

P00424
Cytochrome c oxidase polypeptide 5A, mitochondrial [Saccharomyces cerevisiae S288c]
8556 75 COX5A; YNL052 W metabolic process;transport membrane/mitochondrion catalytic activity;transporter activity 1.31 3.329 2.54

P16387
Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial [Saccharomyces cerevisiae S288c]
8569 25 PDA1; YER178 W cell growth;metabolic process mitochondrion catalytic activity 12.46 31.81 2.55

Q12166
2-isopropylmalate synthase 2, mitochondrial [Saccharomyces cerevisiae S288c]
8542 75 LEU9; YDR10 BW metabolic process mitochondrion catalytic activity;protein binding 1.707 4.367 2.56

P08067
Cytochrome b-c1 complex subunit Rieske, mitochondrial [Saccharomyces cerevisiae S288c]
8566 89 RIP2; YEL024 W metabolic process;transport membrane/mitochondrion catalytic activity;metal ion binding;transporter activity 25.10 67.12 2.67

P41921
Glutathione reductase [Saccharomyces cerevisiae S288c]
8560 14 GLR1; YPL091 W cellular homeostasis;metabolic process;regulation of biological process;response to stimulus cytoplasm;cytosol/mitochondrion;nuclcus antioxidant activity;catalytic activity;nucleotide binding 0.241 0.655 2.72

P15262
Dihydrolipoamide-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex, mitochondrial [Saccharomyces cerevisiae S288c]
8517 26 KGD2; YDR14 BC cell organization and biogenesis;metabolic process mitochondrion catalytic activity;protein binding 5.7 15.49 2.72

P02992
Elongation factor 1A, mitochondrial [Saccharomyces cerevisiae S288c]
8543 59 TUF1; YDR18 7W cell organization and biogenesis;metabolic process mitochondrion catalytic activity;nucleotide binding;RNA binding 12.04 33.55 2.79

P32891
D-lactate dehydrogenase [cytochrome] 1, mitochondrial [Saccharomyces cerevisiae S288c]
8513 80 DLDO1; YDL174 C metabolic process;transport membrane/mitochondrion catalytic activity;nucleotide binding 11.25 32.83 2.92

P38325
Mitochondrial outer membrane protein Omi14 [Saccharomyces cerevisiae S288c]
8525 31 OM14; YBR230 C transport membrane/mitochondrion 6.197 18.30 2.95

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| Gene ID   | Name Description                                                                 | Localization       | Molecular Function                                                                 | Process                                      | BP1       | BP2       | BP3       | BP4       |
|-----------|-----------------------------------------------------------------------------------|--------------------|-------------------------------------------------------------------------------------|----------------------------------------------|-----------|-----------|-----------|-----------|
| Q12230    | Sphingolipid long chain base-responsive protein LPS1                              |                    | regulation of biological process/response to stimulus/transport                      | cytoplasm,membrane,mitochondrion            | 24.11     | 72.56     | 3.01      |           |
| P39728    | Glycine cleavage system H protein, mitochondrial                               |                    |                                      |                                | 6.743     | 20.54     | 3.05      |           |
| P38077    | ATP synthase subunit gamma, mitochondrial                                        |                    |                                      |                                | 9         | 27.48     | 3.05      |           |
| P48239    | Mitochondrial group I intron splicing factor CCM1                                |                    |                                      |                                | 0.044     | 0.136     | 3.09      |           |
| P32191    | Glyceraldehyde 3-phosphate dehydrogenase, mitochondrial                           |                    |                                      |                                | 6.097     | 18.85     | 3.09      |           |
| P40495    | Homocitrate dehydrogenase, mitochondrial                                          |                    |                                      |                                | 3.217     | 10.00     | 3.11      |           |
| P49367    | Homoaconitate, mitochondrial                                                      |                    |                                      |                                | 0.638     | 1.994     | 3.13      |           |
| Q22329    | Uncharacterized protein YDR119W-A                                               |                    |                                      |                                | 1.154     | 3.642     | 3.16      |           |
| P38756    | IRA1 Threonine/Alanine dehydrogenase 1 [Saccharomyces cerevisiae S288c]          |                    |                                      |                                | 1.154     | 3.642     | 3.16      |           |
| P34227    | Mitochondrial peroxidoxin PRX1                                                   |                    |                                      |                                | 5.158     | 17.33     | 3.36      |           |
| Q12165    | ATP synthase subunit delta, mitochondrial                                         |                    |                                      |                                | 1.371     | 4.623     | 3.37      |           |
| P04083    | Tryptophan-irRNA ligase, mitochondrial                                            |                    |                                      |                                | 0.136     | 0.468     | 3.44      |           |
| P53163    | S45 ribosomal protein L12, mitochondrial                                          |                    |                                      |                                | 0.52      | 1.848     | 3.55      |           |
| P36060    | NADH-cytochrome b5 reductase 2 [Saccharomyces cerevisiae S288c]                   |                    |                                      |                                | 10.28     | 36.92     | 3.59      |           |
| P12695    | Dihydroxyphosphino-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial [Saccharomyces cerevisiae S288c] |                    |                                      |                                | 5.898     | 21.63     | 3.67      |           |
| P32340    | Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial                |                    |                                      |                                | 16.43     | 61.10     | 3.72      |           |
| P23181    | Probable oxidoreductase AIM17                                                    |                    |                                      |                                | 2.981     | 11.58     | 3.89      |           |
| P02757    | Cytochrome b-c1 complex subunit 2, mitochondrial                                  |                    |                                      |                                | 21.19     | 82.76     | 3.91      |           |
| P04840    | Mitochondrial outer membrane protein porin 1 [Saccharomyces cerevisiae S288c]     |                    |                                      |                                | 15.23     | 60.58     | 3.98      |           |
| P15450    | fructose-bisphosphate aldolase                                                   |                    |                                      |                                | 0.896     | 3.642     | 4.06      |           |
| P08245    | protein ZEO1 [Saccharomyces cerevisiae S288c]                                     |                    |                                      |                                | 2.162     | 9         | 4.16      |           |
| P00360    | glyceroldehyde-3-phosphate dehydrogenase 1 [Saccharomyces cerevisiae S288c]      |                    |                                      |                                | 1.721     | 7.185     | 4.17      |           |
| P19414    | Acetate synthase, mitochondrial                                                  |                    |                                      |                                | 24.88     | 109.5     | 4.40      |           |
| P00880    | citrate synthase, mitochondrial                                                  |                    |                                      |                                | 8.211     | 36.27     | 4.42      |           |
| P00358    | glyceroldehyde-3-phosphate dehydrogenase 2 [Saccharomyces cerevisiae S288c]      |                    |                                      |                                | 3.489     | 15.49     | 4.44      |           |
| Gene Symbol | Protein Name             | Cellular Location                        | Biological Processes                                      | GO Terms                                              | Enrichment Score |
|-------------|-------------------------|------------------------------------------|-----------------------------------------------------------|--------------------------------------------------------|------------------|
| P00942      | Triosephosphate isomerase| cytoplasm, cytosol, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 0.425            |
| P00942      | Triosephosphate isomerase| cytoplasm, cytosol, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 1.894            |
| P07251      | ATP synthase subunit alpha, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 4.46             |
| P25039      | Elongation factor G, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 12.01            |
| P39518      | Long-chain-fatty-acid-CoA ligase 2 | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 53               |
| P06208-1    | 2-isopropylmalate synthase | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.45             |
| P35252      | sphingolipid long chain base-responsive protein PIL1 | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.57             |
| P06168      | ketol-acid reductoisomerase, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 19.30            |
| P35293      | ATP-binding protein ypt7 | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 9.15             |
| P09624      | Dihydritoloyl dehydrogenase, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 21.53            |
| P35312      | Succinyl-CoA ligase (ADP-forming) subunit beta, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 113.5            |
| P33031      | Succinate/fumarate mitochondrial transporter | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
| P17505      | Malate dehydrogenase, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 21.53            |
| P12709      | glucose-6-phosphate isomerase | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 113.5            |
| P09624      | Dihydritoloyl dehydrogenase, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
| P20967      | 2-oxoglutarate dehydrogenase, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
| P16547      | Mitochondrial outer membrane protein OM45 | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
| P19882      | heat shock protein 60, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
| P46376      | Potassium-activated aldehyde dehydrogenase, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
| P03950      | Heat shock protein Ssc1, mitochondrial | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
| P32316      | acetyl-CoA hydrolase | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
| P18239      | ADP-ATP carrier protein 2 | cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding       | GO:001604, GO:001605, GO:001606                          | 5.27             |
Supplemental Table S7. The relative concentrations of proteins in mitochondria purified from ups1Δ cells cultured with or without LCA. Mitochondria were purified from ups1Δ cells recovered on day 2 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI ups1 | emPAI ups1 + LCA | Ratio ups1 + LCA/ ups1 |
|-----------|-------------|---------------|---------|---------------------|--------------------|---------------------|------------|-----------------|---------------------|
| P00175    | Cytochrome b2, mitochondrial | 85495 | CYB2 | 7 | metabolic process; transport | cytosol; membrane; mitochondrion; nucleus | catalytic activity; metal ion binding; nucleotide binding | 1.371 | 0.159 | 0.04 |
| P16451    | Pyruvate dehydrogenase complex protein X component, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85310 | PDX1; YGR193c | 7 | metabolic process | mitochondrion; organelle lumen | catalytic activity; structural molecule activity | 1.555 | 0.089 | 0.06 |
| P43635    | Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85610 | CIT3; YPK001 | 7 | metabolic process | mitochondrion | catalytic activity | 2.914 | 0.186 | 0.06 |
| P40513    | Mitochondrial acidic protein MAM33 [OS=Saccharomyces cerevisiae S288c] | 85474 | MAM3; YIL070C | 0 | metabolic process; regulation of biological process | mitochondrion; organelle lumen | translation regulator activity | 2.831 | 0.212 | 0.07 |
| P53140    | Protein RM05, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85277 | RM05; YGL107C | 1 | cell differentiation; metabolic process; regulation of biological process | membrane; mitochondrion | RNA binding | 0.668 | 0.053 | 0.08 |
| P81449    | ATP synthase subunit e, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85192 | TIM11; YDR32c | 2 | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrion | catalytic activity; structural molecule activity; transport activity | 9 | 0.778 | 0.09 |
| P00360    | Glyceraldehyde-3-phosphate dehydrogenase 1 [OS=Saccharomyces cerevisiae S288c] | 85339 | TDH1; YIL052 | 5 | metabolic process | cytoplasm; cytosol; membrane; mitochondrion | catalytic activity; nucleotide binding | 3.062 | 0.35 | 0.11 |
| P16547    | Mitochondrial outer membrane protein OM45 [OS=Saccharomyces cerevisiae S288c] | 85467 | OM45; YIL136 | 0 | membrane; mitochondrion | 830.7 64 | 99 | 0.12 |
| P32281    | D-lactate dehydrogenase [cytochrome] 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85138 | LDH1; YDL174C | 0 | metabolic process; transport | membrane; mitochondrion | catalytic activity; nucleotide binding | 11.25 | 3 | 1.412 | 0.13 |
| P43567    | Alamine-glyoxylate aminotransferase 1 [OS=Saccharomyces cerevisiae S288c] | 85051 | AGX1; YFL030 | 4 | metabolic process | cytosol; mitochondrion | catalytic activity | 1.61 | 0.212 | 0.13 |
| P00431    | Cytochrome c peroxidase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85394 | CCP1; YKR066C | 0 | metabolic process; response to stimulus | mitochondrion; organelle lumen | antioxidant activity; catalytic activity; metal ion binding; protein binding | 0.703 | 0.093 | 0.13 |
| P32787    | Mitochondrial genome maintenance protein MGM101 [OS=Saccharomyces cerevisiae S288c] | 85360 | MGM1O1; YIR144 | 9 | cell organization and biogenesis; metabolic process; response to stimulus | chromosome; mitochondrion | DNA binding | 3.281 | 0.438 | 0.13 |
| Q02981    | ABC1 family protein YPL109C, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85599 | YPL109C; YPL109C | 5 | mitochondrion | 0.413 | 0.059 | 0.14 |
| P32393    | GTP-binding protein ypt7 [OS=Saccharomyces cerevisiae S288c] | 85501 | YPT7; YML100Y | 2 | cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport | cytosol; endosome; membrane; mitochondrion; vacuole | catalytic activity; nucleotide binding; protein binding | 1.154 | 0.166 | 0.14 |
| P00927    | Threonine dehydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85681 | ILV1; YER086 | 9 | metabolic process | cytoplasm; mitochondrion | catalytic activity | 1.285 | 0.194 | 0.15 |
| Q02486    | ARS-binding factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85509 | AFB2; YMR072W | 4 | cell organization and biogenesis; metabolic process; regulation of biological process | chromosome; mitochondrion; nucleus | DNA binding | 6.23 | 9 | 7.377 | 0.15 |
| P36521    | 5S ribosomal protein L11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85132 | MRPL11; YDL202W | 5 | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.833 | 0.129 | 0.15 |
| Protein Name                                    | Gene ID | Localization                        | Processes/Activities                                      | Remarks                        |
|------------------------------------------------|---------|-------------------------------------|------------------------------------------------------------|--------------------------------|
| Branched-chain-aminooxylic acid aminotransferase, mitochondrial [S. cerevisiae S288c] | P38891  |                                     | Metabolic process; Regulation of biological process; Response to stimulus | Mitochondrion, Organelle lumen |
| Glycine dehydrogenase (Decarboxylating), mitochondrial [S. cerevisiae S288c] | P48095  |                                     | Metabolic process                                         | Cytosol, Mitochondrion         |
| ATP-dependent RNA helicase MMS16, mitochondrial [S. cerevisiae S288c] | P15424  |                                     | Metabolic process; Regulation of biological process        | Mitochondrion, Organelle lumen |
| Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial [S. cerevisiae S288c] | Q00711  |                                     | Metabolic process; Transport                              | Cytosol, Mitochondrion         |
| Sorting machinery 50 kDa subunit [S. cerevisiae S288c] | P53969  |                                     | Cytosol, Mitochondrion, Nucleus                            | Protein binding, Transporter   |
| Phosphatidylserine decarboxylase proenzyme 1, mitochondrial [S. cerevisiae S288c] | P39006  |                                     | Metabolic process; Regulation of biological process        | Cytosol, Mitochondrion         |
| Hexokinase-2 [S. cerevisiae S288c] | P04807  |                                     | Metabolic process; Communication; Cell organization and biogenesis; Cellular homeostasis | Cytosol, Mitochondrion, Nucleus |
| Mitochondrial inner membrane translocase subunit tim32 [S. cerevisiae S288c] | P32897  |                                     | Transport                                                  | Membrane, Mitochondrion        |
| Dihydroxy-acid dehydrogenase, mitochondrial [S. cerevisiae S288c] | P39522  |                                     | Metabolic process                                         | Mitochondrion                  |
| Rotenone-insensitive NADH:ubiquinone oxidoreductase, mitochondrial [S. cerevisiae S288c] | P32340  |                                     | Metabolic process; Regulation of biological process        | Membrane, Mitochondrion, Organelle lumen |
| Mitochondrial pyruvate carrier 3 [S. cerevisiae S288c] | P35311  |                                     | Transport                                                  | Membrane, Mitochondrion        |
| 2-oxoglutamate dehydrogenase, mitochondrial [S. cerevisiae S288c] | P20967  |                                     | Metabolic process                                         | Cytosol, Mitochondrion, Organelle lumen |
| Cytochrome c oxidase subunit 4, mitochondrial [S. cerevisiae S288c] | P04037  |                                     | Transport                                                  | Membrane, Mitochondrion        |
| NAD-dependent malic enzyme, mitochondrial [S. cerevisiae S288c] | P36013  |                                     | Metabolic process                                         | Mitochondrion, Organelle lumen |
| NADH:cytochrome b5 reductase 2 [S. cerevisiae S288c] | P36060  |                                     | Metabolic process; Response to stimulus                    | Membrane, Mitochondrion        |
| Cytochrome b1-c1 complex subunit 8 [S. cerevisiae S288c] | P08525  |                                     | Metabolic process; Transport                              | Membrane, Mitochondrion        |
| Probable alanine aminotransferase, mitochondrial [S. cerevisiae S288c] | P52893  |                                     | Metabolic process                                         | Mitochondrion                  |
| Isoicrate dehydrogenase [NADP+], mitochondrial [S. cerevisiae S288c] | P31154  |                                     | Metabolic process                                         | Mitochondrion                  |
| Isoicrate dehydrogenase [NAD+] subunit 1, mitochondrial [S. cerevisiae S288c] | P28834  |                                     | Metabolic process; Transport                              | Cytosol, Mitochondrion, Organelle lumen |
| Homoaconitase, mitochondrial [S. cerevisiae S288c] | P49367  |                                     | Metabolic process                                         | Mitochondrion                  |
| Cytochrome c oxidase subunit 6, mitochondrial [S. cerevisiae S288c] | P00427  |                                     | Metabolic process; Transport                              | Membrane, Mitochondrion        |
| Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial [S. cerevisiae S288c] | P35312  |                                     | Metabolic process                                         | Mitochondrion                  |
| ATP synthase subunit alpha, mitochondrial [S. cerevisiae S288c] | P07251  |                                     | Metabolic process; Transport                              | Cytosol, Membrane, Mitochondrion |

**Remarks:***
- **Polar:** Indicates whether the transport is polarized.
- **Protein:** Specifies the protein involved.
- **Localization:** Describes the subcellular localization.
- **Activity:** Indicates the activity associated with the transport.
- **Remarks:** Provides additional information about the transport process.
| P00128 | Cytochrome b-c1 complex subunit 7 | OS=Saccharomyces cerevisiae S288c | BS214 | Q11R7; YDR529C | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity,transporter activity | 11.91 | 5 | 2.594 | 0.22 |
| P0390 | Heat shock protein 30K1C | mitochondrial | OS=Saccharomyces cerevisiae S288c | BS330 | SYL4045C | cell organization and biogenesis;metabolic process;regulation of biological process | membrane;mitochondrion;nucleus;organelle lumen | catalytic activity,enzyme regulator activity,nucleotide binding;protein binding | 67.12 | 9 | 14.647 | 0.22 |
| Q02833 | N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS600 | FMP30; YLP103C | metabolic process | membrane;mitochondrion | catalytic activity,metal ion binding | 0.425 | 0.093 | 0.22 |
| P38969 | Pentamidine resistance factor, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS444 | PINT; YDR268W | cell organization and biogenesis;response to stimulus | membrane;mitochondrion | 0.359 | 0.08 | 0.22 |
| P38088 | Glycine--tRNA ligase 1, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS386 | GRS1 | metabolic process | cytoplasm;mitochondrion;organellar lumen | catalytic activity,nucleotide binding,protein binding | 0.212 | 0.049 | 0.23 |
| P00560 | Phosphoglycerate kinase | OS=Saccharomyces cerevisiae S288c | BS303 | PXG1; YCR012W | metabolic process | cytoplasm;membrane;mitochondrion | catalytic activity,transporter activity | 3.642 | 0.848 | 0.23 |
| P4681 | D-lactate dehydrogenase [cytochrome]2, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS137 | DLO2; YDL178W | metabolic process | mitochondrion;organellar lumen | catalytic activity,nucleotide binding,protein binding | 0.682 | 0.16 | 0.23 |
| P32796-1 | Carnitine O-acetyltransferase, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS496 | CAT2; YML042W | metabolic process;transport | membrane;mitochondrion | catalytic activity | 9.578 | 2.252 | 0.24 |
| P36112 | MTCO3 complex subunit Mic60 | OS=Saccharomyces cerevisiae S288c | BS388 | F1111; MIG60; YKR016W | cell organization and biogenesis;transport | membrane;mitochondrion | 12.85 | 5 | 3.047 | 0.24 |
| P02992 | elongation factor Tu, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS435 | TUF1; YOR187W | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity,nucleotide binding;RNA binding | 9 | 2.162 | 0.24 |
| P39952 | Mitochondrial inner membrane protein OX1 | OS=Saccharomyces cerevisiae S288c | BS689 | OX1; YER154W | cell organization and biogenesis;transport | membrane;mitochondrion | transporter activity | 1.371 | 0.334 | 0.24 |
| P54783 | D-arabino-1,4-lactone oxidase | OS=Saccharomyces cerevisiae S288c | BS488 | ALQ1; YML086C | metabolic process;response to stimulus | membrane;mitochondrion | catalytic activity,nucleotide binding | 5.31 | 1.326 | 0.25 |
| P32316 | acetyl-CoA hydroxilase | OS=Saccharomyces cerevisiae S288c | BS226 | ACH1; YBL015W | metabolic process | cytoplasm;cytosol;mitochondrion | catalytic activity | 20.54 | 4 | 5.136 | 0.25 |
| Q02784 | Monothiol glutaredoxin-5, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS604 | GXX5; YPL059W | cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus | mitochondrion;organellar lumen | catalytic activity,metal ion binding | 1.154 | 0.292 | 0.25 |
| P32317 | Protein AFG1 | OS=Saccharomyces cerevisiae S288c | BS665 | AFG1; YEL052W | cell organization and biogenesis;metabolic process;response to stimulus;transport | membrane;mitochondrion | catalytic activity,nucleotide binding | 0.999 | 0.259 | 0.26 |
| P40502 | Altered inheritance of mitochondria protein 19, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS472 | AIM19; YIL087C | cell organization and biogenesis;metabolic process;response to stimulus;transport | membrane;mitochondrion | 0.999 | 0.259 | 0.26 |
| P53216 | putative cysteine synthase | OS=Saccharomyces cerevisiae S288c | BS289 | MCY1; YGR012C; YGR012W | metabolic process | catalytic activity | 1.555 | 0.407 | 0.26 |
| P12695 | Dihydrolipoamide-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS565 | LAT1; YML071W | metabolic process | mitochondrion;organellar lumen | catalytic activity | 10.60 | 2 | 2.808 | 0.26 |
| P36517 | SAS ribosomal protein L4, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS116 | MRF4; YLR439W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.874 | 0.233 | 0.27 |
| P10507 | mitochondrial-processing peptidase subunit beta | OS=Saccharomyces cerevisiae S288c | BS086 | MAL1; YLR163C | metabolic process;transport | mitochondrion;organellar lumen | catalytic activity,metal ion binding | 0.778 | 0.212 | 0.27 |
| P07246 | Alcohol dehydrogenase 3, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS510 | ADH3; YMR087W | metabolic process | mitochondrion;organellar lumen | catalytic activity,metal ion binding | 11.43 | 2 | 3.16 | 0.28 |
| P34222 | PepD-PepA hydrolase 2 | OS=Saccharomyces cerevisiae S288c | BS222 | FHL2; YBL057 | regulation of biological process | cytoplasm;cytosol;membrane;mitochondrion | catalytic activity,protein binding | 0.702 | 0.154 | 0.28 |
| Q05931 | Heat shock protein Ssp1, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS108 | Ssp1; YLR369W | cell organization and biogenesis;metabolic process | mitochondrion;organellar lumen | nucleotide binding,protein binding | 0.679 | 0.189 | 0.28 |
| P30902 | ATP-synthase subunit d, mitochondrial | OS=Saccharomyces cerevisiae S288c | BS385 | ATP7; YKL016 | metabolic process;transport | membrane;mitochondrion | catalytic activity,transporter activity | 18.30 | 7 | 5.105 | 0.28 |
P09624  Dehydrodipolypetide hydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85052  LEU1; YFD118 C  cellular homeostasis;metabolic process;regulation of biological process  mitochondrion,organelle lumen  catalytic activity;nucleotide binding  43.36  7  12.11  1  0.28

P37267  Assembly factor cpmp4 [OS=Saccharomyces cerevisiae S288c]  CBP4  cell organization and biogenesis  membrane,mitochondrion  1.848  0.52  0.28

P27929  37S ribosomal protein NAM9, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85558  NAM9; YNL137 C  cell organization and biogenesis;metabolic process;regulation of biological process  mitochondrion,ribosome  RNA binding;structural molecule activity  1.062  0.301  0.28

P28241  Isocitrate dehydrogenase (NAD) subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85430  IDH2; YOR13 16W  metabolic process  mitochondrion,organelle lumen  catalytic activity;metal ion binding;metal ion binding;protein binding;DNA binding;RNA binding  7.031  1.994  0.28

P37299  Cytochrome b-c1 complex subunit 10 [OS=Saccharomyces cerevisiae S288c]  85639  QCR10; YHR001W-A  metabolic process;transport  membrane,mitochondrion  catalytic activity;transporter activity  5.31  1.512  0.28

P15414  Aconitate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85101  ACO1; YLR304W C  cell organization and biogenesis;metabolic process;transport  cytoplasm;cytosol;mitochondrion,organelle lumen  catalytic activity;DNA binding;metal ion binding  43.89  3  12.50  3  0.28

P23180  Probable oxidoreductase AIM17 [OS=Saccharomyces cerevisiae S288c]  85636  AIM17; YHL021C  cell organization and biogenesis;metabolic process  mitochondrion  catalytic activity;metal ion binding  3.467  0.995  0.29

P14693  sorting assembly machinery 35 kDa subunit [OS=Saccharomyces cerevisiae S288c]  85648  SAM35; YHR080W 3W  cell organization and biogenesis;transport  membrane,mitochondrion  protein binding  0.54  0.155  0.29

P41735  S-Demethoxydeiquione hydroxylase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85429  CAT5; YOR12 5C  metabolic process  membrane,mitochondrion  catalytic activity;metal ion binding  0.54  0.155  0.29

Q12375  mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c]  85429  ORT1; YOR13 13C  metabolic process;transport  membrane,mitochondrion  structural molecule activity;transporter activity  0.54  0.155  0.29

Q12031  Mitochondrial 2-methylisocitrinate lyase [OS=Saccharomyces cerevisiae S288c]  85611  ICL2; YPR006C  metabolic process  mitochondrion,organelle lumen  catalytic activity  3.281  0.947  0.29

P32387  S4 ribosomal protein 141, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85201  MRP20; YDR405W 5W  cell organization and biogenesis;metabolic process  mitochondrion,ribosome  nucleotide binding;protein binding;RNA binding;structural molecule activity  0.505  0.145  0.29

P47127  Altered inheritance of mitochondria protein 24, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85354  AIM24; YHR080W C  cell organization and biogenesis  mitochondrion  2.562  0.743  0.29

P00401  Cytochrome c oxidase subunit 1 [OS=Saccharomyces cerevisiae S288c]  85459  Cox1; Q0045  metabolic process;transport  membrane,mitochondrion  catalytic activity;metal ion binding;transporter activity  1.61  0.468  0.29

P43617  Uncharacterized mitochondrial carrier YFR045W [OS=Saccharomyces cerevisiae S288c]  85060  YFR045W; YFR045W W  metabolic process;transport  membrane,mitochondrion  structural molecule activity;transporter activity  0.413  0.122  0.30

P32792  UPF0744 protein YSC83 [OS=Saccharomyces cerevisiae S288c]  85641  YSC83; YHR017W 7W  membrane,mitochondrion  0.369  0.11  0.30

P35736  Uncharacterized protein YHR040W [OS=Saccharomyces cerevisiae S288c]  85577  YHR040W 0W; YHR040W 0W  mitochondrial  0.389  0.116  0.30

P35180  mitochondrial import receptor subunit Tom20 [OS=Saccharomyces cerevisiae S288c]  85297  TOM20; YGR082W 2W  cell organization and biogenesis;transport  membrane,mitochondrion  protein binding;transporter activity  1.424  0.425  0.30

P07275  Delta-1-pyruvate-S-carboxylate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85643  PUT2; YHR031W 7W  metabolic process  membrane,mitochondrion,organelle lumen  catalytic activity  4.337  1.31  0.30

P38702  mitochondrial carrier protein LEU15 [OS=Saccharomyces cerevisiae S288c]  85639  LEU15; YHR008G 2W  metabolic process;transport  membrane,mitochondrion  structural molecule activity;transporter activity  0.334  0.101  0.30

P34231  Uncharacterized protein YKL187C [OS=Saccharomyces cerevisiae S288c]  83564  YKL187C; YKL187C  cell organization and biogenesis;transport  membrane,mitochondrion  0.304  0.093  0.31

P48360  Probable NADP+adrenodoxin oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85198  ARH1; YDR37W 6W  cellular homeostasis;metabolic process;transport  cytoplasm;membrane,mitochondrion,organelle lumen  catalytic activity  0.25  0.077  0.31

Q04172  Sensitive to high expression protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85200  SHE9; YDR39  cell organization and biogenesis  membrane,mitochondrion  0.269  0.083  0.31
| [OS=Sacharomyces cerevisiae S288c] | 3W |
|-------------------------------|--------|
| P36775 Lpn protease homolog, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85225 9 | PMI1; YBO022 C | cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus | cytoplasm/mitochondrion;organelle lumen | catalytic activity;DNA binding;nucleotide binding;RNA binding | 0.537 0.166 0.31 |
| P40495 Homosuccinate dehydrogenase, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85471 4 | LYS12; YIL094 C | metabolic process | mitochondrion | catalytic activity | 3.19 1.61 0.31 |
| Q05882 MIOREX complex component 2 [OS=Sacharomyces cerevisiae S288c] | 85099 7 | YLR290 C; YCL111; YLR290 C | metabolic process | mitochondrion | catalytic activity | 1.738 0.54 0.31 |
| P36525 S45 ribosomal protein L24, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85523 1 | MRPL2 4; YMR19 1W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.154 0.359 0.31 |
| Q04728 Arginine biosynthesis bifunctional protein Arg1, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85508 4 | ARG7; YMR062 C | metabolic process | mitochondrion;organelle lumen | catalytic activity | 0.748 0.233 0.31 |
| Q06567 ABC1 family protein MCP2 [OS=Sacharomyces cerevisiae S288c] | 85095 5 | MCP2; YLR253 C | cell organization and biogenesis | membrane/mitochondrion | | 0.218 0.068 0.31 |
| P38722 Mitochondrial Rho GTPase 1 [OS=Sacharomyces cerevisiae S288c] | 85124 9 | GEM1; YAL048 C | cell organization and biogenesis;regulation of biological process;response to stimulus;transport | membrane/mitochondrion | catalytic activity;metal ion binding;nucleotide binding | 0.189 0.059 0.31 |
| P16622 Ferrochelatase, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85434 7 | HEM15 1Y; YOR17 6W | metabolic process | membrane/mitochondrion | catalytic activity | 8.006 2.511 0.31 |
| P38071 Enoyl-[acyl carrier protein] reductase [NADPH, B-specific], mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85231 4 | ETR1; YBR025 C | metabolic process | mitochondrion;organelle lumen | catalytic activity;DNA binding;metal ion binding | 8.006 2.511 0.31 |
| P32898 Mitochondrial presequence protease [OS=Sacharomyces cerevisiae S288c] | 85204 1 | CVM1; YDR43 1C | metabolic process | mitochondrion | catalytic activity;metal ion binding | 0.505 0.16 0.32 |
| P19955 375 ribosomal protein YMR31, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85063 0 | YMR31 0Y; YFR049 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | catalytic activity;protein binding;structural molecule activity | 3.642 1.154 0.32 |
| Q01519 Cytochrome c oxidase subunit 6b [OS=Sacharomyces cerevisiae S288c] | 85072 7 | Cox12; YLR038 C | cell organization and biogenesis;metabolic process;transport | mitochondrion | catalytic activity;transport | 3.642 1.154 0.32 |
| Q38424 Uncharacterized protein YOR020W-A [OS=Sacharomyces cerevisiae S288c] | 14644 8D | YOR02 0W-A; YOR02 0W-A | metabolic process;transport | membrane/mitochondrion | | 3.642 1.154 0.32 |
| Q2V299 Uncharacterized protein YDR119W-A [OS=Sacharomyces cerevisiae S288c] | 37999 70 | COX26; YDR11 1W-A | membrane/mitochondrion | | | 3.642 1.154 0.32 |
| P38771 Ribosome-recycling factor, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85643 3 | RBF1; YHR03 3W | cell organization and biogenesis;metabolic process | mitochondrion | RNA binding | 1.581 0.501 0.32 |
| P19882 Heat shock protein 60, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85096 3 | HSP60; YLR259 C | cell organization and biogenesis;metabolic process;regulation of biological process;transport | cytoplasm;cytosol;membrane;mitochondrion;organelle lumen | catalytic activity;DNA binding;metal ion binding;protein binding | 36.92 7 11.74 3 0.32 |
| P36151 Uncharacterized protein YKR070W [OS=Sacharomyces cerevisiae S288c] | 85394 4 | YKR070 W; YKR070 W | metabolic process | mitochondrion | | 0.833 0.274 0.33 |
| P08417 Fumarate hydratase, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85586 9 | FUM1; YPL262 W | cell organization and biogenesis;metabolic process | cytoplasm;cytosol;mitochondrion;organelle lumen | catalytic activity | 6.88 2.29 0.33 |
| P53292 375 ribosomal protein S35, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85307 5 | MRP53 5; YGR16 5W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.754 0.585 0.33 |
| P16387 Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85695 5 | PDA1; YER178 W | cell growth;metabolic process | mitochondrion;organelle lumen | catalytic activity | 13.49 7 4.52 0.33 |
| P40750 Succinate dehydrogenase (ubiquinone) flavoprotein subunit 2, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85340 5 | YIL045 W; YIL045 W | metabolic process;transport | membrane/mitochondrion | catalytic activity | 2.932 0.983 0.34 |
| P51998 S45 ribosomal protein ynlk, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85498 3 | YML6; YML02 5C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.73 0.245 0.34 |
| P38885 Altered inheritance of mitochondria protein 46, mitochondrial [OS=Sacharomyces cerevisiae S288c] | 85660 6 | AIM46; YHR19 9C | | mitochondrion | catalytic activity | 1.154 0.389 0.34 |
| Gene ID | Name | Description | Localization | Function | GO Terms |
|---------|------|-------------|--------------|----------|----------|
| P00924 | Enolase 1 | [OS=Saccharomyces cerevisiae S288c] | Enolase | Metabolic process; Regulation of biological process | Metabolic process, mitochondrial; Catalytic activity |
| P32191 | Glyceraldehyde-3-phosphate dehydrogenase | [OS=Saccharomyces cerevisiae S288c] | Glyceraldehyde-3-phosphate dehydrogenase | Metabolic process; Membrane | Membrane, mitochondrial; Catalytic activity |
| P07213 | Mitochondrial import receptor subunit 7 | [OS=Saccharomyces cerevisiae S288c] | Mitochondrial import receptor | Membrane | Membrane, mitochondrial; Catalytic activity |
| P25719 | Peptidyl-prolyl cis-trans isomerase C | [OS=Saccharomyces cerevisiae S288c] | Peptidyl-prolyl cis-trans isomerase | Cell death, Metabolic process | Mitochondrion, Organellar lumen; Catalytic activity |
| P04840 | Probable electron transfer flavoprotein subunit 1 | [OS=Saccharomyces cerevisiae S288c] | Probable electron transfer flavoprotein subunit | Cellular homeostasis; Regulation of biological process; Transport | Cytoplasm, Mitochondrion; Catalytic activity |
| P03872 | Glycine cleavage system H protein | [OS=Saccharomyces cerevisiae S288c] | Glycine cleavage system | Metabolic process | Mitochondrion; Catalytic activity |
| P50945 | Mitochondrial uncoupling protein | [OS=Saccharomyces cerevisiae S288c] | Mitochondrial uncoupling protein | Membrane | Membrane, mitochondrial; ATP-binding, Nucleotide binding |
| P08440 | MSR1 | [OS=Saccharomyces cerevisiae S288c] | MSR1 | Metabolic process | Cytoplasm, Membrane, Mitochondrion; Catalytic activity |
| P17505 | Malate dehydrogenase | [OS=Saccharomyces cerevisiae S288c] | Malate dehydrogenase | Metabolic process | Mitochondrion, Organellar lumen; Catalytic activity |

**Note:** The table above represents a portion of the gene information extracted from the document. The complete table can be found in the document. **GOTerms:** The Gene Ontology Terms associated with each gene, indicating the biological processes, molecular functions, and cellular components they are involved in. **GOID:** The Gene Ontology ID for each term.
| Gene ID | Description | Localization | Function |
|---------|-------------|--------------|----------|
| P27892 | Serine hydroxymethyltransferase, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 5.579 | 2.275 | 0.41 |
| P19262 | Dihydrolipoamide-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity;protein binding | 5.7 | 3.235 | 0.41 |
| Q01163 | 37S ribosomal protein S23, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity;nucleotide binding;RNA binding;structural molecule activity | 1.11 | 0.453 | 0.41 |
| P27982 | Altered inherited of mitochondria protein 36, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | membrane/mitochondrion | Catalytic activity | 1.069 | 0.438 | 0.41 |
| P46367 | Potassium-activated aldehyde dehydrogenase, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 50.79 | 5 | 21.02 | 2 | 0.41 |
| P32473 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 9 | 3.833 | 0.43 |
| P33828 | Protein TOM71 ([OS=Saccharomyces cerevisiae][S288c]) | | Protein binding;transporter activity | 0.805 | 0.343 | 0.43 |
| Q06465 | Autophagy-related protein 33 ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.778 | 0.334 | 0.43 |
| P39515 | Mitochondrial import inner membrane translocase subunit Tim17 ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.778 | 0.334 | 0.43 |
| P53889 | Uncharacterized mitochondrial hydrolase FMP41 ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity;metal ion binding | 0.719 | 0.311 | 0.43 |
| P33220 | Mitochondrial import inner membrane translocase subunit Tim21 ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.719 | 0.311 | 0.43 |
| P27758 | 375 ribosomal protein PTET123, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.668 | 0.292 | 0.44 |
| P33752 | 375 ribosomal protein S52, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.668 | 0.292 | 0.44 |
| P33817 | 3-hydroxyisobutyl-CoA hydrolase, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.61 | 0.269 | 0.44 |
| P31668 | 375 ribosomal protein MRPL13, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.585 | 0.259 | 0.44 |
| P32453 | Protein ATP11, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.585 | 0.259 | 0.44 |
| P23641 | Mitochondrial phosphate carrier protein ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 26.82 | 6 | 11.91 | 5 | 0.44 |
| P35881 | 545 ribosomal protein S122, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.551 | 0.245 | 0.44 |
| P32860 | Nfu-1-like protein, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 1.738 | 0.778 | 0.45 |
| P25372 | Thioredoxin-3, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.52 | 0.233 | 0.45 |
| P22136 | ATPase expression protein 2, mitochondrial ([OS=Saccharomyces cerevisiae][S288c]) | | Catalytic activity | 0.506 | 0.227 | 0.45 |
| P40394 | Mitochondrial respiratory chain complexes assembly protein YTA12 | | Catalytic activity;metal ion | 1.579 | 0.707 | 0.45 |
| Protein Name | Organism | EC | Process/Response to Stimulus | Binding | Protein | Gene ID | Log Fold Change |
|--------------|----------|----|------------------------------|--------|---------|---------|---------------|
| P35191       | [OS=Saccharomyces cerevisiae S288c] | 85053 | 0.194 | Cell organization and biogenesis; metabolic process | response to stimulus | mitochondrion, organelle lumen | enzyme regulator activity, metal ion binding, nucleotide binding | binding, protein binding | 1.656 | 0.748 | 0.45 |
| P40416       | Iron-sulfur clusters transporter | 85534 | 7 | Cellular homeostasis, metabolic process | process, transport | membrane, mitochondrion | catalytic activity, nucleotide binding, transport activity | 0.453 | 0.205 | 0.45 |
| P33310       | ATP-dependent permease MDL1 | 85088 | 5 | | transport | membrane, mitochondrion | catalytic activity, nucleotide binding, transport activity | 0.438 | 0.199 | 0.45 |
| Q03327       | Mitochondrial fusion and transport protein Ugo1 | 85208 | 1 | | | membrane, mitochondrion | protein binding, structural molecule activity | 0.425 | 0.194 | 0.46 |
| P52330       | Phosphatidate cytidylyltransferase, mitochondrial | 85293 | 7 | Metabolic process | | membrane, mitochondrion, organelle lumen | catalytic activity | 0.407 | 0.186 | 0.46 |
| P40053       | Altered inheritance of mitochondria | 85681 | 3 | AIA9, YER080 W | | mitochondrion | | 1.938 | 0.891 | 0.46 |
| Q03246       | 37S ribosomal protein S17 | 85522 | 6 | Cell differentiation, cell organization and biogenesis, metabolic process | | mitochondrion, ribosome | RNA binding, structural molecule activity | 0.389 | 0.179 | 0.46 |
| P25039       | Elongation factor G | 85075 | 8 | Cell organization and biogenesis, metabolic process | | cytosol, mitochondrion | catalytic activity, nucleotide binding, RNA binding | 0.326 | 0.151 | 0.46 |
| P41921       | Glutathione reductase | 85601 | 4 | Cellular homeostasis, metabolic process | | cytoplasm, cytosol, mitochondrial, nucleus | antioxidant activity, catalytic activity, nucleotide binding | 0.334 | 0.195 | 0.46 |
| Q04472       | Mitochondrial inner membrane I-AAP protease supercomplex subunit MGR3 | 85514 | 2 | Metabolic process | | membrane, mitochondrion | protein binding | 0.322 | 0.15 | 0.47 |
| P05626       | ATP synthase subunit 4 | 85602 | 7 | Cell organization and biogenesis, metabolic process | | membrane, mitochondrion | catalytic activity, transport activity, protein binding | 7.799 | 3.642 | 0.47 |
| P38910       | 10 kDa heat shock protein, mitochondrial | 85418 | 5 | Cell organization and biogenesis, metabolic process | | cytoplasm, mitochondrion, organelle lumen | metal ion binding, nucleotide binding, protein binding | 4.623 | 2.162 | 0.47 |
| P21306       | ATP synthase subunit epsilon | 85585 | 7 | Metabolic process, transport | | membrane, mitochondrion | catalytic activity, transport activity | 4.623 | 2.162 | 0.47 |
| P48015       | Aminomethyltransferase, mitochondrial | 85158 | 2 | Metabolic process | | mitochondrion | catalytic activity, protein binding | 5.7 | 2.67 | 0.47 |
| P12687       | S4S ribosomal protein 12, mitochondrial | 85572 | 7 | Cell organization and biogenesis, metabolic process | | mitochondrion, ribosome | catalytic activity, RNA binding, structural molecule activity | 0.233 | 0.11 | 0.47 |
| Q06648       | MIDREX complex component 10 | 85187 | 6 | Metabolic process | | membrane, mitochondrion | | 0.222 | 0.105 | 0.47 |
| P36163       | Mitochondrial metalloendopeptidase OMA1 | 85396 | 2 | Metabolic process | | membrane, mitochondrion | catalytic activity, metal ion binding | 0.245 | 0.116 | 0.47 |
| P50110       | Sorting assembly machinery 37 kDa subunit | 85058 | 0 | Cell organization and biogenesis, transport | | membrane, mitochondrion | protein binding | 0.245 | 0.116 | 0.47 |
| P46047       | Aldehyde dehydrogenase 5 | 85680 | 4 | Metabolic process | | mitochondrion, organelle lumen | catalytic activity | 1.762 | 0.84 | 0.48 |
| Q06143       | Mitochondrial dicarboxylate transporter | 85106 | 3 | Metabolic process, transport | | membrane, mitochondrion | structural molecule activity, transport activity | 1.154 | 0.551 | 0.48 |
| P25650       | Acetyl-CoA synthase small subunit, mitochondrial | 85034 | 8 | Metabolic process, regulation of biological process | | mitochondrion | catalytic activity, enzyme regulator activity | 2.793 | 1.336 | 0.48 |
| P32839       | Mitochondrial chaperone BCS1 | 85198 | 1 | Cell organization and biogenesis, metabolic process | | cytosol, membrane, mitochondrion | catalytic activity, nucleotide binding, transport activity | 0.194 | 0.093 | 0.48 |
| P38909       | Cytochrome c mitochondrial import factor CYC2 | 85420 | 2 | Cell organization and biogenesis, metabolic process | | membrane, mitochondrion | catalytic activity | 0.194 | 0.093 | 0.48 |
Q04710  ADP,ATP carrier protein 1 [OS=Saccharomyces cerevisiae S288c]
85507 8 AAC1; YMR056C metabolic process;transport cytosol;membrane;mitochondrion structural molecule activity;transporter activity 7.859 4.456 0.57

Q12233  ATP synthase subunit g, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85613 1 ATPG20; YMR020W cell organization and biogenesis;metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 1.371 0.778 0.57

P36147  Presenilin translocated-associated motor subunit pam17, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85393 9 PAN117; YKR065C transport membrane;mitochondrion 1.371 0.778 0.57

P33303  Succinate/fumarate mitochondrial transporter [OS=Saccharomyces cerevisiae S288c]
85355 8 SFC1; YHR095W metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 15.68 9 0.57

P00830  ATP synthase subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85358 5 ATP2; YLR211W metabolic process;transport cytosol;membrane;mitochondrion catalytic activity;nucleotide binding;protein binding;transporter activity 41.98 24.11 9 0.57

Q03713  Respiratory supercomplex factor 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85497 8 RCF1; YML031W cell organization and biogenesis membrane;mitochondrion 0.995 0.584 0.59

P008B0  Citrate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85573 2 CIT1; YNR001C metabolic process;transport cytosol;mitochondrion;organelle lumen catalytic activity 21.75 8 12.89 5 0.59

P40008  Protein FMP52, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85672 1 FMP52; YER004W endoplasmic reticulum;membrane;mitochondrion catalytic activity 1.738 1.054 0.61

P53721  Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85575 2 RCF2; YNR018B cell organization and biogenesis membrane;mitochondrion 7.111 4.337 0.61

P07253  Cytochrome b pre-mRNA-processing protein 6 [OS=Saccharomyces cerevisiae S288c]
85241 7 CBP6; YBR120C cell organization and biogenesis;metabolic process mitochondrial ribosome 2.728 1.683 0.62

P47045  Mitochondrial import inner membrane translocase subunit TIM54 [OS=Saccharomyces cerevisiae S288c]
85339 2 TIM54; YIL054W cell organization and biogenesis;transport cytosol;membrane;mitochondrion transporter activity 0.54 0.334 0.62

P36534  S45 ribosomal protein l40, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85593 0 MRPL40; YPL173W cell organization and biogenesis;metabolic process mitochondrion;ribosome protein binding;structural molecule activity 0.413 0.259 0.63

P33759  37S ribosomal protein S5, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85255 3 MRPS5; YBR251W cell organization and biogenesis;metabolic process mitochondrion;ribosome RNA binding;structural molecule activity 0.413 0.259 0.63

Q06179  Mitochondrial distribution and morphology protein 38 [OS=Saccharomyces cerevisiae S288c]
85413 0 MDM38; YKLO27C cell organization and biogenesis;cellular homeostasis;regulation of biological process;transport membrane;mitochondrion 3.732 2.35 0.63

P38152  Tricarboxylate transport protein [OS=Saccharomyces cerevisiae S288c]
85259 4 CTPS1; YBR291C metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 0.389 0.245 0.63

P39525  3-oxoacyl-[acyl-carrier-protein] synthase homolog [OS=Saccharomyces cerevisiae S288c]
85679 0 CEM1; YER061C metabolic process mitochondrion catalytic activity 0.369 0.233 0.63

P38797  Protein phosphatase 2C homolog 7, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85647 5 PTPC7; YHR076W metabolic process mitochondrial catalytic activity;metal ion binding;protein binding 0.369 0.233 0.63

P40012  proteophosphinogen oxidase [OS=Saccharomyces cerevisiae S288c]
85673 3 HEM14; YER014W metabolic process membrane;mitochondrion catalytic activity 0.838 0.528 0.63

P36101  TRNA threonylcarbamoylaspartic acid dehydratase 2 [OS=Saccharomyces cerevisiae S288c]
85384 1 TCD2; YKLO27W; YKLO27C metabolic process cytosol;membrane;mitochondrion catalytic activity;nucleotide binding 0.334 0.212 0.63

Q04003  Citrate/oxoglutarate carrier protein [OS=Saccharomyces cerevisiae S288c]
85328 2 YMR224W; YMR241W cell organization and biogenesis;metabolic process membrane;mitochondrion DNA binding;structural molecule activity;transporter activity 4.012 2.548 0.64

P40961  prohibitin-1 [OS=Saccharomyces cerevisiae S288c]
85303 3 PHB1; YGR133C cell organization and biogenesis;metabolic process;transport membrane;mitochondrion protein binding 5.158 3.281 0.64

P38077  ATP synthase subunit gamma, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85232 7 ATP3; YBR039W metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 15.87 6 10.10 3 0.64

Q06150  Lysophosphatidic acid/acyltransferase [OS=Saccharomyces cerevisiae S288c]
85626 2 TAZ1; YPR140W cell organization and biogenesis;metabolic process;transport membrane;mitochondrion catalytic activity 0.304 0.194 0.64

Q01574  acetyl-Coenzyme A synthetase 1 [OS=Saccharomyces cerevisiae S288c]
85124 5 ACS1; YAL054C cell organization and biogenesis;metabolic process cytoplasm;cytosol;endoplasmic reticulum;mitochondrion;nucleus catalytic activity;nucleotide binding 1.482 0.947 0.64
| Gene ID | Description | Function | Localization | Interaction | Score |
|--------|-------------|----------|--------------|-------------|-------|
| P40185 | Protein rnm1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Cell organization and biogenesis;metabolic process | Mitochondrion,organelle lumen | 3.31 | 4.012, 0.76 |
| P32799 | Cytochrome c oxidase subunit 6A, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Cell organization and biogenesis;metabolic process;regulation of biological process;transport | Membrane,mitochondrion | Catalytic activity;enzyme regulator activity;transporter activity | 3.31 | 4.012, 0.76 |
| P50085 | Prohibitin-2 [OS=Saccharomyces cerevisiae S288c] | Cell organization and biogenesis;metabolic process;regulation of biological process | Membrane,mitochondrion | Protein binding | 4.337 | 3.329, 0.77 |
| Q08968 | UPF0061 protein FMP40 [OS=Saccharomyces cerevisiae S288c] | | Mitochondrion | Protein binding | 0.917 | 0.823, 0.90 |
| P07256 | Cytochrome b-1 complex subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Metabolic process;transport | Membrane,mitochondrion | Catalytic activity;metal ion binding;protein binding;transporter activity | 9.89 | 9.89, 1.00 |
| P50088 | Stationary phase gene 1 protein [OS=Saccharomyces cerevisiae S288c] | | Endoplasmic reticulum,membrane,mitochondrion | | 137.4, 89, 137.4, 89 | 1.00 |
| P00410 | Cytochrome c oxidase subunit 2 [OS=Saccharomyces cerevisiae S288c] | Metabolic process;transport | Membrane,mitochondrion | Catalytic activity;metal ion binding;protein binding;transporter activity | 2.831 | 2.831, 1.00 |
| P38325 | Mitochondrial outer membrane protein OM14 [OS=Saccharomyces cerevisiae S288c] | Transport | Membrane,mitochondrion | | 9 | 9, 1.00 |
| P40508 | Uncharacterized protein YL077C [OS=Saccharomyces cerevisiae S288c] | | Mitochondrion | | 0.668 | 0.668, 1.00 |
| P38072 | Protein SCO1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Cell organization and biogenesis;cellular homeostasis;metabolic process;transport | Membrane,mitochondrion | Antioxidant activity;catalytic activity;metal ion binding | 0.73 | 0.73, 1.00 |
| Q08968 | NADH kinase PSSS, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Metabolic process;response to stimulus | Mitochondrion,organelle lumen | Catalytic activity;metal ion binding | 0.369 | 0.369, 1.00 |
| P32445 | Single-stranded DNA-binding protein RIM2 [OS=Saccharomyces cerevisiae S288c] | Cell organization and biogenesis;metabolic process;transport | Membrane,mitochondrion | Structural molecule activity;transporter activity | 0.585 | 0.585, 1.00 |
| P32331 | Carrier protein YMC3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Metabolic process;transport | Membrane,mitochondrion;vacuole | Structural molecule activity;transporter activity | 0.503 | 0.503, 1.00 |
| Q12165 | ATP synthase subunit delta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Metabolic process;transport | Membrane,mitochondrion | Catalytic activity;transporter activity | 1.371 | 1.371, 1.00 |
| P33421 | Succinate dehydrogenase (ubiquinone) cytochrome b subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Cell organization and biogenesis;metabolic process;transport | Membrane,mitochondrion | Catalytic activity;metal ion binding | 0.931 | 0.931, 1.00 |
| Q06668 | Methyltransferase GM51, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Metabolic process | Membrane,mitochondrion | Catalytic activity | 0.303 | 0.303, 1.00 |
| P17695 | Glutaredoxin-2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Cellular homeostasis;metabolic process;regulation of biological process;response to stimulus;transport | Cytoplasm,mitochondrion,nucl eus | Antioxidant activity;catalytic activity | 0.52 | 0.52, 1.00 |
| P34224 | Uncharacterized protein YBLO59W [OS=Saccharomyces cerevisiae S288c] | | Membrane,mitochondrion | | 0.468 | 0.468, 1.00 |
| Q09297 | Mitochondrial 2-oxoacid dehydrogenase carrier 2 [OS=Saccharomyces cerevisiae S288c] | Metabolic process;transport | Membrane,mitochondrion | Structural molecule activity;transporter activity | 0.54 | 0.54, 1.00 |
| Q08223 | ATPase subunit 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | | Cytosol,membrane,mitochondrion | | 0.259 | 0.259, 1.00 |
| P32266 | Dynamin-like GTPase MGM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Cell organization and biogenesis | Membrane,mitochondrion | Catalytic activity;metal ion binding;protein binding | 0.086 | 0.086, 1.00 |
| P19516 | Cytochrome c oxidase assembly protein COX11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | Cell organization and biogenesis;metabolic process | Membrane,mitochondrion,Y-ribosome | Metal ion binding | 0.274 | 0.274, 1.00 |
Q06630  Mitochondrial homologous recombination protein 1 [OS=Saccharomyces cerevisiae S288c]
  85189  0  MHR1; YDR29 W  cell organization and biogenesis;mitochondrion nucleus catalytic activity;DNA binding;structural molecule activity 0.166 0.166 1.00
P00405  Cytochrome c iso-2 [OS=Saccharomyces cerevisiae S288c]
  85667  2  CYC7; YEL039 C  metabolic process;transport mitochondrion metal ion binding 0.259 0.259 1.00
P04039  Cytochrome c oxidase polypeptide VIII, mitochondrial [OS=Saccharomyces cerevisiae S288c]
  85111  1  COX8; YLR035 C  metabolic process;transport membrane,mitochondrion catalytic activity;transporter activity 0.778 0.778 1.00
P40581  Peroxiredoxin HRY1 [OS=Saccharomyces cerevisiae S288c]
  85485  5  HRY1; YDR037 W  metabolic process;response to stimulus cytoplasm;cytosol;mitochondrion;organelle lumen antioxidant activity;catalytic activity 0.259 0.259 1.00
P07236  Threonine–tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c]
  85364  0  MST1; YKL194 C  metabolic process cytoplasm,mitochondrion;organelle lumen catalytic activity;nucleotide binding;RNA binding 0.072 0.072 1.00
P40086  Cytochrome c oxidase assembly protein cox15 [OS=Saccharomyces cerevisiae S288c]
  85688  4  COX15; YLR141 W  cell organization and biogenesis;mitochondrion protein binding membrane,mitochondrion catalytic activity;transporter activity 0.668 0.817 1.22
Q12289  Mitochondrial carnitine carrier [OS=Saccharomyces cerevisiae S288c]
  85426  7  CRC1; YOR10 JC  metabolic process;transport membrane,mitochondrion structural molecule activity;transporter activity 0.931 1.154 1.24
P38523  Gpi1 protein homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c]
  85440  7  MGE1; YDR23 2W  metabolic process;regulation of biological process;transport membrane,mitochondrion;organelle lumen enzyme regulator activity;mitochondrion protein binding 0.624 0.833 1.33
Q04995  Cytochrome c oxidase protein 20, mitochondrial [OS=Saccharomyces cerevisiae S288c]
  85181  7  COX20; YCR23 1C  cell organization and biogenesis;mitochondrion protein binding membrane,mitochondrion catalytic activity;transporter activity 1.031 1.424 1.38
P27697  Atypical kinase COQ8, mitochondrial [OS=Saccharomyces cerevisiae S288c]
  85275  8  COQ8; YLG119 W  metabolic process membrane,mitochondrion;organelle lumen catalytic activity;nucleotide binding 0.133 0.205 1.54
P40496  375 ribosomal protein S25, mitochondrial [OS=Saccharomyces cerevisiae S288c]
  85471  5  RSM25; YIL093 C  cell organization and biogenesis;mitochondrion ribosome structural molecule activity 0.292 0.468 1.60
Q00689  Uncharacterized mitochondrial outer membrane protein YPR098C [OS=Saccharomyces cerevisiae]
  85621  3  YPR098 C; YPR098 membrane,mitochondrion 4.623 9 1.95
| ID     | Gene Name & Description                                                                 | Entrez ID |GO Terms                                                                 | Molecular Function                              | Score 1 | Score 2 | Score 3 |
|--------|-----------------------------------------------------------------------------------------|-----------|-------------------------------------------------------------------------|-------------------------------------------------|----------|----------|----------|
| P21771 | 37S ribosomal protein S28, mitochondrial (OS=Saccharomyces cerevisiae S288c)             | 85193     | cell organization and biogenesis, metabolic process                     | mitochondrion, ribosome                         | 0.129    | 0.274    | 2.12     |
| P32378 | 4-hydroxybenzoate polyphenyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85577     | metabolic process, transport                                            | membrane, mitochondrion                         | 0.136    | 0.292    | 2.15     |
| P42847 | 37S ribosomal protein S18, mitochondrial (OS=Saccharomyces cerevisiae S288c)             | 85541     | cell organization and biogenesis, metabolic process                     | mitochondrion, ribosome                         | 0.155    | 0.334    | 2.15     |
| Q08970 | Mitochondrial metal transporter 2 (OS=Saccharomyces cerevisiae S288c)                    | 85587     | cellular homeostasis, regulation of biological process, response to stimulus, transport | membrane, mitochondrion                         | 0.186    | 0.407    | 2.19     |
| P42949 | Mitochondrial import inner membrane translocase subunit TIM16 (OS=Saccharomyces cerevisiae S288c) | 85334     | transport                                                                | membrane, mitochondrion                         | 0.233    | 0.52     | 2.23     |
| P46998 | mitochondrial membrane protein FMP33 (OS=Saccharomyces cerevisiae S288c)                 | 85327     |                                                                        | membrane, mitochondrion                         | 0.334    | 0.778    | 2.33     |
| Q12032 | Altered inheritance of mitochondria protein 41, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85439     |                                                                        | mitochondrial                                  | 0.468    | 1.154    | 2.47     |
| P00447 | Superoxide dismutase [Mn], mitochondrial (OS=Saccharomyces cerevisiae S288c)             | 85639     | metabolic process, response to stimulus                                 | mitochondrion, organelle lumen                  | 1.894    | 4.878    | 5.58     |
Supplemental Table S8. The relative concentrations of proteins in mitochondria purified from ups1Δ cells cultured with or without LCA. Mitochondria were purified from ups1Δ cells recovered on day 4 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI ups1Δ | emPAI ups1Δ + LCA | Ratio ups1Δ / ups1Δ + LCA |
|-----------|-------------|----------------|---------|-------------------|-------------------|------------------|------------|------------------|------------------------|
| P50088    | Stationary phase gene 1 protein | 85315 | 1 | SPS1 | membrane; mitochondrion | RNA binding; structural molecule activity | 157.4 | 89 | 38.81 | 0.25 |
| P21771    | 37S ribosomal protein S28, mitochondrial | 85193 | 7 | MRPS28 | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | 0.438 | | 0.129 | 0.29 |
| Q2VIP9    | Uncharacterized protein | 37999 | 70 | COX6; YDR119W-A | membrane; mitochondrion | 3.642 | | 1.154 | 0.32 |
| P32387    | 34S ribosomal protein L41, mitochondrial | 85201 | 4 | MRPL20; YDR405W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | 0.968 | | 0.311 | 0.32 |
| Q08245    | protein ZEO1 | 85404 | 0 | ZEO1; YOL109W | cell organization and biogenesis | membrane; mitochondrion | protein binding | 11.58 | 9 | 4.012 | 0.35 |
| P00424    | Cytochrome c oxidase polypeptide SA, mitochondrial | 85567 | 5 | COX5A; YNL052W | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 2.511 | | 0.874 | 0.35 |
| P00044    | Cytochrome c iso-1 | 85350 | 7 | CYC1; YRP048W | metabolic process; transport | mitochondrion | metal ion binding; protein binding | 9 | | 3.217 | 0.36 |
| Q04685    | Autophagy-related protein 33 | 85107 | 0 | ATG33; YLR356W | cell communication; metabolic process; response to stimulus | membrane; mitochondrion | 2.162 | | 0.778 | 0.36 |
| P49334    | Mitochondrial import receptor subunit tom22 | 85559 | 2 | TOM22; YNL131W | cell organization and biogenesis; transport | membrane; mitochondrion | protein binding; transporter activity | 1.783 | | 0.668 | 0.37 |
| Q12359    | Ammonia transport outward protein 1 | 85199 | 2 | ATD3; YDR584C | transport | membrane; mitochondrion | transporter activity | 1.512 | | 0.585 | 0.39 |
| P01097    | ATPase inhibibtor, mitochondrial | 85134 | 7 | RNH1; YDL183W | metabolic process; regulation of biological process | mitochondrion | catalytic activity; enzyme regulator activity; protein binding | 1.154 | | 0.468 | 0.41 |
| Q07914    | mitochondrial import inner membrane translocase subunit TIM14 | 85069 | 4 | PAM18; YLR008C | regulation of biological process; transport | membrane; mitochondrion | enzyme regulator activity; protein binding; transporter activity | 0.778 | | 0.334 | 0.43 |
| P36147    | Presequence translocase-associated motor subunit pam17, mitochondrial | 85393 | 9 | PAM17; YKR065C | transport | membrane; mitochondrion | | 0.778 | | 0.334 | 0.43 |
| P33759    | 37S ribosomal protein S55, mitochondrial | 85255 | 3 | MRPS55; YBR251W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 0.585 | | 0.259 | 0.44 |
| P5198     | 54S ribosomal protein yml6, mitochondrial | 85498 | 3 | YML6; YML025C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 0.551 | | 0.245 | 0.44 |
| P36141    | Putative redox protein fmp46, mitochondrial | 85392 | 3 | FMP46; YKR040C | metabolic process | mitochondrion | catalytic activity; protein binding | 0.52 | | 0.233 | 0.45 |
| P22354    | 54S ribosomal protein L20, mitochondrial | 85396 | 0 | MRPL20; YKR0385C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.389 | | 0.179 | 0.46 |
| P28613    | Accumulation of dyads protein 2 | 85036 | 8 | ADY2; YCR510C | transport | membrane; mitochondrion; vacuole | transporter activity | 9 | | 4.179 | 0.46 |
| P04803    | Tryptophan-4-kinase ligase, mitochondrial | 85186 | 1 | MSW91; YDR268W | metabolic process | cytoplasm; mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 0.292 | | 0.136 | 0.47 |
| Gene ID | Description                                      | Functional category                                      | Localization            | Molecular Activity                  | Fold Change | Gene ID | Description                                      | Functional category                                      | Localization            | Molecular Activity                  | Fold Change |
|--------|--------------------------------------------------|--------------------------------------------------------|-------------------------|-------------------------------|-------------|--------|--------------------------------------------------|--------------------------------------------------------|-------------------------|-------------------------------|-------------|
| P52280 | Mitochondrial import inner membrane translocase subunit TIM21 | cell organization and biogenesis, transport | membrane/mitochondrion | protein binding | 0.311  | P10662 | Protein SCO2, mitochondrial | structural molecular activity, transport activity | membrane/mitochondrion | 13.67  | P40185 | protein Scope | 0.389 |
| P48569 | Uncharacterized protein YDL183C | transport | cytoplasm/mitochondrion | catalytic activity, nucleotide binding, RNA binding | 0.572  | P48527 | Tyrosine-RNA ligase, mitochondrial | metabolism | cytoplasm/mitochondrion | catalytic activity | 0.15 |
| P48568 | Triosephosphate isomerase | metabolic process | cytoplasm/mitochondrion | catalytic activity, nucleotide binding, RNA binding | 0.47  | Q02863 | Ubiquitin carboxyl-terminal hydrolase 16 | metabolism | membrane/mitochondrion | catalytic activity | 0.15 |
| Q04172 | Sensitive to high expression protein 5, mitochondrial | cell organization and biogenesis | membrane/mitochondrion | structural molecular activity, transport activity | 1.48  | P33033 | Succinate/fumarate mitochondrial transporter | metabolism | membrane/mitochondrion | structural molecular activity, transport activity | 0.49 |
| P09624 | Dehydrolipoamide dehydrogenase, mitochondrial | cellular homeostasis, metabolic process, regulation of biological process | mitochondrion | catalytic activity, nucleotide binding, protein binding | 0.50  | P00380 | Glycerolaldehyde-3-phosphate dehydrogenase 1 | metabolism | cytoplasm/mitochondrion | catalytic activity, nucleotide binding | 0.51 |
| P28737 | Protein MSPI | cell organization and biogenesis, metabolic process | membrane/mitochondrion | catalytic activity, nucleotide binding, protein binding, RNA binding | 0.53  | P38072 | Protein SCO2, mitochondrial | antioxidant activity, catalytic activity, metal ion binding | mitochondrial | 0.53 |
| P39525 | 3-oxoacyl (acyl-carrier-protein)-synthase homolog | metabolic process | mitochondrial | catalytic activity | 0.54  | P12695 | Dehydrolipoamide-residue acetyltransferase component of glyoxylate dehydrogenase complex, mitochondrial | metabolism | mitochondrial | catalytic activity | 0.55 |
| P40852 | Glutathione S-transferase 1 | metabolic process | endoplasmic reticulum, mitochondrial | catalytic activity | 0.55  | P12709 | glucose-6-phosphate isomerase | metabolism | mitochondrion | catalytic activity | 0.55 |
| P40815 | Protein mmt1, mitochondrial | cell organization and biogenesis, metabolic process | mitochondrion | catalytic activity | 0.55  | P10662 | 37S ribosomal protein MRPI, mitochondrial | metabolism | mitochondrial | catalytic activity, metal ion binding, structural molecular activity | 0.59 |
| Q03713 | Respiratory supercomplex factor 1, mitochondrial | cell organization and biogenesis | membrane/mitochondrion | antioxidant activity, catalytic activity, metal ion binding, RNA binding | 0.59  | Q3824 | Uncharacterized protein YOR020W-A | metabolism | transport | membrane/mitochondrion | 0.59 |
| P00445 | Superoxide dismutase [Cu-Zn] | cell organization and biogenesis, cellular homeostasis, metabolic process, regulation of biological process | cytoplasm/mitochondrion | catalytic activity, antioxidant activity, metal ion binding, protein binding | 0.59  | P00950 | Phosphoglycerate mutase 1 | metabolism | cytoplasm/mitochondrion | catalytic activity | 0.60 |
| P00942 | Triosephosphate isomerase | metabolic process | cytoplasm/mitochondrion | catalytic activity | 0.61  |
| P38891 | Branched-chain-amino-acid aminotransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS661 5 | BAT1; YHR208 W | metabolic process;regulation of biological process;response to stimulus | mitochondrion,organellar lumen | catalytic activity | 7.111 | 4.926 | 0.69 |
| Q92927 | Mitochondrial 2-oxocarboxylate carrier 2 (OS=Saccharomyces cerevisiae S288c) | BS439 7 | ODC2; YOR222 W | metabolic process;transport | membrane/mitochondrion | structural molecule activity;transport activity | 0.778 | 0.54 | 0.69 |
| P06168 | Ketol-acid reductoisomerase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS106 9 | ELY5; YLR355C | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;DNA binding;metal ion binding | 12.89 | 9 | 0.70 |
| P03539 | Glyceraldehyde-3-phosphate dehydrogenase 3 (OS=Saccharomyces cerevisiae S288c) | BS310 6 | TID3; YGR192 C | cell death;metabolic process | cytoplasm,cytosol;membrane/mitochondrion,nu cleus | catalytic activity;nucleotide de binding;RNA binding | 6.406 | 4.484 | 0.70 |
| P40416 | Iron-sulfur clusters transporter ATM1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS534 7 | ATMI; YMR301 C | cellular homeostasis;metabolic process;transport | membrane/mitochondrion | catalytic activity;nucleotide de binding;transport activity | 0.645 | 0.453 | 0.70 |
| P34365 | Citrate synthase 3, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS610 7 | CIT3; YPR001 W | metabolic process | mitochondrion | catalytic activity | 3.262 | 2.3 | 0.71 |
| Q06892 | NADH kinase POD5, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS591 3 | POD5; YPL188 W | metabolic process;response to stimulus | mitochondrion,organellar lumen | catalytic activity;nucleotide de binding | 0.52 | 0.369 | 0.71 |
| P12792 | UPF0744 protein YSC83 (OS=Saccharomyces cerevisiae S288c) | BS641 0 | YSC83; YHR017 W | membrane/mitochondrion | 0.52 | 0.369 | 0.71 |
| P39726 | Glycine cleavage system H protein, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS125 4 | SGC3; YAL044C | metabolic process | mitochondrion | catalytic activity | 3.642 | 2.594 | 0.71 |
| Q4438 | Stationary phase protein 4 (OS=Saccharomyces cerevisiae S288c) | BS513 4 | SPGA; YMR107 W | 3.642 | 2.594 | 0.71 |
| P12428 | Probable 2-methylcitrate dehydratase (OS=Saccharomyces cerevisiae S288c) | BS610 8 | PDC4; YPR002 W | metabolic process | cytoplasm,membrane/mitochondrion | catalytic activity | 8.306 | 5.978 | 0.72 |
| Q4935 | Cytochrome c oxidase protein 20, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS181 7 | COX20; YDR231 C | cellular organization and biogenesis;metabolic process | membrane/mitochondrion | protein binding | 1.424 | 1.031 | 0.72 |
| P18239 | ADP-ATP carrier protein 2 (OS=Saccharomyces cerevisiae S288c) | BS225 0 | PET9; YBL030C | cell death;metabolic process;transport | membrane/mitochondrion | structural molecule activity;transport activity | 110.0 34 | 80.11 3 | 0.73 |
| P10087 | MICOS subunit MIC26 (OS=Saccharomyces cerevisiae S288c) | BS315 0 | MOS2; MIC26; YGR235 C | cell organization and biogenesis | membrane/mitochondrion | 1.276 | 0.931 | 0.73 |
| Q12230 | Sphingolipid long chain base-responsive protein LSP1 (OS=Saccharomyces cerevisiae S288c) | BS610 3 | LSP1; YPL004C | regulation of biological process;response to stimulus;transport | cytoplasm,membrane/mitochondrion | 33.11 7 | 38.81 1 | 0.75 |
| Q0402 | Nuclear migration protein NUM1 (OS=Saccharomyces cerevisiae S288c) | BS172 7 | NUM1; YDR150 W | cellular organization;cellular component movement;metabolic process;regulation of biological process;transport | endoplasmic reticulum/mitochondrion | catalytic activity;motor activity;protein binding | 0.052 | 0.038 | 0.73 |
| P50403 | Protein SUR7 (OS=Saccharomyces cerevisiae S288c) | BS495 3 | SUR7; YML052 W | cell differentiation;transport | membrane/mitochondrion | 1.154 | 0.848 | 0.73 |
| Q0413 | Citrate/oxoglutarate carrier protein (OS=Saccharomyces cerevisiae S288c) | BS528 2 | YHRM2; YMR241 W | cell organization and biogenesis;metabolic process;transport | membrane/mitochondrion | DNA binding;structural molecule activity;transport activity | 3.467 | 2.548 | 0.73 |
| Q02204 | S45 ribosomal protein L13, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS487 5 | MKPL13; YKR0096C | cell organization and biogenesis;metabolic process | mitochondrion,ribosome | structural molecule activity | 1.054 | 0.778 | 0.74 |
| P0945 | MICO5 complex subunit MIC27 (OS=Saccharomyces cerevisiae S288c) | BS562 3 | AIM37; MIC27; YNL120 W | cell organization and biogenesis | membrane/mitochondrion | 0.968 | 0.719 | 0.74 |
| P15450 | Fructose-bisphosphate aldolase (OS=Saccharomyces cerevisiae S288c) | BS480 5 | FBA1; YKL080C | metabolic process | cytoplasm,cytosol,membrane/mitochondrion | catalytic activity;metal ion binding | 0.896 | 0.668 | 0.75 |
| P40508 | Uncharacterized protein YIL077C (OS=Saccharomyces cerevisiae S288c) | BS473 3 | YIL077C; YIL077C | mitochondrial | 0.896 | 0.668 | 0.75 |
| P40496 | 37S ribosomal protein S25, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BS471 5 | RSM25; YIL099C | cell organization and biogenesis;metabolic process | mitochondrion,ribosome | structural molecule activity | 0.896 | 0.668 | 0.75 |
| Q12166 | 2-isopropylmalate synthase 2, mitochondrial (S. cerevisiae S288c) | 85427 | LEUR, YOR108W | metabolic process | mitochondrial | catalytic activity; protein binding | 2.065 | 1.543 | 0.75 |
| P05650 | Phosphoglycerate kinase (S. cerevisiae S288c) | 85037 | PGI3, YCR012W | metabolic process | cytoplasm; membrane; mitochondrial | catalytic activity; nucleotide binding | 4.412 | 3.299 | 0.75 |
| P34227 | Mitochondrial peroxiredoxin PRX1 (S. cerevisiae S288c) | 85221 | PRX1; YBL064C | cellular homeostasis; metabolic process; regulation of biological processes > response to stimulus | mitochondrial | antioxidant activity; catalytic activity | 5.952 | 4.456 | 0.75 |
| P06208-1 | 2-isopropylmalate synthase (S. cerevisiae S288c) | 85691 | LEU4; YNL104C | metabolic process | cytoplasm; mitochondrial | catalytic activity; protein binding | 6.017 | 4.541 | 0.75 |
| P38855 | Altered inheritance of mitochondria protein 46, mitochondrial (S. cerevisiae S288c) | 85600 | AIM46; YHR199C | mitochondrial | catalytic activity | 0.73 | 0.555 | 0.75 |
| P21801 | Succinate dehydrogenase ubiquinone iron-sulfur subunit, mitochondrial (S. cerevisiae S288c) | 85068 | SDH2; YL041C | metabolic process; transport | membrane; mitochondrial | catalytic activity; metal ion binding | 32.83 | 24.80 | 0.76 |
| P32641 | mitochondrial phosphate carrier protein (S. cerevisiae S288c) | 85354 | MIR1; YIR77C | metabolic process; transport | membrane; mitochondrial | protein binding; structural molecule activity; transport activity | 17.95 | 13.67 | 0.76 |
| P38241 | Isocitrate dehydrogenase (NAD) subunit 2, mitochondrial (S. cerevisiae S288c) | 85430 | IDH2; YOR136W | metabolic process | mitochondrial; organelle lumen | catalytic activity; metal ion binding; nucleotide binding; protein binding; RNA binding | 4.78 | 3.642 | 0.76 |
| P38834 | Isocitrate dehydrogenase (NAD) subunit 1, mitochondrial (S. cerevisiae S288c) | 85669 | IDH1; YNL037C | metabolic process; transport | cytosol; mitochondrial; organelle lumen | catalytic activity; metal ion binding; nucleotide binding; protein binding; RNA binding | 10.28 | 7.859 | 0.76 |
| P32611 | S45 ribosomal protein RML2, mitochondrial (S. cerevisiae S288c) | 85666 | RML2; YL050C | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | catalytic activity; RNA binding; structural molecule activity | 0.509 | 0.389 | 0.76 |
| Q8B223 | Altered inheritance of mitochondria protein 39, mitochondrial (S. cerevisiae S288c) | 85410 | AIM39; YOL053W | cytosol; membrane; mitochondrial | catalytic activity | 0.468 | 0.359 | 0.77 |
| P37956-1 | Camtine O-acetyltransferase, mitochondrial (S. cerevisiae S288c) | 85496 | CAT2; YML042W | metabolic process; transport | membrane; mitochondrial | catalytic activity | 10.18 | 7.938 | 0.78 |
| P198B2 | Heat shock protein 60, mitochondrial (S. cerevisiae S288c) | 85096 | HSP90; YLR259C | cell organization and biogenesis; metabolic process; regulation of biological processes; transport | cytoplasm; cytosol; membrane; mitochondrial; organelle lumen | catalytic activity; DNA binding; nucleotide binding; protein binding | 39.29 | 30.62 | 0.78 |
| P32453 | Protein ATP11, mitochondrial (S. cerevisiae S288c) | 85540 | ATP11; YNL315C | cell organization and biogenesis | mitochondrial | protein binding | 0.995 | 0.778 | 0.78 |
| P38297 | Mitofilin F201 (S. cerevisiae S288c) | 85247 | F201; YBR179C | cell organization and biogenesis | membrane; mitochondrial | catalytic activity; nucleotide binding; protein binding | 0.248 | 0.194 | 0.78 |
| Q6E143 | mitochondrial dicarboxylate transporter (S. cerevisiae S288c) | 85106 | DIC1; YLR348C | metabolic process; transport | membrane; mitochondrial | structural molecule activity; transport activity | 0.931 | 0.73 | 0.78 |
| P49095 | Glycine dehydrogenase (Decarboxylating), mitochondrial (S. cerevisiae S288c) | 85522 | GCV2; YMR189W | metabolic process | cytosol; mitochondrial | catalytic activity | 1.184 | 0.931 | 0.79 |
| P40495 | Homoisocitrate dehydrogenase, mitochondrial (S. cerevisiae S288c) | 85471 | LYS2; YLR094C | metabolic process | mitochondrial | catalytic activity; metal ion binding; nucleotide binding | 4.623 | 3.642 | 0.79 |
| P35191 | Dna1 homolog 1, mitochondrial (S. cerevisiae S288c) | 85053 | MDJ1; YFL016C | cell organization and biogenesis; metabolic process; regulation of biological processes; response to stimulus | mitochondrial; organelle lumen | enzyme regulatory activity; metal ion binding; nucleotide binding | 1.656 | 1.31 | 0.79 |
| Protein ID | Name                                                                 | Interactome | Function                                                                 | Cellular Location | Molecular Activity | Binding Type                | Binding Probability |
|------------|----------------------------------------------------------------------|-------------|--------------------------------------------------------------------------|-------------------|--------------------|----------------------------|---------------------|
| P11914     | Mitochondrial-processing peptide subunit alpha (Saccharomyces cerevisiae S288c) | 85641       | metabolic process, transport                                             | membrane,mitochondrion,organellarum | catalytic activity | metal ion binding | 0.738 0.585 0.79 |
| Q03976     | 37S ribosomal protein S24, mitochondrial (Saccharomyces cerevisiae S288c) | 85175       | cell organization and biogenesis,metabolic process                      | mitochondrion,ribosome | structural molecule activity | 0.738            | 0.585 0.79 |
| P32891     | D-lactate dehydrogenase (Saccharomyces cerevisiae S288c), mitochondrial | 85138       | metabolic process, transport                                             | membrane,mitochondrion | catalytic activity | nuclear binding | 11.25 9 0.80 |
| Q04330     | 37S ribosomal protein RSMQ28, mitochondrial (Saccharomyces cerevisiae S288c) | 85210       | cell organization and biogenesis,metabolic process                      | mitochondrion,ribosome | structural molecule activity | 1.015 0.823 0.81 |
| Q07651     | SUR7 family protein FMP45 (Saccharomyces cerevisiae S288c), mitochondrial | 85130       | cell differentiation,cell organization and biogenesis                  | membrane,mitochondrion | antioxidant activity | catalytic activity | 0.859 0.701 0.82 |
| P04311     | Probable electron transfer flavoprotein subunit beta (Saccharomyces cerevisiae S288c) | 85312       | metabolic process,transport                                              | mitochondrion,organellarum | catalytic activity | protein binding | 3.217 2.652 0.82 |
| P16547     | Mitochondrial outer membrane protein OMA5 (Saccharomyces cerevisiae S288c) | 85467       | memenzyme,mitochondrion                                                  | membrane,mitochondrion | catalytic activity | metal ion binding | 547.4 477.6 0.83 |
| P00175     | Cytchrome b2, mitochondrial (Saccharomyces cerevisiae S288c) | 85495       | metabolic process,transport                                              | cytosol,membrane,mitochondrion,nucleus | catalytic activity | metal ion binding | 0.496 0.413 0.83 |
| P00330     | Alcohol dehydrogenase 1 (Saccharomyces cerevisiae S288c) | 85406       | metabolic process                                                        | cytoplasm,membrane | catalytic activity | metal ion binding | 2.36 1.976 0.84 |
| P00890     | Citrate synthase, mitochondrial (Saccharomyces cerevisiae S288c) | 85573       | metabolic process,transport                                              | cytosol,mitochondrion,organellarum | catalytic activity | 14.08 11.79 0.84 |
| P32191     | Glycerol-3-phosphate dehydrogenase (Saccharomyces cerevisiae S288c) | 85465       | metabolic process                                                        | membrane,mitochondrion | catalytic activity | 5.434 4.555 0.84 |
| Q21091     | Mitochondrial 2-methylisocitrate lyase (Saccharomyces cerevisiae S288c) | 85611       | metabolic process                                                        | mitochondrion,organellarum | catalytic activity | 2.793 2.36 0.84 |
| Q23734     | Nuclear control of ATPase protein 2 (Saccharomyces cerevisiae S288c) | 85627       | metabolic process                                                        | membrane,mitochondrion | catalytic activity | 0.668 0.565 0.85 |
| Q08818     | Meiotic sister-chromatid recombination protein 6, mitochondrial (Saccharomyces cerevisiae S288c) | 85453       | metabolic process                                                        | mitochondrion,organellarum | RNA binding | 0.506 0.431 0.85 |
| P23335     | Protein MS551, mitochondrial (Saccharomyces cerevisiae S288c) | 85090       | metabolic process,regulation of biological process                      | membrane,mitochondrion | protein binding | transducer regulator activity | 0.995 0.848 0.85 |
| Q03028     | Mitochondrial 2-oxoacid:carboxylate carrier 2 (Saccharomyces cerevisiae S288c) | 85596       | metabolic process,transport                                              | membrane,mitochondrion | structural molecule activity | 4.995 4.275 0.86 |
| P23734     | Cysteine desulfurase, mitochondrial (Saccharomyces cerevisiae S288c) | 85034       | cell organization and biogenesis,cellular homeostasis,metabolic process | mitochondrion,nucleus | catalytic activity | metal ion binding | 1.346 1.154 0.86 |
| Q07349     | MIOREX complex component 9 (Saccharomyces cerevisiae S288c) | 85153       | endoplasmic reticulum,membrane,mitochondrion | membrane,mitochondrion | catalytic activity | metal ion binding | 1.276 1.096 0.86 |
| P39522     | Dihydroxy-acid dehydratase, mitochondrial (Saccharomyces cerevisiae S288c) | 85347       | metabolic process                                                        | mitochondrion | catalytic activity | metal ion binding | 13.17 11.32 0.86 |
| P31810     | Probable oxido-reductase AIM17 (Saccharomyces cerevisiae S288c) | 85636       | cell organization and biogenesis,metabolic process                      | mitochondrion | catalytic activity | metal ion binding | 3.467 2.981 0.86 |
| P35292     | 37S ribosomal protein S35, mitochondrial (Saccharomyces cerevisiae S288c) | 85307       | cell organization and biogenesis,metabolic process                      | mitochondrion,ribosome | structural molecule activity | 1.754 1.512 0.86 |
| Gene Symbol | Gene Name | Function | Cellular Location | Activity | Enrichment Score |
|-------------|-----------|----------|-------------------|----------|------------------|
| PDH1        | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process | Mitochondrion, organelle lumen | Catalytic activity | 6.848 5.952 0.87 |
| PEM15       | Ferrochelatase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process | Membrane, Mitochondrion | Catalytic activity | 4.337 3.806 0.88 |
| YOR1176C   | Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process, Transport | Membrane, Mitochondrion | Catalytic activity, Nucleotide binding, Protein binding | 9.578 8.454 0.88 |
| YGC148C    | 37S ribosomal protein S23, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Cell organization and biogenesis, Metabolic process | Mitochondrion, Ribosome | Catalytic activity, Nucleotide binding, RNA binding, Structural molecule activity | 1.11 0.983 0.89 |
| YGR094W    | Valyl-tRNA ligase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process, Regulation of biological process | Cytoplasm, Cytosol, Mitochondrion | Catalytic activity, Nucleotide binding | 0.377 0.334 0.89 |
| YOR086C    | Tricarboxylic acid cycle complexes assembly protein | Metabolic process | Mitochondrion, Organellar lumen | Catalytic activity, Protein binding, RNA binding | 4.059 6.362 0.90 |
| YGR016C    | Malate dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process | Mitochondrion, Organellar lumen | Catalytic activity, Protein binding, RNA binding | 3.359 3.042 0.91 |
| YLR304C    | Aconitate hydratase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process | Cytoplasm, Cytosol, Mitochondrion, Organellar lumen | Catalytic activity, DNA binding, Metal ion binding | 30.62 27.61 0.90 |
| YDR258W    | Heat shock protein 78, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Cell organization and biogenesis, Regulation of biological process | Mitochondrion, Organellar lumen | Catalytic activity, Nucleotide binding, Protein binding | 4.012 3.642 0.91 |
| YGL129C    | External NADH-ubiquinone oxidoreductase 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process | Mitochondrion | Catalytic activity, Nucleotide binding | 12.89 11.79 0.91 |
| YKL085W    | MICO complex subunit Mico60 (OS=Saccharomyces cerevisiae S288c) | Cell organization and biogenesis, Transport | Membrane, Mitochondrion | Catalytic activity, Nucleotide binding, Protein binding, Transport activity | 17.87 16.43 0.92 |
| YML120W    | Retinoic-acid-inensitive NADH-ubiquinone oxidoreductase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process, Regulation of biological process | Membrane, Mitochondrion, Organellar lumen | Catalytic activity, Nucleotide binding | 9 8.284 0.92 |
| YOR176C    | Succinyl-CoA ligase (ADP-forming) subunit beta, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process | Mitochondrion | Catalytic activity, Nucleotide binding | 12.89 11.79 0.91 |
| YKL085W    | Mitochondrial import receptor subunit TOM70 (OS=Saccharomyces cerevisiae S288c) | Cell organization and biogenesis, Transport | Membrane, Mitochondrion | Protein binding, Transport activity | 2.888 2.665 0.92 |
| YOR121W    | ATP synthase subunit beta, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process, Transport | Cytosol, Membrane, Mitochondrion | Catalytic activity, Nucleotide binding, Protein binding, Transport activity | 30.62 28.28 0.92 |
| YML120C    | Mitochondrial respiratory chain complexes assembly protein YTA12 (OS=Saccharomyces cerevisiae S288c) | Cell organization and biogenesis, Metabolic process, Response to stimulus, Transport | Cytoplasm, Membrane, Mitochondrion | Catalytic activity, Metal ion binding, Nucleotide binding, Protein binding | 1.184 1.096 0.93 |
| YOR574W    | Potassium-activated aldehyde dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process | Mitochondrion, Organellar lumen | Catalytic activity | 25.82 24.11 0.93 |
| YOR317W    | Long-chain-fatty-acid-CoA ligase 1 (OS=Saccharomyces cerevisiae S288c) | Metabolic process, Transport | Endoplasmic reticulum, Membrane, Mitochondrion | Catalytic activity, Nucleotide binding | 7.072 7.072 1.00 |
| YMR108W    | Acetyl-CoA synthase catalytic subunit, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process | Mitochondrion | Catalytic activity, Metal ion binding, Nucleotide binding | 4.225 4.225 1.00 |
| YEL024W    | Cytochrome b-c1 complex subunit Flesk, mitochondrial (OS=Saccharomyces cerevisiae S288c) | Metabolic process, Transport | Membrane, Mitochondrion | Catalytic activity, Metal ion binding, Transport activity | 20.54 20.54 1.00 |
| Q0486 | ARS-binding factor 2, mitochondrial (S. cerevisiae) | 85509 | 4 | ABF2; YMRO72 | W | cell organization and biogenesis; metabolic process; regulation of biological process | chromosome, mitochondrion; nucleus | DNA binding | 27.94 | 3 | 27.94 | 3 | 1.00 |
| P04037 | Cytochrome c oxidase subunit 4, mitochondrial (S. cerevisiae) | 85268 | 8 | Cox4; YGL187C | W | cell organization and biogenesis; metabolic process; transport | membrane, mitochondrion | catalytic activity; metal ion binding; transport activity | 17.73 | 8 | 17.73 | 8 | 1.00 |
| P50085 | Prohibitin-2 (S. cerevisiae) | 85314 | 6 | Phb2; YGR231C | W | cell organization and biogenesis; metabolic process; regulation of biological process | membrane, mitochondrion | protein binding | 3.329 | 3.329 | 1.00 |
| P70246 | Alcohol dehydrogenase 3, mitochondrial (S. cerevisiae) | 85510 | 7 | ADH3; YMRO83B | W | metabolic process | mitochondrion, organelle lumen | catalytic activity; metal ion binding | 4.179 | 4.179 | 1.00 |
| P37295 | Mitochondrial inner membrane i-AAA protease supercomplex subunit YME1 (S. cerevisiae) | 85613 | 5 | YME1; YPR024 | W | metabolic process; response to stimulus; transport | membrane, mitochondrion | catalytic activity; metal ion binding; nuclear import protein binding | 0.891 | 0.891 | 1.00 |
| P18988 | Mitochondrial GTPase GDP carrier protein 1 (S. cerevisiae) | 85132 | 9 | GCC1; YDL190C | W | cell organization and biogenesis; cellular homeostasis; metabolic process; regulation of biological process | membrane, mitochondrion | structural molecule activity; transport activity | 4.179 | 4.179 | 1.00 |
| P12480 | Probable electron transfer flavoprotein subunit alpha, mitochondrial (S. cerevisiae) | 85611 | 2 | Aim45; YPR004C | W | metabolic process; transport | mitochondrion, organelle lumen | catalytic activity; nuclear import protein binding | 1.818 | 1.818 | 1.00 |
| P40961 | prohibitin-1 (S. cerevisiae) | 85303 | 9 | PHB1; YGR132C | W | cell organization and biogenesis; metabolic process; regulation of biological process | membrane, mitochondrion | protein binding | 2.793 | 2.793 | 1.00 |
| P6046 | Mitochondrial intermembrane space import and assembly protein 40 (S. cerevisiae) | 85363 | 9 | Mia40; YKL219S | W | cellular component movement; metabolic process; response to stimulus; transport | membrane, mitochondrion | catalytic activity; protein binding; transport activity | 1.555 | 1.555 | 1.00 |
| P55140 | Protein RMD9, mitochondrial (S. cerevisiae) | 85277 | 1 | RMD9; YGL107C | W | cell differentiation; metabolic process; regulation of biological process | membrane, mitochondrion | RNA binding | 0.585 | 0.585 | 1.00 |
| P37521 | Respiratory supercomplex factor 2, mitochondrial (S. cerevisiae) | 85575 | 2 | RCF2; YNR018 | W | cell organization and biogenesis | membrane, mitochondrion | | 5.579 | 5.579 | 1.00 |
| P98297 | Mitochondrial import inner membrane translocase subunit tim23 (S. cerevisiae) | 85575 | 1 | TIM23; YNR017 | W | transport | membrane, mitochondrion | protein binding; transport activity | 2.981 | 2.981 | 1.00 |
| P44116 | Cyto-Uly metalloendopeptidase duc1 (S. cerevisiae) | 85060 | 5 | Duc1; YPR044C | W | metabolic process | cytoplasm, mitochondrion, ribosome | catalytic activity; metal ion binding | 0.711 | 0.711 | 1.00 |
| P00410 | Cytochrome c oxidase subunit 2 (S. cerevisiae) | 85462 | 2 | Cox2; Q0250 | W | metabolic process; transport | membrane, mitochondrion | catalytic activity; metal ion binding; protein binding; transport activity | 1.61 | 1.61 | 1.00 |
| P32331 | Carrier protein YMC1, mitochondrial (S. cerevisiae) | 85617 | 1 | YMC1; YPR058 | W | metabolic process; transport | membrane, mitochondrion, vacuole | structural molecule activity; transport activity | 0.968 | 0.968 | 1.00 |
| P38325 | Mitochondrial outer membrane protein OM14 (S. cerevisiae) | 85253 | 1 | OM14; YBR230C | W | transport | membrane, mitochondrion | | 4.179 | 4.179 | 1.00 |
| P38801 | S45 ribosomal protein L22, mitochondrial (S. cerevisiae) | 85554 | 4 | MRPL22; YNL177C | W | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | RNA binding; structural molecule activity | 0.551 | 0.551 | 1.00 |
| P36444 | Mitochondrial import receptor subunit TOM40 (S. cerevisiae) | 85524 | 3 | TOM40; YMR023 | W | transport | cytosol, membrane, mitochondrion | protein binding; transport activity | 0.896 | 0.896 | 1.00 |
| P10507 | Mitochondrial-processing peptidase subunit beta (S. cerevisiae) | 85086 | 0 | MAS1; YLR163C | W | metabolic process; transport | mitochondrion, organelle lumen | catalytic activity; metal ion binding; protein binding | 0.616 | 0.616 | 1.00 |
| P06493 | LET1 domain-containing protein YLT47, mitochondrial (S. cerevisiae) | 85624 | 3 | YLT47; YPR125 | W | cell organization and biogenesis; transport | membrane, mitochondrion | | 0.61 | 0.61 | 1.00 |
| Q04728 | Arginine biosynthesis bifunctional protein Arg7, mitochondrial (S. cerevisiae) | 85508 | 4 | ARG7; YMRO62 | C | metabolic process | mitochondrion, organelle lumen | catalytic activity | 0.417 | 0.417 | 1.00 |
PS3969  Sorting assembly machinery 50 kDa subunit [OS=Saccharomyces cerevisiae S288c]
85570 5  SAM50; YNL025W  cell organization and biogenesis;transport membrane;mitochondrion protein binding;transporter activity 0.374 0.374 1.00

P25573  Mitochondrial inner membrane i-AAA protease supercomplex subunit MGR1 [OS=Saccharomyces cerevisiae S288c]
85031 3  MGR1; YCL044C  metabolic process membrane;mitochondrion protein binding 0.701 0.701 1.00

P22136  ATPase expression protein 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85532 5  AEP2; YMR282C  metabolic process;regulation of biological process mitochondrion RNA binding 0.292 0.292 1.00

P38910  ID 40 kDa heat shock protein, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85418 5  HSP10; YOR020C  cell organization and biogenesis;metabolic process;response to stimulus;transport cytoplasm;mitochondrion;organellar lumen metal ion binding;nucleroti de binding;protein binding 2.162 2.162 1.00

P38523  GrpE protein homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85440 7  MGE1; YOR232W  metabolic process;regulation of biological process;transport membrane;mitochondrion;organellar lumen enzyme regulator activity;nucleroti de binding;protein binding 0.624 0.624 1.00

P19955  37S ribosomal protein YMR31, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85061 0  YMR31; YFR049W  cell organization and biogenesis;metabolic process mitochondrion;ribosome catalytic activity;protein binding;structural molecule activity 2.594 2.594 1.00

Q03798  Altered inheritance of mitochondria protein 36, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85518 9  AIM36; YMR157C  membrane;mitochondrion 0.624 0.624 1.00

P12482  Mitochondrial aspartate-glutamate transporter AGC1 [OS=Saccharomyces cerevisiae S288c]
85613 2  AGC1; YFR021C  metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 0.238 0.238 1.00

P41921  glutathione reductase [OS=Saccharomyces cerevisiae S288c]
85601 4  GLR1; YPL091W  cellular homeostasis;metabolic process;regulation of biological process;response to stimulus cytoplasm;cytosol;mitochondrion;nucleus antioxidan activity;cellular activity;nucleroti de binding 0.334 0.334 1.00

P38889  uncharacterized mitochondrial hydrolase FMP41 [OS=Saccharomyces cerevisiae S288c]
85555 3  FMP41; YNL168C  metabolic process mitochondrion catalytic activity;metal ion binding 0.501 0.501 1.00

Q14467  multiprotein-bridging factor D subunit 10 [OS=Saccharomyces cerevisiae S288c]
85447 4  MBF1; YOR298C.A  metabolic process;regulation of biological process cytoplasm;mitochondrion;nucleus DNA binding 0.874 0.874 1.00

P37299  cytochrome b-2 complex subunit 10 [OS=Saccharomyces cerevisiae S288c]
85639 0  QCR10; YHR001W.A  metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 2.981 2.981 1.00

Q03327  Mitochondrial fusion and transport protein Ugo1 [OS=Saccharomyces cerevisiae S288c]
85208 1  UGO1; YDR470C  cell organization and biogenesis;metabolic process mitochondrion;mitochondrion protein binding;structural molecule activity 0.701 0.701 1.00

P36151  Uncharacterized protein YKR707W [OS=Saccharomyces cerevisiae S288c]
85394 4  YKR707W; W; YKR707W  metabolic process mitochondrion 0.438 0.438 1.00

P32902  37S ribosomal protein MRP4, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85638 4  MRP4; YHL004W  cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 0.468 0.468 1.00

Q02883  N-acetyl-phosphatidylethanolamine-hydrolyzing phospholipase O, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85600 1  FMP30; YPL103C  metabolic process membrane;mitochondrion catalytic activity;metal ion binding 0.304 0.304 1.00

P17558  37S ribosomal protein PET123, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85432 9  PET123; YOR158W  cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 0.666 0.666 1.00

P40745  mitochondrial import inner membrane translocase subunit TMI54 [OS=Saccharomyces cerevisiae S288c]
85399 2  TMI54; YIL054W  cell organization and biogenesis;transport cytoplasm;membrane;mitochondrion transporter activity 0.334 0.334 1.00

P00401  Cytochrome c oxidase subunit 1 [OS=Saccharomyces cerevisiae S288c]
85459 8  COX1; Q0045  metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding;transporter activity 0.778 0.778 1.00

P38705  Serine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85640 2  DIA4; YHR011W  metabolic process cytoplasm;mitochondrion;organellar lumen catalytic activity;nucleroti de binding 0.15 0.15 1.00

P25038  Translation initiation factor IF-2, mitochondrial [OS=Saccharomyces cerevisiae S288c]
85413 5  IFM1; YOL023W  cell organization and biogenesis;metabolic process mitochondrion;nucleus catalytic activity;nucleroti de binding;RNA binding 0.11 0.11 1.00
| Accession   | Description                                                                 | Organism                                      | Functions                                                                                     | Localization                        | GO Terms                                                                 | Annotation | AA Change | IMI ID |
|-------------|-----------------------------------------------------------------------------|-----------------------------------------------|---------------------------------------------------------------------------------------------|-------------------------------------|-------------------------------------------------------------------------|------------|-----------|---------|
| P3289       | Mitochondrial chaperone BCS1 (S. cerevisiae)                                 |                                               | Cell organization and biogenesis; metabolic process; response to stimuli; transport          | Cytoplasm; membrane; mitochondrion  | catalytic activity; nucleotide binding; transport activity             | 0.194      | 0.194    | 1.00   |
| P38714      | Arginine tRNA ligase, mitochondrial (S. cerevisiae)                          |                                               | Cell organization and biogenesis; metabolic process                                        | Cytoplasm; mitochondrion; organelle lumen | catalytic activity; nucleotide binding                                  | 0.055      | 0.055    | 1.00   |
| Q2375       | Mitochondrial ornithine transporter 1 (S. cerevisiae)                        |                                               | Metabolic process; transport                                                                | Membrane; mitochondrion             | structural molecule activity; transport activity                       | 0.54       | 0.54     | 1.00   |
| P38169      | Kynurenine 3-monooxygenase (S. cerevisiae)                                   |                                               | Metabolic process                                                                           | Membrane; mitochondrion             | catalytic activity; nucleotide binding                                | 0.172      | 0.172    | 1.00   |
| P34222      | Peptidyl-tRNA hydrolase 2 (S. cerevisiae)                                    |                                               | Regulation of biological process                                                           | Cytoplasm; cytosol; membrane; mitochondrion | catalytic activity; protein binding                                  | 0.425      | 0.425    | 1.00   |
| P53732      | 57S ribosomal protein S12, mitochondrial (S. cerevisiae)                    |                                               | Cell organization and biogenesis; metabolic process                                       | Mitochondrion; ribosome             | structural molecule activity                                          | 0.668      | 0.668    | 1.00   |
| P40502      | Altered inheritance of mitochondria protein 19, mitochondrial (S. cerevisiae) |                                               |                                                                                             | Membrane; mitochondrion             |                                                                          | 0.585      | 0.585    | 1.00   |
| P40165      | NADP(H)-glyceraldehyde dehydrogenase (S. cerevisiae)                       |                                               | Metabolic process                                                                           | Cytoplasm; mitochondrion            | catalytic activity; metal ion binding; nucleotide binding             | 0.468      | 0.468    | 1.00   |
| P38172      | MIOREX complex component 3 (S. cerevisiae)                                  |                                               |                                                                                             | Membrane; mitochondrion             |                                                                          | 0.311      | 0.311    | 1.00   |
| P39515      | Mitochondrial import inner membrane translocase subunit Tim17 (S. cerevisiae) |                                               | Cell organization and biogenesis; transport                                                | Membrane; mitochondrion             | protein binding; transport activity                                   | 1.371      | 1.371    | 1.00   |
| P40159      | Uncharacterised protein YNL208W (S. cerevisiae)                             |                                               |                                                                                             | Membrane; mitochondrion; ribosome    |                                                                          | 0.292      | 0.292    | 1.00   |
| P19516      | Cytochrome c oxidase assembly protein Cox11, mitochondrial (S. cerevisiae)  |                                               | Cell organization and biogenesis; metabolic process                                       | Membrane; mitochondrion; ribosome   | Metal ion binding                                                      | 0.274      | 0.274    | 1.00   |
| P48360      | Probable NADPH:adrenodoxin oxidoreductase, mitochondrial (S. cerevisiae)    |                                               |                                                                                             | Cytoplasm; membrane; mitochondrion; organelle lumen | catalytic activity                                                    | 0.16       | 0.16     | 1.00   |
| Q06486      | MIOREX complex component 10 (S. cerevisiae)                                |                                               |                                                                                             | Membrane; mitochondrion             |                                                                          | 0.222      | 0.222    | 1.00   |
| P40530      | Pyruvate dehydrogenase (acyl-transfering) kinase 1, mitochondrial (S. cerevisiae) |                                               |                                                                                             | Mitochondrion; organelle lumen       | catalytic activity; nucleotide binding; protein binding              | 0.245      | 0.245    | 1.00   |
| P22438      | Methionine-tRNA ligase, mitochondrial (S. cerevisiae)                       |                                               | Metabolic process                                                                           | Cytoplasm; cytosol; mitochondrion; organelle lumen | catalytic activity; nucleotide binding                               | 0.136      | 0.136    | 1.00   |
| Q01976      | ADP-ribose pyrophosphatase (S. cerevisiae)                                  |                                               | Metabolic process                                                                           | Cytoplasm; mitochondrion; nucleus    | catalytic activity; metal ion binding                                | 0.194      | 0.194    | 1.00   |
| Q01932-1    | Cysteine dioxygenase 1, mitochondrial (S. cerevisiae)                       |                                               | Metabolic process; regulation of biological process; response to stimuli                   | Cytoplasm; mitochondrion            | catalytic activity; DNA binding; RNA binding                         | 0.179      | 0.179    | 1.00   |
| P23732      | Thioredoxin-3, mitochondrial (S. cerevisiae)                               |                                               |                                                                                             | Cytoplasm; mitochondrion             | catalytic activity                                                   | 0.52       | 0.52     | 1.00   |
| P21306      | ATP synthase subunit epsilon, mitochondrial (S. cerevisiae)                 |                                               | Metabolic process; transport                                                                | Membrane; mitochondrion             | catalytic activity; transport activity                               | 0.778      | 0.778    | 1.00   |
| Q06405      | ATP synthase subunit f, mitochondrial (S. cerevisiae)                       |                                               | Metabolic process; transport                                                                | Membrane; mitochondrion             | catalytic activity; transport activity                               | 1.512      | 1.512    | 1.00   |
| P46998      | Mitochondrial membrane protein FMP33 (S. cerevisiae)                        |                                               |                                                                                             | Membrane; mitochondrion             |                                                                          | 0.334      | 0.334    | 1.00   |
OS=Saccharomyces cerevisiae

54S ribosomal protein L50, mitochondrial

P53463

3.0564

2

ACF1; YKL192C

mitochondrion

0.259

0.259

1.00

Iron-sulfur assembly protein 1

Q07821

3.0563

2

SA1; YL0107 W

cell organization and biogenesis, metabolic process

mitochondrion, organelle lumen

0.136

0.136

1.00

Asparagine--tRNA ligase, mitochondrial

P23435

3.0538

8

SLMS6; YCR0324C

mitochondrion, organelle lumen

0.172

0.172

1.00

Cytochrome b-c1 complex subunit 8

P08525

3.0527

3

QERR; YL0166 W

membrane; mitochrondrion

0.585

0.585

1.00

Uncharacterized protein

P34224

3.0522

1

YBLO59 W; YBLO59 W

membrane; mitochrondrion

0.212

0.212

1.00

Protein OPY1

P38271

3.0524

6

DPY1; YBR129C

cyttoplasm, mitochondrion

0.274

0.274

1.00

Isochirophospholipids phosphohydrolase C

P40015

3.0367

9

5C1; YER019 W

membrane; mitochrondrion

0.212

0.212

1.00

Uncharacterized protein YBR255C-A

Q3E776

3.0255

8

YBR255C -A; YBR255C -A

membrane

0.389

0.389

1.00

Mitochondrial metalloendopeptidase OMA1

P36163

3.0296

2

OMA1; YKR087C

membrane; mitochrondion

0.245

0.245

1.00

3-methyl-2-oxobutanoate hydroxymethyltransferase

P38122

3.0247

4

ECM31; YBR176 W

mitochondrion

0.122

0.122

1.00

4-hydroxybenzoate polyphenoloxidase, mitochondrial

P32378

3.0577

8

COQ2; YBR041 C

membrane; mitochrondion

0.292

0.292

1.00

Hexaprenyl pyrophosphate synthase, mitochondrial

P18900

3.0522

8

COQ1; YBR003 W

membrane; mitochrondion

0.166

0.166

1.00

Ubiquitine-biosynthesis protein COQ9, mitochondrial

Q05779

3.0589

8

COQ9; YLR201C

membrane; mitochrondion

0.166

0.166

1.00

Magnesium-activated aldehyde dehydrogenase, cytosolic

P54115

3.0504

4

ALD6; YPL061 W

cytoplasm, mitochondrion

0.077

0.077

1.00

54s ribosomal protein L32, mitochondrial

P35348

3.0535

9

MRP132; YCR003 W

membrane; mitochondrion, ribosome

0.179

0.179

1.00

MICOS complex subunit MIC12

P38341

3.0526

6

AIM5; YMR262C

cell organization and biogenesis

membrane; mitochondrion

0.292

0.292

1.00

Cytochrome c oxidase subunit 7

P10174

3.0529

8

COX7; YMR256 C

membrane; mitochondrion

1.154

1.154

1.00

Cytochrome c oxidase subunit 7

P40039

3.0511

1

COX8; YLR395C

membrane; mitochondrion

0.778

0.778

1.00

Abhydrolase domain-containing protein INOM32

P35219

3.0529

9

INOM32; YGR031 W

membrane; mitochondrion

0.116

0.116

1.00

Cytochrome c iso-2

P00045

3.0567

2

CVCT; YL0109C

mitochondrion

0.259

0.259

1.00

Probable hydrolase NF3

P49954

3.0516

5

NF3; YLR351C

mitochondrion

0.129

0.129

1.00

COX assembly mitochondrial protein

P36064

3.0572

1

CMC1; YKL137 W

membrane; mitochondrion

0.389

0.389

1.00

Tricarboxylate transport protein

P38152

3.0529

4

CTP1; YBR291C

membrane; mitochondrion

0.245

0.245

1.00

54s ribosomal protein L50, mitochondrial

P35724

3.0575

6

MRP50; YMR022 C

mitochondrion, ribosome

0.585

0.585

1.00
| Q06998 | Putative ATP-dependent RNA helicase YLR419W (S. cerevisiae S288c) | 85113 | YLR419 W; YLR419 W | metabolic process | cytoplasm, mitochondrial, nucleus | catalytic activity, nucleotide binding, protein binding, RNA binding | 0.027 | 0.027 | 1.00 |
| P25578 | CDP-diacetylgllycerol-glycerol-3-phosphate 3-phosphatidyltransferase (S. cerevisiae S288c) | 85035 | PG51; YCL004 C | metabolic process | mitochondrial | catalytic activity, nucleotide binding | 0.083 | 0.083 | 1.00 |
| Q4487 | Mitochondrial inner membrane protein SHH3 (S. cerevisiae S288c) | 85514 | SHH3; YMR118 C | metabolic process | membrane, mitochondrial | catalytic activity, metal ion binding | 0.194 | 0.194 | 1.00 |
| P20967 | 2-oxoglutarate dehydrogenase, mitochondrial (S. cerevisiae S288c) | 85468 | KG61; YIL125W | metabolic process | cytosol, mitochondrial, organelle lumen | catalytic activity, binding, RNA binding | 13.78 | 15 | 1.05 |
| P12843 | Mitochondrial escape protein 2 (S. cerevisiae S288c) | 85534 | YME2; YMR302 C | cell organization and biogenesis, metabolic process | membrane, mitochondrial | nucleotide binding, protein binding | 2.227 | 2.36 | 1.06 |
| P16387 | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial (S. cerevisiae S288c) | 85692 | PD1; YER178 W | cell growth, metabolic process | mitochondrial, organelle lumen | catalytic activity | 11.49 | 12.46 | 1.08 |
| P09440 | C-1,3-bisphosphoglycerate synthase, mitochondrial (S. cerevisiae S288c) | 85237 | MS1; YBR084 W | metabolic process | cytosol, mitochondrial | catalytic activity, nucleotide binding | 0.762 | 0.829 | 1.09 |
| Q01852 | Mitochondrial import inner membrane translocase subunit TIM23 (S. cerevisiae S288c) | 85479 | TIM44; YIL022W | transport | membrane, mitochondrial | nucleotide binding, protein binding | 5.898 | 6.43 | 1.09 |
| P07275 | Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial (S. cerevisiae S288c) | 85643 | PUT2; YHR037 W | metabolic process | membrane, mitochondrial, organelle lumen | catalytic activity | 3.977 | 4.337 | 1.09 |
| P07257 | Cytochrome b-c1 complex subunit 2, mitochondrial (S. cerevisiae S288c) | 85632 | QCR2; YPR191 W | metabolic process, transport | membrane, mitochondrial | catalytic activity, metal ion binding, protein binding, transporter activity | 27.94 | 30.62 | 1.10 |
| P36013 | NAD-dependent malic enzyme, mitochondrial (S. cerevisiae S288c) | 85838 | MAE1; YKL029C | metabolic process | mitochondrial, organelle lumen | catalytic activity, metal ion binding, nucleotide binding | 1.371 | 1.512 | 1.10 |
| P09297 | Threonine dehydratase, mitochondrial (S. cerevisiae S288c) | 85681 | SL1; YER086 W | metabolic process | cytoplasm, mitochondrial | catalytic activity | 1.285 | 1.424 | 1.11 |
| P18077 | ATP synthase subunit gamma, mitochondrial (S. cerevisiae S288c) | 85232 | ATP3; YBR039 W | metabolic process, transport | membrane, mitochondrial | catalytic activity, transporter activity | 11.32 | 12.68 | 1.12 |
| P39925 | Mitochondrial respiratory chain complexes assembly protein AFG3 (S. cerevisiae S288c) | 85673 | AFG3; YER017C | cell organization and biogenesis, metabolic process, response to stimulus, transport | membrane, mitochondrial | catalytic activity, metal ion binding, nucleotide binding, protein binding | 0.734 | 0.823 | 1.12 |
| P48015 | Aminomethyltransferase, mitochondrial (S. cerevisiae S288c) | 85158 | GCVS; YDR019 C | metabolic process | mitochondrial | catalytic activity, protein binding | 6.406 | 7.185 | 1.12 |
| P32898 | Mitochondrial presequence protease (S. cerevisiae S288c) | 85204 | EYM2; YDR430 C | metabolic process | mitochondrial | catalytic activity, metal ion binding | 0.45 | 0.505 | 1.12 |
| P47127 | Altered inheritance of mitochondrial proteins 34, mitochondrial (S. cerevisiae S288c) | 85354 | AIN24; YBR080C | cell organization and biogenesis | mitochondrial | catalytic activity | 1.807 | 2.039 | 1.13 |
| P38071 | Enoyl (acyl-carrier protein) reductase (NADPH, B-specific), mitochondrial (S. cerevisiae S288c) | 85231 | ETR1; YBR026C | metabolic process | mitochondrial, organelle lumen | catalytic activity, DNA binding, metal ion binding | 4.926 | 5.579 | 1.13 |
| P0C90 | Heat shock protein S5C1, mitochondrial (S. cerevisiae S288c) | 85350 | S5C1; YBR045C | cell organization and biogenesis, metabolic process, regulation of biological process, transport | membrane, mitochondrial, nucleus, organelle lumen | catalytic activity, enzyme regulator activity, nucleotide binding, protein binding | 34.93 | 39.84 | 1.14 |
| Gene/Protein Name | Description | Gene ID | IPF | IPG | IPR | Activity | Location | Functions | Comments |
|------------------|-------------|---------|-----|-----|-----|----------|----------|-----------|----------|
| ATP synthase subunit 5, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YDR298C | 8 | 5189 | 2 | catalytic activity;transport | membrane;mitochondrion | metabolic process;transport | 9.0 | 10.36 | S288c | 1.15 |
| Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YDR556W | 8 | 453 | 6 | catalytic activity;metal ion binding;protein binding | membrane;mitochondrion | metabolic process;transport | 1.873 | 2.162 | S288c | 1.15 |
| Mitochondrial distribution and morphology protein 38 | [OS=Saccharomyces cerevisiae S288c] | YOL027C | 0 | 413 | 5 | catalytic activity;protein binding;import | membrane;mitochondrion | cell organization and biogenesis;cellular homeostasis | 3.732 | 4.309 | S288c | 1.15 |
| ATP-dependent permease MOL2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YPL270Y | 8 | 5858 | 5 | catalytic activity;protein binding | membrane;mitochondrion | response to stimulus;transport | 0.535 | 0.619 | S288c | 1.16 |
| External NADH-ubiquinone oxidoreductase 1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YMR145C | 6 | 5517 | 6 | catalytic activity;protein binding | mitochondrial | metabolic process | 4.367 | 5.078 | S288c | 1.16 |
| Protein FMN15, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YLR077W | 6 | 076 | 5 | catalytic activity;metal ion binding;protein binding | membrane;mitochondrion | cell organization and biogenesis | 0.719 | 0.84 | S288c | 1.17 |
| Isocitrate dehydrogenase (NADP), mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YMR012C | 4 | 0534 | 9 | catalytic activity;metal ion binding;protein binding | mitochondrial | metabolic process | 26.12 | 30.62 | S288c | 1.17 |
| Serine hydroxymethyltransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YBR263C | 5 | 256 | 5 | catalytic activity | mitochondrial | metabolic process | 5.136 | 6.055 | S288c | 1.18 |
| Putative cysteine synthase | [OS=Saccharomyces cerevisiae S288c] | YGL002W | 5 | 289 | 5 | catalytic activity | mitochondrial | metabolic process | 0.978 | 1.154 | S288c | 1.18 |
| Alanine--glyoxylate aminotransferase 1 | [OS=Saccharomyces cerevisiae S288c] | YFL030C | 4 | 051 | 4 | catalytic activity | cytosol;mitochondrion | metabolic process | 1.154 | 1.371 | S288c | 1.19 |
| Enolase 1 | [OS=Saccharomyces cerevisiae S288c] | YGR254W | 9 | 316 | 9 | catalytic activity | mitochondrial | metabolic process;regulation of biological process | 0.711 | 0.848 | S288c | 1.19 |
| Protein AFG1 | [OS=Saccharomyces cerevisiae S288c] | YEL052W | 8 | 665 | 8 | catalytic activity;protein binding | membrane;mitochondrion | cell organization and biogenesis;metabolic process;response to stimulus;transport | 0.711 | 0.848 | S288c | 1.19 |
| Mitochondrial genome maintenance protein MGM101 | [OS=Saccharomyces cerevisiae S288c] | YJR144W | 1 | 360 | 9 | catalytic activity;protein binding | chromosome;mitochondrion | cell organization and biogenesis;metabolic process;response to stimulus;transport | 1.976 | 2.36 | S288c | 1.19 |
| ATP synthase subunit d, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YKL016C | 3 | 385 | 3 | catalytic activity;transport | membrane;mitochondrion | metabolic process;transport | 4.179 | 5.105 | S288c | 1.22 |
| D-altarabinono-1,4-lactone aldolase | [OS=Saccharomyces cerevisiae S288c] | YMR066C | 8 | 488 | 8 | catalytic activity;protein binding | membrane;mitochondrion | metabolic process;response to stimulus | 2.415 | 2.981 | S288c | 1.23 |
| Aldehyde dehydrogenase 5, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YER073C | 4 | 680 | 4 | catalytic activity | mitochondrial;organelle lumen | metabolic process | 1.581 | 1.955 | S288c | 1.24 |
| Altered inheritance of mitochondria protein 9, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YER080W | 3 | 681 | 3 | catalytic activity | mitochondrial | metabolic process | 1.938 | 2.403 | S288c | 1.24 |
| Methyltransferase OMS1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YDR316C | 1 | 191 | 1 | catalytic activity | membrane;mitochondrion | metabolic process | 0.389 | 0.484 | S288c | 1.24 |
| Mitochondrial nuclelease | [OS=Saccharomyces cerevisiae S288c] | YIL208C | 2 | 322 | 2 | catalytic activity;metal ion binding | membrane;mitochondrion;nucleus | cell death;metabolic process | 1.969 | 1.336 | S288c | 1.25 |
| Hexokinase 1 | [OS=Saccharomyces cerevisiae S288c] | YR053C | 4 | 961 | 4 | catalytic activity;protein binding | cytoplasm;cytosol;mitochondrion | cell organization and biogenesis | 0.487 | 0.61 | S288c | 1.25 |
| Nif-like protein, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YKL040C | 6 | 382 | 5 | catalytic activity;protein binding | mitochondrion;organelle lumen | cell organization and biogenesis;cellular homeostasis;metabolic process | 1.371 | 1.738 | S288c | 1.27 |
| Homoaconitase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | YER234W | 0 | 182 | 0 | catalytic activity;metal ion binding | mitochondrion | metabolic process | 0.73 | 0.931 | S288c | 1.28 |
| P47293 | N-terminal acetyltransferase 2 | 85405 | NAT2; YGL147 C | cytoplasm,mitochondrion | metabolic process | 0.73 | 0.931 | 1.28 |
| P66775 | Lon protease homolog, mitochondrial | 85225 | PIM1; YBL022C | cell organization and biogenesis,metabolic process;regulation of biological process | cell death,metabolic process | 0.537 | 0.685 | 1.28 |
| P25179 | Peptidyl-prolyl cis-trans isomerase C, mitochondrial | 85489 | CPR3; YML078 W | mitochondrial,organelle lumen | mitochondrial carrier protein RIM2 | 1.512 | 1.929 | 1.28 |
| P38127 | Mitochondrial carrier protein RIM2 (S. cerevisiae) | 85249 | RIM2; YBR192 W | structural molecule activity;transport activity | mitochondrial | 0.778 | 0.995 | 1.28 |
| Q02811 | ABC1 family protein YPL09C | 85599 | YPL09C | mitochondrial | 0.295 | 0.334 | 1.29 |
| P04840 | Mitochondrial outer membrane protein porin 1 | 85666 | POR1; YNL055C | cytoplasm,membrane,mitochondrion | structural molecule activity | 17.33 | 22.35 | 1.29 |
| P33110 | ATP-dependent permease | 85088 | MOL1; YLR188 W | transport | structural molecule activity | 0.274 | 0.354 | 1.29 |
| P36609 | NADH-cytochrome b5 reductase 2 | 85370 | MCR1; YKL130 W | membrane,mitochondrion | mitochondrial | 13.38 | 17.33 | 1.29 |
| P3598 | Succinyl-CoA ligase (ADP-forming) subunit alpha, mitochondrial | 85431 | LSC1; YOR142 C | cytosol,mitochondrion | 9 | 11.74 | 1.30 |
| P04710 | ADP/ATP carrier protein 1 | 85507 | AAC1; YMR056 C | cytoplasm,membrane,mitochondrion | structural molecule activity | 6.848 | 9 | 1.31 |
| P32454 | Aminopeptidase 2, mitochondrial | 85369 | APE2; YKL157 W | cytoplasm,extracellular,membrane,mitochondrion | catalytic activity;metal ion binding | 1.049 | 1.383 | 1.32 |
| P15424 | ATP-dependent DNA helicase | 85177 | MSS116; YDR194 C | mitochondrial,organelle lumen | catalytic activity;metal ion binding | 0.506 | 0.668 | 1.32 |
| P07256 | Cytochrome b-1 complex subunit 1, mitochondrial | 85223 | CDR2; YBL045C | membrane,mitochondrion | catalytic activity,metal ion binding | 8.183 | 10.86 | 1.33 |
| P16354 | 54S ribosomal protein L40, mitochondrial | 85593 | MRPL40; YPL173 W | mitochondrial,ribosome | protein binding;structural molecule activity | 0.585 | 0.778 | 1.33 |
| P38262 | Protein YML1 | 85518 | YML1; YMR152 W | cytoplasm,endoplasmic reticulum,mitochondrion | catalytic activity;metal ion binding | 0.624 | 0.833 | 1.33 |
| P36521 | 54S ribosomal protein L11, mitochondrial | 85132 | MRPL11; YOL202 W | mitochondrial,ribosome | structural molecule activity | 0.624 | 0.833 | 1.33 |
| P28992 | elongation factor Tu, mitochondrial | 85435 | TUF1; YOR187 W | mitochondrial,ribosome | catalytic activity;metal ion binding | 6.667 | 9 | 1.35 |
| P32939 | 60S ribosomal protein y27 | 85601 | YPT7; YML001 W | cytoplasm,mitochondrion | catalytic activity;metal ion binding | 0.848 | 1.154 | 1.36 |
| P36525 | 54S ribosomal protein L24, mitochondrial | 85623 | MRPL24; YMR193 W | mitochondrial,ribosome | RNA binding;structural molecule activity | 0.848 | 1.154 | 1.36 |
| P319987 | Heat shock protein Ssc3, mitochondrial | 85688 | ECM10; YEL030 W | mitochondrial | nucleotide binding;protein binding | 1.198 | 1.637 | 1.37 |
| Q09591 | Heat shock protein Ssc1, mitochondrial | 85108 | SQS1; YLR369 W | mitochondrial,organelle lumen | nucleotide binding;protein binding | 0.496 | 0.679 | 1.37 |
Q12298 uncharacterized ABC transporter ATP-binding protein YDR061W (S=Saccharomyces cerevisiae S288c) 85163 3 YDR061 W; YDR061 W mitochondrial catalytic activity; nucleotide binding 0.194 0.266 1.37

P51266 Cytochrome c oxidase assembly protein SHY1 (S=Saccharomyces cerevisiae S288c) 85000 9 SHY1; YGR112 W cell organization and biogenesis membrane; mitochondrial protein binding 0.978 1.346 1.38

P32799 Cytochrome c oxidase subunit 6A, mitochondrial (S=Saccharomyces cerevisiae S288c) 85268 4 COX13; YGL194 W cell organization and biogenesis membrane; mitochondrial catalytic activity; enzyme regulator activity; transporter activity 2.162 2.981 1.38

Q05677 ABC1 family member MCP2 (S=Saccharomyces cerevisiae S288c) 85095 5 YLR253 W; MCP2; YLR253 W cell organization and biogenesis membrane; mitochondrial 0.218 0.301 1.38

P21375 Fumarate reductase 2 (S=Saccharomyces cerevisiae S288c) 85351 0 OSM1; YBR051 W metabolic process endoplasmic reticulum; mitochondrial catalytic activity; nucleotide binding 0.25 0.346 1.38

P40666 Protein MRG3-like (S=Saccharomyces cerevisiae S288c) 85372 5 YKL133C W YKL133C W metabolic process membrane; mitochondrial protein binding 0.241 0.334 1.39

P47052 Succinate dehydrogenase [ubiquinone] flavoprotein subunit 2, mitochondrial (S=Saccharomyces cerevisiae S288c) 85340 5 YILD045 W; YILD045 W metabolic process; transport membrane; mitochondrial catalytic activity; nucleotide binding 2.695 3.739 1.39

P34231 Uncharacterized protein YKL187C (S=Saccharomyces cerevisiae S288c) 85864 8 FATS; YKL187C W YKL187C W cell organization and biogenesis; transport membrane; mitochondrial 0.304 0.425 1.40

P36101 Fumarate reductase small subunit, mitochondrial (S=Saccharomyces cerevisiae S288c) 85384 1 TCC02; YKL027 W; YKL027 W metabolic process cytosol; membrane; mitochondrial catalytic activity; nucleotide binding 0.334 0.468 1.40

P47015 Altered inheritance of mitochondria protein 23, mitochondrial (S=Saccharomyces cerevisiae S288c) 85131 0 AIM223; YL131C W metabolic process mitochondrial RNA binding 0.35 0.492 1.41

P53326 Uncharacterized protein YGR266W (S=Saccharomyces cerevisiae S288c) 85318 2 YGR266 W; YGR266 W metabolic process membrane; mitochondrial 0.369 0.52 1.41

P40012 Proteoporphyrinogen oxidase (S=Saccharomyces cerevisiae S288c) 85673 3 HEM14; YER014 W metabolic process membrane; mitochondrial catalytic activity 0.947 1.336 1.41

P52605 Acetolactate synthase small subunit, mitochondrial (S=Saccharomyces cerevisiae S288c) 85034 8 ILV6; YCL009C W metabolic process; regulation of biological process mitochondrial catalytic activity; enzyme regulator activity 1.976 2.793 1.41

P50110 Sorting assembly machinery 37 KDa subunit (S=Saccharomyces cerevisiae S288c) 85058 2 SAM37; YMR060 C cell organization and biogenesis; transport membrane; mitochondrial protein binding 0.389 0.551 1.42

P43617 Uncharacterized mitochondrial carrier YPR052W (S=Saccharomyces cerevisiae S288c) 85060 6 YPR045 W; YPR045 W metabolic process; transport membrane; mitochondrial structural molecule activity; transporter activity 0.413 0.585 1.42

P53800 Inner membrane mitobosome receptor MBA1, mitochondrial (S=Saccharomyces cerevisiae S288c) 85248 3 MBA1; YBR185C W cell organization and biogenesis; regulation of biological process membrane; mitochondrial 0.413 0.585 1.42

P33825 Protein TOM71 (S=Saccharomyces cerevisiae S288c) 85651 7 TOM71; YHR117 W transport membrane; mitochondrial protein binding; transporter activity 0.425 0.604 1.42

P32904 S45 ribosomal protein L6, mitochondrial (S=Saccharomyces cerevisiae S288c) 85655 2 MRP16; YHR147 C cell organization and biogenesis; metabolic process mitochondrion; ribosome RNA binding; structural molecule activity 0.54 0.778 1.44

Q02776 Mitochondrial import inner membrane translocase subunit TIM50 (S=Saccharomyces cerevisiae S288c) 85604 2 TIM50; YPL036 W cell organization and biogenesis; metabolic process; transport membrane; mitochondrial catalytic activity; protein binding; transporter activity 2.197 9 1.45

P37298 Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial (S=Saccharomyces cerevisiae S288c) 85175 8 SDH4; YDR178 W metabolic process; transport membrane; mitochondrial catalytic activity; metal ion binding 1.783 2.594 1.45

P19262 Dihydrolipoamide-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (S=Saccharomyces cerevisiae S288c) 85172 6 KG02; YDR148 C cell organization and biogenesis; metabolic process mitochondrion catalytic activity; protein binding 3.062 4.484 1.46

Q03201 S75 ribosomal protein S10, mitochondrial (S=Saccharomyces cerevisiae S288c) 85161 1 RMS10; YDR041 W cell organization and biogenesis; metabolic process mitochondrion; ribosome structural molecule activity 0.701 1.031 1.47
| Uniprot ID  | Protein Name and Description | Gene Symbol(s) | Organism | KEGG Pathways | Gene Ontology Terms |
|------------|-------------------------------|----------------|----------|---------------|---------------------|
| Q12029     | Probable mitochondrial transport protein Rfs1 | YOR271C       | S. cerevisiae | 5.813         | 0.078               |
| P32332     | Mitochondrial oxaloacetate transport protein | YKL120W       | S. cerevisiae | 5.813         | 0.078               |
| P22686     | Dynamin-like GTPase Msma1, mitochondrial | YDR211C       | S. cerevisiae | 5.813         | 0.078               |
| P28817     | 3-Hydroxyisobutyryl-CoA hydrolase, mitochondrial | YPL222C       | S. cerevisiae | 5.813         | 0.078               |
| P39952     | Mitochondrial inner membrane protein Oxa1 | YMR382C       | S. cerevisiae | 5.813         | 0.078               |
| P11325     | Leucine-tRNA ligase, mitochondrial | YLR154C       | S. cerevisiae | 5.813         | 0.078               |
| P15650     | Protein Cbp3, mitochondrial | YPL215S       | S. cerevisiae | 5.813         | 0.078               |
| P24445     | Single-stranded DNA binding protein Rm1, mitochondrial | YCR228C       | S. cerevisiae | 5.813         | 0.078               |
| P25349     | Flavoprotein-like protein Pcr4 | YCR004C       | S. cerevisiae | 5.813         | 0.078               |
| P5166      | ATP-dependent RNA helicase Mrh4, mitochondrial | YLR069C       | S. cerevisiae | 5.813         | 0.078               |
| P42900     | Sigma-like sequence protein 1, mitochondrial | YLR139C       | S. cerevisiae | 5.813         | 0.078               |
| P70236     | Threonine–tRNA ligase, mitochondrial | YKL194C       | S. cerevisiae | 5.813         | 0.078               |
| P39518     | Long-chain-fatty-acid-CoA ligase 2 | YER015C       | S. cerevisiae | 5.813         | 0.078               |
| P25039     | Elongation factor G, mitochondrial | YLR069C       | S. cerevisiae | 5.813         | 0.078               |
| P38702     | Mitochondrial carrier protein Lus | YHR002W       | S. cerevisiae | 5.813         | 0.078               |
| Q06236     | Mitochondrial inner membrane protein Shm4 | YLR164W       | S. cerevisiae | 5.813         | 0.078               |
| Q38797     | Protein phosphatase 2C homolog 7, mitochondrial | YHR076W       | S. cerevisiae | 5.813         | 0.078               |
| Q15799     | Aspartate–tRNA ligase, mitochondrial | YPL104Y       | S. cerevisiae | 5.813         | 0.078               |
| Q36520     | 5S ribosomal protein L10, mitochondrial | YNL284C       | S. cerevisiae | 5.813         | 0.078               |
| Q08668     | UFD1Gel protein Fmp40 | YPL222C       | S. cerevisiae | 5.813         | 0.078               |
| P18496     | Mitochondrial ATPase complex subunit ATP10 | YLR393W       | S. cerevisiae | 5.813         | 0.078               |
| P27697     | Atp6c kinase Cog8, mitochondrial | YGL119W       | S. cerevisiae | 5.813         | 0.078               |
| Gene ID | Description | Function | Localization | Interaction | P-value |
|--------|-------------|----------|--------------|-------------|---------|
| P40035 | Mitochondrial phosphate carrier protein 2 | cellular homeostasis, metabolic process | membrane, mitochondrial | structural molecule activity, transport activity | 0.835 |
| P468B1 | D-lactate dehydrogenase (cytochrome b) | metabolic process | mitochondrial, organelle lumen | catalytic activity, nucleotide binding, protein binding | 0.682 |
| P05626 | ATP synthase subunit 4 | cell organization and biogenesis, metabolic process | membrane, mitochondrial | catalytic activity, transport activity | 3.084 |
| Q03246 | 37S ribosomal protein S17 | cell differentiation, cell organization and biogenesis, metabolic process | mitochondrial, ribosome | RNA binding, structural molecule activity | 0.389 |
| Q06678 | 54S ribosomal protein L35 | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | structural molecule activity | 0.425 |
| P3111 | Mitochondrial pyruvate carrier 3 | transport | membrane, mitochondrial | transporter activity | 0.488 |
| Q12032 | Altered inheritance of mitochondrial protein 41 | | mitochondrial | catalytic activity | 0.488 |
| P27929 | 37S ribosomal protein N49 | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | RNA binding, structural molecule activity | 0.484 |
| P36117 | 54S ribosomal protein L4 | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | structural molecule activity | 0.52 |
| P72767 | Assembly factor cyb4 | cell organization and biogenesis | membrane, mitochondrial | catalytic activity | 0.52 |
| Q02784 | Monothiol glutaredoxin-5 | cell organization and biogenesis, metabolic process | mitochondrial, organelle lumen | catalytic activity, metal ion binding | 0.668 |
| P06169 | Pyruvate dehydrogenase isoform 1 | cell organization and biogenesis, regulation of biological process | cytoplasm, cytosol, nucleus | catalytic activity, metal ion binding | 1.043 |
| P38771 | Ribosome-recycling factor | cell organization and biogenesis, metabolic process | mitochondrial | RNA binding | 0.719 |
| Q0892 | MIOREX complex component 2 | cell organization and biogenesis, metabolic process | mitochondrial | catalytic activity | 0.778 |
| Q12233 | ATP synthase subunit g | cell organization and biogenesis, metabolic process | membrane, mitochondrial | catalytic activity, transport activity | 0.778 |
| P81449 | ATP synthase subunit e | cell organization and biogenesis, metabolic process | membrane, mitochondrial | catalytic activity, structural molecule activity, transport activity | 0.778 |
| P40098 | Uncharacterized mitochondrial membrane protein FMP10 | | membrane, mitochondrial | transport activity | 1.336 |
| Q06VH5 | MIOCS complex subunit Mci10 | cell organization and biogenesis | membrane, mitochondrial | catalytic activity | 0.931 |
| P36516 | 54S ribosomal protein L3 | cell organization and biogenesis, metabolic process | mitochondrial, nucleus, ribosome | catalytic activity, RNA binding, structural molecule activity | 0.269 |
| P01028 | Cytochrome b1 complex subunit 7 | cell organization and biogenesis, metabolic process | membrane, mitochondrial | catalytic activity, transport activity | 3.642 |
| P00427 | Cytochrome c oxidase subunit 6 | cell organization and biogenesis, metabolic process | membrane, mitochondrial | catalytic activity, transport activity | 1.154 |
| P12686 | 37S ribosomal protein MRP13 | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | structural molecule activity | 0.413 |
| Q01574 | acetyl-coenzyme A synthetase 1 (OS=Saccharomyces cerevisiae S288c) | 85124 | 5 | ACS1; YAL054C | cell organization and biogenesis;metabolic process | cytoplasm;cytosol;endoplasmic reticulum;mitochondrion;nucleus | catalytic activity;nucleotide binding | 1.482 | 2.793 | 1.88 |
| Q2289 | mitochondrial carnitine carrier (OS=Saccharomyces cerevisiae S288c) | 85426 | 7 | CRC1; YOR100C | metabolic process;transport | membrane;mitochondrion | structural molecule activity;transport activity | 0.73 | 1.404 | 1.92 |
| Q30104 | Meiotic sister chromatid recombination protein 1 (OS=Saccharomyces cerevisiae S288c) | 85491 | 1 | MSCI; YML128C | metabolic process | endoplasmic reticulum;membrane;mitochondrion | | 1.712 | 3.299 | 1.93 |
| Q2950 | 37S ribosomal protein MRPS1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85598 | 5 | MRPS1; YPL118W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.407 | 0.817 | 2.01 |
| P40008 | Protein MIPS2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85672 | 1 | MIPS2; YER004W | | endoplasmic reticulum;membrane;mitochondrion | catalytic activity | 1.054 | 2.162 | 2.05 |
| P35170 | [Pyruvate dehydrogenase (acetyl-transferring) kinase 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85282 | 1 | PEK2; YGL059W | metabolic process;regulation of biological process | mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | 0.086 | 0.179 | 2.08 |
| Q06510 | Lysophosphatidylcholine acyltransferase (OS=Saccharomyces cerevisiae S288c) | 85626 | 2 | TA2; YPR140W | cell organization and biogenesis;metabolic process | membrane;mitochondrion | catalytic activity | 0.093 | 0.194 | 2.09 |
| P8809 | cytochrome c mitochondrial import factor CYC2 (OS=Saccharomyces cerevisiae S288c) | 85420 | 2 | CYC2; YOR337W | cell organization and biogenesis;metabolic process | membrane;mitochondrion | catalytic activity | 0.093 | 0.194 | 2.09 |
| P41911 | Glycerol-3-phosphate dehydrogenase (NADP+)-dependent (OS=Saccharomyces cerevisiae S288c) | 85409 | 5 | GPDe; YOL059W | metabolic process | cytoplasm;cytosol;mitochondrion | catalytic activity;nucleotide binding;protein binding | 0.089 | 0.186 | 2.09 |
| P35736 | Uncharacterised protein YNR040W (OS=Saccharomyces cerevisiae S288c) | 85577 | 6 | YNR040W; YNR040Y | | mitochondrion | | 0.116 | 0.245 | 2.11 |
| P36528 | 54S ribosomal protein L17, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85546 | 9 | MRPL17; YNL252C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.11 | 0.233 | 2.12 |
| P23821 | Ribosomal protein VAR1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85458 | 6 | VAR1; Q0140 | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.11 | 0.233 | 2.12 |
| P54857 | Ispe 2 (OS=Saccharomyces cerevisiae S288c) | 85162 | 8 | TGL2; YDR008C | metabolic process;transport | mitochondrion | catalytic activity | 0.11 | 0.233 | 2.12 |
| P39722 | Mitochondrial Rho GTPase 1 (OS=Saccharomyces cerevisiae S288c) | 85124 | 9 | GEM1; YAL048C | cell organization and biogenesis;regulation of biological process;response to stimulus;transport | membrane;mitochondrion | catalytic activity;metal ion binding;nucleotide binding | 0.122 | 0.259 | 2.12 |
| P36139 | protein PET10 (OS=Saccharomyces cerevisiae S288c) | 85392 | 0 | PET10; YKR046C | metabolic process | membrane | catalytic activity | 0.122 | 0.259 | 2.12 |
| P90201 | fructose-1,6-bisphosphatase (OS=Saccharomyces cerevisiae S288c) | 85109 | 2 | FBP1; YLR377C | metabolic process | cytosol | catalytic activity;metal ion binding | 0.129 | 0.274 | 2.12 |
| P32570 | tRNA methyltransferase 1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85437 | 6 | MRME1; YOR201C | metabolic process | mitochondrion | catalytic activity;RNA binding | 0.129 | 0.274 | 2.12 |
| P35982 | Isocitrate dehydrogenase (NADP+) (OS=Saccharomyces cerevisiae S288c) | 85572 | 3 | IDP3; YNL009W | metabolic process | cytoplasm;mitochondrion | catalytic activity;metal ion binding;nucleotide binding | 1.371 | 2.924 | 2.13 |
| P38323 | ATP-dependent chaperone, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85252 | 8 | MCK1; YBR227C | metabolic process | membrane;mitochondrion;organelle lumen | catalytic activity;nucleotide binding | 0.145 | 0.311 | 2.14 |
| P38816 | thioredoxin reductase 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 85650 | 6 | TRR2; YHR106W | cellular homeostasis;metabolic process;regulation of biological process;response to stimulus | cytoplasm;mitochondrion | antioxidant activity;catalytic activity | 0.136 | 0.292 | 2.15 |
| Q06830 | Mitochondrial homologous recombination protein 1 (OS=Saccharomyces cerevisiae S288c) | 85189 | 0 | MHR1; YDR296W | cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus | mitochondrion;nucleus | catalytic activity;DNA binding;structural molecule activity | 0.166 | 0.359 | 2.16 |
| P70560 | Cardiolipin synthase (CMP-forming) (OS=Saccharomyces cerevisiae S288c) | 85141 | 3 | CRD1; YOL142C | cell organization and biogenesis;cellular homeostasis;metabolic process | membrane;mitochondrion | catalytic activity | 0.166 | 0.359 | 2.16 |
| P40086 | Cytochrome c oxidase assembly protein Cox15 (OS=Saccharomyces cerevisiae S288c) | 85688 | 4 | COX15; YER141W | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;transport activity | 0.532 | 1.154 | 2.17 |
Supplemental Table S9. The relative concentrations of proteins in mitochondria purified from ups1Δ cells cultured with or without LCA. Mitochondria were purified from ups1Δ cells recovered on day 7 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emP Al ups1 | emP Al ups1 + LCA | Ratio ups1 + LCA / ups1 |
|-----------|-------------|---------------|---------|--------------------|-------------------|------------------|-------------|------------------|--------------------------|
| Q12374    | Nuclear control of ATPase protein 2 | 83627        | NCA2    | metabolic process | membrane; mitochondrion | 1.15          | 0.066         | 0.06         |
| P50088    | Stationary phase gene 1 protein | 85315        | YGR231G | endoplasmic reticulum;membrane;mitochondrion | 1.15          | 0.066         | 0.06         |
| P00128    | Cytochrome b-c1 complex subunit 7 | 85214        | YOR154C | cell organization and biogenesis;transport | membrane;mitochondrion | 15.6         | 1.154         | 0.07         |
| P37298    | Succinate dehydrogenase (ubiquinone) cytochrome b small subunit, mitochondrial | 85175        | YOR181W | metabolic process;transport | membrane;mitochondrion | catalytic activity | 9           | 0.668         | 1.154         |
| P16547    | Mitochondrial outer membrane protein OMA4 | 85467        | YLJ136W | membrane;mitochondrion | 208          | 189.5        | 0.09         |
| P18239    | ADP:ATP carrier protein 2 | 85225        | YLR030C | structure;membrane;mitochondrion | mitochondrion | 591          | 64.79        | 0.11         |
| P39592    | Mitochondrial inner membrane protein OXA1 | 85371        | YLR154C | metabolic process | membrane;mitochondrion | catalytic activity | 1.27         | 1.154         | 0.13         |
| P12687    | S45 ribosomal protein L2, mitochondrial | 85572        | MRPL7F  | cell organization and biogenesis;transport | mitochondrion;ribosome | catalytic activity | 2.65         | 0.334         | 0.13         |
| P39726    | Glycine cleavage system H protein, mitochondrial | 85125        | GCV3    | metabolic process | mitochondrion | 20.5         | 2.594        | 0.13         |
| P33421    | Succinate dehydrogenase (ubiquinone) cytochrome b small subunit, mitochondrial | 85371        | YLR141W | cell organization and biogenesis;transport | membrane;mitochondrion | catalytic activity | 1.27         | 0.179         | 0.14         |
| P32897    | Mitochondrial import inner membrane translocase subunit tim23 | 85575        | TIM23   | membrane;mitochondrion | transport | protein binding;transporter activity | 4.01         | 0.585         | 0.15         |
| P32340    | Rotone- insensitive NADH-ubiquinone oxidoreductase, mitochondrial | 85491        | ND1; YML120C | metabolic process;regulation of biological process | membrane;mitochondrion;organellar lumen | catalytic activity | 61.1       | 0.11         | 0.15         |
| P00424    | Cytochrome c oxidase polypeptide 5A, mitochondrial | 85567        | COX5A,YNL022W | metabolic process | membrane;mitochondrion | catalytic activity | 3.32       | 0.17         | 0.16         |
| Q12165    | ATP synthase subunit delta, mitochondrial | 85156        | ATP16,YOL043W | metabolic process;transport | membrane;mitochondrion | catalytic activity | 4.62       | 0.778         | 0.17         |
| P07251    | ATP synthase subunit alpha, mitochondrial | 85217        | ATP1,YOL099W | metabolic process;transport | cytosol;membrane;mitochondrion | catalytic activity;transporter activity | 120.       | 20.54        | 0.17         |
| P36526    | S45 ribosomal protein L27, mitochondrial | 85328        | MRPL12F 7 | metabolic process;regulation of biological process | mitochondrion;ribosome | structural molecule activity | 1.51         | 0.259         | 0.17         |
| P27697    | Alyolic kinase COQ8, mitochondrial | 85275        | COQ8   | metabolic process | membrane;mitochondrion;organellar lumen | catalytic activity | 0.36       | 0.064         | 0.18         |
| P46367    | Potassium-activated aldehyde dehydrogenase, mitochondrial | 85435        | ALD4,YOR137W | metabolic process | mitochondrion;organellar lumen | catalytic activity | 219.       | 38.81        | 1.15         |
| P32316    | acetyl-CoA dehydrogenase | 85326        | ACH1,YLR031W | metabolic process | cytoplasm;cytosol;mitochondrion | catalytic activity | 99          | 17.73        | 0.18         |
| P33311    | Mitochondrial pyruvate carrier 3 | 85315        | YFL023W | metabolic process | membrane;mitochondrion | transport activity | 1.15        | 0.212         | 0.18         |
| P20967    | 2-oxoglutarate dehydrogenase, mitochondrial | 85468        | KGDL   | metabolic process | cytosol;mitochondrion;organellar lumen | catalytic activity | 55.8       | 10.39        | 0.19         |
| Q04172 | Sensitive to high expression protein 5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85200 2 | SHE9; YDR39 2W | cell organization and biogenesis | membrane/mitochondrion | 0.26 9 | 0.083 | 0.31 |
| P25605 | Acetolactate synthase small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85034 8 | ILV6; YCL009 C | metabolic process, regulation of biological process | mitochrondrion | catalytic activity; enzyme regulator activity | 2.793 3 | 0.31 |
| P33416 | Heat shock protein 78, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85384 5 | HSP78; YDR25 8C | cell organization and biogenesis, metabolic process, regulation of biological process, response to stimulus | mitochrondrion; organelle lumen | catalytic activity; nucleotide binding; protein binding | 3.042 4 | 0.31 |
| P00447 | Superoxide dismutase [Mn], mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85639 9 | SOD2; YHR00 8C | metabolic process, response to stimulus | mitochrondrion; organelle lumen | antioxidant activity; catalytic activity; metal ion binding | 1.894 7 | 0.31 |
| P36060 | NADH-cytochrome b reductase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85370 7 | MCR3; YNL150 W | metabolic process | membrane/mitochondrion | catalytic activity; protein binding | 36.9 27 | 3 | 0.32 |
| P50945 | MICOS complex subunit MIC27, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85662 3 | AIM37; MIC27; YNL100 C | cell organization and biogenesis | membrane/mitochondrion | 0.96 8 | 0.311 | 0.32 |
| P53220 | Mitochondrial import inner membrane translocase subunit TIM21, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85292 1 | TIM21; YGR03 3C | cell organization and biogenesis, transport | membrane/mitochondrion | protein binding | 0.96 8 | 0.311 | 0.32 |
| P40495 | Homoiocitrate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85471 4 | LYS12; YFL04 C | metabolic process | mitochrondrion | catalytic activity; metal ion binding; nucleotide binding | 3.217 3 | 0.32 |
| P08179 | Mitochondrial distribution and morphology protein 3B, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85413 0 | MDM3 8; YOL027 C | cell organization and biogenesis, cell cycle, homeostasis, regulation of biological process, transport | membrane/mitochondrion | 7.91 3 | 2.548 | 0.32 |
| Q03430 | 37S ribosomal protein RSM28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 83210 5 | RSM28; YDR49 4W | cell organization and biogenesis, metabolic process | mitochrondrion; ribosome | structural molecule activity | 2.00 8 | 0.65 | 0.32 |
| Q03711 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85370 9 | SDH1; YNL148 C | metabolic process; transport | membrane/mitochondrion | catalytic activity; nucleotide binding; protein binding | 16.5 35 | 5.381 | 0.33 |
| P36151 | Uncharacterized protein YKR070W, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85394 4 | YKR070 W; YKR070 W | metabolic process | mitochrondrion | 1.33 6 | 0.438 | 0.33 |
| P38523 | GrpE protein homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85440 7 | ME1; YOR23 2W | metabolic process, regulation of biological process, transport | membrane/mitochondrion; organelle lumen | enzyme regulator activity; nucleotide binding; protein binding | 0.83 3 | 0.274 | 0.33 |
| P36013 | NAD-dependent malic enzyme, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85383 9 | MAE1; YOL29 C | metabolic process | mitochrondrion; organelle lumen | catalytic activity; metal ion binding; nucleotide binding | 3.73 2 | 1.239 | 0.33 |
| P16387 | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85692 5 | PDA1; YER178 W | cell growth, metabolic process | mitochrondrion; organelle lumen | catalytic activity | 31.8 19 | 10.60 2 | 0.33 |
| P06208-1 | 2-isopropylmalate synthase [OS=Saccharomyces cerevisiae S288c] | 85661 9 | LEU4; YNL104 C | metabolic process | cytoplasm/mitochrondrion | catalytic activity; protein binding | 19.3 09 | 6.444 | 0.33 |
| P36520 | S45 ribosomal protein L10, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85543 6 | MRPL1 6; YNL284 C | cell organization and biogenesis, metabolic process | mitochrondrion; ribosome | structural molecule activity | 0.73 2 | 0.245 | 0.34 |
| P04037 | cytochrome c oxidase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85268 8 | CYD4; YGL187 C | cell organization and biogenesis, metabolic process, transport | membrane/mitochondrion | catalytic activity; metal ion binding; transporter activity | 42.2 88 | 14.19 9 | 0.34 |
| P51998 | S45 ribosomal protein yw6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85498 3 | YML6; YML02 2C | cell organization and biogenesis, metabolic process | mitochrondrion; ribosome | RNA binding; structural molecule activity | 1.15 4 | 0.389 | 0.34 |
| P32902 | 37S ribosomal protein MRP4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85638 4 | MRP4; YHL004 W | cell organization and biogenesis, metabolic process | mitochrondrion; ribosome | structural molecule activity | 1.37 1 | 0.468 | 0.34 |
| P38891 | Branched-chain amino-acid aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85651 6 | BAT1; YHR20 8W | metabolic process, regulation of biological process, response to stimulus | mitochrondrion; organelle lumen | catalytic activity | 17.7 38 | 6.305 | 0.36 |
| P00427 | Cytochrome c oxidase subunit 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85644 8 | COM6; YHR05 1W | metabolic process; transport | membrane/mitochondrion | catalytic activity; metal ion binding; transporter activity | 2.16 2 | 0.778 | 0.36 |
| P81449 | ATP synthase subunit e, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85192 2 | TIM11; YDR32 2C-A | cell organization and biogenesis, metabolic process, transport | membrane/mitochondrion | catalytic activity; structural molecule activity; transporter activity | 2.16 2 | 0.778 | 0.36 |
| P40098 | uncharacterized mitochondrial membrane protein FMP10, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85693 1 | FMP10; YER182 W | membrane/mitochondrion | | 4.45 6 | 1.637 | 0.37 |
| P38077 | ATP synthase subunit gamma, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85323 7 | ATP3; YBR029 W | metabolic process; transport | membrane/mitochondrion | catalytic activity; transporter activity | 27.4 8 | 10.10 3 | 0.37 |
P19516  Cytochrome c oxidase assembly protein COX11, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85597 1 COX11, YPL3132 W cell organization and biogenesis;metabolic process membrane/mitochondrion;ribosome metal ion binding 0.62 4 0.274 0.44

Q01163  37S ribosomal protein S33, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85274 8 RIM23, YGL129 C cell organization and biogenesis;metabolic process mitochondrial;ribosome catalytic activity;nucleotide binding;RNA binding;structural molecule activity 1.70 7 0.751 0.44

P53969  Sorting assembly machinery 50 kDa subunit [OS=Saccharomyces cerevisiae S288c] 85570 5 SAM50, YNL206 W cell organization and biogenesis;transport membrane/mitochondrion protein binding;transporter activity 0.61 0.269 0.44

P43617  Uncharacterized mitochondrial carrier YFR045W [OS=Saccharomyces cerevisiae S288c] 85060 6 YFR045 W; YFR045 V mitochondrial process;transport metabolic process;transport membrane/mitochondrion structural molecule activity;transporter activity 0.58 5 0.259 0.44

P05626  ATP synthase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85602 7 ATP4, YPL078 C cell organization and biogenesis;metabolic process;transport membrane/mitochondrion catalytic activity;transporter activity 5.81 3 2.594 0.45

P23641  mitochondrial phosphate carrier protein [OS=Saccharomyces cerevisiae S288c] 85354 0 MR31, YJR777 C metabolic process;transport membrane/mitochondrion protein binding;structural molecule activity;transporter activity 30.6 23 13.67 0.45

P17695  Glutaredoxin-2, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85212 4 GRX2, YDR51 3W cellular homeostasis;metabolic process cytoplasm;cytosol;mitochondrion;nucl antioxidant activity;catalytic activity 0.52 0.233 0.45

P43594  MICS complex subunit MIC19 [OS=Saccharomyces cerevisiae S288c] 85056 3 AIM13, MIC19, YFR011 C cell organization and biogenesis cytoplasm;membrane;mitochondrion catalytic activity;nucleotide binding 1.98 8 0.9 0.45

P08440  G-1,3-tetrathiolic oxidoreductase synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85237 8 MRS1, YBR084 W metabolic process cytosol;mitochondrion catalytic activity;nucleotide binding 0.46 8 0.212 0.45

P40165  NAD(P)-hydride epimerase [OS=Saccharomyces cerevisiae S288c] 85552 1 YNL200 C; YNL200 W metabolic process cytoplasm/mitochondrion catalytic activity;metal ion binding;nucleotide binding 0.46 8 0.212 0.45

Q0820D  Iron sulfur cluster assembly protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85596 8 ISU1, YLP135 W cell organization and biogenesis;cellular homeostasis;metabolic process cytoplasm/mitochondrion;organelle lumen catalytic activity;metal ion binding;protein binding 19.6 91 9 0.46

P28834  Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85569 1 IDH1, YNL037 C metabolic process;transport cytosol;mitochondrion;organelle lumen catalytic activity;metal ion binding;nucleotide binding;protein binding;RNA binding 19.6 91 9 0.46

P38169  Kyurenine 3-monooxygenase [OS=Saccharomyces cerevisiae S288c] 85217 9 BNA4, YBL098 W metabolic process membrane/mitochondrion catalytic activity;nucleotide binding 0.37 4 0.172 0.46

P25348  S45 ribosomal protein L32, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85035 9 MRPL3 2, YCR003 W cell organization and biogenesis;metabolic process membrane/mitochondrion;ribosome RNA binding;structural molecule activity 0.38 9 0.179 0.46

P53212  Probable transcriptional regulatory protein HAH1 [OS=Saccharomyces cerevisiae S288c] 85290 4 YGR02 1W; YGR02 1W; YGR02 1W mitochondrial process 0.35 9 0.166 0.46

P07342  Acetolactate synthase catalytic subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85513 5 ILV2, YMR10 8W metabolic process mitochondrial catalytic activity;metal ion binding;nucleotide binding 8.42 7 3.924 0.47

Q12298  Uncharacterized ABC transporter ATP-binding protein YDR061W [OS=Saccharomyces cerevisiae S288c] 85163 3 YDR06 1W; YDR06 1W mitochondrial process catalytic activity;nucleotide binding 0.26 6 0.125 0.47

P40416  Iron-sulfur clusters transporter ATPM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85334 7 YMR330 1C cellular homeostasis;metabolic process;transport membrane/mitochondrion catalytic activity;nucleotide binding;transporter activity 0.28 3 0.133 0.47

P49954  Probable hydroxylase NT3 [OS=Saccharomyces cerevisiae S288c] 85106 5 NT3, YLR351 C metabolic process cytoplasm/mitochondrion catalytic activity 0.27 4 0.129 0.47

P14908  Mitochondrial transcription factor 1 [OS=Saccharomyces cerevisiae S288c] 85526 8 MTF1, YMR22 8W metabolic process;regulation of biological process mitochondrial;organelle lumen catalytic activity;DNA binding;RNA binding 0.25 9 0.122 0.47

P10834  protein PET54 [OS=Saccharomyces cerevisiae S288c] 85313 7 PET54, YGR22 2W metabolic process;regulation of biological process membrane/mitochondrion;organelle lumen structural molecule activity 0.23 3 0.11 0.47

P36528  S45 ribosomal protein L17, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85464 9 MRPL1 7; YNL252 C cell organization and biogenesis;metabolic process mitochondrial;ribosome structural molecule activity 0.23 3 0.11 0.47

P11325  Leucine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85109 8 NAM2, YLR382 C cell organization and biogenesis;metabolic process;regulation of biological process cytosol;mitochondrion;organelle lumen catalytic activity;protein binding;RNA binding 0.25 4 0.12 0.47
Q12166 2-isopropylmalate synthase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85427 5 LEU6; YDR10 YFL055 4C metabolic process mitochondrion catalytic activity;protein binding 4.36 7 2.065 0.47
P53163 S45 ribosomal protein L12, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85281 1 MNP1; YGL208 W metabolic process;organization and biogenesis;metabolic process mitochondrion;ribosome RNA binding;structural molecule activity 1.84 8 0.874 0.47
Q06143 mitochondrial dicarboxylate transporter [OS=Saccharomyces cerevisiae S288c] 85306 3 DCL1; YLR348 C metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 1.15 4 0.551 0.48
Q12201 Mitochondrial 2-methyleneisocitrate lyase [OS=Saccharomyces cerevisiae S288c] 85611 4 IC12; YPR006 C metabolic process mitochondrion;organelle lumen catalytic activity 4.13 5 1.976 0.48
Q08970 Mitochondrial metal transporter 2 [OS=Saccharomyces cerevisiae S288c] 85587 7 MMT2; YPL224 C cellular homeostasis;regulation of biological process;response to stimulus;transport membrane;mitochondrion transporter activity 0.18 6 0.089 0.48
P32839 Mitochondrial chaperone BCS1 [OS=Saccharomyces cerevisiae S288c] 85398 1 BCS1; YOR337 SC cell organization and biogenesis;metabolic process;response to stimulus;transport cytosol;membrane;mitochondrion catalytic activity;nucleotide binding;transporter activity 0.19 4 0.093 0.48
Q06510 Lyosphosphatidylcholine acyltransferase [OS=Saccharomyces cerevisiae S288c] 85626 2 TAZ1; YPR140 W cell organization and biogenesis;metabolic process mitochondrion catalytic activity 0.19 4 0.093 0.48
P07236 Ileucine tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85364 0 MST1; YNL194 C metabolic process cytoplasm;mitochondrion;organelle lumen catalytic activity;protein binding;RNA binding 0.15 0.072 0.48
P42940 Probable electron transfer flavoprotein subunit beta [OS=Saccharomyces cerevisiae S288c] 85312 1 CIR1; YGR20 TC metabolic process;transport mitochondrion;organelle lumen catalytic activity 5.49 4 2.652 0.48
P00401 Cytochrome c oxidase subunit 1 [OS=Saccharomyces cerevisiae S288c] 85459 8 COX11; Q0045 C metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding;transporter activity 1.61 0.778 0.48
P07256 Cytochrome c1 complex subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85223 5 COR1; YBL045 W metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding;transporter activity 24.5 51 11.91 5 0.49
Q07349 MIOX complex component 9 [OS=Saccharomyces cerevisiae S288c] 85153 5 YUL027 C; MRX9; YFL027 C endoplasmic reticulum;membrane;mitochondrion 1.91 3 0.931 0.49
P21801 Succinate dehydrogenase [ubiquinone iron-sulfur] subunits, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85068 5 SDH2; YL041 C metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding 24.8 0.09 12.11 1 0.49
P32445 Single-stranded DNA-binding protein RIM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85039 1 RIM1; YCR028 C metabolic process;organization and biogenesis;metabolic process;regulation of biological process mitochondrial DNA binding 3.64 2 1.783 0.49
P08417 Fumarate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85386 6 FUM1; YFL302 W cell organization and biogenesis;metabolic process cytoplasm;cytosol;mitochondrion;organelle lumen catalytic activity 12.7 38 6.279 0.49
P48526 Isoleucine tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85606 7 ISM1; YPL040 C cell organization and biogenesis;metabolic process;regulation of biological process cytoplasm;cytosol;mitochondrion;organelle lumen catalytic activity;protein binding 0.08 1 0.04 0.49
P53326 Uncharacterized protein YGR266W [OS=Saccharomyces cerevisiae S288c] 85318 2 YGR26 6W; YGR26 6W cell organization and biogenesis;metabolic process;regulation of biological process response to stimulus mitochondrion;organelle lumen enzyme regulator activity;protein binding 3.32 9 1.656 0.50
P35191 Dna1 Homolog 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85053 1 MO1; YFL016 C cell organization and biogenesis;metabolic process;regulation of biological process response to stimulus mitochondrion;organelle lumen enzyme regulator activity;protein binding;RNA binding 3.32 9 0.496 0.50
P00175 Cytochrome b2, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85495 0 CYB2; YML05 4C metabolic process;transport cytosol;membrane;mitochondrion;organelle lumen catalytic activity;metal ion binding;protein binding 0.99 5 0.496 0.50
P15424 ATP-dependent RNA helicase MSS116, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85177 6 MSS11 6; YOR19 4C metabolic process;organization and biogenesis;metabolic process mitochondrion;organelle lumen catalytic activity;nucleotide binding 1.51 2 0.756 0.50
P40047 Aldehyde dehydrogenase 5, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85680 4 ALO5; YER073 W metabolic process mitochondrion;organelle lumen catalytic activity 3.14 6 1.581 0.50
P54783 D-arabinono-1,4-lactone oxidase [OS=Saccharomyces cerevisiae S288c] 85488 8 ALD1; YML08 6C metabolic process;response to stimulus mitochondrion;organelle lumen catalytic activity 5.31 6 2.687 0.51
P08466 mitochondrial nuclease [OS=Saccharomyces cerevisiae S288c] 85322 2 NUC1; YL028 C cell death;metabolic process membrane;mitochondrion;nucleus catalytic activity;metal ion binding 1.63 7 0.833 0.51
Q04548 Fatty aldehyde dehydrogenase HDF1 [OS=Saccharomyces cerevisiae S288c] 85513 7 HDF1; YMR11 OC metabolic process cytosol;membrane;mitochondrion;organelle lumen catalytic activity 4.50 5 2.3 0.51
P32473 Pyruvate dehydrogenase E1 component subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85252 2 PDB1; YBR221 C metabolic process mitochondrion;organelle lumen catalytic activity 13.3 84 6.848 0.51
| Strain          | Genes                                                                 | Classifications                                                                 | Gene ID  |
|----------------|----------------------------------------------------------------------|---------------------------------------------------------------------------------|----------|
| **P.04710**    | ADP-ATP carrier protein 1; mitochondrial outer membrane protein YPR088C | structural molecule activity; transporter activity                              | 85507    |
|                |                                                                       |                                                                                 | AACL1;   |
|                |                                                                       |                                                                                 | YMR085   |
|                |                                                                       |                                                                                 | C       |
| **Q.06089**    | Uncharacterized mitochondrial outer membrane protein YPR088C          | membrane; mitochondrion                                                          | 85621    |
|                |                                                                       |                                                                                 | YPRO088  |
|                |                                                                       |                                                                                 | C        |
| **Q.08822**    | Probable electron transfer flavoprotein-ubiquinone oxidoreductase      | metabolic process; transport                                                    | 85453    |
|                |                                                                       |                                                                                 | CR2;     |
|                |                                                                       |                                                                                 | YOR35    |
|                |                                                                       |                                                                                 | 6W       |
| **P.39522**    | Dihydropyrimidine dehydrogenase; mitochondrial inner mitochondrial     | metabolic process; mitochondrial activity; protein binding                      | 85347    |
|                |                                                                       |                                                                                 | ILV3;    |
|                |                                                                       |                                                                                 | YJR16    |
|                |                                                                       |                                                                                 | C        |
| **P.39523**    | Dihydropyrimidine dehydrogenase; mitochondrial inner mitochondrial     | cell organization and biogenesis; metabolic process                            | 85172    |
|                |                                                                       |                                                                                 | KG02;    |
|                |                                                                       |                                                                                 | YDR14    |
|                |                                                                       |                                                                                 | 8C       |
| **P.43635**    | Citrate synthase 3, mitochondrial                                     | mitochondrial activity; catalytic activity                                       | 85610    |
|                |                                                                       |                                                                                 | CIT3;    |
|                |                                                                       |                                                                                 | YP0001   |
|                |                                                                       |                                                                                 | W        |
| **P.00445**    | Superoxide dismutase (Cu-Zn); mitochondrial                           | cell organization and biogenesis; cellular homeostasis; metabolic process       | 85356    |
|                |                                                                       |                                                                                 | SOD1;    |
|                |                                                                       |                                                                                 | YMR104   |
|                |                                                                       |                                                                                 | C        |
| **P.25719**    | Peptidyl-prolyl cis-trans isomerase C, mitochondrial                   | cell death; mitochondrial activity; organelle lumen                             | 85489    |
|                |                                                                       |                                                                                 | CPR1;    |
|                |                                                                       |                                                                                 | YML07    |
|                |                                                                       |                                                                                 | W        |
| **P.26241**    | NADH dehydrogenase (NADH) subunit 2, mitochondrial                    | mitochondrial activity; organelle lumen                                          | 85430    |
|                |                                                                       |                                                                                 | IP2;     |
|                |                                                                       |                                                                                 | YOR13    |
|                |                                                                       |                                                                                 | 6W       |
| **P.37293**    | N-terminal acetyltransferase 2; mitochondrial                         | cytoplasm; mitochondrial activity; catalytic activity                           | 85305    |
|                |                                                                       |                                                                                 | NAT1;    |
|                |                                                                       |                                                                                 | YGR034   |
|                |                                                                       |                                                                                 | 7C       |
| **P.38332**    | Mitochondrial oxalacetate transport protein; mitochondrial             | structural molecule activity; transporter activity                              | 85373    |
|                |                                                                       |                                                                                 | OAC1;    |
|                |                                                                       |                                                                                 | YLL210   |
|                |                                                                       |                                                                                 | W        |
| **P.43616**    | Cys-Gly metalloendopeptidase dag1                                      | cytoplasm; mitochondrial activity; ribosome                                      | 85600    |
|                |                                                                       |                                                                                 | DGUG1;   |
|                |                                                                       |                                                                                 | YPR044   |
|                |                                                                       |                                                                                 | C        |
| **Q.07500**    | External NADH-ubiquinone oxoreductase 2, mitochondrial                 | mitochondrial activity; catalytic activity; nucleotide binding                  | 85147    |
|                |                                                                       |                                                                                 | NDE2;    |
|                |                                                                       |                                                                                 | YLR068   |
|                |                                                                       |                                                                                 | W        |
| **P.53268**    | Cytochrome oxidase assembly protein SHY1 (OS=Saccharomyces cerevisiae| cell organization and biogenesis; mitochondrial activity; protein binding       | 85300    |
|                |                                                                       |                                                                                 | SHY1;    |
|                |                                                                       |                                                                                 | YGR11    |
|                |                                                                       |                                                                                 | 11       |
| **Q.96069**    | MICO5 complex subunit Mic10; mitochondrial                            | cell organization and biogenesis; mitochondrial activity; protein binding       | 85030    |
|                |                                                                       |                                                                                 | MO51;    |
|                |                                                                       |                                                                                 | MICO10;  |
|                |                                                                       |                                                                                 | YCL057   |
|                |                                                                       |                                                                                 | C-A      |
| **P.19955**    | 37S ribosomal protein YMR31, mitochondrial                            | mitochondrial activity; ribosome; catalytic activity; protein binding; structural| 85061    |
|                |                                                                       |                                                                                 | YMR31    |
|                |                                                                       |                                                                                 | YPR049   |
|                |                                                                       |                                                                                 | W        |
| **P.38825**    | Protein TOM71 (OS=Saccharomyces cerevisiae)                            | cell organization and biogenesis; metabolic process                            | 85651    |
|                |                                                                       |                                                                                 | TOM71    |
|                |                                                                       |                                                                                 | YHR17    |
|                |                                                                       |                                                                                 | 7W       |
| **P.38652**    | S45 ribosomal protein L24, mitochondrial                              | mitochondrial activity; ribosome; RNA binding; structural molecule activity      | 85223    |
|                |                                                                       |                                                                                 | MRP12    |
|                |                                                                       |                                                                                 | 4;       |
|                |                                                                       |                                                                                 | YMR19    |
|                |                                                                       |                                                                                 | 16       |
| **P.43644**    | Mitochondrial peculiar membrane protein 1 (OS=Saccharomyces cerevisiae| mitochondrial activity; protein binding; structural molecule activity            | 85337    |
|                |                                                                       |                                                                                 | MPM1;    |
|                |                                                                       |                                                                                 | YL066    |
|                |                                                                       |                                                                                 | C        |
| **P.38647**    | Presequence translocated-associated motor subunit pam17, mitochondrial| mitochondrial activity; ribosome; RNA binding; structural molecule activity      | 85393    |
|                |                                                                       |                                                                                 | PAM17    |
|                |                                                                       |                                                                                 | YKR065   |
|                |                                                                       |                                                                                 | C        |
| **P.39515**    | Mitochondrial import inner membrane translocase subunit Tim17          | cell organization and biogenesis; transport; mitochondrial activity             | 85329    |
|                |                                                                       |                                                                                 | TIM17;   |
|                |                                                                       |                                                                                 | YLR143   |
|                |                                                                       |                                                                                 | W        |
| **Q.12233**    | ATP synthase subunit 6, mitochondrial                                 | cell organization and biogenesis; metabolic process; transport; mitochondrial   | 85613    |
|                |                                                                       |                                                                                 | ATP20;   |
|                |                                                                       |                                                                                 | YPR020   |
|                |                                                                       |                                                                                 | W        |
| **P.35349**    | Flavoprotein-like protein YCP4 (OS=Saccharomyces cerevisiae)           | cytoplasm; mitochondrial activity; catalytic activity; nucleotide binding; protein binding; RNA binding; structural molecule activity | 85836    |
|                |                                                                       |                                                                                 | YCP4;    |
|                |                                                                       |                                                                                 | YCRO04   |
|                |                                                                       |                                                                                 | C        |
| **P.40341**    | Mitochondrial respiratory chain complex assembly protein YTA12        | mitochondrial activity; catalytic activity; metal ion binding; nucleotide binding; protein binding | 85511    |
|                |                                                                       |                                                                                 | YTA12;   |
|                |                                                                       |                                                                                 | YMR08    |
|                |                                                                       |                                                                                 | 9C       |
| Gene ID | Gene Description | Function | Localization | Binding | Binding Type |
|--------|------------------|----------|--------------|--------|--------------|
| P22136 | ATPase expression protein 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process; regulation of biological process | mitochondrion | RNA binding | 0.50 6 | 0.292 0.58 |
| Q08818 | Mitotic sister-chromatid recombination protein 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion, organelle lumen | RNA binding | 0.50 6 | 0.292 0.58 |
| P00830 | ATP synthase subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process; transport | cytosol, membrane, mitochondrion | catalytic activity; nucleotide binding; protein binding; transporter activity | 91.6 12 | 53.11 7 | 0.58 |
| Q00402 | Nuclear migration protein NUM1 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; cellular component movement; metabolic process; regulation of biological process; transport | endoplasmic reticulum, mitochondrion | catalytic activity; motor activity; protein binding | 0.13 4 | 0.078 0.58 |
| P40185 | Protein YEP1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial, organelle lumen | mitochondrion | catalytic activity; metal ion binding | 0.95 1 | 0.562 0.59 |
| P32898 | Mitochondrial presynaptic protease YME2 [OS=Saccharomyces cerevisiae S288c] | mitochondrial | mitochondrial | catalytic activity; metal ion binding | 1.61 5.17 | 0.64 |
| P36112 | MICS complex subunit Mlc60 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis | membrane, mitochondrion | catalytic activity; nucleotide binding | 19.9 62 | 11.79 8 | 0.59 |
| P33311 | ATP-dependent permease MDL2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | response to stimulus, transport | membrane, mitochondrion | catalytic activity; nucleotide binding; transporter activity | 0.90 1 | 0.535 0.59 |
| P10507 | mitochondrial processing peptidase subunit beta [OS=Saccharomyces cerevisiae S288c] | metabolic process; transport | mitochondrion, organelle lumen | catalytic activity; metal ion binding; protein binding | 1.61 0.957 | 0.59 |
| P35721 | Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis | membrane, mitochondrion | catalytic activity; metal ion binding | 7.11 1 | 4.337 0.61 |
| P32317 | Protein AFG1 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis | membrane, mitochondrion | catalytic activity; nucleotide binding | 1.15 4 | 0.711 0.62 |
| P41735 | S-demethoxyquinone hydroxylase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | catalytic activity | membrane, mitochondrion | catalytic activity; metal ion binding | 0.54 0.334 | 0.62 |
| P35292 | 37S ribosomal protein S45, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; metabolic process; response to stimulus, transport | mitochondrion, ribosome | structural molecule activity | 1.75 4 | 1.089 0.62 |
| P07275 | Delta-1-pyruvate-5-carboxylate dehydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | catalytic activity | membrane, mitochondrion, organelle lumen | catalytic activity | 9.72 3 | 6.055 0.62 |
| P40053 | Altered inheritance of mitochondria protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | mitochondrial | mitochondrial | catalytic activity | 3.34 8 | 2.086 0.62 |
| P35206 | putative cysteine synthase [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion | catalytic activity | 1.55 5 | 0.978 0.63 |
| Q06485 | Autophagy-related protein 33 [OS=Saccharomyces cerevisiae S288c] | cell communication; metabolic process; response to stimulus | membrane, mitochondrion | catalytic activity | 2.16 2 | 1.371 0.63 |
| P29704 | squalene synthase [OS=Saccharomyces cerevisiae S288c] | metabolic process | endoplasmic reticulum, membrane, mitochondrion | catalytic activity | 0.35 0.222 | 0.63 |
| P41911 | Glycerol-3-phosphate dehydrogenase [NAD(+)] 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, cytosol, mitochondrion | catalytic activity; nucleotide binding; protein binding | 0.29 2 | 0.186 0.64 |
| P35140 | Protein YMR059, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell differentiation; metabolic process; regulation of biological process | membrane, mitochondrion | RNA binding | 1.04 7 | 0.668 0.64 |
| P21560 | Protein CBP3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; regulation of biological process | membrane, mitochondrion, ribosome | catalytic activity; nucleotide binding | 0.30 4 | 0.194 0.64 |
| P38604 | Phosphatidylserine decarboxylase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process; regulation of biological process | membrane, mitochondrion | catalytic activity | 0.26 9 | 0.172 0.64 |
| P33843 | Mitochondrial escape protein 2 [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; metabolic process | membrane, mitochondrion | nucleotide binding; RNA binding | 3.28 1 | 2.099 0.64 |
| P47127 | Altered inheritance of mitochondria protein 24, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis | mitochondrion | catalytic activity | 3.17 5 | 2.039 0.64 |
| P48527 | Tyrosine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytosol, cytosol, organelle lumen | catalytic activity; nucleotide binding; RNA binding | 0.23 3 | 0.15 0.64 |

**Biological Processes:**
- Cell organization and biogenesis
- Metabolic process
- Regulation of biological process
- Cellular component movement
- Response to stimulus
- Transport

**Localizations:**
- Mitochondrion
- Organelle lumen
- Membrane
- Cytosol
- Endoplasmic reticulum
- Cytosol; membrane
- Mitochondrion; organelle lumen
- Excised organelle

**Other Properties:**
- Binding interactions
- Molecular functions
- Cellular components
| Gene ID | Symbol | Protein Name | Function | Expression | Binding to RNA | Binding to Protein | Molecule Activity | Catalytic Activity | Localization |
|---------|--------|--------------|----------|------------|----------------|-------------------|--------------------|-------------------|--------------|
| Q03127  | Protein-1 | mitochondrial | metabolic process; regulation of biological process | cytoplasm/mitochondrion; organelle lumen | catalytic activity; nucleotide binding; protein binding | 0.18 | 3 | 0.134 | 0.74 |
| P32904  | 5S4 ribosomal protein L6 | mitochondrial | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | RNA binding; structural molecule activity | 1.05 | 4 | 0.778 | 0.74 |
| P40086  | Cytochrome c oxidase assembly protein cos15 | mitochondrial | cell organization and biogenesis; metabolic process; transport | membrane/mitochondrion | catalytic activity; transporter activity | 1.55 | 5 | 1.154 | 0.74 |
| P34567  | aldehyde dehydrogenase 1 | mitochondrial | metabolic process | cytosol/mitochondrion | catalytic activity | 2.16 | 2 | 1.61 | 0.74 |
| P40908  | Uncarboxylated protein YIL077C | mitochondrial | cell organization and biogenesis; metabolic process; regulation of biological process | membrane/mitochondrion | protein binding | 5.95 | 2 | 4.456 | 0.75 |
| P40961  | prohibitin-1 | mitochondrial | cell organization and biogenesis; metabolic process; regulation of biological process | membrane/mitochondrion | catalytic activity | 0.73 | 6 | 0.551 | 0.75 |
| P38885  | Altered inheritance of mitochondria | mitochondrial | cell organization and biogenesis; metabolic process; regulation of biological process | membrane/mitochondrion | catalytic activity | 0.61 | 6 | 0.468 | 0.76 |
| P36101  | RNA thymidylate synthetase | mitochondrial | cell organization and biogenesis; metabolic process | membrane/mitochondrion | catalytic activity; nucleotide binding | 0.61 | 6 | 0.468 | 0.76 |
| Q03327  | Mitochondrial fusion and transport | mitochondrial | cell organization and biogenesis; metabolic process | membrane/mitochondrion | protein binding; structural molecule activity | 0.55 | 7 | 0.425 | 0.76 |
| P21375  | Fumarate reductase 2 | mitochondrial | cell organization and biogenesis; metabolic process | endoplasmic reticulum; mitochondrion | catalytic activity; nucleotide binding | 0.45 | 3 | 0.346 | 0.77 |
| P36066  | Protein MRG3-like | mitochondrial | cell organization and biogenesis; metabolic process | membrane/mitochondrion | catalytic activity; nucleotide binding | 0.43 | 3 | 0.334 | 0.77 |
| P00657  | ABC1 family protein MIP2 | mitochondrial | cell organization and biogenesis | membrane/mitochondrion | catalytic activity | 0.38 | 9 | 0.301 | 0.77 |
| P25374  | Cysteine desulfurase, mitochondrial | mitochondrial | cell organization and biogenesis; cellular homeostasis; metabolic process | mitochondrial; nucleus | catalytic activity; metal ion binding; protein binding | 2.3 | 5 | 1.783 | 0.78 |
| P39525  | 3-oxoacyl-[acyl-carrier protein] synthase homolog | mitochondrial | cell organization and biogenesis; metabolic process | endoplasmic reticulum; membrane; mitochondrion | catalytic activity | 0.87 | 4 | 0.688 | 0.79 |
| P40008  | Protein YMR352c | mitochondrial | cell organization and biogenesis; metabolic process | endoplasmic reticulum; membrane; mitochondrion | catalytic activity | 1.73 | 8 | 1.371 | 0.79 |
| P39592  | Mitochondrial respiratory chain complexes assembly protein AFG3 | mitochondrial | cell organization and biogenesis; metabolic process; response to stimulus; transport | membrane/mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | 0.82 | 3 | 0.65 | 0.79 |
| P32331  | Carrier protein YMC1, mitochondrial | mitochondrial | cell organization and biogenesis; metabolic process; transport | membrane/mitochondrion; vacuole | structural molecule; activity; transporter activity | 1.58 | 1 | 1.254 | 0.79 |
| P17558  | 37S ribosomal protein PET123, mitochondrial | mitochondrial | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule | 1.44 | 8 | 1.154 | 0.80 |
| P32860  | NTF2-like protein, mitochondrial | mitochondrial | cell organization and biogenesis; cellular homeostasis; metabolic process | mitochondrion; organelle lumen | metal ion binding | 2.65 | 2 | 2.162 | 0.82 |
| Q07601  | SURF family protein SAP45 | mitochondrial | cell organization and biogenesis | membrane/mitochondrion | catalytic activity | 7.37 | 7 | 6.017 | 0.82 |
| P07143  | Cytochrome c1, heme protein, mitochondrial | mitochondrial | cell differentiation; cell organization and biogenesis | cytosol; membrane; mitochondrion | metal ion binding | 13.2 | 51 | 10.93 | 0.83 |
| Q03104  | Metallo-beta lactamase | mitochondrial | cell organization and biogenesis | endoplasmic reticulum; membrane; mitochondrion | catalytic activity | 5.31 | 2 | 4.412 | 0.83 |
| Q01852  | Mitochondrial import inner membrane translocase subunit TIMM44 | mitochondrial | cell organization and biogenesis | membrane/mitochondrion | nucleotide binding; protein binding | 5.40 | 4 | 4.52 | 0.84 |
| P00927  | Threonine dehydratase, mitochondrial | mitochondrial | cell organization and biogenesis | cytosol; mitochondrion; plastid | catalytic activity | 2.25 | 7 | 1.894 | 0.84 |
| Q04013  | Citrate/oxoglutarate carrier protein | mitochondrial | cell organization and biogenesis; metabolic process; transport | membrane/mitochondrion | DNA binding; structural molecule | 4.01 | 2 | 3.467 | 0.86 |
P38988 Mitochondrial GTP/GDP carrier protein 1 [OS=Saccharomyces cerevisiae S288c] 85132 9 GGCl1 YOL118c 0.42 cell organization and biogenesis;cellular homeostasis;metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 3.64 1.00 2.83 0.87
P09457 ATP synthase subunit 5, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85389 2 ATP5 YDR298c 0.17 metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 13.9 15.0 10.36 5.00 0.87
P46681 D-lactate dehydrogenase [cytochrome c] 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85137 1 DLD2 YOL178w 0.66 metabolic process mitochondrion;organelle lumen catalytic activity;nucleotide binding;protein binding 1.26 1.00 1.02 0.87
P50085 Probihom 2 [OS=Saccharomyces cerevisiae S288c] 85314 7 PHB2 YGR231c 0.17 cell organization and biogenesis;metabolic process;regulation of biological process membrane;mitochondrion protein binding 4.33 1.00 3.806 0.88
Q02776 Mitochondrial import inner membrane translocase subunit TIM50 [OS=Saccharomyces cerevisiae S288c] 86364 2 TIM50 YPL063w 0.66 cell organization and biogenesis;metabolic process;transport membrane;mitochondrion catalytic activity;protein binding;transporter activity 9.85 1.00 9.0 0.91
Q08968 UFR0061 protein FMP40 [OS=Saccharomyces cerevisiae S288c] 85587 9 FMP40 YPL222w 1.72 protein binding 1.00 1.00 1.588 0.92
P33598 Succinyl-CoA ligase [ADP-forming] subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85431 0 LSC1 YDR142c 0.58 metabolic process cytosol;mitochondrion catalytic activity;nucleotide binding 11.7 43.0 11.74 3.00 1.00
P04041 Cytochrome c oxidase subunit 2 [OS=Saccharomyces cerevisiae S288c] 85462 2 COX2 YQ0250 0.66 metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding;protein binding;transporter activity 3.64 1.00 3.642 1.00
P40513 Mitochondrial acidic protein MAM33 [OS=Saccharomyces cerevisiae S288c] 85474 0 MAM3 YIL070c 0.38 metabolic process;regulation of biological process mitochondrion;organelle lumen translation regulator activity 2.83 1.00 2.831 1.00
Q08023 Protein FMP25, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85076 6 FMP25 YLR077w 0.71 cell organization and biogenesis membrane;mitochondrion catalytic activity 0.71 0.99 0.719 1.00
Q04728 Arginine biosynthesis bifunctional protein ArgJ, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85508 4 ARG7 YMR062c 0.52 metabolic process organelle lumen;mitochondrion catalytic activity 0.52 1.00 0.52 1.00
P38797 Protein phosphatase 2C homolog 7, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85643 7 PPC2 YHR077w 0.66 metabolic process mitochondrion catalytic activity;metal ion binding;protein binding 0.87 1.00 0.874 1.00
P38517 S45 ribosomal protein L14, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85116 0 MRPL4 YLR439w 0.87 cell organization and biogenesis;metabolic process mitochondrion;ribosome structural molecule activity 0.87 1.00 0.874 1.00
P38709 protein YRI02 [OS=Saccharomyces cerevisiae S288c] 85334 3 YRI02 YBR054w 0.42 transport endoplasmic reticulum;membrane;mitochondrion transporter activity 1.42 1.00 1.424 1.00
P32611 S45 ribosomal protein RN2L1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85666 0 RN2L1 YEL050c 0.63 cell organization and biogenesis;metabolic process mitochondrion;ribosome catalytic activity;RNA binding;structural molecule activity 0.63 1.00 0.638 1.00
Q06668 Methyltransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85191 1 OMS1 YOR316w 0.38 metabolic process membrane;mitochondrion catalytic activity 0.38 0.99 0.389 1.00
P32453 Protein ATP11, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85540 1 ATP11 YNL315c 0.58 ATP11 YNL315c 0.58 metabolic process mitochondrion ATP11 YNL315c 0.58 protein binding 0.58 1.00 0.585 1.00
P35180 mitochondrial import receptor subunit Tom20, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85297 3 TOM20 YIR080w 0.42 cell organization and biogenesis;transport membrane;mitochondrion protein binding;transporter activity 0.42 1.00 0.425 1.00
Q38247 Uncharacterized protein YDR020W-A [OS=Saccharomyces cerevisiae S288c] 14664 80 YDR020w-a YDR020w-a 0.17 metabolic process;transport membrane;mitochondrion 2.16 1.00 2.162 1.00
P37299 cytochrome b-1 complex subunit 10 [OS=Saccharomyces cerevisiae S288c] 85639 0 QCR10 YHR009c 0.17 metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 2.98 1.00 2.981 1.00
P49334 Mitochondrial import receptor subunit tom22, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85559 2 TOM22 YNL311w 0.66 cell organization and biogenesis;transport membrane;mitochondrion protein binding;transporter activity 0.66 1.00 0.668 1.00
P38112 Exoribonuclease II, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85333 1 DSS1 YMR282c 0.74 cell organization and biogenesis;transport membrane;mitochondrion catalytic activity;RNA binding 0.08 0.77 0.087 1.00
P14693 sorting assembly machinery 35 (tm) subunit [OS=Saccharomyces cerevisiae S288c] 86348 3 VAM35 YHR083w 0.31 cell organization and biogenesis;transport membrane;mitochondrion protein binding 0.33 1.00 0.334 1.00
P25345 Asparagine–tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 83038 8 SIM5 YCR024w 0.17 metabolic process cytoplasm;mitochondrion;organelle lumen catalytic activity;nucleotide binding 0.17 0.99 0.172 1.00
P34222 Peptidyl-tRNA hydrolase 2 [OS=Saccharomyces cerevisiae S288c] 85222 3 PTH2 YBR057c 0.42 regulation of biological process cytoplasm;cytosol;membrane;mitochondrion catalytic activity;protein binding 0.42 1.00 0.425 1.00
P28737  Protein MSP1 [OS=Saccharomyces cerevisiae S288c]  85291 5  MSP1;  YGR024W cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport membrane/mitochondrion; nucleus catalytic activity; nucleotide binding; protein binding; RNA binding 0.41 3 0.413 1.00

P23106  ATP synthase subunit epsilon, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85585 7  ATP15;  YPL271W metabolic process; transport membrane/mitochondrion catalytic activity; transporter activity 2.16 2 2.162 1.00

Q01332-1  Cysteine proteinase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85533 8  HER2;  YMR293C cell organization and biogenesis; metabolic process mitochondrion catalytic activity; nucleotide binding 0.16 6 0.166 1.00

P33732  37S ribosomal protein S32, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85577 2  MRPS12;  YNR036C cell organization and biogenesis; metabolic process mitochondrion; ribosome structural molecular activity 0.68 8 0.688 1.00

P32792  UPF0744 protein YSC83 [OS=Saccharomyces cerevisiae S288c]  85641 0  YSC83;  YHR037W membrane/mitochondrion 0.23 3 0.233 1.00

P23833  Protein SCG1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  83232 5  SCD1;  YBR037C cell organization and biogenesis; cellular homeostasis; response to stimulus; transport membrane/mitochondrion antioxidant activity; catalytic activity; metal ion binding 0.46 8 0.468 1.00

Q05648  MIOREX complex component 10 [OS=Saccharomyces cerevisiae S288c]  85187 6  YOR282C;  MRX10;  YDR282C cell organization and biogenesis; metabolic process mitochondrion; ribosome structural molecular activity 0.46 8 0.468 1.00

P40496  37S ribosomal protein S25, mitochondrial [OS=Saccharomyces cerevisiae S288c]  84741 5  RNA25;  YL093C cell organization and biogenesis; metabolic process mitochondrion; ribosome structural molecular activity 0.46 8 0.468 1.00

P50087  MICO5 subunit MIC26 [OS=Saccharomyces cerevisiae S288c]  85315 0  MDS2;  MIC26;  YGR232C cell organization and biogenesis mitochondrion; membrane mitochondrion 0.63 8 0.638 1.00

P33759  37S ribosomal protein S5, mitochondrial [OS=Saccharomyces cerevisiae S288c]  83255 3  MRPS5;  YBR251W cell organization and biogenesis mitochondrion; ribosome RNA binding; structural molecule activity 0.41 3 0.413 1.00

P18496  Mitochondrial ATPase complex subunit ATP10 [OS=Saccharomyces cerevisiae S288c]  83110 9  ATP10;  YLR393W cell organization and biogenesis cytoplasm; membrane; mitochondrion protein binding 0.41 3 0.413 1.00

P18900  Hexamethylene triamine phosphate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85228 8  COQ1;  YBR003W metabolic process membrane; mitochondrion catalytic activity; metal ion binding; protein binding 0.16 6 0.166 1.00

Q07821  Iron-sulfur assembly protein 1 [OS=Saccharomyces cerevisiae S288c]  85063 2  ISA1;  YL027W cell organization and biogenesis; metabolic process mitochondrion; organelle lumen metal ion binding; structural molecular activity 0.13 6 0.136 1.00

Q06630  Mitochondrial homologous recombination protein 1 [OS=Saccharomyces cerevisiae S288c]  85389 0  MHR1;  YDR296W cell organization and biogenesis; metabolic process mitochondrion; nucleus catalytic activity; DNA binding; structural molecular activity 0.35 9 0.359 1.00

P33260  putative mitochondrial translation system component PET127 [OS=Saccharomyces cerevisiae S288c]  85418 2  PET127;  YOR017W cell organization and biogenesis; metabolic process; regulation of biological process mitochondrion 0.09 9 0.099 1.00

P08525  Cytochrome b-c1 complex subunit 8 [OS=Saccharomyces cerevisiae S288c]  83327 3  QC8R;  YLR166W metabolic process; transport membrane; mitochondrion catalytic activity; transporter activity 0.58 5 0.585 1.00

Q02608  37S ribosomal protein S16, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85609 4  MRPS16;  YPL013C cell organization and biogenesis; metabolic process mitochondrion; ribosome structural molecular activity 0.38 9 0.389 1.00

P40581  Peroxiredoxin HYR1 [OS=Saccharomyces cerevisiae S288c]  83485 5  HYR1;  YHR037W metabolic process; response to stimulus cytoplasm; cytosol; mitochondrion; organelle lumen antioxidant activity; catalytic activity 0.25 9 0.259 1.00

P38122  3-methyl-2-oxobutanoate hydroxymethyltransferase [OS=Saccharomyces cerevisiae S288c]  83247 4  ECM31;  YBR176W metabolic process mitochondrion catalytic activity 0.12 2 0.122 1.00

P32463  Acyl carrier protein, mitochondrial [OS=Saccharomyces cerevisiae S288c]  83644 2  ACP1;  YKL192C metabolic process; transport mitochondrion 0.25 9 0.259 1.00

P04039  Cytochrome c oxidase polypeptide VIII, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85111 1  COX8;  YLR395C metabolic process; transport membrane; mitochondrion catalytic activity; transporter activity 0.77 8 0.778 1.00

Q05779  Ubiquinone biosynthesis protein COQ9, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85089 8  COQ9;  YLR201C metabolic process membrane; mitochondrion 0.16 6 0.166 1.00

P03879  Nitron encoded RNA maturase b1 [OS=Saccharomyces cerevisiae S288c]  84548 2  R14;  QO120 metabolic process membrane; mitochondrion catalytic activity; RNA binding 0.17 9 0.179 1.00

P46998  mitochondrial membrane protein FMN33 [OS=Saccharomyces cerevisiae S288c]  83327 9  FMN33;  YL161W membrane; mitochondrion 0.33 4 0.334 1.00

Q12487  54S ribosomal protein L23, mitochondrial [OS=Saccharomyces cerevisiae S288c]  83432 1  MRPL23;  YOR15 cell organization and biogenesis; metabolic process mitochondrion; ribosome; vacuole RNA binding; structural molecular activity 0.23 3 0.233 1.00
| ID   | Protein Name                        | ROC   | FPR   | AUC   |
|------|------------------------------------|-------|-------|-------|
| Q12204 | Probable phospholipase YOR022C, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.05  | 0.11  | 2.04  |
| P22438 | Methionine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.06  | 0.136 | 2.06  |
| P38127 | mitochondrial carrier protein RIM2 [OS=Saccharomyces cerevisiae S288c] | 0.58  | 1.239 | 2.12  |
| P25270 | tRNA methyltransferase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.12  | 0.274 | 2.12  |
| P38816 | thioredoxin reductase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.13  | 0.292 | 2.15  |
| P39722 | Mitochondrial Rho GTPase 1 [OS=Saccharomyces cerevisiae S288c] | 0.05  | 0.189 | 3.20  |
| Q04935 | Cytochrome c oxidase protein 20, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.19  | 0.701 | 3.61  |
| P38705 | Serine--tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 0.07  | 0.322 | 4.47  |
Supplemental Table S10. The relative concentrations of proteins in mitochondria purified from WT or ups2Δ cells cultured without LCA. Mitochondria were purified from WT or ups2Δ cells recovered on day 2 of cell culturing without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI ups2 | Ratio ups2 / WT |
|-----------|-------------|---------------|---------|--------------------|-------------------|-------------------|----------|------------|----------------|
| P00431    | cytochrome c peroxidase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85394 | CCP1; YKR066 C | metabolic process;response to stimulus | mitochondrion;organelle lumen | antioxidant activity;catalytic activity;metal ion binding;protein binding | 2.162 | 0.093 | 0.04 |
| P39522    | Dihydroxy-acid dehydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85347 | ILV3; YJR016 C | metabolic process | mitochondrion | catalytic activity;metal ion binding | 39.37 | 2.054 | 0.05 |
| P25605    | Acetolactate synthase small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85304 | ILV6; YCL009 C | metabolic process;regulation of biological process | mitochondrion | catalytic activity;enzyme regulator activity | 11.74 | 0.624 | 0.05 |
| Q06678    | S45 ribosomal protein L15, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85192 | MRPL3 5; YDR322 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 1.424 | 0.093 | 0.07 |
| P19955    | S75 ribosomal protein YMR31, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85063 | YMR413; YPR049 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | catalytic activity;protein binding;structural molecule activity | 15.68 | 1.154 | 0.07 |
| P35219    | Abyhydrolylase domain-containing protein IM032 [OS=Saccharomyces cerevisiae S288c] | 85291 | IM032; YGR031 W | metabolic process;transport | mitochondrion | catalytic activity | 1.404 | 0.116 | 0.08 |
| P81449    | ATP synthase subunit e, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85192 | TIM11; YDR322 C.A | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;structural molecule activity;transport activity | 9 | 0.778 | 0.09 |
| P19914    | Mitochondrial-processing peptidase subunit alpha [OS=Saccharomyces cerevisiae S288c] | 85641 | MAS2; YHR024 C | metabolic process;transport | membrane;mitochondrion;organelle lumen | catalytic activity;metal ion binding;protein binding | 2.311 | 0.202 | 0.09 |
| Q06892    | NADH kinase POS5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85591 | POS5; YPL188 W | metabolic process;response to stimulus | mitochondrion;organelle lumen | catalytic activity;nucleotide binding | 2.511 | 0.233 | 0.09 |
| P39676    | Flavohemoprotein [OS=Saccharomyces cerevisiae S288c] | 85314 | YBH1; YGR234 W | metabolic process;response to stimulus | cytoplasm;cytosol;mitochondrion;nucleus;organelle lumen | catalytic activity;metal ion binding;protein binding | 4.179 | 0.389 | 0.09 |
| P73767    | Assembly factor cbp4 [OS=Saccharomyces cerevisiae S288c] | 85203 | CBP4 | cell organization and biogenesis | membrane;mitochondrion | | 5.579 | 0.52 | 0.09 |
| P32539    | Elongation factor G, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85075 | MEF1; YLR069 C | cell organization and biogenesis;metabolic process | cytosol;mitochondrion | catalytic activity;nucleotide binding;RNA binding | 1.024 | 0.099 | 0.10 |
| P32445    | Single-stranded DNA-binding protein RIM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85039 | RIM1; YCR028 C.A | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion | DNA binding | 6.743 | 0.668 | 0.10 |
| P38088    | Glycine–tRNA ligase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85318 | GRS1 | metabolic process | cytoplasm;mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | 0.468 | 0.049 | 0.10 |
| Q04866    | ARS binding factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85009 | ABF2; YMR072 W | cell organization and biogenesis;metabolic process;regulation of biological process | chromosome;mitochondrion;nucleus | DNA binding | 69.17 | 7.377 | 0.11 |
| P05252    | Cytochrome b-c1 complex subunit 8 [OS=Saccharomyces cerevisiae S288c] | 85327 | QC48; YIL166 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transport activity | 5.31 | 0.585 | 0.11 |
| P33416    | Heat shock protein 78, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85184 | HSP78; YDR258 C | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion;organelle lumen | catalytic activity;nucleotide binding;protein binding | 12.52 | 5 | 1.383 | 0.11 |
| P23180    | Probable oxidoreductase AIM17 [OS=Saccharomyces cerevisiae S288c] | 85636 | AIM17; YHL021 C | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;metal ion binding | 9 | 0.995 | 0.11 |
| Gene ID | Gene Symbol | Gene Name | Location | Function | PDB Number | Cysteine | Quality |
|--------|-------------|-----------|----------|----------|-------------|----------|---------|
| P08417 | Tumurcata hydratase, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | cell organization and biogenesis;metabolic process | 85586 | FUM1; YPL262 W | 13.87 | 4 | 2.562 | 0.18 |
| P38523 | Gprf protein homolog, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process;regulation of biological process;transport | 85440 | MGR1; YDR232 W | 2.36 | 4 | 0.438 | 0.19 |
| P32787 | Mitochondrial genome maintenance protein MGM101 | [OS=Sacharomyces cerevisiae S288c] | W | cell organization and biogenesis;metabolic process;response to stimulus | 85360 | MGM1; YJR144 W | 4.456 | 3 | 0.833 | 0.19 |
| P3567 | Alamine–glyoxylate aminotransferase 1 | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process | 85051 | AGX1; YFL030 W | 2.481 | 6 | 0.468 | 0.19 |
| P10507 | Mitochondrial-processing peptidase subunit beta | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process;transport | 85086 | MA51; YLR163 C | 2.481 | 6 | 0.468 | 0.19 |
| P47052 | Succinate dehydrogenase (ubiquinone) flavoprotein subunit 2, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process;transport | 85340 | YL045; W; YL045 W | 5.884 | 1 | 1.11 | 0.19 |
| Q09391 | Heat shock protein SSG1, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | cell organization and biogenesis;metabolic process | 85108 | SSG1; YLR369 W | 0.995 | 4 | 0.189 | 0.19 |
| P60208-1 | 2-isopropylmalylate synthase | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process | 85561 | LEU4; YNL104 W | 9 | 1 | 1.728 | 0.19 |
| P3881 | S45 ribosomal protein L22, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | cell organization and biogenesis;metabolic process | 85455 | MRPL2; YNL177 C | 1.994 | 9 | 0.995 | 0.19 |
| P52719 | Peptidyl-prolyl cis-trans isomerase C, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | cell death;metabolic process | 85489 | CPR3; YML07 W | 2.981 | 3 | 0.585 | 0.20 |
| P39525 | 3-oxoacyl (acyl-carrier protein) synthase homolog | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process | 85679 | CEM1; YER061 C | 1.848 | 3 | 0.369 | 0.20 |
| P25372 | Thioredoxin-3, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | cell organization and biogenesis;metabolic process | 85044 | TRX3; YCR083 W | 2.511 | 4 | 0.52 | 0.21 |
| P38122 | 3-methyl-2-oxobutanoate hydroxymethyltransferase | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process | 85247 | ECM3; YBR176 W | 0.585 | 4 | 0.122 | 0.21 |
| P65620 | S45 ribosomal protein L10, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | cell organization and biogenesis;metabolic process | 85543 | MRPL1; YNL284 C | 0.551 | 4 | 0.116 | 0.21 |
| P36013 | NAD-dependent malic enzyme, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process | 85833 | MAE1; YKL229 C | 2.35 | 6 | 0.496 | 0.21 |
| P36528 | S45 ribosomal protein L17, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | cell organization and biogenesis;metabolic process | 85546 | MRPL1; YNL252 C | 0.52 | 6 | 0.11 | 0.21 |
| Q07500 | External NADH-ubiquinone oxidoreductase B, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process | 85147 | ND2; YDL085 W | 12.59 | 4 | 2.687 | 0.21 |
| P40513 | Mitochondrial acetic protein MAM33 | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process;regulation of biological process | 85474 | MAM3; YEL207C | 3.642 | 4 | 0.778 | 0.21 |
| P3289 | Mitochondrial chaperone BCS1 | [OS=Sacharomyces cerevisiae S288c] | W | cell organization and biogenesis;metabolic process;response to stimulus;transport | 85198 | BCS1; YDR375 C | 0.425 | 4 | 0.093 | 0.22 |
| P43635 | Citrate synthase 3, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process | 85610 | GTS3; YPR001 W | 6.11 | 4 | 1.346 | 0.22 |
| P32891 | 2-lactate dehydrogenase [cytochrome] 1, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process;transport | 85138 | DLD1; YDL174 C | 13.03 | 4 | 2.875 | 0.22 |
| P38817 | 3-hydroxyisobutyryl-CoA dehydrogenase, mitochondrial | [OS=Sacharomyces cerevisiae S288c] | W | metabolic process | 85160 | EHD3; YDR036 C | 1.212 | 4 | 0.269 | 0.22 |
OS = Saccharomyces cerevisiae

| Gene Name | Function | Localization | Activity or Process | Score |
|-----------|----------|--------------|---------------------|-------|
| P10662 | 375 ribosomal protein S24, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85175 5 | RSM24; YDR175 C | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | structural molecule activity | 0.905 | 0.202 | 0.22 |
| P07246 | Alcohol dehydrogenase A, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85510 7 | ADH3; YMR08 3W | metabolic process | mitochondrion, organelle lumen | catalytic activity, metal ion binding | 10.15 | 9 | 2.34 | 0.23 |
| P17298 | Succinate dehydrogenase (ubiquione) cytochrome b small subunit, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85175 8 | SDH4; YDR178 W | metabolic process, transport | membrane, mitochondrion | catalytic activity, metal ion binding | 4.995 | 1.154 | 0.23 |
| P16387 | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85692 5 | PDA1; YER178W | cell growth, metabolic process | mitochondrion, organelle lumen | catalytic activity | 25.26 | 4 | 5.898 | 0.23 |
| P13227 | Mitochondrial peroxiredoxin PRX1 (OS=Saccharomyces cerevisiae 5288c) | 85221 5 | PRX1; YBL064 C | cellular homeostasis, metabolic process, regulation of biological process, response to stimulus | mitochondrion | antioxidant activity, catalytic activity | 6.848 | 1.637 | 0.24 |
| P52893 | Probable alanine aminotransferase, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85077 8 | ALT1; YLR083 C | metabolic process | mitochondrion, organelle lumen | catalytic activity | 1.438 | 0.346 | 0.24 |
| P16451 | Pyruvate dehydrogenase complex protein X component, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85310 7 | PDX1; YGR193 C | metabolic process | mitochondrion, organelle lumen | catalytic activity, structural molecule activity | 4.055 | 0.978 | 0.24 |
| P17292 | Seryl hydroxymethyltransferase, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85256 5 | SHM4; YBR263 W | metabolic process | mitochondrion | catalytic activity | 12.21 | 9 | 3.057 | 0.25 |
| P32340 | Rotenone-insensitive NADH: ubiquione oxidoreductase, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85491 9 | ND11; YML12 1C | metabolic process, regulation of biological process | membrane, mitochondrion, organelle lumen | catalytic activity, nucleotide binding | 22.95 | 5.723 | 0.25 |
| P32860 | Neuro-like protein, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85382 6 | NUF1; YKL040 C | cell organization and biogenesis, cellular homeostasis, metabolic process | mitochondrion, organelle lumen | metal ion binding | 5.494 | 1.371 | 0.25 |
| P00427 | Cytochrome c oxidase subunit 6, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85644 8 | COX6; YHR051 W | metabolic process, transport | membrane, mitochondrion | catalytic activity, metal ion binding, transport or activity | 4.623 | 1.154 | 0.25 |
| Q0950 | 375 ribosomal protein MRPS1, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85598 5 | MRPS1; YPL118 W | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 1.154 | 0.292 | 0.25 |
| P53732 | 375 ribosomal protein S12, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85577 2 | MRPS1 2; YNR036 C | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 1.154 | 0.292 | 0.25 |
| P19516 | Cytochrome c oxidase assembly protein COX13, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85597 1 | COX13; YPL132 W | cell organization and biogenesis, metabolic process | membrane, mitochondrion, ribosome | metal ion binding | 1.069 | 0.274 | 0.26 |
| P36251 | 545 ribosomal protein L11, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85132 5 | MRPL1 1; YDL202 W | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 1.069 | 0.274 | 0.26 |
| P40502 | Altered inheritance of mitochondria protein 19, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85472 2 | AIM19; YIL087C | membrane, mitochondrion | | | 0.995 | 0.259 | 0.26 |
| P38300 | Inner membrane mitorsome receptor MBA1, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85248 3 | MBA1; YBR185 C | cell organization and biogenesis, regulation of biological process | membrane, mitochondrion | | 0.995 | 0.259 | 0.26 |
| Q08968 | UPF0081 protein FMP40 (OS=Saccharomyces cerevisiae 5288c) | 85587 9 | FMP40; YPL222 W | mitochondrial | protein binding | 2.495 | 0.65 | 0.26 |
| P10662 | 375 ribosomal protein MRPS1, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85194 8 | MRPS1; YDR347 W | cell organization and biogenesis, metabolic process, response to stimulus | mitochondrion, ribosome | antioxidant activity, catalytic activity, metal ion binding, structural molecule activity | 2.981 | 0.778 | 0.26 |
| P23833 | Protein SC01, mitochondrial (OS=Saccharomyces cerevisiae 5288c) | 85232 5 | SC01; YBR037 C | cell organization and biogenesis, cellular homeostasis, response to | membrane, mitochondrion | antioxidant activity, catalytic activity | 1.783 | 0.468 | 0.26 |
| P31998 | 54S ribosomal protein ym1, mitochondrial (S. cerevisiae) | 85498 | 3 | YMR66; YML025C | stimulus/transport | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 0.931 | 0.245 | 0.26 |
| Q32029 | Probable mitochondrial transport protein ftf1 (S. cerevisiae) | 85444 | 5 | FISF1; YDR271C | transport | membrane; mitochondrion | transporter activity | 2.36 | 0.624 | 0.26 |
| P38797 | Protein phosphatase 2C homolog 7, mitochondrial (S. cerevisiae) | 85647 | 5 | PTC7; YLR076W | metabolic process | mitochondrion | catalytic activity; metal ion binding; protein binding | 0.874 | 0.233 | 0.27 |
| P32191 | Glycerol-3-phosphate dehydrogenase, mitochondrial (S. cerevisiae) | 85465 | 1 | GUT2; YIL155C | metabolic process | membrane; mitochondrion | catalytic activity | 9.502 | 2.574 | 0.27 |
| P2453 | Protein ATP11, mitochondrial (S. cerevisiae) | 85540 | 1 | ATP11; YNL315C | cell organization and biogenesis | mitochondrion | protein binding | 1.512 | 0.413 | 0.27 |
| P46367 | Potassium-activated aldehyde dehydrogenase, mitochondrial (S. cerevisiae) | 85415 | 6 | ALD4; YMR374W | metabolic process | mitochondrion; organelle lumen | catalytic activity | 58.07 | 5 | 15.92 | 7 | 0.27 |
| P35180 | Mitochondrial import receptor subunit 1, mitochondrial (S. cerevisiae) | 85297 | 3 | TOM20; YGR082W | cell organization and biogenesis; transport | membrane; mitochondrion | protein binding; transporter activity | 0.701 | 0.194 | 0.28 |
| P40053 | Altered inheritance of mitochondria protein 9, mitochondrial (S. cerevisiae) | 85683 | 1 | AIM9; YER080W | mitochondrial | mitochondrial | 4.289 | 1.19 | 0.28 |
| P33003 | Succinate:fumarate mitochondrial transporter (S. cerevisiae) | 85358 | 8 | SFC1; YGR095W | metabolic process; transport | membrane; mitochondrion | structural molecule activity; transporter activity | 17.95 | 7 | 4.995 | 0.28 |
| Q04728 | Arginine biosynthesis bifunctional protein ArgJ, mitochondrial (S. cerevisiae) | 85508 | 4 | ARG7; YMR006C | metabolic process | mitochondrion; organelle lumen | catalytic activity | 1.154 | 0.322 | 0.28 |
| P00445 | Superoxide dismutase (Cu-Zn) (S. cerevisiae) | 85356 | 8 | SOD1; YJR110C | cell organization and biogenesis; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus | cytoplasm; cytosol; mitochondrion; nucleus | antioxidant activity; catalytic activity; metal ion binding; protein binding | 1.848 | 0.52 | 0.28 |
| P07275 | Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial (S. cerevisiae) | 85643 | 2 | PUR2; YHR037W | metabolic process | membrane; mitochondrion; organelle lumen | catalytic activity | 6.565 | 1.848 | 0.28 |
| P24940 | Probable electron transfer flavoprotein subunit beta (S. cerevisiae) | 85312 | 1 | CIR1; YGR207C | metabolic process; transport | mitochondrion; organelle lumen | 7.66 | 2.162 | 0.28 |
| P29399 | GTP-binding protein yph7 (S. cerevisiae) | 85501 | 2 | YPT7; YML001W | cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport | cytosol; endosome; membrane; mitochondrion; nucleus | catalytic activity; nucleotide binding; protein binding | 0.585 | 0.166 | 0.28 |
| Q06630 | Mitochondrial homologous recombination protein 1 (S. cerevisiae) | 85189 | 0 | NMR1; YDR296W | cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus | mitochondrion; nucleus | catalytic activity; DNA binding; structural molecule activity | 0.585 | 0.166 | 0.28 |
| Q2480 | Probable electron transfer flavoprotein subunit alpha, mitochondrial (S. cerevisiae) | 85613 | 2 | AIM45; YPR004C | metabolic process; transport | mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 3.467 | 0.995 | 0.29 |
| P41735 | S-demethoxysaliquinone hydroxylase, mitochondrial (S. cerevisiae) | 85249 | 2 | CAT5; YOR125C | metabolic process | membrane; mitochondrion | catalytic activity; metal ion binding | 0.54 | 0.155 | 0.29 |
| P07806 | Valine–tRNA ligase, mitochondrial (S. cerevisiae) | 85298 | 6 | VAS1; YGR094W | metabolic process; regulation of biological process | cytoplasm; cytosol; mitochondrion | catalytic activity; nucleotide binding | 0.722 | 0.212 | 0.29 |
| P36775 | Ion transport homolog, mitochondrial (S. cerevisiae) | 85215 | 9 | PIM1; YBL022C | cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus | cytoplasm; mitochondrion; organelle lumen | catalytic activity; DNA binding; nucleotide binding; RNA binding | 1.222 | 0.359 | 0.29 |
| P07256 | Cytochrome b-c1 complex subunit 1, mitochondrial (S. cerevisiae) | 85223 | 5 | COR1; YBL045C | metabolic process; transport | membrane; mitochondrion | catalytic activity; metal ion binding; protein binding; transporter activity | 18.78 | 3 | 5.529 | 0.29 |
| P38910 | 10 kDa heat shock protein, mitochondrial (S. cerevisiae) | 85418 | 5 | HSP10; YMR020C | cell organization and biogenesis; metabolic process; response to stimulus; transport | cytoplasm; mitochondrion; organelle lumen | metal ion binding; nucleotide binding | 4.623 | 1.371 | 0.30 |
|ID| Description                                                                 | Gene(s) | Binding | Process | Localization | Activity | Regulation | mole  | Wt  | Zn  | 
|---|---|---|---|---|---|---|---|---|---|---|
|P22354| 54S ribosomal protein L20, mitochondrial (OS=Saccharomyces cerevisiae S288c) | MRPl20 | | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural  | 1.276 | 0.389 | 0.30 |
|P23242| Probable 2-methylcitrate dehydratase (OS=Saccharomyces cerevisiae S288c) | Pmhl1; Vpr002 | | metabolic process | cytoplasm;membrane;mitochondrion | catalytic  | 19.53 | 5 | 5.978 | 0.31 |
|P40047| Aldehyde dehydrogenase 5, mitochondrial (OS=Saccharomyces cerevisiae S288c) | ALC5; YER073 | | metabolic process | mitochondrial;organellar lumen | catalytic  | 3.146 | 0.968 | 0.31 |
|P40769| Kynurenine 3-monooxygenase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | BNA4; YBL098 | | metabolic process | membrane;mitochondrion | catalytic  | 0.269 | 0.083 | 0.31 |
|P48015| Aminomethyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | GCVL1; YDR019 | | metabolic process | mitochondrial | catalytic  | 11.21 | 7 | 3.489 | 0.31 |
|P41921| Glutathione reductase (OS=Saccharomyces cerevisiae S288c) | GLO1; YPL091 | | cellular homeostasis;metabolic process;regulation of biological process;response to stimulus | cytoplasm;cytosol;mitochondrion;nucleus | antioxidant  | 0.241 | 0.075 | 0.31 |
|Q05667| ABC1 family protein MCP2 (OS=Saccharomyces cerevisiae S288c) | YLR253; YCR99 | | cell organization and biogenesis | membrane;mitochondrion | 0.218 | 0.068 | 0.31 |
|P5191| Dna1 homolog 1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | MDG1; YFL016 | | cell organization and biogenesis;metabolic process | mitochondrial;organellar lumen | enzyme regulator  | 4.722 | 1.477 | 0.31 |
|P52374| Cysteine desulfurase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | NPS1; YCL017 | | cell organization and biogenesis;cellular homeostasis;metabolic process | mitochondrial;nucleus | catalytic  | 2.594 | 0.817 | 0.31 |
|P08624| Dihydrolipoamide dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | LPD1; YFL018 | | cellular homeostasis;metabolic process;regulation of biological process | mitochondrial;organellar lumen | catalytic  | 30.62 | 3 | 9.701 | 0.32 |
|P38172| MIOREX complex component 3 (OS=Saccharomyces cerevisiae S288c) | YBL095 | | | membrane;mitochondrion | 0.968 | 0.311 | 0.32 |
|P7558| 375 ribosomal protein PET123, mitochondrial (OS=Saccharomyces cerevisiae S288c) | PET123; YOR115 | | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural  | 1.448 | 0.468 | 0.32 |
|P27929| 375 ribosomal protein NAM9, mitochondrial (OS=Saccharomyces cerevisiae S288c) | NAM9; YNL137 | | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion;ribosome | RNA  | 0.931 | 0.301 | 0.32 |
|P17505| Malate dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | MDH1; YKL085 | | metabolic process | mitochondrial;organellar lumen | catalytic  | 99 | 32.40 | 5 | 0.33 |
|Q05892| MIOREX complex component 2 (OS=Saccharomyces cerevisiae S288c) | YLR290; C; COO11; YLR290 | | | | catalytic  | 3.217 | 1.054 | 0.33 |
|P21771| 375 ribosomal protein S258, mitochondrial (OS=Saccharomyces cerevisiae S288c) | MRPS12; YDR337 | | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA  | 0.833 | 0.274 | 0.33 |
|P30902| ATP synthase subunit d, mitochondrial (OS=Saccharomyces cerevisiae) | ATP7; YKL016 | | metabolic process;transport | membrane;mitochondrion | catalytic  | 5.105 | 1.683 | 0.33 |
P4917  Uncharacterized mitochondrial carrier YNO45W [OS=Saccharomyces cerevisiae S288c]    85060  6  YPR045 W; YPR045 W  metabolic process, transport     membrane, mitochondrial    structural molecule activity, transport activity 0.778 0.259 0.33
P53736  Uncharacterized protein YNR040W [OS=Saccharomyces cerevisiae S288c]    85577  6  YNR040 W; YNR040 W  mitochondrial  1.154 0.389 0.34
P53326  Uncharacterized protein YGR266W [OS=Saccharomyces cerevisiae S288c]    85318  2  YGR266 W; YGR266 W  membrane, mitochondrial  1.081 0.369 0.34
P56950  Heat shock protein SSc1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85350  3  SSc1; YPR045 C  cell organization and biogenesis, metabolic process, regulation of biological process, transport     membrane, mitochondrial, nucleus, organelle lumen    catalytic activity, enzyme regulator activity, nucleotide binding, protein binding 51.75 17.95 0.35
P56406  Mitochondrial intermembrane space import and assembly protein A0 [OS=Saccharomyces cerevisiae S288c]  85363  9  MIA40; YKL195 W  cellular component movement, metabolic process, response to stimulus, transport     membrane, mitochondrial    catalytic activity, protein binding, transport activity 2.3 0.817 0.36
Q6485  Autophagy-related protein 33 [OS=Saccharomyces cerevisiae S288c]    85107  0  ATG33; YLR356 W  cell communication, metabolic process, response to stimulus     membrane, mitochondrial    catalytic activity, transport activity 2.162 0.778 0.36
P21306  ATP synthase subunit epsilon, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85585  7  ATP15; YPL271 W  metabolic process, transport     membrane, mitochondrial    catalytic activity, transport activity 2.162 0.778 0.36
P21101  Succinate dehydrogenase (ubiquinone) iron-sulfur subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85068  5  SDH2; YLL041 C  metabolic process, transport     membrane, mitochondrial    catalytic activity, metal ion binding 32.83 9 12.11 0.37
Q3E824  Uncharacterized protein YOR020W-A [OS=Saccharomyces cerevisiae S288c]  14664  80  YOR020 W-A  mitochondrial, transport     membrane, mitochondrial    5.813 2.162 0.37
P32473  Pyruvate dehydrogenase E1 component subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85252  2  PDH1; YBR221 C  metabolic process     mitochondrial, organelle lumen    catalytic activity 10.28 8 3.833 0.37
P46841  D-lactate dehydrogenase [cytochrome b] 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85137  6  DLD2; YDL178 W  metabolic process     mitochondrial, organelle lumen    catalytic activity, nucleotide binding, protein binding 1.829 0.682 0.37
P53266  Cytochrome oxidase assembly protein SHY1 [OS=Saccharomyces cerevisiae S288c]  85300  9  SHY1; YGR112 W  cell organization and biogenesis     membrane, mitochondrial    protein binding 1.783 0.668 0.37
P50044  Cytochrome c iso-1 [OS=Saccharomyces cerevisiae S288c]    85350  7  CYC1; YVR048 W  metabolic process, transport     mitochondrial    metal ion binding, protein binding 12.33 5 4.623 0.37
Q12374  Nuclear control of ATPase protein 2 [OS=Saccharomyces cerevisiae S288c]    85627  8  NCA2; YPR155 W  metabolic process     membrane, mitochondrial    0.565 0.212 0.38
P20967  2-oxoglutarate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]    85468  1  KG01; YIL125 W  metabolic process     cytosol, mitochondrial, organelle lumen    catalytic activity 13.78 5 5.201 0.38
P28241  Isocitrate dehydrogenase (NAD) subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]    85430  3  IDH2; YOR136 W  metabolic process     mitochondrial, organelle lumen    catalytic activity, metal ion binding, nucleotide binding, protein binding, RNA binding 6.197 2.34 0.38
P509440  C-1-tetrahydrofolate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c]    85237  8  MIS1; YBR084 W  metabolic process     cytosol, mitochondrial    catalytic activity, nucleotide binding 1.668 0.693 0.38
P40945  Homoisocitrate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85471  4  LYS12; YIL094 C  metabolic process     mitochondrial    catalytic activity, metal ion binding, nucleotide binding 6.499 2.481 0.38
P07143  Cytochrome c1, heme protein, mitochondrial [OS=Saccharomyces cerevisiae S288c]    85423  1  CYT1; YDR065 W  metabolic process, transport     cytosol, mitochondrial    metal ion binding 19.30 9 7.377 0.38
P23641  Mitochondrial phosphate carrier protein [OS=Saccharomyces cerevisiae S288c]    85354  0  MPI1; YJR077 C  metabolic process, transport     membrane, mitochondrial    protein binding, structural molecule activity, transport activity 26.82 6 10.36 0.39
P16622  Ferrochelatase, mitochondrial [OS=Saccharomyces cerevisiae S288c]    85434  7  HEM15; YOR176 W  metabolic process     membrane, mitochondrial    catalytic activity 5.579 2.162 0.39
P40172  Sensitive to high expression protein 9, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85200  2  SIE9; YDR393 W  cell organization and biogenesis membrane,mitochondrion  0.374  0.172  0.46
P22353  S45 ribosomal protein L8, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85338  2  MRPL8; YL063 C  cell organization and biogenesis;metabolic process mitochondrion,ribosome structural molecule activity  0.359  0.166  0.46
P39925  Mitochondrial respiratory chain complexes assembly protein AFG3 (OS=Saccharomyces cerevisiae S288c)  85673  7  AFG3; YER017 C  cell organization and biogenesis;metabolic process;response to stimulus,transport membrane,mitochondrion catalytic activity;metal ion binding;protein binding  1.228  0.569  0.46
P38884  Altered inheritance of mitochondria protein 18, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85660  5  AIM18; YHR198 C  mitochondrion catalytic activity  0.311  0.145  0.47
Q06493  LETM1 domain-containing protein YLH47, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85624  3  YLH47; YPR125 W  cell organization and biogenesis;transport membrane,mitochondrion catalytic activity  1.043  0.487  0.47
P80711  Enoyl-[acyl-carrier protein] reductase (NADPH, B-specific), mitochondrial (OS=Saccharomyces cerevisiae S288c)  85231  4  ETR1; YBR206 C  metabolic process mitochondrion,organellle lumen catalytic activity;DNA binding;metal ion binding  7.111  3.329  0.47
P32335  Protein MSS51, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85090  0  MSS51; YLR203 C  metabolic process;regulation of biological process membrane,mitochondrion protein binding;translation regulator activity  1.512  0.711  0.47
Q01532-1  Cysteine proteinase 1, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85439  0  AIM41; YDR215 C  mitochondrial catalytic activity  1.61  0.778  0.48
Q07349  MIOREX complex component 9 (OS=Saccharomyces cerevisiae S288c)  85153  5  YDL027 C; MRK9; YDL027 C  endoplasmic reticulum;membrane,mitochondrion catalytic activity  1.913  0.931  0.49
P40008  Protein FMP52, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85672  1  FMP52; YER004 W  endoplasmic reticulum,membrane,mitochondrion catalytic activity  2.162  1.054  0.49
P53292  375 ribosomal protein S35, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85307  5  MRPS3 5; YER165 W  cell organization and biogenesis;metabolic process mitochondrion,ribosome structural molecule activity  1.512  0.738  0.49
Q08822  Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85453  8  CIR2; YDR356 W  metabolic process;transport membrane,mitochondrion catalytic activity;metal ion binding;nucleotide binding  3.019  1.488  0.49
P19882  Heat shock protein 60, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85096  3  HSP90; YLR259 C  cell organization and biogenesis;metabolic process;regulation of biological process,transport cytoplasm,cytosol,membrane,mitochondrion ,organellle lumen catalytic activity;DNA binding;nucleotide binding;protein binding  23.81  11.74  0.49
P34241  Succinate dehydrogenase (ubiquinone) cytochrome b subunit, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85371  6  SDH3; YKL141 W  cell organization and biogenesis;metabolic process;regulation of biological process,transport membrane,mitochondrion catalytic activity;metal ion binding  1.276  0.638  0.50
Q02776  Mitochondrial import inner membrane translocase subunit TIM50 (OS=Saccharomyces cerevisiae S288c)  85604  2  TIM50; YPL063 W  cell organization and biogenesis;metabolic process;transport membrane,mitochondrion catalytic activity;protein binding;transport er activity  7.483  3.771  0.50
P43616  Cys-Gly metalloprotease dag1 (OS=Saccharomyces cerevisiae S288c)  85060  5  DUG1; YFR044 C  metabolic process cytoplasm,mitochondrion,ribosome catalytic activity;metal ion binding  1.354  0.585  0.51
P00950  Phosphoglycerate mutase 1 (OS=Saccharomyces cerevisiae S288c)  85370  5  GPM1; YKL152 C  metabolic process;regulation of biological process cytoplasm,cytosol,membrane,mitochondrion catalytic activity  2.981  1.512  0.51
P07342  Acetolactate synthase catalytic subunit, mitochondrial (OS=Saccharomyces cerevisiae S288c)  85513  5  ILV2; YMR110 BW  metabolic process mitochondrion catalytic activity;metal ion binding;nucleotid e binding;protein binding  5.236  2.665  0.51
P50085  Prohibitin-2 (OS=Saccharomyces cerevisiae S288c)  85314  6  PHB2; YGR231 C  cell organization and biogenesis;metabolic process;regulation of biological process membrane,mitochondrion protein binding  4.926  2.511  0.51
| S288c | [OS=Saccharomyces cerevisiae] oxodicarboxylate carrier 2 | 85462 2 | COX2; Q0250 | metabolic process, transport | membrane, mitochondrion | catalytic activity, metal ion binding, protein binding, transport activity | 3.642 | 2.162 | 0.59 |
|-------|----------------------------------------------------------|----------|-------------|---------------------------|------------------------|-------------------------------------------------|---------|---------|-------|
| Q08179 | Mitochondrial distribution and morphology protein 38 [OS=Saccharomyces cerevisiae S288c] | 85413 0 | MDM3; R; YOL027 C | cell organization and biogenesis, cellular homeostasis; regulation of biological process; transport | membrane, mitochondrion | 5.683 | 3.467 | 0.61 |
| Q03798 | Altered inheritance of mitochondrial protein 36, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85518 9 | AIM19; YMR157C | metabolic process, transport | membrane, mitochondrion | 1.336 | 0.833 | 0.62 |
| Q2298 | uncharacterized ABC transporter ATP-binding protein YDR616W [OS=Saccharomyces cerevisiae S288c] | 85163 3 | YDR061 W; YDR061 W | metabolic process, transport | membrane, mitochondrion | catalytic activity, nucleotide binding | 0.425 | 0.266 | 0.63 |
| P31332 | Mitochondrial oxaloacetate transport protein [OS=Saccharomyces cerevisiae S288c] | 85373 9 | DAC1; YKL120 W | metabolic process, transport | membrane, mitochondrion | structural molecule activity, transport activity | 3.813 | 3.642 | 0.63 |
| P31815 | Tricarboxylate transport protein [OS=Saccharomyces cerevisiae S288c] | 85259 4 | CTP1; YBR291 C | metabolic process, transport | membrane, mitochondrion | structural molecule activity, transport activity | 0.389 | 0.245 | 0.63 |
| Q0643 | mitochondrial dicarboxylate transporter [OS=Saccharomyces cerevisiae S288c] | 85106 3 | DSC1; YLR348 C | metabolic process, transport | membrane, mitochondrion | structural molecule activity, transport activity | 1.154 | 0.73 | 0.63 |
| Q0648 | MIOREX complex component 10 [OS=Saccharomyces cerevisiae S288c] | 85187 6 | YDR282 C; MRX10; YDR282 C | metabolic process, transport | membrane, mitochondrion | 0.35 | 0.222 | 0.63 |
| P38702 | mitochondrial carrier protein LEU5 [OS=Saccharomyces cerevisiae S288c] | 85639 1 | LEU5; YHR002 W | metabolic process, transport | membrane, mitochondrion | structural molecule activity, transport activity | 0.334 | 0.212 | 0.63 |
| P40012 | protoporphyrinogen oxidase [OS=Saccharomyces cerevisiae S288c] | 85673 3 | HEM14; YER014 W | metabolic process | membrane, mitochondrion | catalytic activity | 1.482 | 0.947 | 0.64 |
| P32266 | Dinamin-like GTPase MGM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85438 6 | MGM1; YDR211 C | cell organization and biogenesis | membrane, mitochondrion | catalytic activity, nucleotide binding, protein binding | 0.28 | 0.179 | 0.64 |
| P38669 | Pentamidine resistance factor, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85444 0 | PNT1; YDR266 W | cell organization and biogenesis, response to stimulus | membrane, mitochondrion | 0.259 | 0.166 | 0.64 |
| P47236 | Threonine–tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85364 0 | MSL1; YKL194 C | metabolic process | cytoplasm, mitochondrion, organelle lumen | catalytic activity, nucleotide binding, RNA binding | 0.233 | 0.15 | 0.64 |
| P46945 | ATP synthase subunit 5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85189 2 | ATP5; YDR298 C | metabolic process, transport | membrane, mitochondrion | catalytic activity, transport activity | 9 | 5.813 | 0.65 |
| P47873 | D-arabinose 1,4-lactone oxidase [OS=Saccharomyces cerevisiae S288c] | 85488 8 | ALO1; YML086C | metabolic process, response to stimulus | membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding | 3.299 | 2.162 | 0.66 |
| Q08223 | Altered inheritance of mitochondrial protein 39, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85410 3 | AIM39; YOL053 W | cytoplasm, membrane, mitochondrion | 0.711 | 0.468 | 0.66 |
| P07123 | Mitochondrial import receptor subunit TOM70 [OS=Saccharomyces cerevisiae S288c] | 85560 2 | TOM70; YNL212 W | cell organization and biogenesis, transport | membrane, mitochondrion | protein binding, transport activity | 1.728 | 1.154 | 0.67 |
| P33111 | Mitochondrial pyruvate carrier 3 [OS=Saccharomyces cerevisiae S288c] | 85315 8 | FMP43; MPC3; YDR243 W | transport | membrane, mitochondrion | transporter activity | 3.154 | 0.778 | 0.67 |
| P03539 | Glyceraldehyde-3-phosphate dehydrogenase 3 [OS=Saccharomyces cerevisiae S288c] | 85310 6 | TDM3; YGR192 C | cell death, metabolic process | cytoplasm, cytosol, membrane, mitochondrion, nucleus | catalytic activity, nucleotide binding, RNA binding | 3.962 | 2.675 | 0.68 |
| P38225 | Mitochondrial outer membrane protein OM14 [OS=Saccharomyces cerevisiae S288c] | 85253 1 | OM14; YBR230 C | transport | membrane, mitochondrion | 9 | 6.197 | 0.69 |
| P54003 | Protein SUR7 [OS=Saccharomyces cerevisiae S288c] | 85495 3 | SUR7; YML052W | cell differentiation, transport | membrane, mitochondrion | 0.848 | 0.583 | 0.69 |
| Q09297 | Mitochondrial 2-oxocarboxylate carrier 2 [OS=Saccharomyces cerevisiae S288c] | 85419 7 | ODC2; YDR222 W | metabolic process, transport | membrane, mitochondrion | structural molecule activity, transport activity | 0.778 | 0.54 | 0.69 |
| ID     | Name and Description                                                                 | Function(s)                                 | Localization                  | Molecular Weight (kDa) | Protein Binding | Activity Category                        | Activity Value |
|--------|--------------------------------------------------------------------------------------|---------------------------------------------|--------------------------------|------------------------|-----------------|-------------------------------------------|----------------|
| P53220 | Mitochondrial import inner membrane translocate subunit TIM21 (S. cerevisiae)         | cell organization and biogenesis; transport | membrane, mitochondrion      | 80.5                   | 0.317 | structural molecule activity; transport activity | 0.596          |
| Q12251 | Uncharacterized mitochondrial carrier YPR011C (S. cerevisiae)                         | metabolic process; transport                | membrane, mitochondrion      | 94.1                   | 0.283 | catalytic activity; metal ion binding     | 0.283          |
| P53163 | mitochondrial metalloendopeptidase OMA1 (S. cerevisiae)                              | metabolic process                           | membrane, mitochondrion      | 3.64                   | 0.254 | catalytic activity; metal ion binding     | 0.254          |
| P00424 | Cytochrome c oxidase poly peptide 5A, mitochondrial (S. cerevisiae)                  | metabolic process; transport                | membrane, mitochondrion      | 8.0                    | 0.187 | catalytic activity; transport activity     | 0.187          |
| Q03327 | Mitochondrial fusion and transport protein Ugo1 (S. cerevisiae)                      | cell organization and biogenesis; metabolic process | membrane, mitochondrion      | 17.3                   | 0.183 | protein binding; structural molecule activity | 0.183          |
| Q02883 | N-acetyl-phosphatidylethanolamine-hydrorylating phospholipase D, mitochondrial (S. cerevisiae) | metabolic process                           | membrane, mitochondrion      | 6.9                    | 0.183 | catalytic activity; metal ion binding     | 0.183          |
| P39869 | Sorting assembly machinery 50 kDa subunit (S. cerevisiae)                            | cell organization and biogenesis; transport | membrane, mitochondrion      | 5.4                    | 0.183 | catalytic activity; transport activity     | 0.183          |
| P40215 | External NADH-ubiquinone oxidoreductase 1, mitochondrial (S. cerevisiae)             | cell organization and biogenesis; transport | mitochondrion                | 4.3                    | 0.183 | catalytic activity; NADH binding           | 0.183          |
| P38988 | Mitochondrial GTP/GDP carrier protein 1 (S. cerevisiae)                              | cell organization and biogenesis; regulatory | membrane, mitochondrion      | 3.4                    | 0.183 | structural molecule activity; transport activity | 0.183          |
| P49435 | Cytochrome c oxidase protein 20, mitochondrial (S. cerevisiae)                       | cell organization and biogenesis; transport | membrane, mitochondrion      | 2.5                    | 0.183 | catalytic activity; transport activity     | 0.183          |
| P49458 | Fatty aldehyde dehydrogenase HFD1 (S. cerevisiae)                                    | cell organization and biogenesis; molecular homeostasis; metabolic process; transport | membrane, mitochondrion      | 2.2                    | 0.183 | catalytic activity; endoplasmic reticulum endosome; membrane; mitochondrial | 0.183          |
| P25087 | Sterol 24-C-methyl transferase (S. cerevisiae)                                       | cell organization and biogenesis; transport | membrane, mitochondrion      | 2.1                    | 0.183 | catalytic activity; endoplasmic reticulum | 0.183          |
| P03721 | Respiratory supercomplex factor 2, mitochondrial (S. cerevisiae)                     | cell organization and biogenesis            | membrane, mitochondrion      | 2.0                    | 0.183 | catalytic activity; transport activity     | 0.183          |
| P07253 | cytochrome B pre-mRNA-processing protein 6 (S. cerevisiae)                           | cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrion, ribosome      | 2.0                    | 0.183 | catalytic activity; transport activity     | 0.183          |
| P18077 | ATP synthase subunit gamma, mitochondrial (S. cerevisiae)                            | metabolic process; transport                | membrane, mitochondrion      | 2.0                    | 0.183 | catalytic activity; transport activity     | 0.183          |
| P40508 | Uncharacterized protein YLO77C (S. cerevisiae)                                       | cell organization and biogenesis; transport | mitochondrion                | 1.9                    | 0.183 | catalytic activity; transport activity     | 0.183          |
| P38127 | mitochondrial carrier protein RIM2 (S. cerevisiae)                                    | cell organization and biogenesis; metabolic process; transport | membrane, mitochondrion      | 1.8                    | 0.183 | catalytic activity; nuclear export binding | 0.183          |
| P27697 | Atypical kinase COQ8, mitochondrial (S. cerevisiae)                                  | metabolic process                           | membrane, mitochondrion, organelle lumen | 1.8                    | 0.183 | catalytic activity; nuclear export binding | 0.183          |
| P38239 | ADP,ATP carrier protein 2 (S. cerevisiae)                                            | cell death; metabolic process; transport    | membrane, mitochondrion      | 1.8                    | 0.183 | catalytic activity; transport activity     | 0.183          |
| P53206 | putative cysteine synthase (S. cerevisiae)                                            | metabolic process                           | membrane, mitochondrion      | 1.8                    | 0.183 | catalytic activity; transport activity     | 0.183          |
| P33110 | ATP-dependent permease MDL1, mitochondrial (S. cerevisiae)                           | metabolic process                           | membrane, mitochondrion      | 1.8                    | 0.183 | catalytic activity; nuclear export binding | 0.183          |
| [OS=Saccharomyces cerevisiae S288c] | C | process;transport | cytoplasm;membrane;mitochondrion | catalytic activity;metabolite binding | 6.743 | 5.813 | 0.86 |
|-------------------------------------|---|------------------|-------------------------------|----------------------------------|--------|--------|-----|
| P25349 | flavoprotein-like protein YCP4 [OS=Saccharomyces cerevisiae S288c] | 85036 0 | YCP4; YCR004 C | metabolic process;regulation of biological process | cytoplasm;mitochondrion | catalytic activity;transport activity | 1.555 | 1.346 | 0.87 |
| P40886 | cytochrome c oxidase assembly protein cox15 [OS=Saccharomyces cerevisiae S288c] | 85688 4 | COX15; YER141 W | cell organization and biogenesis;membrane transport | membrane;mitochondrion | catalytic activity;transport activity | 4.125 | 3.758 | 0.91 |
| Q01852 | mitochondrial import inner membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c] | 85479 0 | TIM44; YIL022 W | transport | membrane;mitochondrion | nucleotide binding;protein binding | 11.79 8 | 10.78 8 | 0.91 |
| P00890 | citrate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85573 2 | CIT1; YMR001 C | metabolic process;transport | cytosol;mitochondrion;organellar lumen | catalytic activity | 0.968 | 0.968 | 1.00 |
| Q08023 | protein FMP25, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85076 6 | FMP25; YLR077 W | cell organization and biogenesis | membrane;mitochondrion | catalytic activity;protein binding | 0.701 | 0.701 | 1.00 |
| P25573 | mitochondrial inner membrane 1-AAD protease supercomplex subunit MAG1 [OS=Saccharomyces cerevisiae S288c] | 85031 3 | MAG1; YCL044 C | metabolic process | membrane;mitochondrion | catalytic activity;protein binding | 0.484 | 0.484 | 1.00 |
| P08466 | mitochondrial nuclease [OS=Saccharomyces cerevisiae S288c] | 85322 2 | NUC1; YLR208 C | cell death;metabolic process | membrane;mitochondrion;nucleus | catalytic activity;metal ion binding | 1.336 | 1.336 | 1.00 |
| P00360 | glyceroldehyde-3-phosphate dehydrogenase 1 [OS=Saccharomyces cerevisiae S288c] | 85339 5 | TDH1; YIL052 W | metabolic process | cytoplasm;cytosol;mitochondrion | catalytic activity;metal ion binding | 0.823 | 0.823 | 1.00 |
| Q01574 | acetyl-Coenzyme A synthetase 1 [OS=Saccharomyces cerevisiae S288c] | 85124 5 | ACS1; YAL054 C | cell organization and biogenesis;membrane transport | cytoplasm;cytosol;endoplasmic reticulum;mitochondrion;nucleus | catalytic activity;metal ion binding | 0.624 | 0.624 | 1.00 |
| P06668 | methyltransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85191 1 | OMS1; YDR316 W | metabolic process | membrane;mitochondrion | catalytic activity | 0.484 | 0.484 | 1.00 |
| Q12375 | mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c] | 85429 7 | ORT1; YDR130 W | metabolic process;transport | membrane;mitochondrion | structural molecule activity;transport activity | 0.54 | 0.54 | 1.00 |
| P53163 | S45 ribosomal protein L12, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85281 1 | MPM1; YGL068 W | cell organization and biogenesis;membrane transport | mitochondrial;ribosome | structural molecule activity | 1.31 | 1.31 | 1.00 |
| P40496 | 37S ribosomal protein S25, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85471 5 | RSM25; YIL093C | cell organization and biogenesis;membrane transport | mitochondrial;ribosome | structural molecule activity | 0.468 | 0.468 | 1.00 |
| P39533 | Homocitrate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85323 0 | ACO2; YIL200 C | metabolic process | mitochondrial | catalytic activity;metal ion binding | 0.17 | 0.17 | 1.00 |
| P34224 | Uncharacterized protein YBL059W [OS=Saccharomyces cerevisiae S288c] | 85222 1 | YBL059 W; YBL059 W | membrane;mitochondrion | catalytic activity;protein binding | 0.468 | 0.468 | 1.00 |
| P34222 | Peptidyl-tRNA hydrolase 2 [OS=Saccharomyces cerevisiae S288c] | 85222 3 | PTI2; YBL057 W | regulation of biological process | cytoplasm;cytosol;mitochondrion | catalytic activity;protein binding | 0.425 | 0.425 | 1.00 |
| Q02999 | Uncharacterized protein YDR119W-A [OS=Saccharomyces cerevisiae S288c] | 37999 70 | COX26; YDR119 W-A | metabolic process | membrane;mitochondrion | structural molecule activity | 1.154 | 1.154 | 1.00 |
| Q06510 | lysophosphatidylcholine acyltransferase [OS=Saccharomyces cerevisiae S288c] | 85626 2 | TAZ1; YPR140 W | cell organization and biogenesis;membrane transport | membrane;mitochondrion | catalytic activity | 0.194 | 0.194 | 1.00 |
| P54857 | lipase 2 [OS=Saccharomyces cerevisiae S288c] | 85162 8 | TGL2; YDR058 C | metabolic process;transport | mitochondrial | catalytic activity | 0.369 | 0.369 | 1.00 |
| P32463 | Acyl carrier protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85364 2 | ACP1; YKL102 C | metabolic process;transport | mitochondrial | catalytic activity | 0.259 | 0.259 | 1.00 |
| Q05867 | Uncharacterized protein YLR283W, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85098 8 | YLR283 W; YLR283 W | endoplasmic reticulum;membrane;mitochondrion | catalytic activity | 0.11 | 0.11 | 1.00 |
| P40581 | pentiredoxin HYK1 [OS=Saccharomyces cerevisiae S288c] | 85485 5 | HYK1; YBR037 W | metabolic process;response to stimulus | cytoplasm;cytosol;mitochondrion;organellar lumen | catalytic activity | 0.259 | 0.259 | 1.00 |
| Q12328 | mitochondrial import inner membrane translocase subunit TIM22 [OS=Saccharomyces cerevisiae S288c] | 85130 9 | TIM22; YDL217 C | cell organization and biogenesis;transport | cytosol;membrane;mitochondrion | catalytic activity;protein binding | 0.233 | 0.233 | 1.00 |
| P04039 | cytochrome c oxidase polypeptide VIII, mitochondrial | 85111 1 | COM8; YLR395 | metabolic process;transport | membrane;mitochondrion | catalytic activity | 0.778 | 0.778 | 1.00 |
| Gene ID  | Description                                                                 | Cellular Localization                  | Interaction              | Remarks                                                                 | C      | Score 1 | Score 2 |
|---------|------------------------------------------------------------------------------|----------------------------------------|--------------------------|------------------------------------------------------------------------|-------|--------|--------|
| P38816  | Thioredoxin reductase 2, mitochondrial                                       | cytoplasm/mitochondrion               | antioxidant activity     | catalytic activity                                                     | 0.136 | 0.136  | 1.00   |
| P14693  | Sorting assembly machinery 35 kDa subunit                                    | membrane/mitochondrion               | protein binding          | catalytic activity                                                     | 0.334 | 0.334  | 1.00   |
| Q20863  | Ubiquitin carboxyl-terminal hydrolase 16                                     | membrane/mitochondrion               | catalytic activity       |                                                                         | 0.072 | 0.072  | 1.00   |
| P00358  | Glyceraldehyde-3-phosphate dehydrogenase 2                                   | cytoplasm/cytosol/membrane/mitochondrion | catalytic activity       | nuclear                                                    | 1.721 | 2.008  | 1.17   |
| P21560  | Protein CBP3, mitochondrial                                                  | membrane/mitochondrion/mitosomes     | catalytic activity       | catalytic activity/metal ion binding/nucleotide e binding/protein binding | 0.682 | 0.812  | 1.19   |
| P08539  | Guanine nucleotide-binding protein alpha-1 subunit                           | cytosol/endosome/membrane             | catalytic activity       | catalytic activity/metal ion binding/nucleotide e binding/protein binding | 0.359 | 0.431  | 1.20   |
| P22136  | ATPase expression protein 2, mitochondrial                                    | mitochondrion                         | RNA binding              |                                                                         |       | 2.398  | 1.23   |
| P40416  | Iron-sulfur clusters transporter ATM1, mitochondrial                         | membrane/mitochondrion               | catalytic activity       | nuclear binding/protein binding                                        | 0.035 | 0.546  | 1.21   |
| P39882  | Isocitrate dehydrogenase [NADP] [OS=Saccharomyces cerevisiae S288c]           | cytoplasm/mitochondrion               | catalytic activity       | nuclear binding/mitochondrion                                         |       | 1.943  | 2.398  |
| P05060  | Phosphoglycerate kinase                                                       | cytoplasm/mitochondrion               | catalytic activity       | nuclear binding/mitochondrion                                         |       | 2.415  | 2.981  |
| Q07651  | SUR7 family protein FMN45                                                     | membrane/mitochondrion               |                                                                         |                                                                         |       | 3.125  | 3.924  |
| P10823  | Guanine nucleotide-binding protein alpha-2 subunit                           | cytosol/mitochondrion                 | catalytic activity       | catalytic activity/metal ion binding/nucleotide e binding/protein binding | 0.978 | 1.346  | 1.38   |
| P53230  | Phosphatidate cytidylyltransferase, mitochondrial                            | membrane/mitochondrion/organellar lumen | catalytic activity       |                                                                         |       | 0.292  | 0.407  |
| P50887  | MICOS subunit MIC26                                                          | membrane/mitochondrion               |                                                                         |                                                                         |       | 0.638  | 0.931  |
| P37292  | UPP0744 protein YSC83                                                        | membrane/mitochondrion               |                                                                         |                                                                         |       | 0.233  | 0.369  |
| P32738  | 4-hydroxybenzoate polyphenyltransferase, mitochondrial                      | membrane/mitochondrion               |                                                                         |                                                                         |       | 0.292  | 0.468  |
| Q12289  | Mitochondrial carnite carrier                                                 | membrane/mitochondrion               |                                                                         |                                                                         |       | 0.931  | 1.683  |
| Q08245  | protein ZEO1 [OS=Saccharomyces cerevisiae S288c]                             | membrane/mitochondrion               |                                                                         |                                                                         |       | 2.362  | 4.012  |
| P12230  | Sphingolipid long chain base responsive protein LSP1                         | cytoplasm/mitochondrion               |                                                                         |                                                                         | 14.84 | 28.28  | 1.90   |
| Q12466  | triCAB-1 [OS=Saccharomyces cerevisiae S288c]                                 | endoplasmic reticulum/membrane/mitochondrion |                                                                         |                                                                         | 0.191 | 0.369  | 1.93   |
| Q00405  | ATP synthase subunit f, mitochondrial                                         | membrane/mitochondrion               |                                                                         |                                                                         |       | 1.512  | 2.981  |
| P8809   | Cytochrome c mitochondrial import factor CYC2                                 | membrane/mitochondrion               |                                                                         |                                                                         |       | 0.093  | 0.194  |
| P0472 | Mitochondrial inner membrane i-AAA protease supercomplex subunit MGR3 (S. cerevisiae) | 85514 2 | MGR3; YMR115W | metabolic process | membrane, mitochondrion | protein binding | 0.15 | 0.322 | 2.15 |
| P29311 | Protein BMH1 (S. cerevisiae) | 85692 4 | BMH1; YER177W | cell differentiation, cell growth, cell organization and biogenesis, metabolic process, regulation of biological process, response to stimulus | cytoplasm, membrane, nucleus | DNA binding; protein binding | 0.136 | 0.282 | 2.15 |
| Q00873 | Cytochrome c heme lyase (S. cerevisiae) | 85737 5 | CTR2; YKL087C | cell organization and biogenesis, metabolic process | membrane, mitochondrion | catalytic activity, metal ion binding | 0.166 | 0.359 | 2.16 |
| P38526 | NADH-cytochrome b5 reductase 1 (S. cerevisiae) | 85476 8 | CIB1; YDL43C | metabolic process | endoplasmic reticulum, membrane, mitochondrion, nucleus | catalytic activity | 0.334 | 0.778 | 2.33 |
| P16603 | NADPH-cytochrome P450 reductase (S. cerevisiae) | 85643 8 | NCP1; YHR042W | metabolic process | cytoplasm, cytosol, endoplasmic reticulum, membrane, mitochondrion | catalytic activity, metal ion binding, nucleotide binding | 0.194 | 0.604 | 3.11 |
| Q02191 | ABC1 family protein YPL109C, mitochondrial (S. cerevisiae) | 85599 5 | YPL109C; YPL109C | mitochondrial | 0.059 | 0.219 | 4.39 |
| P54115 | Magnesium-activated aldehyde dehydrogenase, cytosolic (S. cerevisiae) | 85604 4 | ALD6; YPL061W | metabolic process, response to stimulus | cytoplasm, cytosol, mitochondrial | catalytic activity | 0.077 | 0.346 | 4.49 |
| P34231 | Uncharacterized protein YKL187C (S. cerevisiae) | 85364 8 | FAT3; YKL187C; YKL187C | cell organization and biogenesis, transport | membrane, mitochondrion | 0.093 | 0.425 | 4.57 |
| P38373 | Protein M5P1 (S. cerevisiae) | 85291 5 | M5P1; YGR028W | cell organization and biogenesis, metabolic process, regulation of biological process, response to stimulus, transport | membrane, mitochondrion, nucleus | catalytic activity, metal ion binding, protein binding, RNA binding | 0.122 | 0.585 | 4.80 |
| P38825 | Protein TOM71 (S. cerevisiae) | 85651 7 | TOM71; YHR117W | transport | membrane, mitochondrion | protein binding, transport activity | 0.061 | 0.512 | 8.39 |
| P39518 | Long-chain fatty acid --CoA ligase 2 (S. cerevisiae) | 85673 4 | FAA2; YER015W | metabolic process, transport | cytoplasm, mitochondrion | catalytic activity, metal ion binding | 0.055 | 0.619 | 11.25 |
| Q03940 | Trkalpha-3 (S. cerevisiae) | 85490 3 | TC83; YML007C | cell organization and biogenesis, regulation of biological process | endoplasmic reticulum, membrane, mitochondrion | metal ion binding, protein binding | 0.032 | 0.365 | 11.41 |
Supplemental Table S11. The relative concentrations of proteins in mitochondria purified from WT or ups2Δ cells cultured without LCA. Mitochondria were purified from WT or ups2Δ cells recovered on day 4 of cell culturing without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI ups2 | Ratio ups2 / WT |
|-----------|-------------|----------------|---------|--------------------|--------------------|-------------------|----------|-------------|----------------|
| P37267    | Assembly factor etp4 ([S]-Saccharomyces cerevisiae S288c) | 85192 2 | CBP4 | cell organization and biogenesis | membrane/mitochondrion | catalytic activity; structural activity; transport | 7.111 | 0.233 | 0.03 |
| P81449    | ATP synthase subunit e, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85241 7 | CBP6, YBR120C | cell organization and biogenesis; metabolic process; transport | membrane/mitochondrion | catalytic activity; structural activity; transport | 9 | 0.334 | 0.04 |
| P07253    | Cytochrome b pre-rRNA-processing protein 6 ([S]-Saccharomyces cerevisiae S288c) | 85060 0 | YMR331, YFR049W | cell organization and biogenesis; metabolic process | mitochondrion/ribosome | catalytic activity; protein binding; structural activity; transport | 4.179 | 0.179 | 0.04 |
| P19955    | 37S ribosomal protein YMR31, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85241 7 | CBP6, YBR120C | cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrion/ribosome | catalytic activity; protein binding; structural activity | 26.82 6 | 1.154 | 0.04 |
| P00128    | Cytochrome b-1 complex subunit 7 ([S]-Saccharomyces cerevisiae S288c) | 85214 2 | QCR7, YDR520C | cell organization and biogenesis; metabolic process; transport | membrane/mitochondrion | catalytic activity; structural activity; transport | 34.93 8 | 1.783 | 0.05 |
| P37299    | Cytochrome c oxidase subunit 6A, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85268 4 | COX3, YGL191W | cell organization and biogenesis; metabolic process; transport | membrane/mitochondrion | catalytic activity; structural activity; transport | 18.95 3 | 0.995 | 0.05 |
| P34594    | MIC65 complex subunit MIC65 ([S]-Saccharomyces cerevisiae S288c) | 85006 3 | AIM11, MIC19, YOR011C | cell organization and biogenesis | cytoplasm/mitochondrion | catalytic activity | 4.337 | 0.233 | 0.05 |
| Q12265    | ATP synthase subunit delta, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85156 0 | ATP5A, YDL004W | metabolic process; transport | membrane/mitochondrion | catalytic activity; structural activity; transport | 4.623 | 0.334 | 0.07 |
| P38885    | Altered inheritance of mitochondria protein 46, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85660 6 | AIM46, YHR199C | mitochondrial | catalytic activity | 2.728 | 0.245 | 0.09 |
| P40165    | NAD(P)H-dehydrogenase (complex I) ([S]-Saccharomyces cerevisiae S288c) | 85552 1 | YNL200C, YNL200C | metabolic process | cytoplasm/mitochondrion | catalytic activity; metal ion binding; nucleotide binding | 2.162 | 0.212 | 0.10 |
| P4037     | Cytochrome c oxidase subunit 4, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85268 8 | COX4, YGL187C | cell organization and biogenesis; metabolic process; transport | membrane/mitochondrion | catalytic activity; metal ion binding; nucleotide binding | 42.28 8 | 4.337 | 0.10 |
| P35736    | Uncharacterized protein YKLO10C ([S]-Saccharomyces cerevisiae S288c) | 85381 6 | YKLO10C, YKLO10C | cell organization and biogenesis | membrane | catalytic activity | 0.374 | 0.04 | 0.11 |
| P27068    | Cytochrome c oxidase subunit 6, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85444 8 | COX6, YHR051W | metabolic process; transport | membrane/mitochondrion | catalytic activity; metal ion binding; transport | 7.254 | 0.778 | 0.11 |
| P36141    | Putative redox protein fmp46, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85392 3 | FMP46, YKR049C | metabolic process | mitochondrial | catalytic activity; protein binding | 4.337 | 0.52 | 0.12 |
| Q06481    | Cytochrome c oxidase subunit 5 ([S]-Saccharomyces cerevisiae S288c) | 85030 0 | YOR051, YOR051W | cell organization and biogenesis | membrane/mitochondrion | catalytic activity; protein binding | 6.197 | 0.931 | 0.15 |
| P01175    | Cytochrome b2, mitochondrial ([S]-Saccharomyces cerevisiae S288c) | 85493 3 | CYB2, YMR054C | metabolic process; transport | cytosol/mitochondrion | catalytic activity; metal ion binding; nucleotide binding | 1.639 | 0.189 | 0.15 |
| P38341    | MIC65 complex subunit MIC65 ([S]-Saccharomyces cerevisiae S288c) | 85256 6 | AIM45, MIC12, YBR262C | cell organization and biogenesis | membrane/mitochondrion | catalytic activity | 1.783 | 0.292 | 0.16 |
| Q0892 | MIOREX complex component 2 [OS=Saccharomyces cerevisiae S288c] | B5099 | YLR290C; YCA11; YLR290C | metabolic process | mitochondrion | catalytic activity | 3.217 | 0.54 | 0.17 |
| P40502 | Altered inheritance of mitochondria protein 19, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5472 | AIM115; YIL087C | metabolic process | membrane/mitochondrion | catalytic activity | 1.512 | 0.259 | 0.17 |
| P39525 | 3-o-oxacyl-[acyl-carrier-protein] synthase homolog [OS=Saccharomyces cerevisiae S288c] | B5679 | CEM11; YER060C | metabolic process | mitochondrion | catalytic activity | 2.899 | 0.52 | 0.18 |
| P22353 | 54S ribosomal protein L8, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5338 | MRP8; YIL063C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.848 | 0.166 | 0.20 |
| P08252 | Cytochrome b-c1 complex subunit 8 [OS=Saccharomyces cerevisiae S288c] | B5327 | QCR8; YIL166W | metabolic process; transport | membrane/mitochondrion | catalytic activity; transporter activity | 2.981 | 0.585 | 0.20 |
| P02992 | elongation factor Tu, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5435 | TUF1; YDR187W | cell organization and biogenesis; metabolic process | mitochondrion | catalytic activity; nucleotide binding; RNA binding | 30.62 | 0.017 | 0.20 |
| P08667 | cytochrome b-c1 complex subunit Rieske, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5668 | RIF1; YEL024W | metabolic process; transport | membrane/mitochondrion | catalytic activity; metal ion binding; transporter activity | 55.23 | 4.11 | 0.20 |
| P3823 | Gsp6 protein homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5440 | MGE1; YOR232W | metabolic process; regulation of biological process; transport | membrane/mitochondrion; organelle lumen | enzyme regulator activity; nucleotide binding; protein binding | 1.336 | 0.274 | 0.21 |
| P00424 | Cytochrome c oxidase polypeptide 5A, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5667 | COXSA; YNL052W | metabolic process; transport | membrane/mitochondrion | catalytic activity; transporter activity | 2.511 | 0.52 | 0.21 |
| P23572 | Thioesterase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5044 | TRX3; YCR083W | cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport | cytoplasm; mitochondrion | catalytic activity | 2.511 | 0.52 | 0.21 |
| P04689 | Altered inheritance of mitochondria protein 32 [OS=Saccharomyces cerevisiae S288c] | B5495 | AIM32; YML050W | metabolic process | membrane/mitochondrion | 0.52 | 0.11 | 0.21 |
| P31305 | Mitochondrial 37S ribosomal protein S27 [OS=Saccharomyces cerevisiae S288c] | B5312 | RSM27; YGR215W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 2.162 | 0.468 | 0.22 |
| P08970 | Mitochondrial metal transporter 2 [OS=Saccharomyces cerevisiae S288c] | B5857 | MMT2; YPL224C | cellular homeostasis; regulation of biological process; response to stimulus; transport | membrane/mitochondrion | transporter activity | 0.407 | 0.089 | 0.22 |
| P02608 | 37S ribosomal protein S16, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5609 | MRPS16; YPL013C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 1.683 | 0.389 | 0.23 |
| P1034 | protein PET54 [OS=Saccharomyces cerevisiae S288c] | B5313 | PET54; YGR222W | metabolic process; regulation of biological process | membrane/mitochondrion; organelle lumen | nucleotide binding; RNA binding; translation regulator activity | 1.565 | 0.369 | 0.24 |
| P07500 | External NADH-dequinone oxidoreductase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5147 | NDE2; YDL068W | metabolic process | mitochondrion | catalytic activity; nucleotide binding | 13.67 | 0.329 | 0.24 |
| P06236 | Mitochondrial inner membrane protein SHH4 [OS=Saccharomyces cerevisiae S288c] | B5086 | SHH4; YLR164W | metabolic process | membrane/mitochondrion | catalytic activity; metal ion binding | 3.217 | 0.778 | 0.24 |
| P00127 | Cytochrome b-c1 complex subunit 6 [OS=Saccharomyces cerevisiae S288c] | B5099 | GCR6; YFR033C | metabolic process; transport | membrane/mitochondrion | catalytic activity; transporter activity | 1.371 | 0.334 | 0.24 |
| Q32428 | Probable 2-methylcitrate dehydratase [OS=Saccharomyces cerevisiae S288c] | B5610 | PDH1; YPR002W | metabolic process | cytoplasm; membrane; mitochondrion | catalytic activity | 18.11 | 4.423 | 0.26 |
| P48569 | Uncharacterized protein YDL183C [OS=Saccharomyces cerevisiae S288c] | B5134 | YDL183C; YDL183C | transport | mitochondrion | 1.069 | 0.274 | 0.26 |
| P19516 | Cytochrome c oxidase assembly protein COXK1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5957 | COXK1; YPL132W | cell organization and biogenesis; metabolic process | membrane/mitochondrion; ribosome | metal ion binding | 1.069 | 0.274 | 0.26 |
| P25573 | Mitochondrial inner membrane I-AAA protease supercomplex subunit MGR1 [OS=Saccharomyces cerevisiae S288c] | B5011 | MGR1; YCL044C | metabolic process | membrane/mitochondrion | protein binding | 1.649 | 0.425 | 0.26 |
| P53219 | Abhydrolase domain-containing protein IMO32 [OS=Saccharomyces cerevisiae S288c] | B5291 | IMO32; YGR031W | metabolic process; transport | mitochondrion | catalytic activity | 0.931 | 0.245 | 0.26 |
Q03798 Altered inheritance of mitochondrial protein 36, mitochondrial (Saccharomyces cerevisiae S288c)

B5518 9 AIM36, YMR157C membrane/mitochondrion 1.637 0.438 0.27

P53326 Uncharacterized protein YKR266W (Saccharomyces cerevisiae S288c)

B5318 2 YGR266W; YR266W membrane/mitochondrion 1.081 0.299 0.28

Q03201 37S ribosomal protein S10, mitochondrial (Saccharomyces cerevisiae S288c)

B5161 1 RMS10, YDR041W cell organization and biogenesis/metabolic process mitochondrial/ribosome structural molecule activity 0.701 0.194 0.28

P31875 37S ribosomal protein MRP21, mitochondrial (Saccharomyces cerevisiae S288c)

B5218 2 MRP21; YLR090W cell organization and biogenesis/metabolic process mitochondrial/ribosome structural molecule activity 0.701 0.194 0.28

P00445 Superoxe dismutase [Cu-Zn] (Saccharomyces cerevisiae S288c)

B5356 6 SOD1; YJR104C cell organization and biogenesis/cellular homeostasis/metabolic process/regulation of biological process/response to stimulus cytoplasm/mitochondrion antioxidant activity; catalytic activity; metal ion binding; protein binding 1.848 0.52 0.28

Q06892 NADH kinase POS5, mitochondrial (Saccharomyces cerevisiae S288c)

B5591 3 POS5; YPL188W metabolic process/response to stimulus mitochondrial/organellar lumen catalytic activity/nucleotide binding 1.31 0.369 0.28

P25719 Peptidyl-prolyl cis-trans isomerase C, mitochondrial (Saccharomyces cerevisiae S288c)

B5489 7 CPR3; YML078W metabolic process cytosol/mitochondrion catalytic activity 2.981 0.848 0.28

P43567 Alanine–glyoxylate aminotransferase 1, mitochondrial (Saccharomyces cerevisiae S288c)

B5011 4 AGX1; YLP030W metabolic process mitochondrial/organellar lumen catalytic activity 2.162 0.616 0.28

Q04935 Cytochrome c oxidase protein 20, mitochondrial (Saccharomyces cerevisiae S288c)

B5181 7 COX20; YDR231C cell organization and biogenesis/metabolic process membrane/mitochondrion protein binding 2.455 0.701 0.29

P14693 Sorting assembly machinery 35 kDa subunit (Saccharomyces cerevisiae S288c)

B5448 3 SAM35; YHR083W cell organization and biogenesis/transport membrane/mitochondrion protein binding 0.54 0.155 0.29

P42847 37S ribosomal protein S18, mitochondrial (Saccharomyces cerevisiae S288c)

B5141 0 MRPL18; YNL308W cell organization and biogenesis/metabolic process mitochondrial/ribosome RNA binding/structural molecule activity 0.54 0.155 0.29

Q04472 Mitochondrial inner membrane i-AAA protease supercomplex subunit MGR3 (Saccharomyces cerevisiae S288c)

B5154 2 MGR3; YMR115W metabolic process membrane/mitochondrion protein binding 0.52 0.15 0.29

P25605 Acetolactate synthase small subunit, mitochondrial (Saccharomyces cerevisiae S288c)

B5034 8 ILV6; YCL009C metabolic process/regulation of biological process mitochondrial catalytic activity/enzyme regulator activity 6.848 1.976 0.29

P00401 Cytochrome c oxidase subunit 1 (Saccharomyces cerevisiae S288c)

B5409 8 COX1; Q0045 metabolic process/transport membrane/mitochondrion catalytic activity;metal ion binding;transport activity 1.61 0.468 0.29

P00927 Threonine dehydratase, mitochondrial (Saccharomyces cerevisiae S288c)

B5681 9 ILV1; YER086W metabolic process cytoplasm/mitochondrion catalytic activity 3.125 0.914 0.29

Q06678 54S ribosomal protein L35, mitochondrial (Saccharomyces cerevisiae S288c)

B5192 1 MRPL35; YDR322W cell organization and biogenesis/metabolic process mitochondrial/ribosome structural molecule activity 1.031 0.304 0.29

P38122 3-methyl-J-oxobutanoate hydroxymethyltransferase (Saccharomyces cerevisiae S288c)

B547 4 ECM31; YBR176W metabolic process mitochondrial catalytic activity 0.413 0.122 0.30

P21954 Isocitrate dehydrogenase (NADP), mitochondrial (Saccharomyces cerevisiae S288c)

B5149 3 IDP1; YDL066W metabolic process mitochondrial catalytic activity;metal ion binding;transport activity 38.81 11.58 0.30

P38120 37S ribosomal protein S9, mitochondrial (Saccharomyces cerevisiae S288c)

B5244 3 MRPS9; YBR146W cell organization and biogenesis/metabolic process mitochondrial/ribosome RNA binding/structural molecule activity 2.384 0.719 0.30

Q02117 Protein ARS56, mitochondrial (Saccharomyces cerevisiae S288c)

B5580 0 ARS56; YER069W metabolic process/regulation of biological process cytoplasm/mitochondrion/organellar lumen catalytic activity;metal ion binding;protein binding 0.286 0.087 0.30

Q02446 37S ribosomal protein S17, mitochondrial (Saccharomyces cerevisiae S288c)

B5522 6 MRPS17; YMR188C cell differentiation/cell organization and biogenesis/metabolic process mitochondrial/ribosome RNA binding/structural molecule activity 1.276 0.389 0.30
| Gene ID | Description                                                                 | GO Terms                                                                 | Cellular Location                      | Activity                                                                 | Log2 Fold Change | P-Value 1 | P-Value 2 |
|--------|------------------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------|--------------------------------------------------------------------------|-----------------|-----------|-----------|
| P22354 | S45 ribosomal protein L20, mitochondrial [Saccharomyces cerevisiae S288c]   | -                                                                        | -                                      | structural molecule activity                                              | 1.273           | 0.389     | 0.30      |
| P09950 | S-aminoacetaldehyde synthase, mitochondrial [Saccharomyces cerevisiae S288c] | -                                                                        | -                                      | catalytic activity                                                        | 0.28            | 0.086     | 0.31      |
| P00830 | ATP synthase subunit beta, mitochondrial [Saccharomyces cerevisiae S288c]    | -                                                                        | cytoplasm, membrane, mitochondrial     | catalytic activity, nucleotide binding, protein binding, transport activity | 78.43           | 24.11     | 9         |
| P07236 | Threonine-tRNA ligase, mitochondrial [Saccharomyces cerevisiae S288c]        | -                                                                        | -                                      | DNA binding                                                               | 3.642           | 1.154     | 0.32      |
| P32445 | Single-stranded DNA-binding protein RIM1, mitochondrial [Saccharomyces cerevisiae S288c] | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.642           | 1.154     | 0.32      |
| P32837 | S45 ribosomal protein L42, mitochondrial [Saccharomyces cerevisiae S288c]    | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 1.581           | 0.501     | 0.32      |
| P32445 | Single-stranded DNA-binding protein RIM1, mitochondrial [Saccharomyces cerevisiae S288c] | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 1.054           | 0.334     | 0.32      |
| P7298 | Succinate dehydrogenase (ubiquinone) cytochrome b small subunit, mitochondrial [Saccharomyces cerevisiae S288c] | -                                                                        | -                                      | catalytic activity, metal ion binding                                      | 1.448           | 0.468     | 0.32      |
| P81451 | ATP synthase subunit K, mitochondrial [Saccharomyces cerevisiae S288c]       | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 0.896           | 0.292     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0250  | COX2; YGR132C                                                                | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q0140  | VAR1; WYOR222                                                                  | -                                                                        | -                                      | catalytic activity, transport protein activity                            | 3.217           | 1.054     | 0.33      |
| Q02883 | N-acetyl-phosphatidylethanolamine-hydrolizing phospholipase D, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5600 1 | FMP30; YPL103C | metabolic process | membrane, mitochondrial | catalytic activity; metal ion binding | 0.557 | 0.194 | 0.35 |
| P32860 | NID-like protein, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5382 6 | NUF1; YKL040C | cell organization and biogenesis;cellular homeostasis; metabolic process | mitochondrion, organelle lumen | metal ion binding | 3.87 | 1.371 | 0.35 |
| P18900 | hexaprenyl pyrophosphatase synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5228 8 | COQ1; YBR003W | metabolic process | membrane, mitochondrial | catalytic activity; metal ion binding; protein binding | 0.468 | 0.166 | 0.35 |
| P39726 | Glycine cleavage system H protein, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5125 4 | GCY3; YAL044C | metabolic process | mitochondrion | catalytic activity | 4.995 | 1.783 | 0.36 |
| P00044 | Cytochrome c iso-1 [OS=Saccharomyces cerevisiae S288c]| B5380 7 | CYC1; YIR048W | metabolic process; transport | mitochondrion | metal ion binding; protein binding | 9 | 3.217 | 0.36 |
| P49367 | Homoaconitase, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5182 0 | LYS4; YDR234W | metabolic process | mitochondrion | catalytic activity; metal ion binding; protein binding | 1.54 | 0.551 | 0.36 |
| P21306 | ATP synthase subunit epsilon, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5385 7 | ATP15; YPL271W | metabolic process; transport | membrane, mitochondrial | catalytic activity; transp onter activity | 2.162 | 0.778 | 0.36 |
| P31710 | [Pyruvate dehydrogenase (acetyl-transferring)] kinase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5282 8 | PKP2; YGL059W | metabolic process; regulation of biological process | mitochondrion, organelle lumen | catalytic activity; nucleotide binding; protein binding | 0.778 | 0.28 | 0.36 |
| Q58824 | Uncharacterized protein YOR020W-A [OS=Saccharomyces cerevisiae S288c]| 14664 80 | YDR020W A; YDR020W A | metabolic process; transport | membrane, mitochondrial | | 5.813 | 2.162 | 0.37 |
| Q50784 | Monothiol glutaredoxin-5, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5604 8 | GRXS; YPL059W | cell organization and biogenesis; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus | mitochondrion, organelle lumen | catalytic activity; metal ion binding | 1.783 | 0.668 | 0.37 |
| Q6Q560 | Protein idS1 [OS=Saccharomyces cerevisiae S288c]| B5677 6 | ISD11; YER048W A | cell organization and biogenesis; metabolic process | organelle, mitochondrial | catalytic activity; protein binding | 1.783 | 0.668 | 0.37 |
| P68417 | fumarate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5586 6 | FUM1; YPL262W | cell organization and biogenesis; metabolic process | cytoplasm, cytosol, mitochondrion, organelle lumen | catalytic activity | 13.87 | 5.21 | 0.38 |
| P23574 | Cysteine desulfurase, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5034 3 | NFS1; YCL017C | cell organization and biogenesis; cellular homeostasis; metabolic process | mitochondrion, nucleus | catalytic activity; metal ion binding; protein binding | 2.594 | 0.978 | 0.38 |
| G12298 | uncharacterized ABC transporter ATP-binding protein YDR061W [OS=Saccharomyces cerevisiae S288c]| B5163 5 | YDR061W W; YDR061W W | | mitochondrion | catalytic activity; nucleotide binding | 0.512 | 0.194 | 0.38 |
| P32891 | D-lactate dehydrogenase (cytochrome 1), mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5138 0 | DLD1; YDL174C | metabolic process; transport | membrane, mitochondrial | catalytic activity; nucleotide binding | 18.68 | 7.161 | 0.38 |
| P33416 | Heat shock protein 78, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5184 5 | HSP78; YDR238C | cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus | mitochondrion, organelle lumen | catalytic activity; nucleotide binding; protein binding | 7.929 | 3.042 | 0.38 |
| P36625 | S45 ribosomal protein L24, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5223 1 | MRPL24; YMR193W | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | RNA binding; structural molecule activity | 1.512 | 0.585 | 0.39 |
| P54003 | Protein SUR7 [OS=Saccharomyces cerevisiae S288c]| B5405 3 | SUR7; YML052W | cell differentiation; transport | membrane, mitochondrial | | 1.512 | 0.585 | 0.39 |
| P00431 | cytochrome c peroxidase, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5394 0 | CCP1; YKR066C | metabolic process; response to stimulus | mitochondrion, organelle lumen | antioxidant activity; catalytic activity; metal ion binding; protein binding | 1.424 | 0.557 | 0.39 |
| P21560 | Protein CBP3, mitochondrial [OS=Saccharomyces cerevisiae S288c]| B5858 6 | CBP3; YPL215W | cell organization and biogenesis; regulation of biological process | membrane, mitochondrial, ribosome | catalytic activity | 1.424 | 0.557 | 0.39 |
| P37293 | N-terminal acetyltransferase 2 [OS=Saccharomyces cerevisiae S288c]| B5305 0 | NAT2; YGR147C | metabolic process | cytoplasm, mitochondrial | catalytic activity | 1.404 | 0.551 | 0.39 |
P4053  Altered inheritance of mitochondria protein 9; mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85681 3  AIM9; YER080W  
mitochondrion  
4.555 1.798 0.39

P53163  5 S45 ribosomal protein L12, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85287 1  MNP1; YGL068W  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
RNA binding;structural molecule activity  
1.31 0.52 0.40

P47052  Succinate dehydrogenase (ubiquinone) flavoprotein subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85340 5  YL045W; YL045Y  
metabolic process;transport  
membrane;mitochondrion  
catalytic activity;nuclear molecule binding  
4.732 1.88 0.40

Q01574  Acetyl-CoA synthetase 1 [OS=Saccharomyces cerevisiae S288c]  
85154 5  ACS1; YAL054C  
cell organization and biogenesis;metabolic process  
cytosol;cytosol;endoplasmic reticulum;mitochondrion;nucleus  
catalytic activity;nuclear molecule binding  
2.36 0.947 0.40

P40185  Protein mrf1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85476 0  MMF1; YL051C  
cell organization and biogenesis;metabolic process  
mitochondrion;organellar lumen  
antioxidant activity;catalytic activity;metal ion binding  
5.31 2.162 0.41

PO0447  Superoxide dismutase [Mn], mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85639 9  SOD2; YHR008C  
metabolic process;response to stimulus  
mitochondrion;organellar lumen  
antioxidant activity;catalytic activity;metal ion binding  
8.017 2.455 0.41

Q04599  5 S45 ribosomal protein L1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85658 4  MRPL1; YDR116C  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
RNA binding;structural molecule activity  
1.069 0.438 0.41

P36066  Protein MRG3-like [OS=Saccharomyces cerevisiae S288c]  
85372 5  YK1133C; YKL133C  
metabolic process  
membrane;mitochondrion  
protein binding  
1.054 0.433 0.41

P07246  Alcohol dehydrogenase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85510 7  ADH3; YMR083W  
metabolic process  
mitochondrion;organellar lumen  
catalytic activity;metal ion binding  
10.15 9 4.179 0.41

P35180  Mitochondrial import receptor subunit Tom20 [OS=Saccharomyces cerevisiae S288c]  
85297 3  TOM20; YGR082W  
cell organization and biogenesis;transport  
membrane;mitochondrion  
protein binding;transporter activity  
1.031 0.425 0.41

Q03799  5 37S ribosomal protein 58, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85519 0  MRPS8; YMR158W  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
structural molecule activity  
1.031 0.425 0.41

P46367  Potassium-activated aldehyde dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85455 6  ALD4; YOR374W  
metabolic process  
mitochondrion;organellar lumen  
catalytic activity  
47.49 7 19.62 0.41

P43617  Uncharacterized mitochondrial carrier YFR045W [OS=Saccharomyces cerevisiae S288c]  
85060 6  YFR045W; YFR045W  
metabolic process;transport  
membrane;mitochondrion  
structural molecule activity;transporter activity  
0.995 0.413 0.42

P32796-1  Carnitine O-acetyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85496 5  CAT2; YMO422W  
metabolic process;transport  
membrane;mitochondrion  
catalytic activity  
13.81 6 5.749 0.42

P36101  tRNA threonylcarbamoyladenosine dehydratase 2 [OS=Saccharomyces cerevisiae S288c]  
85384 1  TCD2; YKL027W; YKL027W  
metabolic process  
cytosol;membrane;mitochondrion  
catalytic activity;nuclear molecule binding  
0.778 0.334 0.43

Q07914  Mitochondrial import inner membrane translocase subunit TIM14 [OS=Saccharomyces cerevisiae S288c]  
85069 4  PAM138; YLR008C  
regulation of biological process;transport  
membrane;mitochondrion  
enzyme regulator activity;protein binding;transporter activity  
0.778 0.334 0.43

P50526  ATP synthase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85062 7  ATP4; YPL078C  
cell organization and biogenesis;metabolic process;transport  
membrane;mitochondrion  
catalytic activity;transporter activity  
4.995 2.162 0.43

P40159  Uncharacterized protein YNL208W [OS=Saccharomyces cerevisiae S288c]  
85501 3  YNL208W; YNL208W  
membrane;mitochondrion;ribosome  
0.668 0.292 0.44

P36331  5 S45 ribosomal protein L36, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85341 9  MRPL36; YBR122C  
cell organization and biogenesis;metabolic process  
mitochondrion;ribosome  
structural molecule activity  
0.668 0.292 0.44

Q04585  Fatty aldehyde dehydrogenase [OS=Saccharomyces cerevisiae S288c]  
85513 7  HDF1; YMR110C  
metabolic process  
deplasmic reticulum;endosome;membrane;mitochondrion  
catalytic activity  
4.055 1.783 0.44

P38325  Mitochondrial outer membrane protein OM14 [OS=Saccharomyces cerevisiae S288c]  
85233 1  OM14; YBR230C  
transport  
membrane;mitochondrion  
catalytic activity  
6.197 2.728 0.44

P32317  Protein AFG1 [OS=Saccharomyces cerevisiae S288c]  
85665 8  AFG1; YEL052W  
cell organization and biogenesis;metabolic process;response to stimulus;transport  
membrane;mitochondrion  
catalytic activity;nuclear molecule binding  
1.326 0.585 0.44

P53140  Protein RMD9, mitochondrial [OS=Saccharomyces cerevisiae S288c]  
85277 1  RMD9; YGL1107C  
cell differentiation;metabolic process;regulation of biological process  
membrane;mitochondrion  
RNA binding  
1.512 0.668 0.44
| Gene Name | Description | GO Terms | Accession Numbers | Function | Localization | Activity | Binding | 1.512 | 5.158 | 0.448 | 2.981 | 3.962 | 1.349 | 1.276 | 1.637 | 0.498 | 0.33.55 | 0.51 | 0.778 | 0.222 | 0.105 | 0.47 | 0.212 | 0.101 | 0.48 | 3.262 | 1.555 | 0.48 | 1.154 | 0.551 | 0.48 | 1.61 | 0.778 | 0.48 | 1.047 | 0.506 | 0.48 | 0.931 | 0.456 | 0.49 | 9 | 4.456 | 0.50 | 3.281 | 1.637 | 0.50 | 1.276 | 0.638 | 0.50 | 3.962 | 2.008 | 0.51 | 11.74 | 3 | 5.952 | 0.51 | 2.981 | 1.512 | 0.51 | 0.448 | 0.228 | 0.51 | 4.926 | 2.511 | 0.51 | 5.158 | 2.643 | 0.51 | 9 | 4.623 | 0.51 | 1.532 | 0.778 | 0.51 |
| Accession | Description | Synonym | Gene Symbol | Molecular Function | Cellular Component | Subcellular Location | Entry Terms | Enzyme Activity | Molecular Activity | Protein Binding | cis-Regulatory Activity | Translational Efficiency | 0.6 | 0.3 | 0.54 |
|-----------|-------------|---------|-------------|-------------------|-------------------|---------------------|--------------|----------------|-------------------|----------------|----------------------|------------------------|------|-----|------|
| P32335    | Protein MSD1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85900   | Mss51       | Ylr202c          | metabolic process | membrane/mitochondrion | protein-binding, translocation regulation | 1.929 | 0.995 | 0.52 |
| P3888     | Uncharacterized mitochondrial hydrolase FMP41 [OS=Saccharomyces cerevisiae S288c] | 85555   | Fmp41       | Ynl168c          | metabolic process | mitochondrial       | catalytic activity, metal ion binding | 0.968 | 0.501 | 0.52 |
| P46881    | D-lactate dehydrogenase   | 85187   | Dld2        | Ydl178w          | metabolic process | mitochondrial/organellar lumen | catalytic activity, nucleotide binding, protein binding | 1.829 | 0.951 | 0.52 |
| P36151    | Uncharacterized protein YKR070W [OS=Saccharomyces cerevisiae S288c] | 85394   | Ykr070w     | Ykr070w          | metabolic process | mitochondrial       | 0.833 | 0.438 | 0.53 |
| P40495    | Homolysiotrate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85471   | Yls12       | Yil204c          | metabolic process | mitochondrial       | catalytic activity, metal ion binding, nucleotide binding, protein binding | 4.109 | 2.162 | 0.53 |
| P07256    | Cytochrome b-c1 complex subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85223   | Cor1        | Ybl045c          | metabolic process | membrane/mitochondrion | catalytic activity, metal ion binding, nucleotide binding, protein binding, translocation regulation | 18.78 | 9.89 | 0.53 |
| P34635    | Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85610   | Cit3       | Ypr001w          | metabolic process | mitochondrial       | catalytic activity | 5.529 | 2.914 | 0.53 |
| P40634    | 545 ribosomal protein L40, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85593   | Mrpl40      | Ypl173w          | cell organization and biogenesis, metabolic process | mitochondrial/ribosome | protein binding, structural molecule activity | 0.778 | 0.413 | 0.53 |
| P33769    | 37S ribosomal protein S5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85255   | Mrps5      | Ybr251w          | cell organization and biogenesis, metabolic process | mitochondrial/ribosome | RNA binding, structural molecule activity | 0.778 | 0.413 | 0.53 |
| P36163    | Mitochondrial metalloendopeptidase OMA1 [OS=Saccharomyces cerevisiae S288c] | 85396   | Oma1       | Ykr087c          | metabolic process | membrane/mitochondrion | catalytic activity, metal ion binding | 0.73 | 0.389 | 0.53 |
| P32191    | Glyceraldehyde-3-phosphate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85465   | Gut2       | Yil155c          | metabolic process | membrane/mitochondrion | catalytic activity | 8.522 | 4.955 | 0.53 |
| P38797    | Protein phosphatase 2C homolog 7, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85647   | Ptc7       | Yhr076w          | metabolic process | mitochondrial       | catalytic activity, metal ion binding, nucleotide binding, protein binding | 0.688 | 0.369 | 0.54 |
| Q12031    | Mitochondrial 2-methylisocitraterase lyase [OS=Saccharomyces cerevisiae S288c] | 85611   | Icl2       | Ypr006c          | metabolic process | mitochondrial/organellar lumen | catalytic activity | 5.158 | 2.793 | 0.54 |
| P38088    | Metabolic process | 85618   | 0.6         | 0.3 | 0.54 |
| P32902    | 37S ribosomal protein MRB4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85638   | Mrb4       | Yhl004w          | cell organization and biogenesis, metabolic process | mitochondrial/ribosome | structural molecule activity | 0.616 | 0.334 | 0.54 |
| P32316    | Acetyl-CoA hydrolase [OS=Saccharomyces cerevisiae S288c] | 85226   | Achi1      | Ybl015w          | metabolic process | cytoplasm/cytosol/mitochondrion | catalytic activity | 15.29 | 8.326 | 0.54 |
| P35191    | Dna1 homolog 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85033   | Dna1       | Yfl016c          | cell organization and biogenesis, metabolic process, regulation of biological process, response to stimulus | mitochondrial/organellar lumen | enzyme regulator activity, metal ion binding, nucleotide binding, protein binding | 3.037 | 1.696 | 0.55 |
| P38071    | Enoyl-acyl-carrier protein reductase [NADPH, β-specific], mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85231   | Etr1       | Ybr026c          | metabolic process | mitochondrial/organellar lumen | catalytic activity, DNA binding, metal ion binding | 9.426 | 4.926 | 0.55 |
| P32795    | Mitochondrial inner membrane I-AAA protease supercomplex subunit YME1 [OS=Saccharomyces cerevisiae S288c] | 85613   | Yme1       | Ypr024w          | metabolic process, response to stimulus, transport | membrane/mitochondrion | catalytic activity, metal ion binding, nucleotide binding, protein binding | 1.798 | 0.986 | 0.55 |
| P00359    | Glyceraldehyde-3-phosphate dehydrogenase 3 | 85310   | Tdh3       | Ygr192c          | cell death, metabolic process | cytoplasm/cytosol/mitochondrion/nucleus | catalytic activity, nucleotide binding | 7.185 | 3.962 | 0.55 |
| Gene | Symbol | Protein Name | Localization | Function | GO Terms | tSIDE 3.424 | Fold 0.63  |
|------|--------|--------------|--------------|----------|----------|-------------|-----------|
| P40582 | GSH5 | Glutathione S-transferase 1 | mitochondrial | metabolic process | antioxidant activity; catalytic activity; protein binding; RNA binding | 1.683 | 0.931 5.469 0.63 |
| P50087 | MICOS subunit MIC26 | mitochondrial | cell organization and biogenesis | membrane; mitochondrial | 1.683 | 0.931 5.469 0.63 |
| P39987 | Heat shock protein SSC3 | mitochondrial | cell organization and biogenesis; metabolic process; transport | mitochondrion | 2.162 | 1.198 5.469 0.63 |
| P15108 | ATP-dependent molecular chaperone HSC82 | mitochondrial | cell organization and biogenesis; metabolic process; response to stimulus | cytoplasm; membrane; mitochondrial | 1.081 | 0.602 5.469 0.63 |
| P40364 | Mitochondrial peculiar membrane protein 1 | mitochondrial | membrane; mitochondrial | 1.512 | 0.848 5.469 0.63 |
| P37299 | cytochrome b-c1 complex subunit 10 | mitochondrial | metabolic process; transport | membrane; mitochondrial | 5.31 | 2.981 5.469 0.63 |
| P12233 | ATP synthase subunit g | mitochondrial | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrial | 1.371 | 0.778 5.469 0.63 |
| P36147 | Presequence translocated-associated motor subunit pam17 | mitochondrial | transport | membrane; mitochondrial | 1.371 | 0.778 5.469 0.63 |
| P06485 | Autophagy-related protein 33 | mitochondrial | cell communication; metabolic process; response to stimulus | membrane; mitochondrial | 1.371 | 0.778 5.469 0.63 |
| P17505 | Malate dehydrogenase | mitochondrial | metabolic process | mitochondrion; organelle lumen | 56.79 7.31 5.469 0.63 |
| P42940 | Probable electron transfer flavoprotein subunit beta | mitochondrial | metabolic process; transport | mitochondrion; organelle lumen | 4.623 | 2.652 5.469 0.63 |
| P16387 | Pyruvate dehydrogenase E1 component subunit alpha | mitochondrial | cell growth; metabolic process | mitochondrion; organelle lumen | 21.63 8.12 5.469 0.63 |
| P67675 | Lon protease homolog | mitochondrial | cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus | cytoplasm; mitochondrial; organelle lumen | 1.362 | 0.792 5.469 0.63 |
| P04710 | ADP, ATP carrier protein 1 | mitochondrial | metabolic process; transport | cytosol; membrane; mitochondrial | 11.74 3.71 5.469 0.63 |
| P28834 | Isocitrate dehydrogenase (NAD) subunit 1 | mitochondrial | metabolic process; transport | cytosol; mitochondrial; organelle lumen | 15.23 8.12 5.469 0.63 |
| P36527 | 54S ribosomal protein L28 | mitochondrial | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | 0.874 | 0.57 5.469 0.63 |
| P16622 | Ferrichelatase | mitochondrial | metabolic process | membrane; mitochondrial | 6.305 | 3.806 5.469 0.63 |
| P40012 | Protoporphyrinogen oxidase | mitochondrial | metabolic process | membrane; mitochondrial | 2.162 | 1.336 5.469 0.63 |
| P32453 | Protein ATP11 | mitochondrial | cell organization and biogenesis | mitochondrion | 1.239 | 0.778 5.469 0.63 |
| P40215 | External NADH-ubiquinone oxidoreductase 1 | mitochondrial | metabolic process | mitochondrion | 5.469 | 3.453 5.469 0.63 |
| C00822 | Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial | mitochondrial | metabolic process; transport | membrane; mitochondrial | 3.424 | 2.162 5.469 0.63 |
| Gene Product | Function | Location | GO Terms | Gene Product | Function | Location | GO Terms |
|--------------|----------|----------|----------|--------------|----------|----------|----------|
| Lipase 2 | | | | Saccharomyces cerevisiae S288c | | | | |
| 54S ribosomal protein YM1 | | | | Saccharomyces cerevisiae S288c | | | | |
| ATP-dependent permease MDL1 | | | | Saccharomyces cerevisiae S288c | | | | |
| 3-hydroxyisobutyl-CoA hydrolase | | | | Saccharomyces cerevisiae S288c | | | | |
| Cytochrome c oxidase assembly subunit A | | | | Saccharomyces cerevisiae S288c | | | | |
| Intron-encoded RNA maturease b14 | | | | Saccharomyces cerevisiae S288c | | | | |
| Protein disulfide-isoamerase | | | | Saccharomyces cerevisiae S288c | | | | |
| mitochondrial transcription factor 2 | | | | Saccharomyces cerevisiae S288c | | | | |
| Glutamyl-RNA(Gln) amidotransferase subunit A | | | | Saccharomyces cerevisiae S288c | | | | |
| Serine-RNA ligase, mitochondrial | | | | Saccharomyces cerevisiae S288c | | | | |
| Probable oxidoreductase AIM17 | | | | Saccharomyces cerevisiae S288c | | | | |
| 375 ribosomal protein S12 | | | | Saccharomyces cerevisiae S288c | | | | |
| Ribosome-releasing factor 2, mitochondrial | | | | Saccharomyces cerevisiae S288c | | | | |
| Phosphatidylinositol decarboxylase | | | | Saccharomyces cerevisiae S288c | | | | |
| Sorting assembly machinery 50 kDA subunit | | | | Saccharomyces cerevisiae S288c | | | | |
| Arginine biosynthesis bifunctional protein Arg1 | | | | Saccharomyces cerevisiae S288c | | | | |
| mitochondrial dicarboxylate transporter | | | | Saccharomyces cerevisiae S288c | | | | |
| 545 ribosomal protein L25 | | | | Saccharomyces cerevisiae S288c | | | | |
| Valine-RNA ligase, mitochondrial | | | | Saccharomyces cerevisiae S288c | | | | |
| Gene ID  | Enzyme Name                        | GO Terms                              | Subcellular Location | Molecular Activity | Activity Type         | Enzymatic Activity | 3.299 | 2.981 | 2.665 | 6.565 | 2.162 | 2.433 | 0.848 | 3.299 | 2.162 |
|---------|------------------------------------|---------------------------------------|----------------------|-------------------|----------------------|-------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| P16451  | Pyruvate dehydrogenase complex protein X component, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5310    | PDK1; YGR193C                      | metabolic process                     | mitochondrion;organelle lumen | catalytic activity;structural molecule activity | 2.594 | 1.783 | 0.69 |
| P18869  | Pentamidine resistance factor, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5444    | PNT1; YDR266W                      | cell organization and biogenesis;response to stimulus | membrane;mitochondrion | catalytic activity | 0.848 | 0.585 | 0.69 |
| P49095  | Glycine dehydrogenase (Decarboxylating), mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5522    | GCV1; YMR189W                      | metabolic process                     | cytosol;mitochondrion | catalytic activity | 2.433 | 1.683 | 0.69 |
| P07257  | Cytochrome b-c1 complex subunit 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5632    | GCR2; YPR191W                      | metabolic process;transport            | membrane;mitochondrion | catalytic activity;metal ion binding;protein binding | 36.75 | 1 | 25.49 | 0.69 |
| Q06688  | Methyltransferase OMS1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5191    | OMS1; YDR316W                      | metabolic process                     | membrane;mitochondrion | catalytic activity | 0.693 | 0.484 | 0.70 |
| P19262  | Dihydroxyphenylalanine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5712    | KG62; YDR148C                      | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;protein binding | 6.406 | 4.484 | 0.70 |
| P38891  | Branched-chain amino-acid aminotransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5661    | BAT1; YHR208W                      | metabolic process;regulation of biological process;response to stimulus | mitochondrion;organelle lumen | catalytic activity | 9 | 6.305 | 0.70 |
| P11914  | Mitochondrial-processing peptidase subunit alpha (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5441    | MASS2; YHR024AC                    | metabolic process;transport            | membrane;mitochondrion;organelle lumen | catalytic activity;metal ion binding;protein binding | 1.291 | 0.905 | 0.70 |
| P38152  | Tricarboxylate transport protein (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5294    | CTP1; YBR291C                      | metabolic process;transport            | membrane;mitochondrion | structural molecule activity | 0.551 | 0.389 | 0.71 |
| Q08179  | Mitochondrial distribution and morphology protein 3B (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5433    | MSM38; YOL027C                     | cell organization and biogenesis;cellular homeostasis;regulation of biological process;transport | membrane;mitochondrion | catalytic activity | 6.079 | 4.309 | 0.71 |
| P88077  | ATP synthase subunit gamma, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5232    | ATP3; YBR093W                      | metabolic process;transport            | membrane;mitochondrion | catalytic activity;transport | 12.68 | 9 | 0.71 |
| P36528  | S45 ribosomal protein L17, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5466    | MRPL17; YNL252C                    | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.52 | 0.369 | 0.71 |
| P48015  | Aminomethyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5158    | GCV1; YDR091C                      | metabolic process                     | mitochondrion | catalytic activity;protein binding | 9 | 6.406 | 0.71 |
| P38702  | mitochondrial carrier protein LEU5 (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5639    | LEU5; YHR002W                      | metabolic process;transport            | membrane;mitochondrion | structural molecule activity;transport | 0.468 | 0.334 | 0.71 |
| Q04172  | Sensitive to high expression protein 9, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5200    | SHE9; YDR393W                      | cell organization and biogenesis      | membrane;mitochondrion | catalytic activity | 0.374 | 0.269 | 0.72 |
| P48077  | Hexokinase-2 (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5263    | HKX2; YGL253W                      | cell communication;cell organization and biogenesis;cellular homeostasis;metabolic process;regulation of biological process;response to stimulus;transport | cytosol;mitochondrion | catalytic activity;nucleotide binding | 0.359 | 0.259 | 0.72 |
| P32897  | Mitochondrial import inner membrane translocase subunit tim23 (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5757    | TIM23; YNR017W                     | transport                             | membrane;mitochondrion | protein binding;transport | 2.981 | 2.162 | 0.73 |
| P37292  | Seryl hydroxymethyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5256    | SHM1; YBR263W                      | metabolic process                     | mitochondrion | catalytic activity | 9 | 6.565 | 0.73 |
| P07213  | Mitochondrial import receptor subunit TOM70 (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5500    | TOM70; YNL121C                     | cell organization and biogenesis;transport | membrane;mitochondrion | protein binding;transport | 3.642 | 2.665 | 0.73 |
| P54783  | D-arabino-1,4-lactone oxidase (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5488    | ALD1; YML086C                      | metabolic process;response to stimulus | membrane;mitochondrion | catalytic activity;nucleotide binding | 3.299 | 2.415 | 0.73 |
| P43616  | Cys-Gly metalloendopeptidase dag1 (OS=Saccharomyces cerevisiae S288c) | | | | | | | | | | | | | | | |
| B5060    | DUG1; YFR044C                      | metabolic process                     | cytoplasm;mitochondrion;ribosome | catalytic activity;metal ion binding | 1.154 | 0.848 | 0.73 |
| Gene Symbol | Protein Name | GO Term | Cellular Component | Molecular Function | Biological Process | Gene Ontology Score |
|-------------|--------------|---------|--------------------|--------------------|--------------------|---------------------|
| F3751 | Aft1 | protein | - | - | - | - |
| P69045 | MICOS complex subunit MEC17 | protein | - | - | - | - |
| P28625 | Protein YIM1 | protein | - | - | - | - |
| P3736 | Uncharacterized protein YMR140W | protein | - | - | - | - |
| P3613 | NAD-dependent malic enzyme, mitochondrial | protein | - | - | - | - |
| P3612 | MICOS complex subunit MGD1 | protein | - | - | - | - |
| P2751 | ATP synthase subunit alpha, mitochondrial | protein | - | - | - | - |
| P3904 | S45 ribosomal protein L6, mitochondrial | protein | - | - | - | - |
| P3850 | Heat-shock protein SIC1, mitochondrial | protein | - | - | - | - |
| P3680 | NASH-cytochrome b5 reductase subunit 2 | protein | - | - | - | - |
| P3877 | Ribosome recycling factor, mitochondrial | protein | - | - | - | - |
| P2344 | Mitochondrial import receptor subunit TOM40 | protein | - | - | - | - |
| P3652 | S45 ribosomal protein L11, mitochondrial | protein | - | - | - | - |
| Q0071 | Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial | protein | - | - | - | - |
| Q0823 | Protein FMP25, mitochondrial | protein | - | - | - | - |
| P48526 | Isoleucine-tRNA ligase, mitochondrial | protein | - | - | - | - |
| P3261 | S45 ribosomal protein RML2, mitochondrial | protein | - | - | - | - |
| Q0693 | LETM1 domain-containing protein YLR47, mitochondrial | protein | - | - | - | - |
| Q0823 | Altered inheritance of mitochondria protein 39, mitochondrial | protein | - | - | - | - |
| P48527 | Tyrosine-tRNA ligase, mitochondrial | protein | - | - | - | - |
| P3823 | ATP-dependent clpX-like chaperone, mitochondrial | protein | - | - | - | - |
| Q0823 | Altered inheritance of mitochondria protein 39, mitochondrial | protein | - | - | - | - |
| P48527 | Tyrosine-tRNA ligase, mitochondrial | protein | - | - | - | - |
| P3823 | ATP-dependent clpX-like chaperone, mitochondrial | protein | - | - | - | - |
| **P3881** | 545 ribosomal protein L22, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5544 4 | MRPL22; YNL177C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | RNA binding; structural molecule activity | 1.154 | 0.931 | 0.81 |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **P3311** | ATP-dependent permease MDL2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5885 8 | MDL2; YPL270W | response to stimulus; transport | membrane; mitochondrion | catalytic activity; nucleotide binding; transporter activity | 1.116 | 0.901 | 0.81 |
| **Q03976** | 375 ribosomal protein S24, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5175 5 | RSM24; YDR175C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.905 | 0.738 | 0.82 |
| **P08466** | mitochondrial nuclease [OS=Saccharomyces cerevisiae S288c] | B5322 2 | NUC1; YIL208C | cell death; metabolic process | membrane; mitochondrion; nucleus | catalytic activity; metal ion binding | 1.637 | 1.336 | 0.82 |
| **P30902** | ATP synthase subunit d, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5385 3 | ATP7; YK1016C | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 5.105 | 4.179 | 0.82 |
| **P36116** | 545 ribosomal protein L3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5303 9 | MRPL3; YMR024W | cell organization and biogenesis; metabolic process; response to stimulus | mitochondrion; nucleus; ribosome | catalytic activity; RNA binding; structural molecule activity | 0.743 | 0.61 | 0.82 |
| **P74045** | mitochrondial import inner membrane translocase subunit TIM54 [OS=Saccharomyces cerevisiae S288c] | B5339 2 | TIM54; YIL054W | cell organization and biogenesis; transport | cytosol; membrane; mitochondrion | transporter activity | 0.655 | 0.54 | 0.82 |
| **Q21266** | 2-isopropylmalate synthase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5427 5 | LEU9; YDR108W | metabolic process | mitochondrion | catalytic activity; protein binding | 2.472 | 2.065 | 0.84 |
| **P06168** | ketoaldehyde reductoisomerase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5106 9 | ILV5; YLR355C | cell organization and biogenesis; metabolic process | mitochondrion | catalytic activity; DNA binding; metal ion binding | 12.89 | 10.78 | 0.84 |
| **P15424** | ATP-dependent RNA helicase MISS116, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5177 5 | MSSL16; YDR194C | metabolic process; regulation of biological process | mitochondrion; organelle lumen | catalytic activity; nucleotide binding; RNA binding | 1.644 | 1.387 | 0.84 |
| **P07275** | Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5463 2 | PUT2; YHR057W | metabolic process | membrane; mitochondrion; organelle lumen | catalytic activity | 6.055 | 5.136 | 0.85 |
| **P00360** | glyceric aldehyde-3-phosphate dehydrogenase 1 [OS=Saccharomyces cerevisiae S288c] | B5339 5 | TDH1; YIL052W | metabolic process | cytoplasm; cytosol; membrane; mitochondrion | catalytic activity; nucleotide binding | 1.721 | 1.462 | 0.85 |
| **P09440** | C-1-terahydrofolate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5237 8 | M551; YBR084W | metabolic process | cytosol; mitochondrion | catalytic activity; nucleotide binding | 1.049 | 0.9 | 0.86 |
| **P09457** | ATP synthase subunit 5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5189 2 | ATP5; YDR298C | metabolic process; transport | membrane; mitochondrion | catalytic activity; transporter activity | 9 | 7.799 | 0.87 |
| **P04840** | Mitochondrial outer membrane protein porin 1 [OS=Saccharomyces cerevisiae S288c] | B5566 9 | PDR1; YNL055C | cell death; cell organization and biogenesis; cellular homeostasis; regulation of biological process; transport | cytoplasm; membrane; mitochondrion | transporter activity | 15.23 | 13.38 | 0.88 |
| **P04341** | Mitochondrial respiratory chain complexes assembly protein YTA12 [OS=Saccharomyces cerevisiae S288c] | B5511 4 | YTA12; YMR080C | cell organization and biogenesis; metabolic process; response to stimulus; transport | cytoplasm; membrane; mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | 1.371 | 1.276 | 0.93 |
| **P06208-1** | 2-isopropylmalate synthase [OS=Saccharomyces cerevisiae S288c] | B5661 9 | LEUA; YNL104C | metabolic process | cytoplasm; mitochondrion | catalytic activity; protein binding | 5.236 | 4.878 | 0.93 |
| **P19414** | Aconitate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5101 3 | ACO1; YLR304C | cell organization and biogenesis; metabolic process; transport | cytoplasm; cytosol; mitochondrion; organelle lumen | catalytic activity; DNA binding; metal ion binding | 48.53 | 46.19 | 0.95 |
| **P07342** | Aconitate synthase catalytic subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5513 5 | ILV2; YMR108W | metabolic process | mitochondrion | catalytic activity; metal ion binding; nucleotide binding | 4.223 | 4.123 | 1.00 |
| **P47127** | Altered inheritance of mitochondria protein 24, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5354 3 | AIM24; YJR080C | cell organization and biogenesis | mitochondrion | antioxidant activity; catalytic activity | 2.857 | 2.857 | 1.00 |
| **P34227** | Mitochondrial peroxiredoxin PRX1 [OS=Saccharomyces cerevisiae S288c] | B5223 5 | PRX1; YBL064C | cellular homeostasis; metabolic process; regulation of biological process; response to stimulus | mitochondrion | antioxidant activity; catalytic activity | 5.158 | 5.158 | 1.00 |
### Q03028
**Mitochondrial 2-oxoacid:carboxylate carrier 1**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5956   | QDC1   | GTP/GDP carrier | Membrane, Mitochondrion | Structural activity | Protein binding | 5.813 1.00 |
| B5077   | ALT1   | 2-oxoacid:carboxylate carrier | Mitochondrion, Organelle lumen | Catalytic activity | 1.102 1.00 |
| B5132   | GGC1   | 2-oxoacid:carboxylate carrier | Membrane, Mitochondrion | Structural activity | 3.16 1.00 |

### Q02709
**Probable mitochondrial transport protein ftx1**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5444   | F5F1   | Transporter | Membrane, Mitochondrion | Transporter activity | 2.36 1.00 |

### Q07349
**MRX complex component 9**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5153   | YDL027C| Membrane | Mitochondrion | Endoplasmic reticulum | 1.913 1.00 |

### P39518
**Long-chain fatty-acid-CoA ligase 2**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5673   | MRX3   | Cytoplasm | Mitochondrion | Catalytic activity | 0.619 1.00 |

### P32331
**Ceramyl protein YMC1, mitochondrial**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5617   | YMC1   | Membrane | Mitochondrion, Vacuole | Structural activity | 1.581 1.00 |

### P38825
**Protein TOMT1**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5651   | TOMT1  | Transport | Membrane, Mitochondrion | Protein binding | 0.512 1.00 |

### P40508
**Uncharacterized protein YIL077C**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5473   | YIL077C| Mitochondrion | 0.896 1.00 |

### P15179
**Aspartate–tRNA ligase, mitochondrial**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5400   | YPL104W| Metabolic process | Cytoplasm, Mitochondrion, Organelle lumen | Catalytic activity | 0.379 1.00 |

### P00950
**Phosphoglycerate mutase 1**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5370   | YGR033C| Metabolic process | Cytoplasm, Mitochondrion | Catalytic activity | 1.929 1.00 |

### P40416
**Iron-sulfur clusters transporter ATM1, mitochondrial**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5344   | YMR301C| Cellular homeostasis | Mitochondrion | Catalytic activity | 0.453 1.00 |

### P38626
**NADH-cytochrome b5 reductase 1**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5476   | CBR1   | Metabolic process | Endoplasmic reticulum, Mitochondrion, Nucleus | Catalytic activity | 0.957 1.00 |

### P32330
**Phosphatidate cytidylyltransferase, mitochondrial**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5293   | TAM411 | Membrane | Mitochondrion, Organelle lumen | Catalytic activity | 0.668 1.00 |

### P27697
**Atypical kinase COQ8**, mitochondrial

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5275   | YGL119W| Metabolic process | Membrane, Mitochondrion, Organelle lumen | Catalytic activity | 0.453 1.00 |

### P47039
**Probable kynurenine--oxoglutarate transaminase BNA3**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5338   | BNA3   | Metabolic process | Cytoplasm, Mitochondrion | Catalytic activity | 0.468 1.00 |

### P25626
**S45 ribosomal protein IMG1, mitochondrial**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5041   | IMG1   | Cell organization | Mitochondrion, Ribosome | Structural activity | 1.031 1.00 |

### P35220
**Mitochondrial import inner membrane translocase subunit TIM21**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5292   | TIM21  | Cell organization | Mitochondrion | Protein binding | 0.719 1.00 |

### P32939
**GTP-binding protein ypt 2**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5501   | YPF7   | Cell communication | Cytoplasm, Endosome, Mitochondrion, Vacuole | Catalytic activity | 0.585 1.00 |

### P48360
**Probable NADPH-adrenodoxin oxidoreductase, mitochondrial**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5198   | ARH1   | Cellular homeostasis | Cytoplasm, Mitochondrion, Organelle lumen | Catalytic activity | 0.346 1.00 |

### P35270
**mRNA methyltransferase 1, mitochondrial**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5437   | MRM1   | Metabolic process | Mitochondrion | Catalytic activity | 0.274 1.00 |

### P38172
**MIOREX complex component 3**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5218   | YBL095W| Membrane | Mitochondrion | 0.501 1.00 |

### P09201
**fructose-1,6-bisphosphatase**

| Gene ID | Symbol | Description | Localization | Molecular Function | Biological Process | Specificity |
|---------|--------|-------------|--------------|--------------------|--------------------|-------------|
| B5109   | FBP1   | Metabolic process | Cytosol | Catalytic activity | 0.274 1.00 |
Octanoyltransferase, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85094 0 LIP2; YLR239C metabolic process cytoplasm;mitochondrion catalytic activity 0.245 0.245 1.00
Mitochondrial homologous recombination protein 1
[OS=Saccharomyces cerevisiae S288c] 85189 0 NRH1; YDR296W cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus mitochondrion catalytic activity;DNA binding;structural molecule activity 0.359 0.359 1.00
Mitochondrial distribution and morphology protein 10
[OS=Saccharomyces cerevisiae S288c] 85122 3 MIM410; YAL010C cell organization and biogenesis;transport membrane;mitochondrion protein binding 0.16 0.16 1.00
4-hydroxybenzoate polyphenyltransferase, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85577 8 COQ2; YMR041C metabolic process;transport membrane;mitochondrion catalytic activity 0.292 0.292 1.00
ATPase expression protein 1, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85508 6 AEP1; YMR064W regulation of biological process mitochondrion translation regulator activity 0.15 0.15 1.00
Iron-sulfur assembly protein 1
[OS=Saccharomyces cerevisiae S288c] 85603 2 ISA1; YIL027W cell organization and biogenesis;metabolic process mitochondrion;organelle lumen metal ion binding;structural molecule activity 0.136 0.136 1.00
Nuclear migration protein NUM1
[OS=Saccharomyces cerevisiae S288c] 85172 7 NUM1; YDR130W cell organization and biogenesis;cellular component movement;metabolic process;regulation of biological process;transport endoplasmic reticulum;mitochondrion catalytic activity;motor activity;protein binding 0.025 0.025 1.00
Uncharacterized protein YKL187C
[OS=Saccharomyces cerevisiae S288c] 85364 8 FAT3; YKL187C; YKL187C cell organization and biogenesis;transport membrane;mitochondrion 0.194 0.194 1.00
Mitochondrial import inner membrane translocase subunit Tim17
[OS=Saccharomyces cerevisiae S288c] 85329 8 TIM17; YIL143W cell organization and biogenesis;transport membrane;mitochondrion protein binding;transporter activity 0.778 0.778 1.00
Altered inheritance of mitochondria protein 18, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85660 5 AIM18; YHR198C mitochondrion catalytic activity 0.145 0.145 1.00
Uncharacterized protein YDR119W-A
[OS=Saccharomyces cerevisiae S288c] 37999 70 COX26; YDR119W-A cell organization and biogenesis;cellular component movement;metabolic process;regulation of biological process;transport membrane;mitochondrion 1.154 1.154 1.00
Acyl carrier protein, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85304 2 ACP1; YKL192C metabolic process;transport mitochondrion 0.259 0.259 1.00
Putative transferase CAF17, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85358 6 IBA57; YIR122W cell organization and biogenesis;metabolic process mitochondrion;organelle lumen catalytic activity 0.075 0.075 1.00
Intermediate cleaving peptidase 55
[OS=Saccharomyces cerevisiae S288c] 85681 1 ICP55; YER078C metabolic process;regulation of biological process membrane;mitochondrion catalytic activity;metal ion binding 0.077 0.077 1.00
thioredoxin reductase 2, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85600 6 TRB2; YHR106W cellular homeostasis;metabolic process;regulation of biological process;response to stimulus cytoplasm;mitochondrion antioxidant activity;catalytic activity 0.136 0.136 1.00
Lysophosphatidylcholine acyltransferase
[OS=Saccharomyces cerevisiae S288c] 85626 2 TA21; YPR140W cell organization and biogenesis;metabolic process;transport membrane;mitochondrion catalytic activity 0.093 0.093 1.00
Cytochrome c oxidase polypeptide VIII, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85111 1 COX8; YLR399C metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 0.778 0.778 1.00
Cytochrome c oxidase subunit 7
[OS=Saccharomyces cerevisiae S288c] 85239 8 COX7; YMR256C metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 1.154 1.154 1.00
DNA-directed RNA polymerase, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85050 7 RPO41; YFL039W cell organization and biogenesis;metabolic process cytoplasm;mitochondrion;organelle lumen catalytic activity;DNA binding 0.056 0.056 1.00
Ubiquinone biosynthesis protein COQ9, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85089 8 COQ9; YLR201C metabolic process membrane;mitochondrion 0.166 0.166 1.00
Ubiquitin carboxyl-terminal hydrolase 16
[OS=Saccharomyces cerevisiae S288c] 85063 2 UB16; YPL072W metabolic process membrane;mitochondrion catalytic activity 0.072 0.072 1.00
Thrreonine-tRNA ligase, cytoplasmic
[OS=Saccharomyces cerevisiae S288c] 85473 2 THS1; YIL078W metabolic process cytoplasm;mitochondrion catalytic activity;nucleotide binding;RNA binding 0.05 0.05 1.00
Dihydrolipoamide dehydrogenase, mitochondrial
[OS=Saccharomyces cerevisiae S288c] 85092 7 LPD1; YLI038C cellular homeostasis;metabolic process;regulation of biological process mitochondrion;organelle lumen catalytic activity;nucleotide binding 21.53 9 23.11 9 1.07
| P16547 | Mitochondrial outer membrane protein OM45 [OS=Saccharomyces cerevisiae S288c] | B5467 | 0 | OM45; YIL136W | membrane/mitochondrion | 250.1 89 | 274.4 23 | 1.10 |
|---|---|---|---|---|---|---|---|---|
| Q12466 | tricatin-1 [OS=Saccharomyces cerevisiae S288c] | B5425 | 3 | TC61; YDR086C | cell organization and biogenesis; regulation of biological process | endoplasmic reticulum/mitochondrion | 0.417 0.468 | 1.12 |
| P2332 | Mitochondrial oxaloacetate transport protein [OS=Saccharomyces cerevisiae S288c] | B5733 | 9 | OAC1; YKL112O | metabolic process; transport | membrane/mitochondrion | 4.999 5.813 | 1.16 |
| Q12482 | Mitochondrial aspartate-glutamate transporter AGC1 [OS=Saccharomyces cerevisiae S288c] | B5613 | 2 | AGC1; YPR021C | metabolic process; transport | membrane/mitochondrion | 0.348 0.407 | 1.17 |
| P00924 | Eno1p 1 [OS=Saccharomyces cerevisiae S288c] | B5316 | 9 | ENO1; YGR254W | metabolic process; regulation of biological process | cytoplasm; cytosol; membrane/mitochondrion | 0.848 0.995 | 1.17 |
| P12695 | Dihydrolipoamide-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5665 | 3 | LAT1; YNL071W | metabolic process | mitochondrial; organelle lumen | 8.43 7.62 | 1.19 |
| P40035 | Mitochondrial phosphate carrier protein 2 [OS=Saccharomyces cerevisiae S288c] | B5677 | 9 | PIC2; YER053C | cellular homeostasis; metabolic process | membrane/mitochondrion | 1.637 1.976 | 1.21 |
| Q12374 | Nuclear control of ATPase protein 2 [OS=Saccharomyces cerevisiae S288c] | B5627 | 8 | NCA2; YPR155C | metabolic process | membrane/mitochondrion | 0.468 0.565 | 1.21 |
| P07651 | Sur7p family protein FMP45 [OS=Saccharomyces cerevisiae S288c] | B5130 | 4 | FMP45; YDL222C | differential cell organization and biogenesis | membrane/mitochondrion | 4.878 6.017 | 1.23 |
| Q1852 | Mitochondrial import inner membrane translocase subunit Tim44 [OS=Saccharomyces cerevisiae S288c] | B5479 | 0 | TIM44; YIL022W | transport | membrane/mitochondrion | 3.758 4.946 | 1.32 |
| P33303 | Succinate/fumarate mitochondrial transporter [OS=Saccharomyces cerevisiae S288c] | B5355 | 8 | SFC1; YJR095W | metabolic process; transport | membrane/mitochondrion | 9 11.91 5 | 1.32 |
| P25087 | Sterol 24-C-methyltransferase [OS=Saccharomyces cerevisiae S288c] | B5500 | 3 | ERG6; YML088C | metabolic process | endoplasmic reticulum; membrane/mitochondrion | 1.424 1.894 | 1.33 |
| Q4013 | Citrate/oxoglutarate carrier protein [OS=Saccharomyces cerevisiae S288c] | B5528 | 2 | YHM2; YMR241W | cell organization and biogenesis | membrane/mitochondrion | 3.467 4.623 | 1.33 |
| P53292 | 37S ribosomal protein S35, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5307 | 5 | MRPS35; YGR165W | cell organization and biogenesis | mitochondrial; ribosome | 1.512 2.02 | 1.34 |
| P53266 | Cytochrome oxidase assembly protein SHY1 [OS=Saccharomyces cerevisiae S288c] | B5300 | 9 | SHY1; YIR112W | cell organization and biogenesis | membrane/mitochondrion | 1.154 1.555 | 1.35 |
| P42900 | Sigma-like sequence protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5083 | 0 | SLS1; YLR199C | cell organization and biogenesis; metabolic process | membrane/mitochondrion | 0.194 0.266 | 1.37 |
| P54115 | Magnesium-activated aldehyde dehydrogenase, cytosolic [OS=Saccharomyces cerevisiae S288c] | B5604 | 4 | ALD6; YPL061W | metabolic process; response to stimulus | cytoplasm; cytosol; mitochondrial | 0.25 0.346 | 1.38 |
| P20967 | 2-oxoglutarate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5648 | 1 | KG01; YIL125W | metabolic process | cytosol; mitochondrial; organelle lumen | 11.42 6 15.84 3 | 1.39 |
| P53206 | Putative cysteine synthase [OS=Saccharomyces cerevisiae S288c] | B5289 | 5 | YGR012W; YGR012W | metabolic process | mitochondrial; ribosome | 0.837 1.154 | 1.41 |
| Q12289 | mitochondrial carnitine carrier [OS=Saccharomyces cerevisiae S288c] | B5426 | 7 | CRC1; YDR100C | metabolic process; transport | membrane/mitochondrion | 1.404 1.994 | 1.42 |
| P21771 | 37S ribosomal protein S28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5193 | 7 | MRPS28; YDR337W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | 0.438 0.624 | 1.42 |
| Q06367 | ABC1 family protein MCP2 [OS=Saccharomyces cerevisiae S288c] | B5095 | 5 | YLR235W; MCP2; YLR235W | cell organization and biogenesis | membrane/mitochondrion | 0.484 0.693 | 1.43 |
| P08090 | Citrate synthase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | B5573 | 2 | CIT1; YNR003C | metabolic process; transport | cytosol; mitochondrial; organelle lumen | 9 12.89 5 | 1.43 |
| Q0163 | 37S ribosomal protein S23, mitochondrial (OS=Saccharomyces cerevisiae S288c) | B5274 8 | RSM23, YGL129C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | catalytic activity; nucleo tide binding; RNA binding; structural molecule activity | 0.983 | 2.065 | 2.10 |
| P32792 | UPF0744 protein YSCB3 (OS=Saccharomyces cerevisiae S288c) | B5441 0 | YSCB3, YHR017 W | membrane; mitochondrion | | | 0.11 | 0.233 | 2.12 |
| P49954 | Probable hydrolase NIT3 (OS=Saccharomyces cerevisiae S288c) | B5106 5 | NIT3, YLR351C | metabolic process | | cytoplasm; mitochondrion | catalytic activity | 0.129 | 0.274 | 2.12 |
| P38297 | Mitofusin FZO1 (OS=Saccharomyces cerevisiae S288c) | B5247 7 | FZO1, YBR179C | cell organization and biogenesis | | membrane; mitochondrion | catalytic activity; nucleo tide binding; protein binding | 0.142 | 0.304 | 2.14 |
| Q08926 | ULP1-interacting protein 4 (OS=Saccharomyces cerevisiae S288c) | B5591 6 | ULP4, YPL188C | | endoplasmic reticulum; membrane; mitochondrion; nucleus | | | 0.136 | 0.292 | 2.15 |
| P1921 | Glutathione reductase (OS=Saccharomyces cerevisiae S288c) | B5001 4 | GLR1, YPL091W | | | | cytoplasm; cytosol; mitochondrion; nuclear | antioxidant activity; catalytic activity; nucleo tide binding | 0.155 | 0.334 | 2.15 |
| P12709 | Glucose-6-phosphate isomerase (OS=Saccharomyces cerevisiae S288c) | B5249 5 | PG11, YBR196C | | | | | catalytic activity | 0.166 | 0.359 | 2.16 |
| P3166 | ATP-dependent RNA helicase mrh4, mitochondrial (OS=Saccharomyces cerevisiae S288c) | B5281 2 | MRH4, YGL064C | cell organization and biogenesis; metabolic process | | | | catalytic activity; nucleo tide binding; RNA binding | 0.225 | 0.501 | 2.23 |
| P50110 | Sorting assembly machinery 37 KDA subunit (OS=Saccharomyces cerevisiae S288c) | B5508 2 | SAM37, YMR080C | | cell organization and biogenesis; transport | | | membrane; mitochondrion | protein binding | 0.245 | 0.551 | 2.25 |
| P22136 | ATPase expression protein 2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | B5532 5 | AEP2, YMR282C | metabolic process; regulation of biological process | | | | | RNA binding | 0.292 | 0.668 | 2.29 |
| P40803 | Tryptophan-tRNA ligase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | B5186 1 | MSW1, YDR296W | | | | | cytoplasm; mitochondrion; organellar lumen | catalytic activity; nucleo tide binding | 0.292 | 0.668 | 2.29 |
| P40496 | 37S ribosomal protein S23, mitochondrial (OS=Saccharomyces cerevisiae S288c) | B5471 5 | RSM23, YIL093C | | | | | structural molecule activity | 0.292 | 0.668 | 2.29 |
| Q03430 | 37S ribosomal protein RSM28, mitochondrial (OS=Saccharomyces cerevisiae S288c) | B5210 5 | RSM28, YDR404 W | cell organization and biogenesis; metabolic process | | | | structural molecule activity | 1.462 | 3.489 | 2.39 |
| P56350 | S45 ribosomal protein L10, mitochondrial (OS=Saccharomyces cerevisiae S288c) | B5433 6 | MRPL10, YNL284C | | | | | structural molecule activity | 0.551 | 1.404 | 2.55 |
| Q03653 | protein EFR3 (OS=Saccharomyces cerevisiae S288c) | B5252 2 | EFR3, YMR231C | | | | | membrane; mitochondrion | | 0.096 | 0.259 | 2.70 |
| P19952 | Mitochondrial inner membrane protein OXA1 (OS=Saccharomyces cerevisiae S288c) | B5689 8 | OXA1, YER154W | | | | | membrane; mitochondrion | transporter activity | 1.371 | 3.87 | 2.82 |
| P38169 | Kynurenine 3-monooxygenase (OS=Saccharomyces cerevisiae S288c) | B5217 9 | BNA4, YBL098W | | | | | membrane; mitochondrion | catalytic activity; nucleo tide binding | 0.172 | 0.487 | 2.83 |
| P38640 | Trrcabin-3 (OS=Saccharomyces cerevisiae S288c) | B5490 3 | TCB3, YML072C | | | | | endoplasmic reticulum; membrane; mitochondrion | metal ion binding; protein binding | 0.283 | 0.806 | 2.85 |
| P56517 | S45 ribosomal protein L4, mitochondrial (OS=Saccharomyces cerevisiae S288c) | B5116 0 | MRPL4, YLR439W | | | | | | structural molecule activity | 0.369 | 1.081 | 2.93 |
| Q12251 | Uncharacterized mitochondrial carrier YPR011C (OS=Saccharomyces cerevisiae S288c) | B5612 1 | YPR011C, YPR011C | | | | | structural molecule activity; transporter activity | | 0.245 | 0.73 | 2.98 |
| P28737 | Protein MSR1 (OS=Saccharomyces cerevisiae S288c) | B5291 5 | MSR1, YGR028 W | | | | | membrane; mitochondrion; nucleus | catalytic activity; nucleo tide binding; protein binding | 0.239 | 0.778 | 3.00 |
| P40015 | Inositol phosphoplipids phospholipase C (OS=Saccharomyces cerevisiae S288c) | B5673 9 | ISP1, YER019W | | | | | | | 0.101 | 0.334 | 3.31 |
| Q03327 | Mitochondrial fusion and transport protein Ugo1 (OS=Saccharomyces cerevisiae S288c) | B5208 1 | UGD1, YDR470C | | | | | membrane; mitochondrion | protein binding; structural molecule activity | 0.425 | 1.424 | 3.35 |
| Accession | Description                                                                 | Gene ID     | Organism                  | GO Terms                                             | p-value | q-value | Fold Change |
|-----------|------------------------------------------------------------------------------|-------------|---------------------------|------------------------------------------------------|---------|---------|-------------|
| P25038    | Translation initiation factor IF-2, mitochondrial                            | B54135      | *Saccharomyces cerevisiae* | mitochondrion; nucleus; cellular process             | 0.11    | 0.369   | 3.35        |
| Q12117    | Protein MRH1                                                                  | B51597      | *Saccharomyces cerevisiae* | endoplasmic reticulum; membrane; mitochondrial       | 2.162   | 7.254   | 3.36        |
| P49334    | Mitochondrial import receptor subunit tom22                                 | B55592      | *Saccharomyces cerevisiae* | membrane; mitochondrial; protein binding; transport | 0.292   | 1.154   | 3.95        |
| P25578    | CDP-diacylglycerol–glycerol-3-phosphate 3-phosphatidylyltransferase           | B50352      | *Saccharomyces cerevisiae* | mitochondrial; metabolic process                    | 0.083   | 0.374   | 4.51        |
Supplemental Table S12. The relative concentrations of proteins in mitochondria purified from WT or ups2Δ cells cultured without LCA. Mitochondria were purified from WT or ups2Δ cells recovered on day 7 of cell culturing without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI WT | emPAI ups2 | Ratio ups2 / WT |
|-----------|-------------|---------------|--------|--------------------|-------------------|------------------|----------|-------------|-----------------|
| P38120    | 37S ribosomal protein S9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85244 3 | MRPS9; YBR146W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 3.437 | 0.145 | 0.04 |
| P12687    | 54S ribosomal protein L2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85572 7 | MRPL2; YNL005C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | catalytic activity;RNA binding;structural molecule activity | 1.848 | 0.11 | 0.06 |
| P08525    | Cytochrome b-c1 complex subunit 8 [OS=Saccharomyces cerevisiae S288c] | 85327 3 | QCR8; YLJ168W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 5.31 | 0.585 | 0.11 |
| P48527    | Tyrosine-tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85600 7 | MSR1; YPL097W | metabolic process | cytoplasm;cytosol;mitochondrion;organellar lumen | catalytic activity;nucleotide binding;RNA binding | 0.63 | 0.072 | 0.11 |
| Q03430    | 37S ribosomal protein MRPS18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85210 5 | MRPS18; YDR494W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 3.062 | 0.35 | 0.11 |
| P36141    | Putative redox protein fmp6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85392 3 | FMPP46; YKR049C | metabolic process | mitochondrion | catalytic activity;protein binding | 4.337 | 0.52 | 0.12 |
| P38885    | Altered inheritance of mitochondria protein 46, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85660 6 | AIM46; YHR199C | mitochondrial | catalytic activity | 1.594 | 0.245 | 0.12 |
| P38797    | Protein phosphatase 2C homolog 7, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85647 5 | PTC7; YMR076W | metabolic process | mitochondrion | catalytic activity;metal ion binding;protein binding | 0.874 | 0.11 | 0.13 |
| P25605    | Acetolactate synthase small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85034 8 | ILV6; YCL009C | metabolic process;regulation of biological process | mitochondrion | catalytic activity;enzyme regulator activity | 10.28 | 0.346 | 0.13 |
| P40165    | NAD(P)H:quinone oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85552 1 | YNL200C; YNL200C | metabolic process | cytoplasm;mitochondrion | catalytic activity;metal ion binding;nucleotide de binding | 1.61 | 0.212 | 0.13 |
| Q23449    | ATP synthase subunit 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85110 2 | ATP14; YLR295C | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 2.728 | 0.389 | 0.14 |
| P24847    | 37S ribosomal protein S18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85541 0 | MRPS18; YNL306W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 1.054 | 0.155 | 0.15 |
| P00128    | Cytochrome b-c1 complex subunit 7 [OS=Saccharomyces cerevisiae S288c] | 85214 2 | QCR7; YDR527C | cell organization and biogenesis;metabolic process | membrane;mitochondrion | catalytic activity;transporter activity | 11.91 | 1.783 | 0.15 |
| P91449    | ATP synthase subunit e, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85192 2 | TIM11; YDR332C-A | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | catalytic activity;structural molecule activity | 9 | 1.371 | 0.15 |
| P56521    | 54S ribosomal protein L11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85132 5 | MRPL11; YDL202W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.833 | 0.129 | 0.15 |
| P37267    | Assembly factor clbp4 [OS=Saccharomyces cerevisiae S288c] | 85526 8 | CBP4 | cell organization and biogenesis | membrane;mitochondrion | 3.329 | 0.52 | 0.16 |
| P14908    | Mitochondrial transcription factor 1 [OS=Saccharomyces cerevisiae S288c] | 85526 8 | MTFL1; YMR228W | metabolic process;regulation of | mitochondrion;organellar lumen | catalytic activity;DNA | 0.778 | 0.122 | 0.16 |

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| Loci | Biological Process | Binding | RNA Binding | Metabolic Score | GO Terms |
|------|--------------------|---------|-------------|-----------------|----------|
| Q02486 | ARS-binding factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | AFB2, YMR072W | cell organization and biogenesis, metabolic process, regulation of biological process | chromosome, mitochondrial, nucleus | DNA binding | 69.17 | 10.93 | 0.16 |
| P36520 | S45 ribosomal protein L10, mitochondrial [OS=Saccharomyces cerevisiae S288c] | MRP3L30, YNL284C | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | structural molecule activity | 0.73 | 0.116 | 0.16 |
| P40159 | Uncharacterized protein YNL208W, YNL208W [OS=Saccharomyces cerevisiae S288c] | YNL208W, YNL208W | membrane, mitochondrial, ribosome | | | 1.783 | 0.292 | 0.16 |
| P19955 | 37S ribosomal protein YMR31, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YMR31, YFR040W | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | catalytic activity, protein binding, structural molecule activity | 15.68 | 1 | 2.594 | 0.17 |
| P36517 | S45 ribosomal protein L4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | MRP4L4, YLR039W | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | structural molecule activity | 2.162 | 0.369 | 0.17 |
| P40502 | Altered inheritance of mitochondria protein 19, mitochondrial [OS=Saccharomyces cerevisiae S288c] | AIM19, YIL087C | membrane, mitochondrial | | | 1.512 | 0.259 | 0.17 |
| P00045 | Cytochrome c iso-2 [OS=Saccharomyces cerevisiae S288c] | CYC7, YEL035C | metabolic process, transport | mitochondrial | metal ion binding | 1.512 | 0.259 | 0.17 |
| P36526 | S45 ribosomal protein L27, mitochondrial [OS=Saccharomyces cerevisiae S288c] | MRPL27, YBR282W | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | structural molecule activity | 1.512 | 0.259 | 0.17 |
| Q01683 | 37S ribosomal protein S23, mitochondrial [OS=Saccharomyces cerevisiae S288c] | RSM23, YGL129C | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | catalytic activity, nucleotide binding, RNA binding, structural molecule activity | 4.367 | 0.751 | 0.17 |
| P51998 | S45 ribosomal protein YML6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | YML6, YML025C | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | RNA binding, structural molecule activity | 1.404 | 0.245 | 0.17 |
| P32799 | Cytochrome c oxidase subunit 6A, mitochondrial [OS=Saccharomyces cerevisiae S288c] | COX13, YGL191W | cell organization and biogenesis, metabolic process, regulation of biological process | membrane, mitochondrial | catalytic activity, enzyme regulator activity, transporter activity | 11.58 | 9 | 2.162 | 0.19 |
| P07253 | Cytochrome B pre-mRNA processing protein 6 [OS=Saccharomyces cerevisiae S288c] | CBP6, YBR120C | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | | 3.394 | 0.638 | 0.19 |
| P35180 | Mitochondrial transport receptor subunit Tom20 [OS=Saccharomyces cerevisiae S288c] | TOM20, YGR082W | cell organization and biogenesis, metabolic process, regulation of biological process | membrane, mitochondrial | protein binding, transporter activity | 1.031 | 0.194 | 0.19 |
| P11914 | Mitochondrial processing peptidase subunit alpha [OS=Saccharomyces cerevisiae S288c] | MASA2, YHR024C | metabolic process, transport | membrane, mitochondrial, organelle lumen | catalytic activity, metal ion binding, protein binding | 2.311 | 0.445 | 0.19 |
| P22353 | S45 ribosomal protein S18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | MRPL8, YIL063C | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | structural molecule activity | 0.848 | 0.166 | 0.20 |
| P21771 | S35 ribosomal protein S28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | MRPS28, YDR337W | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | RNA binding, structural molecule activity | 0.624 | 0.129 | 0.21 |
| P02381 | Ribosomal protein VAR1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | VAR1, Q0140 | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | structural molecule activity | 0.52 | 0.11 | 0.21 |
| Q0818 | Meiotic sister-chromatid recombination protein 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | MRC6, YGR354C | metabolic process | mitochondrial, organelle lumen | RNA binding | 1.047 | 0.227 | 0.22 |
| P39676 | Flavochromoprotein [OS=Saccharomyces cerevisiae S288c] | YHR1, YGR234W | metabolic process, response to stimulus | cytoplasm, cytosol, mitochondrial, nucleus, organelle lumen | catalytic activity, metal ion binding, protein binding | 4.179 | 0.931 | 0.22 |
| P38884 | S45 ribosomal protein L22, mitochondrial [OS=Saccharomyces cerevisiae S288c] | MRPL22, YNL177C | cell organization and biogenesis, metabolic process | mitochondrial, ribosome | RNA binding, structural molecule activity | 1.683 | 0.389 | 0.23 |
| Gene | Function | Subcellular Location | Activity | EMBL/GenBank/Protein ID | Log2(FC) |
|------|----------|---------------------|----------|-------------------------|----------|
| P28917 | 3-Hydroxyisobuteryl-CoA hydrolase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion | 85160 | 0.743 |
| Q04728 | Arginine biosynthesis bifunctional protein ArgJ, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion, organelle lumen | 85508 | 0.63 |
| P38323 | ATP-dependent zipA-like chaperone, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | membrane, mitochondrion, organelle lumen | 85252 | 0.607 |
| P38977 | Mitochondrial import inner membrane translocase subunit tim23 [OS=Saccharomyces cerevisiae S288c] | transport | membrane, mitochondrion | 85575 | 4.012 |
| P38088 | Glucose-6-phosphate isomerase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, mitochondrion, organelle lumen | 86343 | 0.636 |
| P23833 | Protein SOD1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; cellular homeostasis; response to stimulus | membrane, mitochondrion | 85232 | 1.154 |
| P38771 | Ribosome-recycling factor, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrion | 85643 | 1.955 |
| P17558 | ATP-dependent mitochondrial protein PET113, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | 85432 | 2.594 |
| P40581 | Peroxiredoxin HYR1 [OS=Saccharomyces cerevisiae S288c] | metabolic process; response to stress | cytoplasm, mitochondrial, organelle lumen | 85485 | 0.995 |
| P17695 | Glutaredoxin-2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cellular homeostasis; metabolic process; regulation of biological process; response to stimulus | cytoplasm, mitochondrial, nucleus | 85212 | 0.874 |
| P00927 | Threonine dehydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, mitochondrion | 85681 | 2.257 |
| P38860 | NFU1-like protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; metabolic process | mitochondrion, organelle lumen | 85382 | 3.87 |
| Q05892 | MIDREX complex component 2 [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrial | 85099 | 3.87 |
| P40513 | Mitochondrial acyl-CoA dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process; regulation of biological process | mitochondrion, organelle lumen | 85474 | 2.831 |
| P00427 | Cytochrome c oxidase subunit 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process; transport | membrane, mitochondrion | 85644 | 2.831 |
| P00445 | Superoxide dismutase [Cu-Zn] [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; cellular homeostasis; metabolic process; response to stress | cytoplasm, mitochondrial, nucleus | 85356 | 1.848 |
| P42900 | Sigma-like sequence protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis; metabolic process | membrane, mitochondrion | 85083 | 0.425 |
| P40582 | Glutathione S-transferase 1 [OS=Saccharomyces cerevisiae S288c] | metabolic process | endoplasmic reticulum, membrane, mitochondrion, nucleus | 85485 | 2.162 |
| P41911 | Glycerol-3-phosphate dehydrogenase [NAD(+)] [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, mitochondrial | 85409 | 0.292 |
| P38169 | Kynurenine 3-dehydroxynase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | metabolic process | membrane, mitochondrion | 85217 | 0.269 |
| Q03557 | Glutamyl-tRNA(s)amidotransferase subunit A, mitochondrial [OS=Saccharomyces cerevisiae] | 85533 | HER2; YMR293C | cell organization and biogenesis; metabolic process | mitochondrion | catalytic activity; nucleotide binding | 0.259 | 0.08 | 0.31 |
| Q02863 | Ubiquitin carboxyl-terminal hydrolase 16 [OS=Saccharomyces cerevisiae] | 85603 | 2 | UBP13; YPLD72W | metabolic process | membrane; mitochondrion | catalytic activity | 0.233 | 0.072 | 0.31 |
| P37298 | Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial [OS=Saccharomyces cerevisiae] | 85175 | 8 | SDH4; YDR178W | metabolic process; transport | membrane; mitochondrion | catalytic activity; metal ion binding | 3.642 | 1.154 | 0.32 |
| P36066 | Protein MRG3 like [OS=Saccharomyces cerevisiae] | 85372 | 5 | YKL133C; YKL133C | metabolic process | membrane; mitochondrion | protein binding | 1.054 | 0.334 | 0.32 |
| P50945 | MICOS complex subunit MIC27 [OS=Saccharomyces cerevisiae] | 85562 | 4 | AIM37; MIC27; YNL100W | cell organization and biogenesis | membrane; mitochondrion | RNA binding; structural molecule activity | 0.968 | 0.311 | 0.32 |
| P27929 | 37S ribosomal protein NAM9, mitochondrial [OS=Saccharomyces cerevisiae] | 85558 | 5 | NAM9; YNL137C | cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrion; ribosome | 1.202 | 0.389 | 0.32 |
| P12787 | Mitochondrial genome maintenance protein MGM101 [OS=Saccharomyces cerevisiae] | 85360 | 9 | MGM101; YIR144W | cell organization and biogenesis; metabolic process; response to stimulus | chromosome; mitochondrion | DNA binding | 3.281 | 1.069 | 0.33 |
| P30437 | Cytochrome c oxidase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae] | 85268 | 8 | COX4; YGL187C | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrion | catalytic activity; metal ion binding; transporter activity | 27.48 | 9 | 0.33 |
| P51615 | Uncharacterized protein YKR070W [OS=Saccharomyces cerevisiae] | 85394 | 4 | YKR070W; YKR070W | metabolic process | mitochondrion | 1.336 | 0.438 | 0.33 |
| P15424 | ATP-dependent RNA helicase MMS516, mitochondrial [OS=Saccharomyces cerevisiae] | 85177 | 5 | MMS516; YDR194C | metabolic process; regulation of biological process | mitochondrion; organelle lumen | catalytic activity; nucleotide binding; RNA binding | 1.783 | 0.585 | 0.33 |
| Q00892 | NADH kinase POSS, mitochondrial [OS=Saccharomyces cerevisiae] | 85591 | 3 | POSS; YPL138W | metabolic process; response to stimulus | mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 1.565 | 0.52 | 0.33 |
| P12866 | 37S ribosomal protein MRPL13, mitochondrial [OS=Saccharomyces cerevisiae] | 85297 | 5 | MRPL13; YGR084C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.778 | 0.259 | 0.33 |
| P38300 | Inner membrane mitochondrion receptor MRB1, mitochondrial [OS=Saccharomyces cerevisiae] | 85248 | 3 | MRB1; YBR185C | cellorganization and biogenesis; regulation of biological process | membrane; mitochondrion | 0.778 | 0.259 | 0.33 |
| P39525 | 3-oxoacyl [acyl-carrier-protein] synthase homolog [OS=Saccharomyces cerevisiae] | 85679 | 0 | CEM2; YER061C | metabolic process | mitochondrion | catalytic activity | 1.081 | 0.369 | 0.34 |
| Q06678 | 34S ribosomal protein L35, mitochondrial [OS=Saccharomyces cerevisiae] | 85192 | 1 | MRPL35; YDR322W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 1.219 | 0.425 | 0.35 |
| P29092 | 37S ribosomal protein MRP4, mitochondrial [OS=Saccharomyces cerevisiae] | 85638 | 4 | MRP4; YHL004W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.957 | 0.334 | 0.35 |
| P21954 | Nicotinamide dehydrogenase [NADP], mitochondrial [OS=Saccharomyces cerevisiae] | 85149 | 3 | IDP1; YDL066W | metabolic process | mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | 33.134 | 11.589 | 0.35 |
| P25719 | Polypl-prolyl cis-trans isomerase C, mitochondrial [OS=Saccharomyces cerevisiae] | 85489 | 7 | CPR3; YMR278W | cell death; metabolic process | mitochondrion; organelle lumen | catalytic activity | 2.415 | 0.848 | 0.35 |
| P23747 | Cysteine desulfurase, mitochondrial [OS=Saccharomyces cerevisiae] | 85034 | 3 | NFS1; YCL017C | cell organization and biogenesis; cellular homeostasis; metabolic process | mitochondrion; nucleus | catalytic activity; metal ion binding; protein binding | 2.3 | 0.817 | 0.36 |
| Accession | Symbol | Gene Name | Function | Localization | GO Terms | P-value | q-value |
|-----------|--------|-----------|----------|--------------|-----------|---------|---------|
| P36516    | SPS3   | SPS3      | cell organization and biogenesis | mitochondrion; nucleus; ribosome | catalytic activity; RNA binding; structural molecule activity | 1.043 | 0.374 | 0.36 |
| P3567     | aln1   | ALN1      | metabolic process | cytosol; mitochondrion | catalytic activity | 2.162 | 0.778 | 0.36 |
| P23006    | ATP5    | ATP5      | metabolic process | membrane; mitochondrion | catalytic activity; transporter activity | 2.162 | 0.778 | 0.36 |
| P02992    | sll1   | SLL1      | cell organization and biogenesis | mitochondrion | catalytic activity; nucleotide binding; RNA binding | 12.04 | 3 | 4.38 | 0.36 |
| P38969    | pent1  | PENT1     | cell organization and biogenesis | membrane; mitochondrion | | 0.711 | 0.259 | 0.36 |
| P18900    | npe1   | NPE1      | metabolic process | membrane; mitochondrion | catalytic activity; metal ion binding; protein binding | 0.711 | 0.259 | 0.36 |
| P32898    | mpq1   | MPQ1      | metabolic process | mitochondrion | catalytic activity; metal ion binding | 0.812 | 0.297 | 0.37 |
| P25038    | rif4   | RIF4      | cell organization and biogenesis | mitochondrion; nucleus | catalytic activity; nucleotide binding; RNA binding | 0.299 | 0.11 | 0.37 |
| P34146    | hsp70   | HSP70     | cell organization and biogenesis | mitochondrion; organelle lumen | catalytic activity; nucleotide binding; protein binding | 4.264 | 1.569 | 0.37 |
| Q04935    | cco1   | COX1      | cell organization and biogenesis | membrane; mitochondrion | protein binding | 1.894 | 0.701 | 0.37 |
| P32445    | srs2   | SRS2      | cell organization and biogenesis | mitochondrion | DNA binding | 1.783 | 0.668 | 0.37 |
| P00044    | sfs1   | SFS1      | metabolic process | mitochondrion | metal binding; protein binding | 12.33 | 5 | 4.623 | 0.37 |
| P07806    | val1   | VAL1      | metabolic process; regulation of biological process | cytoplasm; cytosol; mitochondrion | catalytic activity; nucleotide binding | 0.668 | 0.251 | 0.38 |
| Q08968    | ump1   | UMP1      | mitochondrial | protein binding | | 2.162 | 0.823 | 0.38 |
| P40053    | alp1   | ALP1      | mitochondrial | | | 4.036 | 1.537 | 0.38 |
| P33226    | unr1   | UNR1      | membrane; mitochondrion | | | 0.778 | 0.299 | 0.38 |
| P39726    | gcv3   | GCV3      | metabolic process | mitochondrion | catalytic activity | 6.743 | 2.594 | 0.38 |
| P08417    | fum1   | FUM1      | cell organization and biogenesis | cytoplasm; cytosol; mitochondrion; organelle lumen | catalytic activity | 8.237 | 3.175 | 0.39 |
| P32453    | atp5   | ATP5      | cell organization and biogenesis | mitochondrion | protein binding | 1.512 | 0.585 | 0.39 |
| Q03713    | res2   | RES2      | cell organization and biogenesis | membrane; mitochondrion | | 1.512 | 0.585 | 0.39 |
| P50088    | stp1   | STP1      | endoplasmic reticulum; membrane; mitochondrion | | | 157.4 | 89 | 62.09 | 0.39 |
| Accession | Description                                                                 | Localization                                                                 | GO Terms                                                                 | p-value   |
|-----------|------------------------------------------------------------------------------|------------------------------------------------------------------------------|--------------------------------------------------------------------------|-----------|
| P18152    | Tricarboxylate transport protein                                            | mitochondrial                                                               | de binding, protein binding                                              | 0.551     |
| P18628    | SAS ribosomal protein L17, mitochondrial                                    | mitochondrial                                                               | cell organization and biogenesis, metabolic process                     | 0.52      |
| Q07349    | MIOREX complex component 9                                                  | mitochondrial                                                               | catalytic activity, RNA binding                                          | 2.433     |
| P28289    | Mitochondrial chaperone BCS1                                               | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.425     |
| Q01976    | ADP ribose pyrophosphatase                                                  | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.425     |
| P30879    | Intron encoded RNA matruse BI4                                              | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.389     |
| P54115    | Magnesium-activated aldehyde dehydrogenase, cytosolic                       | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.346     |
| P56252    | SAS ribosomal protein L15, mitochondrial                                     | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.334     |
| P58297    | Mitofusin F201, mitochondrial                                               | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.304     |
| Q05931    | Heat shock protein S5Q1, mitochondrial                                      | organelle lumen                                                             | catalytic activity, RNA binding                                          | 0.884     |
| Q06089    | Uncharacterized mitochondrial outer membrane protein YPR098C                | mitochondrial                                                               | catalytic activity, RNA binding                                          | 4.623     |
| Q08223    | Altered inheritance of mitochondria-transport protein 39                   | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.995     |
| P10662    | SAS ribosomal protein MRP1, mitochondrial                                    | mitochondrial                                                               | catalytic activity, RNA binding                                          | 1.239     |
| P52893    | Probable alanine aminotransferase, mitochondrial                            | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.951     |
| P31911    | Dna1 homolog 1, mitochondrial                                               | mitochondrial                                                               | enzyme regulator activity, RNA binding, mitochondrial                    | 2.765     |
| P36008    | Elongation factor 1-gamma 2                                                 | mitochondrial                                                               | catalytic activity, RNA binding                                          | 0.202     |
| Q12029    | Probable mitochondrial transport protein ftf1                               | mitochondrial                                                               | transporter activity, RNA binding                                        | 2.793     |
| P18409    | Mitochondrial distribution and morphology protein 10                        | mitochondrial                                                               | protein binding                                                          | 0.16      |
P0047
Super oxide dismutase (Mn), mitochondrial [OS=Saccharomyces cerevisiae S288c]

85639 9 SOD2; YHR008C metabolic process;response to stimulus mitochondrion;organelle lumen antioxidant activity;catalytic activity;metal ion binding 3.924 1.894 0.48

P00401
Cytochrome c oxidase subunit 1 [OS=Saccharomyces cerevisiae S288c]

85459 8 COX1; Q0045 metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding;transporter activity 1.61 0.778 0.48

Q23480
Probable electron transfer flavoprotein subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85611 2 AIM45; YPR004C metabolic process;transport mitochondrion;organelle lumen catalytic activity;nucleotide de binding 2.548 1.239 0.49

P38714
Arginine-decarboxylase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85649 1 MSK1; YHR091C cell organization;development;metabolic process cytoplasm;mitochondrion;organelle lumen catalytic activity;metal ion binding;nucleotide de binding 0.113 0.055 0.49

P38834
Isocitrate dehydrogenase (NAD) subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85569 1 IDH1; YNL037C metabolic process;transport cytosol;mitochondrion;organelle lumen catalytic activity;metal ion binding;protein binding;RNA binding 7.859 3.833 0.49

P38825
Protein TOM71 [OS=Saccharomyces cerevisiae S288c]

85651 7 TOM71; YHR117W transport membrane;mitochondrion protein binding;transporter activity 0.701 0.343 0.49

P43635
Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85610 7 CIT3; YPR001W metabolic process mitochondrion catalytic activity 3.642 1.783 0.49

P07275
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85643 2 PUT2; YHR037W metabolic process membrane;mitochondrion;organelle lumen catalytic activity 5.579 2.765 0.50

P38921
D-lactate dehydrogenase [cytochrome] 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85138 0 OLD1; YDL174C metabolic process transport membrane;mitochondrion catalytic activity;metal ion binding 11.25 3 5.661 0.50

P53140
Protein RM90D, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85277 1 RM90D; YGL107C cell differentiation;metabolism regulation of biological process membrane;mitochondrion RNA binding 1.154 0.585 0.51

P32317
Protein AFG1 [OS=Saccharomyces cerevisiae S288c]

85665 8 AFG1; YEL052W cell organization and biogenesis;metabolic process;response to stimulus;transport membrane;mitochondrion catalytic activity;protein binding;RNA binding 1.154 0.585 0.51

P36525
SAS ribosomal protein L24, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85523 1 MRPL24; YMR193W cell organization and biogenesis;metabolic process mitochondrion;ribosome RNA binding;structural organization 1.154 0.585 0.51

P40752
Succinate dehydrogenase [ubiquinone] flavoprotein subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85340 5 YIL045W; YIL045W metabolic process transport membrane;mitochondrion catalytic activity;metal ion binding 4.043 2.065 0.51

Q22091
Mitochondrial 2-methylisocitrate lyase [OS=Saccharomyces cerevisiae S288c]

85611 4 ICL2; YPR006C metabolic process mitochondrion;organelle lumen catalytic activity 3.833 1.976 0.52

P40008
Protein FMP52L, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85672 1 FMP52L; YER004W endoplasmic reticulum;membrane;mitochondrion catalytic activity 2.652 1.371 0.52

P40098
Cytochrome c oxidase assembly protein cox15 [OS=Saccharomyces cerevisiae S288c]

85688 4 COX15; YER141W cell organization and biogenesis;metabolic process;transport membrane;mitochondrion catalytic activity;transporter activity 2.594 1.346 0.52

P4098
Uncharacterized mitochondrial membrane protein FMP10 [OS=Saccharomyces cerevisiae S288c]

85693 1 FMP10; YER182W membrane;mitochondrion structural molecule activity;transporter activity 4.436 2.36 0.53

P43617
Uncharacterized mitochondrial carrier YPR045W [OS=Saccharomyces cerevisiae S288c]

85106 6 YPR045W; YPR045W metabolic process transport membrane;mitochondrion structural molecule activity;transporter activity 0.778 0.413 0.53

P38891
Branched-chain-aminoo acid aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

85661 5 BAT1; YHR208W metabolic process;regulation of biological process;response to stress mitochondrion;organelle lumen catalytic activity 7.111 3.806 0.54
| Gene Symbol | Description                                      | Function                               | Cellular Location | Biological Process                  | Molecular Function                  | Log2 Fold Change |
|-------------|--------------------------------------------------|----------------------------------------|-------------------|-------------------------------------|-------------------------------------|-----------------|
| P10834      | Protein P654                                      | Metabolic process; regulation of biological process | Membrane, Mitochondrion, Organelle lumen | Metabolism; Development; Cell Cycle | Catalytic activity; Protein binding | 0.688           |
| P19262      | Dihydrolipoamide-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial | Cell organization and biogenesis; Metabolic process | Mitochondrion     | Metabolism; Development; Cell Cycle | Catalytic activity; Protein binding | 5.7             |
| Q05648      | MID1 complex component 10                        |                                        | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Catalytic activity; Protein binding | 0.65            |
| P34227      | Mitochondrial peroxiredoxin PX1                  | Cellular homeostasis; Metabolic process; Regulation of biological process | Mitochondrion     | Oxidative stress; Hypoxia; Response to stress | Antioxidant activity; Catalytic activity | 5.158           |
| P40961      | Prohibitin-1                                     | Cell organization and biogenesis; Metabolic process; Regulation of biological process | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Protein binding                    | 5.158           |
| P39006      | Phosphotyrosine deacetylase pseudomyosin 1, mitochondrial | Metabolic process; Regulation of biological process | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Catalytic activity               | 0.487           |
| Q06VH5      | MICO5 complex subunit Mic10                      | Cell organization and biogenesis | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Metabolism; Development; Cell Cycle | 1.683           |
| P342940     | Probable electron transfer flavoprotein subunit beta | Metabolic process; Transport          | Mitochondrion, Organelle lumen | Metabolism; Development; Cell Cycle | Metabolism; Development; Cell Cycle | 3.87            |
| P04472      | Mitochondrial inner membrane I-AAA protease supercomplex subunit MG3 | Metabolic process | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Metabolism; Development; Cell Cycle | 0.417           |
| Q06567      | ABC11 family protein MCP2                        | Cell organization and biogenesis | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Metabolism; Development; Cell Cycle | 0.389           |
| P09457      | ATP synthase subunit 5, mitochondrial             | Metabolic process; Transport          | Mitochondrion, Organelle lumen | Metabolism; Development; Cell Cycle | Catalytic activity; Transport activity | 10.36           |
| P37299      | Cytochrome b-1 complex subunit 10                 | Metabolic process; Transport          | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Catalytic activity; Transport activity | 5.31            |
| P12374      | Nuclear control of ATPase protein 2              | Metabolic process | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Metabolism; Development; Cell Cycle | 0.668           |
| P40047      | Aldehyde dehydrogenase 5, mitochondrial          | Metabolic process | Mitochondrion, Organelle lumen | Metabolism; Development; Cell Cycle | Catalytic activity               | 1.995           |
| P12333      | ATP synthase subunit 6, mitochondrial             | Cell organization and biogenesis; Metabolic process; Transport | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Catalytic activity; Transport activity | 1.371           |
| P36147      | Prescence translocated-associated motor subunit 17, mitochondrial | Transport | Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Catalytic activity               | 1.371           |
| P24228      | Probable 2-methylcitrate dehydratase              | Metabolic process; Transport          | Cytoplasm, Membrane, Mitochondrion | Metabolism; Development; Cell Cycle | Catalytic activity               | 12.33           |
| P53732      | 37S ribosomal protein S12, mitochondrial          | Cell organization and biogenesis; Metabolic process | Mitochondrion, Ribosome | Metabolism; Development; Cell Cycle | Structural molecule activity       | 1.154           |
cerevisiae S288c mitochondrial assembly protein COX11, Cytochrome c oxidase
mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl cerevisiae S288c subunit 2 Cytochrome c oxidase mitochondria protein 36, Altered inheritance of FMP41 mitochondrial hydrolase uncharacterized
NADPH, B Enoyl
| Accession | Symbol | Description | Localization | Function | KEGG ID | ## | ## | ## |
|-----------|--------|-------------|--------------|----------|---------|----|----|----|
| P38271    | OPY1   | Protein OPY1 | cytoplasm, mitochondrial | catalytic activity, protein binding | | 0.438 | 0.274 | 0.63 |
| P48015    | Amino| Aminotransferase, mitochondrial | cytoplasm, mitochondrial | catalytic activity, protein binding | | 8.047 | 5.062 | 0.63 |
| Q07500    | External | Ubiquinone oxidoreductase 2, mitochondrial | cytoplasm, mitochondrial | catalytic activity, nucleotide binding | | 6.356 | 4.012 | 0.63 |
| P32792    | UPP0744 | Protein YOS3, mitochondrial | cytoplasm, mitochondrial | catalytic activity, protein binding | | 0.369 | 0.233 | 0.63 |
| P37923    | SWI4 | Cytochrome b | cytoplasm, mitochondrial | catalytic activity, protein binding | | 1.154 | 0.73 | 0.63 |
| Q00155    | Methyltransferase | Methyltransferase | cytoplasm, mitochondrial | catalytic activity, protein binding | | 0.334 | 0.212 | 0.63 |
| Q07011    | Succinate dehydrogenase | Succinate dehydrogenase | mitochondrial | catalytic activity, protein binding | | 8.454 | 5.381 | 0.64 |
| Q01532-1  | Cysteine proteinase | Cysteine proteinase 1 | mitochondrial | catalytic activity, DNA binding, RNA binding | | 0.28 | 0.179 | 0.64 |
| P41921    | Glutathione reductase | Glutathione reductase | cytoplasm, mitochondrial | antioxidant activity, catalytic activity, nucleotide binding | | 0.241 | 0.155 | 0.64 |
| P38705    | Serine-tRNA ligase, mitochondrial | Serine-tRNA ligase, mitochondrial | cytoplasm, mitochondrial, organelle lumen | catalytic activity, nucleotide binding | | 0.233 | 0.15 | 0.64 |
| P07236    | Threonine-tRNA ligase, mitochondrial | Threonine-tRNA ligase, mitochondrial | cytoplasm, mitochondrial, organelle lumen | catalytic activity, nucleotide binding, RNA binding | | 0.233 | 0.15 | 0.64 |
| P53266    | Cytochrome oxidase | Cytochrome oxidase | membrane, mitochondrial | protein binding | | 1.783 | 1.154 | 0.65 |
| P32340    | Rotenone-insensitive | Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial | cytoplasm, mitochondrial, organelle lumen | catalytic activity, nucleotide binding | | 16.43 | 10.72 | 1 | 0.65 |
| P36013    | NAD-dependent malic enzyme, mitochondrial | NAD-dependent malic enzyme, mitochondrial | cytoplasm, mitochondrial, organelle lumen | catalytic activity, metabolic activity, nucleotide binding | | 1.512 | 0.995 | 0.66 |
| P38127    | Mitochondrial carrier protein | Mitochondrial carrier protein | membrane, mitochondrial | structural molecule activity, transmembrane activity | | 1.512 | 0.995 | 0.66 |
| Q06668    | Methyltransferase | Methyltransferase | membrane, mitochondrial | catalytic activity, structural molecule activity, transmembrane activity | | 0.585 | 0.389 | 0.66 |
| P04710    | ADP-ATP carrier protein | ADP-ATP carrier protein | cytoplasm, mitochondrial | structural molecule activity, transmembrane activity | | 10.28 | 8 | 0.67 |
| P3641     | Mitochondrial phosphatase carrier protein | Mitochondrial phosphatase carrier protein | membrane, mitochondrial | protein binding, structural molecule activity, transmembrane activity | | 20.54 | 13.67 | 8 | 0.67 |
| P08667    | Cytochrome b-c1 complex subunit Rieske | Cytochrome b-c1 complex subunit Rieske, mitochondrial | membrane, mitochondrial | catalytic activity, metal binding | | 25.10 | 16.78 | 3 | 0.67 |
| P38910 | 30 kDa heat shock protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85418 5 | HSP10; YOR620C | cell organization and biogenesis; metabolic process; response to stimulus; transport | cytoplasm; mitochondrial; organelle lumen | metal ion binding; nucleotide binding; protein binding | 3.217 | 2.162 | 0.67 |
| P00830 | ATP synthase subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85358 5 | ATP2; YJR121W | metabolic process; transport | cytosol; membrane; mitochondrial | catalytic activity; nucleotide binding; protein binding | 38.81 | 26.12 | 0.67 |
| P21560 | Protein CBP3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85588 6 | CBP3; YPL215W | cell organization and biogenesis; regulation of biological process | membrane; mitochondrial; ribosome | catalytic activity; protein binding; transport | 1.031 | 0.701 | 0.68 |
| P15108 | ATP-dependent molecular chaperone HSC82 [OS=Saccharomyces cerevisiae S288c] | 85522 4 | HSC82; YMR186W | cell organization and biogenesis; metabolic process; response to stimulus | cytoplasm; membrane; mitochondrial | catalytic activity; nucleotide binding; protein binding | 1.565 | 1.081 | 0.69 |
| P40955 | Glycerol-3-phosphate dehydrogenase (Decarboxylating), mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85522 7 | GCV2; YMR189W | metabolic process | cytosol; mitochondrial | catalytic activity | 1.575 | 1.096 | 0.70 |
| P46046 | Mitochondrial intermembrane space import and assembly protein 40 [OS=Saccharomyces cerevisiae S288c] | 85363 9 | MIA40; YKL195W | cellular compartment movement; metabolic process; response to stimulus | membrane; mitochondrial | catalytic activity; protein binding; transport | 2.914 | 2.03 | 0.70 |
| P23287 | 44S ribosomal protein L41, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85201 4 | MRFP20; YDR405W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | nucleotide binding; protein binding; RNA binding; structural molecule activity | 0.719 | 0.501 | 0.70 |
| P32191 | Glycerol-3-phosphate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85465 1 | GUT2; YL155C | metabolic process | membrane; mitochondrial | catalytic activity | 6.097 | 4.289 | 0.70 |
| Q22531 | Uncharacterized mitochondrial carrier YPR011C [OS=Saccharomyces cerevisiae S288c] | 85612 1 | YPR011C; YPR011C | metabolic process; transport | membrane; mitochondrial | structural molecule activity; transport | 0.551 | 0.389 | 0.71 |
| P40035 | Mitochondrial phosphate carrier protein 2 [OS=Saccharomyces cerevisiae S288c] | 85677 9 | PIC2; YER053C | cellular homeostasis; metabolic process; transport | membrane; mitochondrial | structural molecule activity; transport | 2.793 | 1.976 | 0.71 |
| Q44568 | Fatty aldehyde dehydrogenase HFD1 [OS=Saccharomyces cerevisiae S288c] | 85513 7 | HFD1; YMR11OC | metabolic process | endoplasmic reticulum; endosome; membrane; mitochondrial | catalytic activity | 3.642 | 2.594 | 0.71 |
| P38702 | Mitochondrial carrier protein LEUS [OS=Saccharomyces cerevisiae S288c] | 85639 1 | LEUS; YDR002W | metabolic process; transport | membrane; mitochondrial | structural molecule activity; transport | 0.468 | 0.334 | 0.71 |
| Q28970 | Mitochondrial metal transporter 2 [OS=Saccharomyces cerevisiae S288c] | 85587 7 | MMMT2; YPL224C | cellular homeostasis; regulation of biological process; response to stimulus; transport | membrane; mitochondrial | transporter activity | 0.407 | 0.292 | 0.72 |
| P39925 | Mitochondrial respiratory chain complexes assembly protein AFG3 [OS=Saccharomyces cerevisiae S288c] | 85673 7 | AFG3; YER017C | cell organization and biogenesis; metabolic process; response to stimulus; transport | membrane; mitochondrial | catalytic activity; metal ion binding; nucleotide binding; protein binding | 1.015 | 0.734 | 0.72 |
| P33421 | Succinate dehydrogenase [ubiquinone cytochrome b subunit], mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85371 6 | SDH3; YKL141W | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrial | catalytic activity; metal ion binding | 1.276 | 0.931 | 0.73 |
| Q12166 | 2-isopropylmalate synthase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85427 5 | LEU9; YOR108W | metabolic process | mitochondrial | catalytic activity; protein binding | 1.707 | 1.246 | 0.73 |
| P19414 | Aconitate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85101 3 | ACO1; YLR304C | cell organization and biogenesis; metabolic process; transport | cytoplasm; cytosol; mitochondrial; organelle lumen | catalytic activity; DNA binding; metal ion binding | 24.88 | 18.16 | 0.73 |
| Gene ID       | Description                                                                 | GO Terms                                                                 | GO Score (with Organism) |
|--------------|------------------------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------|
| P40215       | External NADH-ubiquinone oxido-reductase 1, mitochondrial                    | metabolic process                                                       | 5.078                    |
| P32904       | 54S ribosomal protein L6, mitochondrial                                      | cell organization and biogenesis; metabolic process                     | 1.054                    |
| P60208-1     | 2-isopropylmalate synthase                                                  | metabolic process                                                        | 4.223                    |
| P38444       | Mitochondrial import receptor subunit TOM40                                | cell organization and biogenesis; metabolic process                     | 0.896                    |
| P38523       | Gpr1 protein homolog, mitochondrial                                          | metabolic process                                                        | 0.833                    |
| P70256       | Cytochrome b-c1 complex subunit 1, mitochondrial                            | metabolic process                                                        | 9.89                     |
| P36534       | 54S ribosomal protein L40, mitochondrial                                    | cell organization and biogenesis; metabolic process                     | 0.778                    |
| P32473       | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial             | metabolic process                                                        | 6.848                    |
| P53736       | Uncharacterized protein YNR040W                                            | cell organization and biogenesis; metabolic process                     | 0.73                     |
| P50085       | Prohibitin-2                                                                | cell organization and biogenesis; metabolic process; regulation of biological process | 3.806                    |
| P70251       | ATP synthase subunit alpha, mitochondrial                                   | metabolic process                                                        | 26.82                    |
| P36112       | MIC10 complex subunit Mic60                                                 | cell organization and biogenesis; transport                              | 11.79                    |
| P40058       | Uncharacterized protein YIL077C                                             | cell organization and biogenesis; transport                              | 1.154                    |
| Q01574       | acetyl-coenzyme A synthetase 1                                               | cell organization and biogenesis; metabolic process                     | 3.281                    |
| P40012       | pyrroloporphyrinogen oxidase                                                 | metabolic process                                                        | 1.198                    |
| P36101       | IRNA threonylcarbamoyladenosine dehydrogenase 2                            | metabolic process                                                        | 0.778                    |
| P10507       | mitochondrial-processing peptidase subunit beta                             | metabolic process                                                        | 0.778                    |
| P53969       | Sorting assembly machinery 50 S0 da subunit                                 | cell organization and biogenesis; transport                              | 0.61                     |
| Q02981       | ABC1 family protein YPL109C, mitochondrial                                  | mitochondrial                                                            | 0.413                    |
| P46367       | Potassium-activated aldehyde dehydrogenase, mitochondrial                  | metabolic process                                                        | 24.11                    |
| Gene Symbol | Description | Function | Localization | Metabolic Process | Gene Symbol | Description | Function | Localization | Metabolic Process | Gene Symbol | Description | Function | Localization | Metabolic Process |
|-------------|-------------|----------|--------------|-----------------|-------------|-------------|----------|--------------|-----------------|-------------|-------------|----------|--------------|-----------------|
| TIM54       | mitochondrial import inner membrane translocase subunit | cell organization and biogenesis, transport | cytosol, membrane, mitochondrion | transporter activity | 0.655      | 0.54      | 0.82      |             |                 |             |             |             |             |                 |                 |
| MGR1       | Mitochondrial inner membrane i-AAA protease supercomplex subunit | metabolic process | membrane, mitochondrion | protein binding | 1.031      | 0.859      | 0.83      |             |                 |             |             |             |             |                 |                 |
| TIM44       | inner membrane translocase subunit | metabolic process | mitochondrion | catalytic activity; nucleotide binding | 7.003      | 5.898      | 0.84      |             |                 |             |             |             |             |                 |                 |
| LSC2       | translocase subunit | cellular homeostasis, metabolic process, transport | membrane, mitochondrion | catalytic activity; nucleotide binding | 0.645      | 0.546      | 0.85      |             |                 |             |             |             |             |                 |                 |
| MDH1       | glyceraldehyde-3-phosphate dehydrogenase 1 | metabolic process | cytoplasm, cytosol, membrane, mitochondrion | catalytic activity; nucleotide binding | 1.721      | 1.462      | 0.85      |             |                 |             |             |             |             |                 |                 |
| YGR012W     | putative cysteine synthase | metabolic process | membrane, mitochondrion | catalytic activity | 1.346      | 1.154      | 0.86      |             |                 |             |             |             |             |                 |                 |
| ILV2       | Acetolactate synthase catalytic subunit | metabolic process | mitochondrion | catalytic activity; metal ion binding, nucleotide binding | 4.223      | 3.642      | 0.86      |             |                 |             |             |             |             |                 |                 |
| SDH2       | Succinate dehydrogenase | metabolic process, transport | membrane, mitochondrion | catalytic activity; metal ion binding | 18.68      | 16.19      | 0.87      |             |                 |             |             |             |             |                 |                 |
| YLR086C     | D-arabinono-1,4-lactone oxidase | metabolic process, response to stimulus | membrane, mitochondrion | catalytic activity; nucleotide binding | 3.299      | 2.981      | 0.90      |             |                 |             |             |             |             |                 |                 |
| ILV5       | Ketol acid reductoisomerase, mitochondrial | cell organization and biogenesis, metabolic process | mitochondrion | catalytic activity; DNA binding, metal ion binding | 9.000      | 8.211      | 0.91      |             |                 |             |             |             |             |                 |                 |
| LAT1       | Dihydroxyphenylalanine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial | metabolic process | mitochondrion, organelle lumen | catalytic activity | 5.898      | 5.404      | 0.92      |             |                 |             |             |             |             |                 |                 |
| YER178W     | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial | cell growth, metabolic process | mitochondrion, organelle lumen | catalytic activity | 12.46      | 11.49      | 0.92      |             |                 |             |             |             |             |                 |                 |
| YLR355C     | Heat shock protein SS15, mitochondrial | cell organization and biogenesis, metabolic process, regulation of biological process, transport | membrane, mitochondrion, nucleus, organelle lumen | catalytic activity; enzyme regulator activity; nucleotide binding, protein binding | 26.82      | 25.10      | 0.94      |             |                 |             |             |             |             |                 |                 |
| YPR191W     | Cytochrome b-1 complex subunit 2, mitochondrial | metabolic process | transport | catalytic activity; metal ion binding, protein binding, regulator activity | 21.19      | 21.19      | 1.00      |             |                 |             |             |             |             |                 |                 |
| YCR012W     | Phosphoglycerate kinase | metabolic process | cytoplasm, membrane, mitochondrion | catalytic activity; nucleotide binding | 4.843      | 4.843      | 1.00      |             |                 |             |             |             |             |                 |                 |
| YCL    | Mitochondrial import inner membrane translocase subunit | transport | membrane, mitochondrion | nucleotide binding, protein binding | 4.125      | 4.125      | 1.00      |             |                 |             |             |             |             |                 |                 |
| YLR150W     | NADH-cytochrome b5 reductase | metabolic process; response to stimulus | membrane, mitochondrion | catalytic activity; protein binding | 10.28      | 10.28      | 1.00      |             |                 |             |             |             |             |                 |                 |
P28241  Isocitrate dehydrogenase [NAD] subunit 2, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85430 3  IDH2; YOR136W  metabolic process  mitochondrion;organelle lumen  catalytic activity;metal ion binding;protein binding;RNA binding  4.179  4.179  1.00

Q07651  SUR7 family protein FMF45 [Os=Saccharomyces cerevisiae S288c]
85130 4  FMF45; YDL222C  cell differentiation;cell organization and biogenesis  membrane/mitochondrion  6.017  6.017  1.00

P09440  1,3-tetrahydrofuran synthase, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85237 8  MSL1; YBR084W  metabolic process  cytosol;mitochondrion  catalytic activity;nucleotides nucleotide binding  0.9  0.9  1.00

P36148  Glycerol-3-phosphate O-acetyltransferase 2 [Os=Saccharomyces cerevisiae S288c]
85394 1  GPT2; YKR067W  metabolic process  cytoplasm;endoplasmic reticulum;membrane  catalytic activity  1.116  1.116  1.00

P23335  Protein M5551, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85090 0  M5551; YLR203C  metabolic process;regulation of biological process  membrane/mitochondrion  protein binding;translation;translational activity  1.154  1.154  1.00

P23332  Mitochondrial oxaloacetate transport protein [Os=Saccharomyces cerevisiae S288c]
85373 9  OAC1; YKL110W  metabolic process;transport  membrane/mitochondrion  structural molecule activity;transporter activity  2.594  2.594  1.00

P3721  Respiratory supercomplex factor 2, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85575 2  RCF2; YMR018W  cell organization and biogenesis  membrane/mitochondrion  7.111  7.111  1.00

P38325  Mitochondrial outer membrane protein OM14 [Os=Saccharomyces cerevisiae S288c]
85253 1  OM14; YBR230C  transport  membrane/mitochondrion  6.197  6.197  1.00

P38626  NADH-cytochrome b5 reductase 1 [Os=Saccharomyces cerevisiae S288c]
85476 8  CBR1; YIL043C  metabolic process  endoplasmic reticulum;membrane;mitochondrion;nucleus  catalytic activity  1.61  1.61  1.00

P40364  Mitochondrial peculiar membrane protein 1 [Os=Saccharomyces cerevisiae S288c]
85337 9  MPM1; YIL066C  membrane/mitochondrion  1.512  1.512  1.00

P2266  Dynamin-like GTPase MGM1, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85438 6  MGM1; YDR211C  cell organization and biogenesis  membrane/mitochondrion  0.389  0.389  1.00

P33331  Carrier protein YMC1, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85617 1  YMC1; YPR058W  metabolic process;transport  membrane/mitochondrion;vacuole  structural molecule activity;transporter activity  1.254  1.254  1.00

Q0493  LETM1 domain-containing protein YLH47, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85624 3  YLH47; YPR125W  cell organization and biogenesis;transport  membrane/mitochondrion  0.61  0.61  1.00

P38072  Protein SCD2, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85231 2  SCD2; YBR024W  cell organization and biogenesis;cellular homeostasis;metabolic process;transport  membrane/mitochondrion  antioxidant activity;catalytic activity;metal ion binding  0.73  0.73  1.00

P21375  Fumarate reductase 2 [Os=Saccharomyces cerevisiae S288c]
85351 0  OSM1; YIR051W  metabolic process  endoplasmic reticulum;mitochondrion  catalytic activity;nucleotides nucleotide binding  0.346  0.346  1.00

Q03976  37s ribosomal protein S24, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85175 5  RSM24; YDR175C  cell organization and biogenesis;metabolic process  mitochondrion;ribosome  structural molecule activity  0.585  0.585  1.00

P27697  Atypical kinase COQ8, mitochondrial [Os=Saccharomyces cerevisiae S288c]
85275 8  COQ8; YUL119W  metabolic process  membrane/mitochondrion;organelle lumen  catalytic activity;nucleotides nucleotide binding  0.365  0.365  1.00

Q09297  Mitochondrial 2-oxoacid carboxylate carrier 2 [Os=Saccharomyces cerevisiae S288c]
85439 7  ODC2; YOR222W  metabolic process;transport  membrane/mitochondrion  structural molecule activity;transporter activity  0.778  0.778  1.00

Q0685  Autophagy-related protein 33 [Os=Saccharomyces cerevisiae S288c]
85107 0  ATG33; YLR356W  cell communication;metabolic process;response to stimulus  membrane/mitochondrion  1.371  1.371  1.00

P30087  MICS subunit MCIC26 [Os=Saccharomyces cerevisiae S288c]
85315 0  MCIC26; YGR235C  cell organization and biogenesis  membrane/mitochondrion  0.931  0.931  1.00

Q12298  Uncharacterized ABC transporter ATP-binding protein YDR061W [Os=Saccharomyces cerevisiae S288c]
85163 3  YDR061W; YDR061W  mitochondrial  catalytic activity;nucleotide binding  0.266  0.266  1.00

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| Gene ID | Description | Function | Localization | Activity | Score |
|--------|-------------|----------|--------------|----------|-------|
| Q02883 | N-acetyl-phenylphosphonoamidate hydrolase | catalytic activity | membrane, mitochondrial | 0.304 0.304 | 1.00 |
| P34224 | Uncharacterized protein | catalytic activity | membrane, mitochondrial | 0.468 0.468 | 1.00 |
| P34222 | Peptidyl-tRNA hydrolase | catalytic activity | membrane, mitochondrial | 0.425 0.425 | 1.00 |
| P38122 | 3-methyl-2-oxobutanoate hydroxymethyltransferase | catalytic activity | membrane, mitochondrial | 0.259 0.259 | 1.00 |
| YDR610W | Lysophosphatidylcholine acyltransferase | catalytic activity | membrane, mitochondrial | 0.194 0.194 | 1.00 |
| Q04205 | ATP synthase subunit f | catalytic activity | membrane, mitochondrial | 2.981 2.981 | 1.00 |
| Q05610 | Uncharacterized mitochondrial outer membrane protein | catalytic activity | membrane, mitochondrial | 0.389 0.389 | 1.00 |
| Q05867 | Uncharacterized protein | catalytic activity | membrane, mitochondrial | 0.11 0.11 | 1.00 |
| Q2V09 | Uncharacterized protein | catalytic activity | membrane, mitochondrial | 1.154 1.154 | 1.00 |
| P48526 | Isoleucine -tRNA ligase, mitochondrial | catalytic activity | membrane, mitochondrial | 0.04 0.04 | 1.00 |
| P42378 | 4-hydroxybenzoate polyprenyltransferase, mitochondrial | catalytic activity | membrane, mitochondrial | 0.292 0.292 | 1.00 |
| YPR090C | Cytochrome c oxidase assembly protein | catalytic activity | membrane, mitochondrial | 0.194 0.194 | 1.00 |
| YDR119W-A | Cytochrome c oxidase assembly protein | catalytic activity | membrane, mitochondrial | 0.389 0.389 | 1.00 |
| CMC1 | Acyl carrier protein, mitochondrial | Catalytic activity | membrane, mitochondrial | 0.259 0.259 | 1.00 |
| P42463 | Acyl carrier protein, mitochondrial | Catalytic activity | membrane, mitochondrial | 0.778 0.778 | 1.00 |
| P49103 | Cytochrome c oxidase assembly protein | Catalytic activity | membrane, mitochondrial | 0.585 0.585 | 1.00 |
| Q00873 | Cytochrome c1, heme lyase | Catalytic activity | membrane, mitochondrial | 0.359 0.359 | 1.00 |
| P33220 | Mitochondrial carrier protein, mitochondrial | Structural activity | membrane, mitochondrial | 0.11 0.11 | 1.00 |
| P40341 | Mitochondrial respiratory chain complexes assembly protein | Catalytic activity | membrane, mitochondrial | 1.184 1.276 | 1.08 |
| P32795 | Mitochondrial inner membrane | Catalytic activity | membrane, mitochondrial | 1.3 1.415 | 1.09 |
| ID     | Gene Name                      | Protein Name                       | Stimulus/Transport | Metabolic Process | Mitochondrial Import | Catalytic Activity | Metal Ion Binding | Nucleotide Binding | Protein Binding |
|--------|--------------------------------|------------------------------------|--------------------|-------------------|-----------------------|--------------------|-------------------|-------------------|------------------|
| P16547 | Mitochondrial outer membrane protein OM45 | [OS=Saccharomyces cerevisiae S288c] | membrane/mitochondrion | endoplasmic reticulum;membrane;mitochondrion | Metal ion binding;protein binding | 300.9 | 95 | 330.1 | 31 | 1.10 |
| Q2466  | Tricarbamy I | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis;regulation of biological process | endoplasmic reticulum;membrane;mitochondrion | metal ion binding;protein binding | 0.52 | 0.574 | 1.10 |
| P17505 | Malate dehydrogenase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrial;organelle lumen | Catalytic activity;protein binding;RNA binding | 28.93 | 6 | 32.40 | 5 | 1.12 |
| P16622 | Ferrochelatase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | membrane;mitochondrion | Catalytic activity | 4.337 | 4.926 | 1.14 |
| P49367 | Homoaconditase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | mitochondrial | Catalytic activity;metal ion binding;protein binding | 0.638 | 0.73 | 1.14 |
| Q08222 | Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process,transport | membrane;mitochondrion | Catalytic activity;metal ion binding;protein binding | 2.162 | 2.481 | 1.15 |
| P25087 | Sterol 24-C-methyltransferase | [OS=Saccharomyces cerevisiae S288c] | metabolic process | endoplasmic reticulum;membrane;mitochondrion | Catalytic activity | 1.424 | 1.649 | 1.16 |
| Q24822 | Mitochondrial aspartate-glutamate transporter | [OS=Saccharomyces cerevisiae S288c] | metabolic process,transport | membrane;mitochondrion | Structural molecule activity;transporter activity | 0.348 | 0.407 | 1.17 |
| P07213 | Mitochondrial import receptor subunit TOM70 | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis;transport | membrane;mitochondrion | Protein binding;transporter activity | 2.665 | 3.125 | 1.17 |
| Q04922 | Nuclear migration protein NUM1 | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis;cellular component movement;metabolic process;regulation of biological process;transport | endoplasmic reticulum;mitochondrion | Catalytic activity;motor activity;protein binding | 0.065 | 0.078 | 1.20 |
| P33110 | ATP-dependent permease MD1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | transport | membrane;mitochondrion | Catalytic activity;nucleotide binding;transporter activity | 0.438 | 0.528 | 1.21 |
| P07143 | Cytochrome C1, heme protein, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytosol;membrane;mitochondrion | Metal ion binding | 13.25 | 1 | 16.01 | 13 | 1.21 |
| P20967 | 2-oxoglutarate dehydrogenase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytosol;mitochondrion;organelle lumen | Catalytic activity | 8.168 | 9.908 | 1.21 |
| P00358 | Glyceraldehyde-3-phosphate dehydrogenase 2 | [OS=Saccharomyces cerevisiae S288c] | cell death;metabolic process | cytoplasm;cytosol;membrane;mitochondrion;nucleus | Catalytic activity;nucleotide binding;protein binding | 3.489 | 4.484 | 1.29 |
| P04840 | Mitochondrial outer membrane protein porin 1 | [OS=Saccharomyces cerevisiae S288c] | cell death;cell organization and biogenesis;cellular homeostasis;regulation of biological process;transport | cytoplasm;membrane;mitochondrion | Transporter activity | 15.23 | 8 | 19.69 | 1 | 1.29 |
| P53230 | Phosphatidate cytidylyltransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | membrane;mitochondrion;organelle lumen | Catalytic activity | 0.407 | 0.532 | 1.31 |
| Q02776 | Mitochondrial import inner membrane translocase subunit TIM50 | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis;metabolic process,transport | membrane;mitochondrion | Catalytic activity;protein binding;transporter activity | 7.483 | 9.857 | 1.32 |
| P28737 | Protein MSP1 | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis;metabolic process | membrane;mitochondrion;nucleus | Catalytic activity;nucleotide binding | 0.585 | 0.778 | 1.33 |
| Gene Symbol | Description | GO Terms | Organism | GO ID |
|-------------|-------------|----------|----------|-------|
| P3303       | Succinate/fumarate mitochondrial transporter | transport, metabolic process | S. cerevisiae 288c | F08466 |
| P39722      | Mitochondrial RhG TPase 1 | transport | S. cerevisiae 288c | P33759 |
| P25039      | Elongation factor 6, mitochondrial | regulation, cellular process | S. cerevisiae 288c | Q0413 |
| P05626      | ATP synthase subunit 4, mitochondrial | transport, metabolic process | S. cerevisiae 288c | P04172 |
| P38077      | ATP synthase subunit 7, mitochondrial | transport, metabolic process | S. cerevisiae 288c | P00424 |
| P37559      | ATP synthase subunit 10, mitochondrial | transport, metabolic process | S. cerevisiae 288c | Q08179 |
| P40495      | Homoisocitrate dehydrogenase, mitochondrial | metabolic process | S. cerevisiae 288c | P08466 |
| P00950      | Mitochondrial nucleoside diphosphate kinase | transport, metabolic process | S. cerevisiae 288c | P39158 |
| P25349      | Flavoprotein-like protein | transport, metabolic process | S. cerevisiae 288c | P16603 |
| P29704      | Squalene synthase | transport, metabolic process | S. cerevisiae 288c | Q03028 |
| P099190     | Very-long-chain enoyl-CoA reductase | transport, metabolic process | S. cerevisiae 288c | P14540 |

**GO Terms**:
- **Regulation of metabolic process**
- **Transport**
- **Biological process**
- **Response to stimulus**
- **Cell organization and biogenesis**
- **Metabolic process**
- **Disease**
- **Morphology**
- **Membrane**
- **Mitochondrion**
- **Nucleus**
- **Endoplasmic reticulum**
- **Cytosol**
- **Cytosol**
- **Cytoplasm**
- **Mitochondrion**
- **Ribosome**
- **Nucleotide binding**
- **Metal ion binding**
- **Transmembrane receptor activity**
- **DNA binding**
- **Ion binding**
- **Catalytic activity**
- **Nucleic acid binding**
- **Molecular function**
- **Protein family**
| Gene Name   | Gene Symbol | Gene Description | Cellular Component | Function                                      | Binding Activity | Description |
|------------|-------------|------------------|--------------------|------------------------------------------------|-----------------|-------------|
| ATPase expression protein 2, mitochondrial | ATP2 | [OS=Saccharomyces cerevisiae S288c] | **| metabolite process, regulation of biological process, mitochondrial | RNA binding | 0.359 0.585 1.63 |
| Trisphosphate isomerase | YPR050C | [OS=Saccharomyces cerevisiae S288c] | **| metabolic process | cytoplasm, cytosol, membrane, mitochondrial | catalytic activity | 0.425 0.701 1.65 |
| Elissosome protein 1 | YML031C | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, metabolic process, transport | cytoplasm, extracellular, membrane, mitochondrial | RNA binding, structural molecule activity | 0.52 0.874 1.68 |
| S45 (ribosomal protein L12, mitochondrial) | YGL068W | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, metabolic process | mitochondrial, ribosome | RNA binding | 0.821 14.08 6 1.72 |
| Citrate synthase, mitochondrial | CIT1 | [OS=Saccharomyces cerevisiae S288c] | **| metabolic process, transport | cytosol, mitochondrial, organelle lumen | catalytic activity | 3.16 5.449 1.72 |
| Mitochondrial GTP/GDP carrier protein 1 | YDR010C | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, metabolic process, transport | membrane, mitochondrial | structural molecule activity, transport | 0.778 1.371 1.76 |
| Mitochondrial import inner membrane translocase subunit Tim17 | YIL143W | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, transport | membrane, mitochondrial | protein binding, transport | 47.06 89.06 3 1.89 |
| Mitochondrial carnitine carrier | YOR100C | [OS=Saccharomyces cerevisiae S288c] | **| metabolic process, transport | membrane, mitochondrial | structural molecule activity, transport | 9 18.30 7 2.03 |
| Heat shock protein 26 | YBR072W | [OS=Saccharomyces cerevisiae S288c] | **| metabolic process, response to stimulus | cytoplasm, mitochondrial, nucleus | protein binding, RNA binding | 4.878 9 1.85 |
| Mitochondrial fusion and transport protein Ugo1 | YDR470C | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, cellular homeostasis, metabolic process, transport | membrane, mitochondrial | protein binding, structural molecule activity | 0.557 1.031 1.85 |
| ADP/ATP carrier protein 2 | YCR010C | [OS=Saccharomyces cerevisiae S288c] | **| cell death, metabolic process, transport | membrane, mitochondrial | structural molecule activity, transport | 0.093 1.94 2.09 |
| Accumulation of dyads protein 2 | YCR010C | [OS=Saccharomyces cerevisiae S288c] | **| transport | membrane, mitochondrial | transporter activity | 9 18.30 7 2.03 |
| Sphingolipid long chain base-responsive protein PlL1 | YPL030C | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, regulation of biological process | cytoplasm, membrane, mitochondrial | protein binding | 10.45 21.53 9 2.06 |
| Uncharacterized protein | YMR048C | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, transport | membrane, mitochondrial | protein binding | 0.089 0.186 2.09 |
| Proline dehydrogenase, mitochondrial | YLR142W | [OS=Saccharomyces cerevisiae S288c] | **| metabolic process | mitochondrial, organelle lumen | catalytic activity | 0.093 0.194 2.09 |
| LAS seventeen-binding protein 3 | YHR024C-A | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, regulation of biological process | cytoplasm, mitochondrial | protein binding | 0.08 0.186 2.09 |
| GTP-binding protein ypk7 | YMR001C | [OS=Saccharomyces cerevisiae S288c] | **| cell communication, cell organization and biogenesis, metabolic process, regulation of biological process, response to stimulus, transport | cytosol, endosome, membrane, mitochondrial, vacuole | catalytic activity, nucleotide binding, protein binding | 0.166 0.359 2.16 |
| Ipase 2 | YDR058C | [OS=Saccharomyces cerevisiae S288c] | **| metabolic process, transport | mitochondrial | catalytic activity | 0.233 0.52 2.23 |
| Mitochondrial import receptor subunit tom22 | YNL131W | [OS=Saccharomyces cerevisiae S288c] | **| cell organization and biogenesis, transport | membrane, mitochondrial | protein binding, transport | 0.292 0.668 2.29 |
| Heat shock protein 60, mitochondrial | YOL039C | [OS=Saccharomyces cerevisiae S288c] | **| metabolic process, transport | cytoplasm, cytosol, mitochondrial, organelle lumen | catalytic activity, DNA binding, nucleotide binding, protein binding | 0.138 0.325 8 2.44 |
| Sphingolipid long chain base-responsive protein Lsp1 | YPL040C | [OS=Saccharomyces cerevisiae S288c] | **| regulation of biological process, response to stimulus, transport | cytoplasm, membrane, mitochondrial | protein binding | 0.216 5.31 2.46 |
| Sphingolipid long chain base-responsive protein Lsp1 | YPL040C | [OS=Saccharomyces cerevisiae S288c] | **| regulation of biological process | cytoplasm, membrane, mitochondrial | catalytic activity | 24.11 62.09 6 2.57 |
| Accession | Name | Description | GO Terms | Kegg Pathway | Score | 0.05 | 2.00 |
|-----------|------|-------------|----------|--------------|-------|------|------|
| P12709    | glucose-6-phosphate isomerase | [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, membrane, mitochondrion | catalytic activity | 0.166 | 0.468 | 2.82 |
| P39952    | Mitochondrial inner membrane protein OXA1 | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, transport | membrane, mitochondrion | transporter activity | 1.054 | 3.217 | 3.05 |
| P05019    | Sorting assembly machinery 37 kDa subunit | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, transport | membrane, mitochondrion | protein binding | 0.116 | 0.389 | 3.35 |
| P04803    | Tryptophan-tRNA ligase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | metabolic process | cytoplasm, mitochondrion, organelle lumen | catalytic activity, nucleotide binding | 0.136 | 0.468 | 3.44 |
| Q00955    | Acetyl-CoA carboxylase | [OS=Saccharomyces cerevisiae S288c] | cell organization and biogenesis, metabolic process, transport | cytoplasm, cytosol, endoplasmic reticulum, membrane, mitochondrion | catalytic activity, metal ion binding, nucleotide binding | 0.032 | 0.271 | 8.47 |
Supplemental Table S13. The relative concentrations of proteins in mitochondria purified from ups2Δ cells cultured with or without LCA. Mitochondria were purified from ups2Δ cells recovered on day 2 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | Entrez Gene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI ups2 | emPAI ups2 + LCA | Ratio ups2 + LCA / ups2 |
|-----------|-------------|---------------|---------|-------------------|-------------------|------------------|-----------|----------------|----------------------|
| P40251    | Mitochondrial acidic protein MAM33 (Saccharomyces cerevisiae S288c) | 85475 | MAM33; YIL70 C | metabolic process;regulation of biological process | mitochondrion;organelle lumen | translation regulator activity | 0.778 | 0.212 | 0.37 |
| P17558    | 37S ribosomal protein PET123, mitochondrial (Saccharomyces cerevisiae S288c) | 85432 | PET123; YDR15 8W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.468 | 0.136 | 0.29 |
| P46861    | D-lactate dehydrogenase (cytochrome c) 2, mitochondrial (Saccharomyces cerevisiae S288c) | 85137 | DLO2; YDL178 W | metabolic process | mitochondrion;organelle lumen | catalytic activity;protein binding | 0.682 | 0.25 | 0.37 |
| P32387    | 54S ribosomal protein L41, mitochondrial (Saccharomyces cerevisiae S288c) | 85201 | MRP20; YDR40 5W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | nucleotide binding;protein binding | 0.719 | 0.311 | 0.43 |
| P23572    | Thioredoxin-3, mitochondrial (Saccharomyces cerevisiae S288c) | 85044 | TRX3; YCR083 W | cellular homeostasis;metabolic process;response to stimulus;transport | cytoplasm/mitochondrion | catalytic activity | 0.52 | 0.233 | 0.45 |
| P00441    | Superoxide dismutase (Cu-Zn) (Saccharomyces cerevisiae S288c) | 85356 | SOD1; YIR104 C | cell organization and biogenesis;cellular homeostasis;metabolic process;response to stimulus | cytoplasm/mitochondrion;nucl eus | antioxidant activity;protein binding | 0.52 | 0.233 | 0.45 |
| P14963    | sorting assembly machinery 35 subunit (Saccharomyces cerevisiae S288c) | 85648 | SAM35; YHR08 3W | cell organization and biogenesis;transport | membrane/mitochondrion | protein binding | 0.334 | 0.155 | 0.46 |
| P22998    | uncharacterized ABC transporter ATP-binding protein YDR061W (Saccharomyces cerevisiae S288c) | 85163 | YDR06 1W; YDR06 1W | cell organization and biogenesis;metabolic process | mitochondrion | catalytic activity;protein binding | 0.266 | 0.125 | 0.47 |
| P21771    | 37S ribosomal protein S28, mitochondrial (Saccharomyces cerevisiae S288c) | 85193 | MRP52; YDR33 7W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.274 | 0.129 | 0.47 |
| P38797    | Protein phosphatase 2C homolog 7, mitochondrial (Saccharomyces cerevisiae S288c) | 85647 | PTC7; YHR07 6W | metabolic process | mitochondrion | catalytic activity;protein binding | 0.233 | 0.11 | 0.47 |
| P36517    | 54S ribosomal protein L4, mitochondrial (Saccharomyces cerevisiae S288c) | 85116 | MRP4; YJR439 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.233 | 0.11 | 0.47 |
| P35998    | 54S ribosomal protein yml106, mitochondrial (Saccharomyces cerevisiae S288c) | 85498 | YML6; YML2 5C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.245 | 0.116 | 0.47 |
| P35140    | Protein RMD9, mitochondrial (Saccharomyces cerevisiae S288c) | 85277 | YLR107 5C | cell differentiation;metabolic process;regulation of biological process | membrane/mitochondrion | RNA binding | 0.227 | 0.108 | 0.48 |
| P07236    | Threonine--RNA ligase, mitochondrial (Saccharomyces cerevisiae S288c) | 85364 | MST1; YKL194 C | metabolic process | cytoplasm/mitochondrion;organellar lumen | catalytic activity;protein binding | 0.15 | 0.072 | 0.48 |
| P23323    | Mitochondrial oxaloacetate transport protein (Saccharomyces cerevisiae S288c) | 85373 | GAC1; YKL120 W | metabolic process;transport | membrane/mitochondrion | structural molecule activity;transporter activity | 3.642 | 1.783 | 0.49 |
| P07275    | Delta-1-pyrroline-5-carboxylate dehydratase, mitochondrial (Saccharomyces cerevisiae S288c) | 85643 | PUT2; YHR03 7W | metabolic process | membrane/mitochondrion;organellar lumen | catalytic activity | 1.848 | 1.009 | 0.55 |
| P00950    | Phosphoglycerate mutase 1 (Saccharomyces cerevisiae S288c) | 85370 | GPM1; YKL152 C | metabolic process;regulation of biological process | cytoplasm/mitochondrion;membrane/mitochondrion | catalytic activity | 1.512 | 0.848 | 0.56 |
| P32860    | Nfu-like protein, mitochondrial (Saccharomyces cerevisiae S288c) | 85382 | NFIU1; YKL040 D | cell organization and biogenesis;cellular homeostasis;metabolic process | mitochondrion;organellar lumen | metal ion binding | 1.371 | 0.778 | 0.57 |
| P43635    | Citrate synthase 3, mitochondrial (Saccharomyces cerevisiae S288c) | 85610 | CIT3; YPR001 W | metabolic process | mitochondrion | catalytic activity | 1.346 | 0.817 | 0.61 |
| P40086    | Cytochrome c oxidase assembly protein cox15 (Saccharomyces cerevisiae S288c) | 85688 | COX15; YER141 | cell organization and biogenesis;metabolic process | membrane/mitochondrion | catalytic activity;transporter activity | 1.346 | 0.817 | 0.61 |
| Gene ID | Name                                       | W   | process/transport | activity                              | p-value 1 | p-value 2 |
|--------|-------------------------------------------|-----|------------------|---------------------------------------|-----------|-----------|
| P36525 | S45 ribosomal protein L24, mitochondrial  | 85231 | MRPL2 1-4         | mitochondrial ribosome                 | 0.585     | 0.359     |
|        |                                           |     |                  | RNA binding; structural molecule activity | 0.61      |           |
| P39525 | 3-oxoacyl (acyl carrier protein) synthase homolog | 85679 | CAD1, YER061 1-4   | mitochondrial                           | 0.369     | 0.233     |
|        |                                           |     |                  | catalytic activity                     | 0.63      |           |
| P32898 | Mitochondrial presequence protease         | 85204 | CYR4 1-8          | mitochondrial                           | 0.25      | 0.16      |
|        |                                           |     |                  | catalytic activity; metal ion binding  | 0.64      |           |
| P28706 | Valine-tRNA ligase, mitochondrial         | 85298 | VAS1, YGR097 1-4   | mitochondrial                           | 0.212     | 0.136     |
|        |                                           |     |                  | catalytic activity; nucleotide binding | 0.64      |           |
| P00931 | Heat shock protein SSG1, mitochondrial    | 85108 | SSG1, YER069 1-4   | mitochondrial; organelle lumen         | 0.189     | 0.122     |
|        |                                           |     |                  | nucleotide binding; protein binding    | 0.65      |           |
| P18071 | Enoyl-(acyl-carrier protein) reductase     | 85231 | ETR1, YBR026 1-4   | mitochondrial                           | 3.329     | 2.162     |
|        | (NADPH, B-specific), mitochondrial        |     |                  | catalytic activity; DNA binding; metal ion binding |           |           |
| P15424 | ATP-dependent RNA helicase MMS116,        | 85177 | MMS116 1-4         | mitochondrial; organelle lumen         | 0.166     | 0.108     |
|        | mitochondrial                            |     |                  | catalytic activity; nucleotide binding; RNA binding |           |           |
| P23574 | Cysteine desulfurase, mitochondrial       | 85034 | NCS1, YCL017 1-4   | mitochondrial; nucleus                  | 0.817     | 0.532     |
|        |                                           |     |                  | catalytic activity; metal ion binding; protein binding |           |           |
| P88825 | Protein TOM71 (Saccharomyces cerevisiae   | 85667 | TOM71, YHR111 1-4  | mitochondrial; protein binding;        | 0.512     | 0.343     |
|        | S288c)                                    |     |                  | transporter activity                    | 0.67      |           |
| P33110 | ATP-dependent permease MDL1, mitochondrial| 85088 | MDL1, YLR188 1-4   | membrane; mitochondrial                | 0.528     | 0.354     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity; nucleotide binding; transporter activity |           |           |
| P38325 | Mitochondrial outer membrane protein OMM1| 85253 | OMM1, YBR230 1-4   | membrane; mitochondrial                | 6.197     | 4.179     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | 0.67                                  |           |           |
| P29094 | S45 ribosomal protein L6, mitochondrial   | 85655 | MRPL6, YHR141 1-4  | mitochondrial; ribosome                | 0.778     | 0.54      |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | RNA binding; structural molecule activity | 0.69      |           |
| P33416 | Heat shock protein 78, mitochondrial      | 85184 | HSP78, YDR253 1-4  | mitochondrial; organelle lumen         | 1.383     | 0.973     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity; nucleotide binding; protein binding |           | 0.70      |
| P16603 | NADPH-cytochrome P450 reductase           | 85643 | NCP1, YHR04 1-4    | membrane; mitochondrial                | 0.695     | 0.425     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity; metal ion binding; nucleotide binding |           | 0.70      |
| P49367 | Homeocintase, mitochondrial               | 85182 | LYS4, YDR23 1-4    | mitochondrial                           | 0.551     | 0.389     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity; metal ion binding; protein binding |           | 0.71      |
| P35675 | alanine-glyoxylate aminotransferase 1      | 85051 | ALG1, YFL030 1-4   | cytosol; mitochondrial                 | 0.468     | 0.334     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity                     | 0.71      |           |
| P10507 | mitochondrial processing peptidase subunit beta | 85086 | MAS1, YLR163 1-4   | mitochondrial; organelle lumen         | 0.468     | 0.334     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity; metal ion binding; protein binding |           | 0.71      |
| Q08970 | Mitochondrial metal transporter 2         | 85887 | MM212, YPL224 1-4  | membrane; mitochondrial                | 0.407     | 0.292     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | transporter activity                    | 0.72      |           |
| P00447 | Superoxide dismutase [Mn], mitochondrial  | 85639 | SOD2, YHR00 1-4    | mitochondrial; organelle lumen         | 1.424     | 1.031     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | antioxidant activity; catalytic activity; metal ion binding |           | 0.72      |
| P09440 | C-1-tetrathydrofuranolate synthase,       | 85237 | MIG1, YBR084 1-4   | cytosol; mitochondrial                 | 0.633     | 0.459     |
|        | mitochondrial                           |     |                  | catalytic activity; nucleotide binding | 0.73      |           |
| P27979 | Cytochrome c oxidase subunit 6A, mitochondrial | 85268 | CXX13, YGL191 1-4  | mitochondrial; organelle lumen         | 2.981     | 2.162     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity; enzyme regulator activity; transporter activity |           | 0.73      |
| Q04568 | Fatty aldehyde dehydrogenase HFD1         | 85513 | HFD1, YMR111 1-4   | mitochondrial                           | 1.346     | 0.978     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity                     | 0.73      |           |
| P33112 | Succinyl-CoA ligase [Acp-forming] subunit beta, mitochondrial | 85315 | LSC2, YGR24 1-4    | mitochondrial                           | 3.417     | 2.355     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity; nucleotide binding | 0.74      |           |
| P40185 | Protein mmn1, mitochondrial               | 85476 | MMN1, YIL051 1-4   | mitochondrial; organelle lumen         | 4.012     | 2.981     |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | catalytic activity                     | 0.74      |           |
| P00410 | Cytochrome c oxidase subunit 2            | 85462 | CXX2, Q0250       | mitochondrial; protein binding;        | 2.162     | 1.61      |
|        | (Saccharomyces cerevisiae S288c)          |     |                  | mitochondrial; catalytic activity; metal ion binding |           | 0.74      |
| Gene ID | Protein Name | Molecular Function | Location | Expression | Binding Activity  |
|---------|--------------|--------------------|----------|------------|------------------|
| P40053 | Altered inheritance of mitochondria | 9, mitochondrial (Saccharomyces cerevisiae S288c) | 85381 | AIM9; YER080C | 1.19 | 0.891 | 0.75 |
| Q03798 | Altered inheritance of mitochondria | 36, mitochondrial (Saccharomyces cerevisiae S288c) | 85158 | AIM16; YMR157C | 0.833 | 0.624 | 0.75 |
| P16062 | 37S ribosomal protein MRPI, mitochondrial (Saccharomyces cerevisiae S288c) | | 85194 | MRPI1; YDR234W | 0.778 | 0.585 | 0.75 |
| Q06143 | mitochondrial dicarboxylate transporter | (Saccharomyces cerevisiae S288c) | 85106 | DIC1; YLR348C | 0.73 | 0.551 | 0.75 |
| P08890 | Citrate synthase, mitochondrial (Saccharomyces cerevisiae S288c) | | 85573 | CIT1; YNR001C | 10.78 | 8.211 | 0.76 |
| P19882 | Heat shock protein 60, mitochondrial (Saccharomyces cerevisiae S288c) | | 85096 | HIS20; YLR259C | 11.74 | 3.9 | 0.77 |
| P27697 | Atypical kinase COQ8, mitochondrial (Saccharomyces cerevisiae S288c) | | 85275 | COQ8; YGL119W | 0.365 | 0.283 | 0.78 |
| Q01163 | 37S ribosomal protein S23, mitochondrial (Saccharomyces cerevisiae S288c) | | 85274 | RSM23; YGL129C | 0.365 | 0.283 | 0.78 |
| P07253 | Cytochrome B pre-mRNA-processing protein 6 (Saccharomyces cerevisiae S288c) | | 85241 | CBP6; YBR120C | 2.162 | 1.683 | 0.78 |
| Q12480 | Probable electron transfer flavoprotein subunit alpha, mitochondrial (Saccharomyces cerevisiae S288c) | | 85611 | AIM46; YPR004C | 0.995 | 0.778 | 0.78 |
| P53292 | 37S ribosomal protein S35, mitochondrial (Saccharomyces cerevisiae S288c) | | 85307 | MRPS3; YER165W | 0.738 | 0.585 | 0.79 |
| P09570 | Heat shock protein SSC1, mitochondrial (Saccharomyces cerevisiae S288c) | | 85350 | SSC1; YPR045C | 17.95 | 7 | 0.82 |
| P40035 | Mitochondrial phosphate carrier protein 2 (Saccharomyces cerevisiae S288c) | | 85677 | PIC2; YER053C | 1.637 | 1.336 | 0.82 |
| P22136 | ATPase expression protein 2, mitochondrial (Saccharomyces cerevisiae S288c) | | 85532 | AEP2; YMR282C | 0.431 | 0.359 | 0.83 |
| P32473 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (Saccharomyces cerevisiae S288c) | | 85252 | PDB1; YBR221C | 3.833 | 3.281 | 0.86 |
| P33111 | ATP-dependent permease MDL2, mitochondrial (Saccharomyces cerevisiae S288c) | | 85585 | MDL2; YPL270W | 0.708 | 0.619 | 0.87 |
| P48015 | Aminonitriletransferase, mitochondrial (Saccharomyces cerevisiae S288c) | | 85158 | GCCV1; YDR019C | 3.489 | 3.062 | 0.88 |
| Q12031 | Mitochondrial 2-methylisocitrate lyase (Saccharomyces cerevisiae S288c) | | 85611 | ICL2; YPR006C | 0.947 | 0.833 | 0.88 |
| P67765 | Lon protease homolog, mitochondrial (Saccharomyces cerevisiae S288c) | | 85225 | PIM1; YBL022C | 0.359 | 0.318 | 0.89 |
| P35151 | DnaJ homolog 1, mitochondrial (Saccharomyces cerevisiae S288c) | | 85053 | MDJ1; YFL016C | 1.477 | 1.31 | 0.89 |
| P54783 | D-arabino-1,4-lactone oxidase (Saccharomyces cerevisiae S288c) | | 85488 | ALD1; YML086C | 2.162 | 1.929 | 0.89 |
| P17505 | Malate dehydrogenase, mitochondrial (Saccharomyces cerevisiae S288c) | | 85377 | MDH1; YKL085W | 32.40 | 5 | 0.89 |
| P47282 | Serine hydroxymethyltransferase, mitochondrial (Saccharomyces cerevisiae S288c) | | 85256 | SHM1; YBR263W | 3.037 | 2.765 | 0.91 |

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P16387  Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85692 5  PDA1, YER178 W  cell growth, metabolic process  mitochondrial, organelle lumen  catalytic activity 5.898 5.404 0.92
Q12428  Probable 2-methylisovalerate dehydrogenase [OS=Saccharomyces cerevisiae S288c]  85610 8  PDH1, YMR002 W  metabolic process  cytoplasm, membrane, mitochondrial  catalytic activity 5.978 5.494 0.92
P07342  Acetolactate synthase catalytic subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85513 5  ILV2, YMR189 W  metabolic process  mitochondrial  catalytic activity, metal ion binding, nucleotide binding 2.665 2.455 0.92
P07251  ATP synthase subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85217 7  ATP1, YBL099 W  metabolic process, transport  cytosol, membrane, mitochondrial  catalytic activity, nucleotide binding, transporter activity 13.67 8 13.67 8 1.00
Q08179  Mitochondrial distribution and morphology protein 38 [OS=Saccharomyces cerevisiae S288c]  85413 0  MDM3 0 B, YOL027 C  cell organization and biogenesis, cellular homeostasis; regulation of biological process, transport  membrane, mitochondrial 3.467 3.467 1.00
P20992  elongation factor Tu, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85435 9  TUF1, YOR187 W  cell organization and biogenesis, metabolic process  mitochondrial  catalytic activity, nucleotide binding, RNA binding 3.924 3.924 1.00
P25349  Flavoprotein-like protein YCP4 [OS=Saccharomyces cerevisiae S288c]  85036 0  YCP4, YCR004 C  metabolic process, regulation of biological process  cytoplasm, membrane, mitochondrial  catalytic activity, nucleotide binding, protein binding 5.813 5.813 1.00
Q03028  Mitochondrial 2-oxoacid:coenzyme A ligase carrier 1 [OS=Saccharomyces cerevisiae S288c]  85596 9  ODC1, YPL134 C  metabolic process, transport  membrane, mitochondrial  structural molecule activity, transporter activity 4.275 4.275 1.00
P37295  Mitochondrial inner membrane i-AAA protease supercomplex subunit YME1 [OS=Saccharomyces cerevisiae S288c]  85613 5  YME1, YPL024 W  metabolic process, response to stimulus, transport  membrane, mitochondrial  catalytic activity, metal ion binding, nucleotide binding, protein binding 0.8 0.8 1.00
P28834  Isocitrate dehydrogenase (NAD) subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85659 1  IDH1, YNL037 C  metabolic process, transport  cytoplasm, mitochondrial, organelle lumen  catalytic activity, metal ion binding, nucleotide binding, protein binding, transporter activity 2.36 2.36 1.00
P40637  cytochrome c oxidase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85688 8  COX4, YGL187 C  cell organization, biogenesis, metabolic process, transport  membrane, mitochondrial  catalytic activity, metal ion binding, transporter activity 5.579 5.579 1.00
Q08968  UFM1 Fatty Acid 0.995 0.624 2.162 0.546 0.701 0.484 0.823 0.823 1.00
P03721  Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85575 2  RCF2, YNR01 8W  cell organization and biogenesis, transport  membrane, mitochondrial 5.579 5.579 1.00
P04866  mitochondrial nuclease [OS=Saccharomyces cerevisiae S288c]  85322 2  NUC1, YIL208 C  cell death, metabolic process  membrane, mitochondrial  catalytic activity, metal ion binding, transporter activity 1.336 1.336 1.00
P40508  Uncharacterized protein YIL077C [OS=Saccharomyces cerevisiae S288c]  85473 3  YIL077 C, YIL077 N  mitochondrial 1.154 1.154 1.00
P03900  glycerolaldehyde-3-phosphate dehydrogenase 1 [OS=Saccharomyces cerevisiae S288c]  85539 5  TDP1, YIL052 W  metabolic process  cytoplasm, cytosol, membrane, mitochondrial  catalytic activity, nucleotide binding 0.823 0.823 1.00
P16451  Pyruvate dehydrogenase complex protein X component, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85310 7  PDX1, YGR19 3C  metabolic process  mitochondrial, organelle lumen  catalytic activity, structural molecule activity 0.978 0.978 1.00
P39726  Glycolytic cleavage system H protein, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85125 4  GCV3, YAL044 C  metabolic process  mitochondrial  catalytic activity 1.154 1.154 1.00
Q06688  Methyltransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85191 1  OMS1, YDR31 6W  metabolic process  membrane, mitochondrial  catalytic activity 0.484 0.484 1.00
P25573  Mitochondrial inner membrane i-AAA protease supercomplex subunit MGR1 [OS=Saccharomyces cerevisiae S288c]  85031 3  MGR1, YCL044 C  metabolic process  membrane, mitochondrial  protein binding 0.701 0.701 1.00
P40416  Iron-sulfur clusters transporter ATM1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85334 7  ATM1, YMR30 1C  cellular homeostasis, metabolic process, transport  membrane, mitochondrial  catalytic activity, nucleotide binding, transporter activity 0.546 0.546 1.00
P24940  Probable electron transfer flavoprotein subunit beta [OS=Saccharomyces cerevisiae S288c]  85312 1  CIR1, YGR20 7C  metabolic process, transport  mitochondrial, organelle lumen  catalytic activity 2.162 2.162 1.00
P25605  Acetolactate synthase small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85034 8  ILV6, YCL009 C  metabolic process, regulation of biological process  mitochondrial  catalytic activity, enzyme regulator activity 0.624 0.624 1.00
P18127  mitochondrial carrier protein RIM2 [OS=Saccharomyces cerevisiae S288c]  85249 1  RIM2, YBR192 W  cell organization and biogenesis, metabolic process, transport  membrane, mitochondrial  structural molecule activity, transporter activity 0.995 0.995 1.00
| Gene ID | Description                              | Localization                           | Metabolic Process                                                                 | Catalytic Activity |
|--------|------------------------------------------|----------------------------------------|-----------------------------------------------------------------------------------|--------------------|
| P38626 | NADH-cytochrome b5 reductase 1           | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial, cytosol, mitochondrial, ER                              | 0.778              |
| P38072 | Protein SCD2, mitochondrial              | [OS=Saccharomyces cerevisiae S288c]    | cell organization and biogenesis, mitochondrial, cytosol, transport               | 0.73               |
| P40008 | Protein FMF52, mitochondrial             | [OS=Saccharomyces cerevisiae S288c]    | endoplasmic reticulum, membrane, mitochondrial                                   | 1.094              |
| P32331 | Carrier protein YMC1, mitochondrial      | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial, vacuole, structural molecule, mitochondrial, transport  | 0.968              |
| Q04472 | Mitochondrial inner membrane iAAA protease supercomplex subunit MGR3 | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.322              |
| P38079 | protein YRC2 [OS=Saccharomyces cerevisiae cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]    | transport, endoplasmic reticulum, membrane, mitochondrial, transporter activity   | 1.424              |
| P31287 | Mitochondrial genome maintenance protein MGMT101 | [OS=Saccharomyces cerevisiae cerevisiae S288c] | transport, endoplasmic reticulum, membrane, mitochondrial, transporter activity | 0.833              |
| Q04935 | Cytochrome c oxidase protein 20, mitochondrial | [OS=Saccharomyces cerevisiae cerevisiae S288c] | membrane, mitochondrial                                                          | 1.424              |
| P30087 | MICOS subunit MIC26                      | [OS=Saccharomyces cerevisiae S288c]    | chromosome, mitochondrial                                                       | 0.931              |
| P36151 | Magnesium-activated aldehyde dehydrogenase, cytosolic | [OS=Saccharomyces cerevisiae S288c]    | cytoplasm, cytosol, mitochondrial                                              | 0.346              |
| P28737 | Protein MSHF1 [OS=Saccharomyces cerevisiae cerevisiae S288c] | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial, nucleus, mitochondrial, cytosol, DNA binding           | 0.585              |
| Q5892  | MIOREM complex component 2               | [OS=Saccharomyces cerevisiae S288c]    | mitochondrial, mitochondrial, cytosol, mitochondrial                               | 1.054              |
| Q3824  | Uncharacterized protein YFR070W-A        | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.274              |
| P36151 | Stationary phase protein 4               | [OS=Saccharomyces cerevisiae S288c]    | mitochondrial, mitochondrial, cytosol, mitochondrial                               | 1.783              |
| Q34246 | 37S ribosomal protein S17, mitochondrial | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.389              |
| P38910 | 10 kDa heat shock protein, mitochondrial | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 1.371              |
| P32792 | UPT074 protein YSC83                    | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.369              |
| P25179 | Peptidyl-prolyl cis-trans isomerase C, mitochondrial | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.585              |
| P36163 | Mitochondrial metalloendopeptidase OMA1 | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.389              |
| P53230 | Phosphatidate cytidylyltransferase, mitochondrial | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.407              |
| P34231 | Uncharacterized protein YK127B            | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.425              |
| Q06VH5 | MICOS complex subunit Mic1D              | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.931              |
| Q23743 | Nuclear control of ATPase protein 2      | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.212              |
| P17695 | Glutaredoxin-2, mitochondrial            | [OS=Saccharomyces cerevisiae S288c]    | membrane, mitochondrial                                                          | 0.52               |

**Metabolic Processes:**
- Endoplasmic reticulum
- Membrane
- Mitochondrion
- Peroxisome
- Cytosol
- Nucleus
- Cytoskeleton
- Cell organelles
- Cell differentiation
- Cell death
- Transport
- Catalytic activity
- Metal ion binding
- DNA binding
- Protein binding
- RNA binding

**Catalytic Activity:**
- 0.212
- 0.274
- 0.346
- 0.369
- 0.407
- 0.425
- 0.585
- 1.00
- 2.162
- 1.424
- 1.054
- 1.783
- 1.371
| QJ2375 | mitochondrial omithine transporter 1 | [Os-Saccharomyces cerevisiae S288c] |
| 85429 | ORT1; YDR133C | metabolic process,transport | membrane/mitochondrion | structural molecule activity,transporter activity | 0.54 | 0.54 | 1.00 |
| P28117 | 3-hydroxyisobutyryl-CoA-hydrolyase, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85160 | EHD3; YDR036C | metabolic process | mitochondrion | catalytic activity | 0.269 | 0.269 | 1.00 |
| P51110 | Sorting assembly machinery 37 kDa subunit | [Os-Saccharomyces cerevisiae S288c] |
| 85508 | SAM37; YMR060C | cell organization and biogenesis,transport | membrane/mitochondrion | protein binding | 0.245 | 0.245 | 1.00 |
| P40496 | 37S ribosomal protein S25, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85471 | KSM25; YIL093C | cell organization and biogenesis,metabolic process | mitochondrion,ribosome | structural molecule activity | 0.468 | 0.468 | 1.00 |
| P34222 | Peptidyl-tRNA hydroxide 2 | [Os-Saccharomyces cerevisiae S288c] |
| 85222 | PTH2; YBL027C | regulation of biological process | cytoplasm,cytosol,membrane/mitochondrion | catalytic activity,protein binding | 0.425 | 0.425 | 1.00 |
| Q05648 | MIOREX complex component 10 | [Os-Saccharomyces cerevisiae S288c] |
| 85187 | YDR282C; YMR10 ; YDR282C | metabolic process,transport | membrane/mitochondrion | structural molecule activity,transporter activity | 0.222 | 0.222 | 1.00 |
| P81152 | Tricarboxylate transport protein | [Os-Saccharomyces cerevisiae S288c] |
| 85259 | CTP1; YBR291C | metabolic process,transport | membrane/mitochondrion | structural molecule activity,transporter activity | 0.245 | 0.245 | 1.00 |
| P25039 | Elongation factor G, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85075 | MEF1; YLR069C | cell organization and biogenesis,metabolic process | cytosol/mitochondrion | catalytic activity,nucleotide binding,interaction | 0.099 | 0.099 | 1.00 |
| P34224 | Uncharacterized protein YBL059W | [Os-Saccharomyces cerevisiae S288c] |
| 85222 | YBL059W; YBL059W | metabolic process,transport | membrane/mitochondrion | structural molecule activity,transporter activity | 0.468 | 0.468 | 1.00 |
| P12686 | 37S ribosomal protein MRP13, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85297 | MRP13; YGR084C | cell organization and biogenesis,metabolic process | mitochondrion,ribosome | structural molecule activity | 0.259 | 0.259 | 1.00 |
| P36147 | Presequence translocated-associated motor subunit pam17, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85393 | PAM17; YKR065C | transport | membrane/mitochondrion | protein binding | 0.501 | 0.501 | 1.00 |
| P53220 | Mitochondrial import inner membrane translocase subunit TIM21 | [Os-Saccharomyces cerevisiae S288c] |
| 85292 | TIM21; YGR030C | cell organization and biogenesis,transport | membrane/mitochondrion | protein binding | 0.501 | 0.501 | 1.00 |
| P81172 | MIOREX complex component 3 | [Os-Saccharomyces cerevisiae S288c] |
| 85218 | YBR095W; YBR095W | metabolic process,transport | membrane/mitochondrion | structural molecule activity,transporter activity | 0.311 | 0.311 | 1.00 |
| P38702 | mitochondrial carrier protein LEU5 | [Os-Saccharomyces cerevisiae S288c] |
| 85639 | LEU5; YMR020W | metabolic process,transport | membrane/mitochondrion | structural molecule activity,transporter activity | 0.212 | 0.212 | 1.00 |
| P11914 | Mitochondrial-processing peptidase subunit alpha | [Os-Saccharomyces cerevisiae S288c] |
| 85641 | MAS2; YHR024C | metabolic process,transport | membrane/mitochondrion,organellar lumen | catalytic activity,metal ion binding,protein binding | 0.202 | 0.202 | 1.00 |
| P38088 | Glycine-\(\text{H}^+\) antiporter 1, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85656 | GRS1 | metabolic process | cytoplasm/mitochondrion,organellar lumen | catalytic activity,nucleotide binding,interaction | 0.049 | 0.049 | 1.00 |
| Q06510 | Lyophosphatidylcholine acetyltransferase | [Os-Saccharomyces cerevisiae S288c] |
| 85626 | TAIZ1; YPR1400W | cell organization and biogenesis,metabolic process,transport | membrane/mitochondrion | catalytic activity | 0.194 | 0.194 | 1.00 |
| P22553 | 54S ribosomal protein L8, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85338 | MRPL8; YIL063C | cell organization and biogenesis,metabolic process | mitochondrion,ribosome | structural molecule activity | 0.166 | 0.166 | 1.00 |
| Q12251 | Uncharacterized mitochondrial carrier | [Os-Saccharomyces cerevisiae S288c] |
| 85612 | YPR0111C; YPR0111C | metabolic process,transport | membrane/mitochondrion | structural molecule activity,transporter activity | 0.389 | 0.389 | 1.00 |
| P50127 | Cytochrome b-c1 complex subunit 6 | [Os-Saccharomyces cerevisiae S288c] |
| 85609 | OCR6; YFR0333C | metabolic process,transport | membrane/mitochondrion | catalytic activity,transporter activity | 0.334 | 0.334 | 1.00 |
| Q12233 | ATP synthase subunit g, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85613 | ATP20; YPR0200W | cell organization and biogenesis,metabolic process,transport | membrane/mitochondrion | catalytic activity,transporter activity | 0.778 | 0.778 | 1.00 |
| Q02950 | 37S ribosomal protein MRP51, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85598 | MRP51; YPL118W | cell organization and biogenesis,metabolic process | mitochondrial,ribosome | structural molecule activity | 0.292 | 0.292 | 1.00 |
| Q22979 | Uncharacterized protein YDR119W-A | [Os-Saccharomyces cerevisiae S288c] |
| 37999 | COX26; YDR119W-A | metabolic process,transport | membrane/mitochondrion | structural molecule activity,transporter activity | 1.154 | 1.154 | 1.00 |
| Q05867 | Uncharacterized protein YLR283W, mitochondrial | [Os-Saccharomyces cerevisiae S288c] |
| 85698 | YLR283W; YLR283W | endoplasmic reticulum,membrane/mitochondrion | | | 0.11 | 0.11 | 1.00 |
| Gene ID  | Description                                                                 | Accession Numbers | Function                                                                 | Location          | Activity/Binding                      |
|---------|------------------------------------------------------------------------------|-------------------|---------------------------------------------------------------------------|-------------------|---------------------------------------|
| P19516  | Cytochrome c oxidase assembly protein COX11, mitochondrial                   | YOR37      | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P38323  | ATP-dependent citP-like chaperone, mitochondrial                            | YKR066      | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P40530  | (Pyruvate dehydrogenase (acetyl-transferring) kinase 1, mitochondrial       | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P40581  | Peroxisome HPR1                                                             | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P46528  | 545 ribosomal protein L17, mitochondrial                                     | YPL072      | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P53732  | 375 ribosomal protein S12, mitochondrial                                     | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| Q01322  | Cysteine proteinase 1, mitochondrial                                         | YOR37      | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P32463  | Acyl carrier protein, mitochondrial                                          | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| Q38816  | Thioredoxin reductase 2, mitochondrial                                        | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| Q35577  | Protein fmp32, mitochondrial                                                 | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P31822  | 3-methyl-2-oxobutanoyl hydroxyymethyltransferase                             | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P48322  | Peptidyl-prolyl cis-trans isomerase                                          | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P4039   | Cytochrome c oxidase polypeptide VII, mitochondrial                          | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| Q07984  | Monothiol glutaredoxin-5, mitochondrial                                      | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| Q06630  | Mitochondrial homologous recombination protein 1                             | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P36520  | 545 ribosomal protein L10, mitochondrial                                     | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| Q09176  | 375 ribosomal protein S24, mitochondrial                                     | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P88909  | Cytochrome c mitochondrial import factor CYC2                                 | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| Q2863   | Ubiquitin carboxyl-terminal hydrolase 16                                     | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P00431  | Cytochrome c peroxidase, mitochondrial                                        | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P10834  | Protein PET54                                                               | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P46387  | Potassium-activated aldehyde dehydrogenase, mitochondrial                   | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
| P40215  | External NADH-ubiquinone oxidoreductase 1, mitochondrial                     | YPR12       | catalytic activity                                                        | mitochondrial     | 1.00                                  |
2-oxoglutarate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P20967   | cytosol/mitochondrion,organelle lumen | catalytic activity: 5.201 3.764 1.11 |

External NADH-quinone oxidoreductase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| Q07500   | mitochondrion,activity:nucleotide binding | catalytic activity: 2.687 2.981 1.11 |

ATP synthase subunit gamma, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P38077   | membrane/mitochondrion,activity:transporter activity | 9 10 10 3 1.12 |

Protoporphyrinogen oxidase [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P40102   | membrane/mitochondrion | catalytic activity: 0.947 1.069 1.13 |

Mitochondrial escape protein 2 [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P3843    | mitochondrion,nucleotide binding | catalytic activity: 1.637 1.859 1.14 |

Homosuccinate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P40495   | mitochondrion,activity:metal ion binding,nucleotide binding | catalytic activity: 2.481 2.831 1.14 |

Altered inheritance of mitochondria protein 24, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P47127   | mitochondrion | catalytic activity: 1.395 1.593 1.14 |

Aldehyde dehydrogenase 5, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P40047   | mitochondrion,organelle lumen | catalytic activity: 0.968 1.106 1.14 |

Mitochondrial phosphate carrier protein 3 [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P3641    | protein binding:structural molecule activity:transporter activity | 10.36 5 11.91 5 1.15 |

Succinyl-CoA ligase [ADP-forming] subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P51958   | mitochondrion,nucleotide binding | catalytic activity: 5.18 5.952 1.15 |

Branch-chain amino-acid aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P38891   | mitochondrion,organelle lumen | catalytic activity: 2.511 2.899 1.15 |

Prohibitin 2 [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P50085   | protein binding | catalytic activity: 2.511 2.899 1.15 |

Succinate dehydrogenase [ubiquione] iron-sulfur subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P21801   | catalytic activity:metal ion binding | 12.11 1 14.01 3 1.16 |

Mitochondrial GTP/GDP carrier protein 1 [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P8898    | structural molecule activity:transporter activity | 2.728 3.16 1.16 |

Succinate:fumarate mitochondrial transporter [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P3303    | structural molecule activity:transporter activity | 4.995 5.813 1.16 |

Alcohol dehydrogenase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P07246   | catalytic activity:metal ion binding | 2.34 2.728 1.17 |

Carnitine O-acetyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P32796-1 | catalytic activity:transporter activity | 2.44 2.849 1.17 |

ATP synthase subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P0830    | catalytic activity:nucleotide binding:protein binding:transporter activity | 17.47 8 20.54 4 1.18 |

Uncharacterized protein YGR262W [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P53326   | membrane/mitochondrion | catalytic activity: 0.369 0.442 1.20 |

Glycerol-3-phosphate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P32191   | membrane/mitochondrion | catalytic activity: 2.574 3.14 1.22 |

ARS-binding factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| Q2046    | chromosome/mitochondrion,nucleus,DNA binding | 7.377 9 1.22 |

Phosphoglycerate kinase [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P0560    | cytoplasm/mitochondrion | catalytic activity: 2.981 3.642 1.22 |

Dehydroxy-acid dehydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| P39522   | mitochondrion,activity:metal ion binding | catalytic activity: 2.054 2.511 1.22 |

Metabolite aspartate glutamate transporter AGC1 [OS=Saccharomyces cerevisiae S288c]

| SC       | binding                        |
|----------|--------------------------------|
| Q12482   | structural molecule activity:transporter activity | 0.238 0.292 1.23 |

Note: The binding information provided may be incomplete or inaccurate as it is derived from a text-mining process. The actual biological context and experimental data should be consulted for accurate interpretation.
Q00711  Succinate dehydrogenase (ubiquitone) flavoprotein subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85370 9 SDH1, YKL148 C metabolic process;transport membrane,mitochondrion catalytic activity;nucleotide binding;protein binding 3.072 3.819 1.24
Q08223  Altered inheritance of mitochondria protein 39, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85410 3 AIM35, YDL053 W cytosol;membrane,mitochondrion 0.468 0.585 1.25
Q04002  Nuclear migration protein NUM1 [OS=Saccharomyces cerevisiae S288c]  85172 7 NUM1, YDR150W cell organization and biogenesis;cellular component movement;metabolic process;regulation of biological process;transport endoplasmic reticulum,mitochondrion catalytic activity;motor activity;protein binding 0.052 0.066 1.25
Q12166  2-isopropylmalate synthase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85427 5 LEU9, YDR180W metabolic process mitochondrion 1.11 1.39 1.25
Q04933  LET1 domain-containing protein YLH47, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85624 3 YLH47, YPL125W cell organization and biogenesis;transport membrane,mitochondrion 0.487 0.61 1.25
Q12117  Protein MRH1 [OS=Saccharomyces cerevisiae S288c]  85159 7 MRH1, YDR83W transport endoplasmic reticulum,membrane,mitochondrion transporter activity 2.831 3.642 1.29
P27929  375 ribosomal protein NAM9, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85558 5 NAM9, YNL137C cell organization and biogenesis mitochondrion,ribosome RNA binding;structural molecule activity 0.301 0.389 1.29
Q08023  Protein FMP25, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85076 6 FMP25, YOR077W cell organization and biogenesis membrane,mitochondrion 0.968 1.254 1.30
P39518  Long-chain-fatty-acid-CoA ligase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85673 4 FAA2, YER015W metabolic process;transport cytoplasm,mitochondrion catalytic activity;nucleotide binding 0.619 0.802 1.30
P47045  mitochondrial import inner membrane translocase subunit TIM54 [OS=Saccharomyces cerevisiae S288c]  85339 2 TIM54, YIL054W cell organization and biogenesis;transport cytosol,membrane,mitochondrion transporter activity 0.334 0.433 1.30
P53893  probable alanine aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85077 8 ALT1, YLR089C metabolic process mitochondrion,organelle lumen catalytic activity 0.346 0.45 1.30
P38921  D-lactate dehydrogenase [cytochrome c] 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85138 0 DLO1, YDL174C metabolic process;transport membrane,mitochondrion catalytic activity;nucleotide binding 2.875 3.748 1.30
P04840  Mitochondrial outer membrane protein porin 1 [OS=Saccharomyces cerevisiae S288c]  85666 9 POR1, YNL055C cell death;cell organization and biogenesis;cellular homeostasis;regulation of biological process;transport cytoplasm,membrane,mitochondrion transporter activity 9.117 1.39
P12695  Dihydrolipoyl-pimeloyl residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85665 3 LAT1, YNL071W metabolic process mitochondrion,organelle lumen catalytic activity 3.758 4.946 1.32
P09624  Dihydrolipoyl dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85052 7 LPO1, YFL018C cellular homeostasis;metabolic process;regulation of biological process mitochondrion,organelle lumen catalytic activity;nucleotide binding 9.701 13.03 1.34
P07113  Mitochondrial import receptor subunit TOM70 [OS=Saccharomyces cerevisiae S288c]  85660 2 TOM70, YNL121C cell organization and biogenesis;transport membrane,mitochondrion protein binding;transporter activity 1.154 1.572 1.36
P36013  NAD-dependent malic enzyme, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85383 9 MAE1, YKL029C metabolic process mitochondrion,organelle lumen catalytic activity;metal ion binding;nucleotide binding 0.496 0.679 1.37
Q07349  MIOX complex component 9 [OS=Saccharomyces cerevisiae S288c]  85153 5 YDL027C, MRX9, YDL027C endoplasmic reticulum,membrane,mitochondrion 0.931 1.276 1.37
P08417  fumarate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85856 6 FUM1, YPL262W cell organization and biogenesis;metabolic process cytoplasm;cytosol,mitochondrion,organelle lumen catalytic activity 2.562 3.52 1.37
P05626  ATP-synthase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85602 7 ATP4, YPL078C cell organization and biogenesis;metabolic process;transport membrane,mitochondrion catalytic activity;transporter activity 3.084 4.275 1.39
P47052  succinate dehydrogenase (ubiquitone) flavoprotein subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85340 5 YL045W, YL045W metabolic process;transport membrane,mitochondrion catalytic activity;nucleotide binding 1.11 1.543 1.39
P53969  Sorting assembly machinery 50 kDa subunit [OS=Saccharomyces cerevisiae S288c]  85370 5 SAM50, YNL026W cell organization and biogenesis;transport membrane,mitochondrion protein binding;transporter activity 0.269 0.374 1.39
Q12289  mitochondrial carnitine carrier [OS=Saccharomyces cerevisiae S288c]  85426 7 CRC1, YDR10OC metabolic process;transport membrane,mitochondrion structural molecule activity;transporter activity 1.683 2.34 1.39
P00427  Cytochrome c oxidase subunit 6, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85644 8 COX6, YHR051W metabolic process;transport membrane,mitochondrion catalytic activity;metal ion binding;transporter activity 1.154 1.61 1.40
Q02883  N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85600 1 FMP30, YPL103C metabolic process membrane,mitochondrion catalytic activity;metal ion binding 0.304 0.425 1.40
ADP/ATP carrier protein 2
[OS=Saccharomyces cerevisiae S288c]

PET9; YBL030C

cell death; metabolic process; transport

membrane; mitochondrion

structural molecule activity; transporter activity

110.6 34

167.7 61

1.52

Ferrochelatase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

HEM15; YOR176W

metabolic process

membrane; mitochondrion

catalytic activity

2.162 3.329

1.54

Succinate dehydrogenase (ubiquinone) cytochrome b subunit, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

SDH4; YOR176W

metabolic process; transport

membrane; mitochondrion

catalytic activity; metal ion binding

1.154 1.783

1.55

Protein CBP3, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

CBP3; YPL215W

cell organization and biogenesis; regulation of biological process

membrane; mitochondrion; ribosome

metal ion binding; protein binding

0.369 0.574

1.56

Triplet-1 [OS=Saccharomyces cerevisiae S288c]

TCB1; YOR086C

cell organization and biogenesis; regulation of biological process

endoplasmic reticulum; membrane; mitochondrion

metal ion binding; protein binding; RNA binding

0.34 3.642

1.56

Isocitrate dehydrogenase (NAD) subunit 2, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

IDH2; YOR137W

metabolic process

mitochondrion; organelle lumen

catalytic activity; metal ion binding; nucleotide binding; protein binding

0.172 0.269

1.56

54S ribosomal protein L3, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

MRPL10; YMR024C

cell organization and biogenesis; metabolic process; response to stimulus

mitochondrion; nucleus; ribosome

catalytic activity; RNA binding; structural molecule activity

0.179 0.28

1.56

Dynamin-like GTPase MGM1, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

MG1M1; YGR210C

cell organization and biogenesis

membrane; mitochondrion

catalytic activity; nucleotide binding; protein binding

0.222 0.35

1.58

squalene synthase
[OS=Saccharomyces cerevisiae S288c]

ERG9; YHR19W

metabolic process

endoplasmic reticulum; membrane; mitochondrion

catalytic activity

0.233 0.369

1.58

NADH kinase PS5, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

PO55; YPL188W

metabolic process; response to stimulus

mitochondrion; organelle lumen

catalytic activity; nucleotide binding

0.245 0.389

1.59

Altered inheritance of mitochondria protein 46, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

AIM46; YHR19W

mitochondrion

catalytic activity

0.259 0.413

1.59

ABC1 family protein YPL109C, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

YPL109C; YPL109C

mitochondrion

0.259 0.413

1.59

Uncharacterized mitochondrial carrier YFR045W [OS=Saccharomyces cerevisiae S288c]

YFR045W; YFR045W

metabolic process; transport

membrane; mitochondrion

structural molecule activity; transporter activity

0.259 0.413

1.59

54S ribosomal protein L40, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

MRPL40; YPL173W

cell organization and biogenesis; metabolic process

mitochondrion; ribosome

protein binding; structural molecule activity

0.259 0.413

1.59

Inner membrane mito ribosome receptor MBA1, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

MBA1; YBR135C

cell organization and biogenesis; regulation of biological process

membrane; mitochondrion

0.259 0.413

1.59

Protein OPY1, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

OPY1; YBR125C

cytoplasm; mitochondrion

0.274 0.438

1.60

Squalene synthase
[OS=Saccharomyces cerevisiae S288c]

ERG9; YHR19W

metabolic process

endoplasmic reticulum; membrane; mitochondrion

catalytic activity

0.274 0.438

1.60

Cytochrome c1 heme lyase [OS=Saccharomyces cerevisiae S288c]

CPY7; YKL078C

cell organization and biogenesis; metabolic process

membrane; mitochondrion

catalytic activity; metal ion binding

0.359 0.588

1.63

Glyoxylate dehydrogenase (Dehydroxylation), mitochondrial
[OS=Saccharomyces cerevisiae S288c]

GCV2; YMR188W

metabolic process

cytosol; mitochondrion

catalytic activity

0.388 0.638

1.64

Theonine dehydratase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

ILV1; YER098W

metabolic process

cytosol; mitochondrion

catalytic activity

0.425 0.701

1.65

Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

CI2; YDR335W

metabolic process; transport

membrane; mitochondrion

catalytic activity; metal ion binding; nucleotide binding

1.488 2.481

1.67

Mitochondrial peroxiredoxin PRX1, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

PRX1; YBL064C

cellular homeostasis; metabolic process; regulation of biological process; response to stimulus

mitochondrion

antioxidant activity; catalytic activity

1.637 2.793

1.71

Aconitate hydratase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

ACO1; YJR304C

cell organization and biogenesis; metabolic process; transport

cytosol; cytosol; mitochondrion; organelle lumen

catalytic activity; DNA binding; metal ion binding

10.05 3

17.23 3

1.71

Single-stranded DNA-binding protein RIM1, mitochondrial
[OS=Saccharomyces cerevisiae S288c]

RIM1; YCR028C

cell organization and biogenesis; metabolic process; regulation of biological process

mitochondrion

DNA binding

0.668 1.154

1.73
P30624
Long-chain fatty-acid-CoA ligase 1
[OS=Saccharomyces cerevisiae S288c]
P30624

P0465
Autophagy-related protein 33
[OS=Saccharomyces cerevisiae S288c]
P0465

P81449
ATP synthase subunit e, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
P81449

P19262
Dihydrolipoamide-residue
succinylltransferase component of 2-
(thenylurate dehydrogenase complex, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
P19262

P37299
Cytochrome b-2 complex subunit 10
[OS=Saccharomyces cerevisiae S288c]
P37299

P04005
ATP synthase subunit f, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
P04005

P09457
ATP synthase subunit 5, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
P09457

P36101
1RNAS*threonylcarbamoyladenosine
dehydratase 2 [OS=Saccharomyces cerevisiae S288c]
P36101

P37293
N-terminal acetyltransferase 2
[OS=Saccharomyces cerevisiae S288c]
P37293

P57376
Uncharacterized protein YMR040W
[OS=Saccharomyces cerevisiae S288c]
P57376

P16547
Mitochondrial outer membrane protein OM45 [OS=Saccharomyces cerevisiae S288c]
P16547

P36112
Mitochondrial inner membrane
[OS=Saccharomyces cerevisiae S288c]
P36112

P50945
Mitochondrial DNA, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
P50945

P36066
Protein MRG3-1ke [OS=Saccharomyces cerevisiae S288c]
P36066

P4013
Citrate/malate transporter carrier protein
[OS=Saccharomyces cerevisiae S288c]
P4013

P33421
Succinate dehydrogenase [ubiquinone] cytochrome b subunit, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
P33421

P06168
Ketol-acid reductoisomerase, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
P06168

P53266
Cytochrome oxidase assembly protein SHY1 [OS=Saccharomyces cerevisiae S288c]
P53266

P41921
Glutathione reductase
[OS=Saccharomyces cerevisiae S288c]
P41921

P12032
Altered inheritance of mitochondria
protein 41, mitochondrial
[OS=Saccharomyces cerevisiae S288c]
P12032

P38169
Prohibitin 1 [OS=Saccharomyces cerevisiae S288c]
P38169

P41921
Glutathione reductase
[OS=Saccharomyces cerevisiae S288c]
P41921

P39061
Prohibitin 1 [OS=Saccharomyces cerevisiae S288c]
P39061
| Gene ID | Description | Interaction | Interaction | Function | Interaction | References |
|---------|-------------|-------------|-------------|----------|-------------|------------|
| P40015  | Fatty acid binding protein, mitochondrial |  |  |  |  |  |
| P38771  | Ribosome-replicating factor, mitochondrial |  |  |  |  |  |
| P38884  | Mitochondrial biogenesis protein |  |  |  |  |  |
| P12939  | GTP-binding protein |  |  |  |  |  |
| P07143  | Cytochrome c1, heme protein, mitochondrial |  |  |  |  |  |
| Q04172  | Sensitive to high expression protein |  |  |  |  |  |
| P31580  | Mitochondrial import receptor |  |  |  |  |  |
| P19955  | 37S ribosomal protein |  |  |  |  |  |
| P18496  | Mitochondrial ATP synthase complex subunit |  |  |  |  |  |
| P28625  | Protein YMR1 |  |  |  |  |  |
| P08676  | Cytochrome b-c1 complex subunit |  |  |  |  |  |
| Q07651  | SUR7 family protein |  |  |  |  |  |
| Q03327  | Mitochondrial fusion and transport protein |  |  |  |  |  |
| P46998  | Mitochondrial membrane protein |  |  |  |  |  |
| P36060  | NADH-cytochrome b5 reductase |  |  |  |  |  |
| P72677  | Assembly factor cbp4 |  |  |  |  |  |
| P40096  | Uncpharnected mitochondrial membrane protein |  |  |  |  |  |
| Q21029  | Probable mitochondrial transport protein |  |  |  |  |  |
| P21306  | ATP synthase subunit epsilon, mitochondrial |  |  |  |  |  |
| P38969  | Pentamidine resistance factor, mitochondrial |  |  |  |  |  |
| P19254  | Toxidate dehydrogenase (NADP), mitochondrial |  |  |  |  |  |
| Q06567  | ABC1 family protein |  |  |  |  |  |
| P39006  | Phosphatidylserine decarboxylase |  |  |  |  |  |
| P32839  | Mitochondrial chaperone |  |  |  |  |  |
| Q06678  | S45 ribosomal protein |  |  |  |  |  |
| P42949  | Mitochondrial import inner membrane translocase subunit |  |  |  |  |  |

**References:**

1. 3.27
2. 6.848
3. 2.45
4. 0.254
5. 0.101
| Gene ID  | Description                                                                 | Accession 1 | Accession 2 | Function                                | Category                   | Value 1   | Value 2   | Value 3   |
|---------|-----------------------------------------------------------------------------|-------------|-------------|-----------------------------------------|----------------------------|-----------|-----------|-----------|
| P39515  | Mitochondrial import inner membrane translocase subunit Tim17 (OS=S. cerevisiae S288c) | BS329       | TIM17       | cell organization and biogenesis;transport | membrane;mitochondrion    | 0.334     | 1.371     | 4.10      |
| P39952  | Mitochondrial inner membrane protein Oxa1 (OS=S. cerevisiae S288c)           | BS689       | Oxa1;      | cell organization and biogenesis;transport | membrane;mitochondrion    | 0.778     | 3.217     | 4.13      |
| P25087  | Sterol 24-C-methyltransferase (OS=S. cerevisiae S288c)                       | BS5000      | ERG6;     | metabolic process                       | endoplasmic reticulum;membrane;mitochondrion | 0.425     | 1.894     | 4.46      |
| Q01574  | Acetyl-CoA synthase 1 (OS=S. cerevisiae S288c)                               | BS124       | ACS1;     | cell organization and biogenesis;metabolic process | cytoplasm;cytosol;endoplasmic reticulum;mitochondrion;nucleus | 0.624     | 2.793     | 4.48      |
| P08525  | Cytochrome b-c1 complex subunit 8 (OS=S. cerevisiae S288c)                   | BS327       | OCR8;     | metabolic process;transport              | membrane;mitochondrion    | 0.585     | 2.981     | 5.10      |
| P30902  | ATP synthase subunit 8, mitochondrial (OS=S. cerevisiae S288c)               | BS385       | ATP7;     | metabolic process;transport              | membrane;mitochondrion    | 1.683     | 9         | 5.35      |
| Q07914  | Mitochondrial import inner membrane translocase subunit Tim14 (OS=S. cerevisiae S288c) | BS069       | PAM18;    | regulation of biological process;transport | membrane;mitochondrion    | 0.334     | 3.217     | 9.63      |
Supplemental Table S14. The relative concentrations of proteins in mitochondria purified from *ups2Δ* cells cultured with or without LCA. Mitochondria were purified from *ups2Δ* cells recovered on day 4 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description | EntrezGene ID | Gene ID | Biological Process | Cellular Component | Molecular Function | emPAI ups2 | emPAI ups2 + LCA | RATIO ups2 + LCA / ups2 |
|-----------|-------------|---------------|---------|-------------------|-------------------|-------------------|-------------|-------------------|-----------------------|
| P25578    | CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase [OS=Saccharomyces cerevisiae S288c] | 85035 2 | PIGS1; YCL004 W | metabolic process | mitochondrion | catalytic activity; nucleotide binding | 0.374 | 0.083 | 0.22 |
| P36526    | 545 ribosomal protein L27, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85258 5 | MRPL2 7; YBR282W W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecular activity | 0.995 | 0.259 | 0.26 |
| P24720    | Protein MNE1 [OS=Saccharomyces cerevisiae S288c] | 85451 2 | MNE1; YDR351C | metabolic process | cytoplasm; mitochondrial; organelle lumen | 0.194 | 0.061 | 0.31 |
| Q01574    | acetyl-CoA synthetase 1 [OS=Saccharomyces cerevisiae S288c] | 85124 5 | ACS1; YALO54 | cell organization and biogenesis; metabolic process | cytoplasm; cytosol; endoplasmic reticulum; mitochondrial; nucleus | catalytic activity; nucleotide binding | 0.947 | 0.354 | 0.37 |
| P36527    | 545 ribosomal protein L28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85207 3 | MRPL2 8; YDR464W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecular activity | 0.52 | 0.233 | 0.45 |
| P12687    | 545 ribosomal protein L2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85572 7 | MRPS7; YNL005 C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | catalytic activity; RNA binding; structural molecular activity | 2.899 | 1.31 | 0.45 |
| Q03799    | 375 ribosomal protein S8, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85519 0 | MRPS8; YMR158W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecular activity | 0.425 | 0.194 | 0.46 |
| Q06630    | Mitochondrial homologous recombination protein 1 [OS=Saccharomyces cerevisiae S288c] | 85189 0 | MHR1; YDR297W | cell organization and biogenesis; metabolic process | mitochondrion; nucleus | catalytic activity; DNA binding; structural molecular activity | 0.359 | 0.166 | 0.46 |
| P41154    | Magnesium-activated aldehyde dehydrogenase, cytosolic [OS=Saccharomyces cerevisiae S288c] | 85604 4 | ALD6; YPL061W | metabolic process; response to stimulus | cytoplasm; cytosol; mitochondrial | catalytic activity | 0.346 | 0.16 | 0.46 |
| P23738    | 4-hydroxybenzoate polyphenyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85778 8 | COQ2; YMR004C | metabolic process; transport | membrane; mitochondrial | catalytic activity | 0.292 | 0.136 | 0.47 |
| P49954    | Probable hydroxaldehyde dehydrogenase [OS=Saccharomyces cerevisiae S288c] | 85106 5 | NTS; YLR351C | metabolic process | cytoplasm; mitochondrial | catalytic activity | 0.274 | 0.125 | 0.47 |
| P38746    | Oligo-A TPase homolog [OS=Saccharomyces cerevisiae S288c] | 85637 2 | YFG3; YHR014C | mitochondrial | nucleotide binding | 0.194 | 0.093 | 0.48 |
| P38705    | Serine-tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85640 2 | DUA4; YHR0011W | metabolic process | cytoplasm; mitochondrial; organelle lumen | catalytic activity; nucleotide binding | 0.15 | 0.072 | 0.48 |
| P36056    | 375 ribosomal protein S22, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85370 1 | RSM22; YKL155C | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | catalytic activity; structural molecular activity | 0.125 | 0.061 | 0.49 |
| P15108    | ATP-dependent molecular chaperone Hsc82 [OS=Saccharomyces cerevisiae S288c] | 85522 4 | HSC82; YMR188W | cell organization and biogenesis; metabolic process | cytoplasm; membrane; mitochondrial | catalytic activity; nucleotide binding; protein binding | 0.602 | 0.299 | 0.50 |
| P08223    | Altered inheritance of mitochondria protein 39, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85410 3 | AIM39; YOL053W | metabolic process | cytosol; membrane; mitochondrial | catalytic activity | 0.468 | 0.259 | 0.55 |
| P39112    | Exoribonuclease II, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85533 1 | DSS1; YMR287C | metabolic process | mitochondrion; organelle lumen | catalytic activity; RNA binding | 0.233 | 0.134 | 0.58 |
| P02486    | ARS-binding factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85509 4 | ABF2; YMR007W | cell organization and biogenesis; metabolic process | chromosome; mitochondrial; nucleus | DNA binding | 33.55 | 19.30 | 0.58 |
| P04340    | 375 ribosomal protein RSM28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85210 5 | RSM28; YDR494W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecular activity | 3.489 | 2.008 | 0.58 |
Mitochondrial import receptor subunit tom22 [Os=Saccharomyces cerevisiae S288c]

85559 2 TOM22 ; YNL131 W cell organization and biogenesis;transport membrane;mitochondrion protein binding,transporter activity 1.154 0.668 0.58

37S ribosomal protein S12, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85577 2 MRPS1 2; YNR03 6C cell organization and biogenesis;metabolic process mitochondrion,ribosome structural molecule activity 1.154 0.668 0.58

37S ribosomal protein rsm18, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85677 6 RMPL18; YER050 C cell organization and biogenesis;metabolic process mitochondrion,ribosome structural molecule activity 0.995 0.585 0.59

545 ribosomal protein L25, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85296 7 MRPL25 5; YGR07 6C cell organization and biogenesis;metabolic process mitochondrion,ribosome structural molecule activity 0.874 0.52 0.59

Succinate dehydrogenase [ubiquinone] cytochrome b subunit, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85371 6 SDH3; YKL141 W cell organization and biogenesis;metabolic process;transport cytosol,endosome,membrane,mitochondrion;vacuole catalytic activity;metal ion binding 0.638 0.389 0.61

GTP-binding protein vps7 [Os=Saccharomyces cerevisiae S288c]

85501 2 VPS7; YML001 W cell communication;cell organization and biogenesis;metabolic process;response to stimulus;transport cytosol,mitochondrion catalytic activity;protein binding 0.585 0.359 0.61

Atypical kinase COQ8, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85275 8 COQ8; YGL119 W metabolic process membrane;mitochondrion;organellar lumen catalytic activity;nucleotide binding 0.453 0.283 0.62

4W ribosomal protein L1, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85169 4 MRPL1 1; YDR11 6C cell organization and biogenesis;metabolic process mitochondrion,ribosome RNA binding;structural molecule activity 0.438 0.274 0.63

Tricarboxylate transport protein [Os=Saccharomyces cerevisiae S288c]

85254 4 CTP1; YBR291 C metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 0.389 0.245 0.63

Mitochondrial peculiar membrane protein 1 [Os=Saccharomyces cerevisiae S288c]

85646 9 MRPL1 7; YNL252 C cell organization and biogenesis;metabolic process mitochondrion,ribosome structural molecule activity 0.369 0.233 0.63

10 kDa heat shock protein, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85418 5 HSP10; YDR02 0C cell organization and biogenesis;metabolic process;response to stimulus;transport cytosol,mitochondrion;organellar lumen metal ion binding;protein binding 2.162 1.371 0.63

Mitochondrial carrier protein LEU5 [Os=Saccharomyces cerevisiae S288c]

85639 1 LEU5; YHR002W metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 0.334 0.212 0.63

Autophagy-related protein 32 [Os=Saccharomyces cerevisiae S288c]

85466 0 ATG32; YIL146C metabolic process membrane;mitochondrion;vacuole protein binding 0.318 0.202 0.64

Methionine–tRNA ligase, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85308 1 MSM1; YGR17 C metabolic process cytosol,mitochondrion;organellar lumen catalytic activity;nucleotide binding 0.212 0.136 0.64

Mitochondrial ribosomal protein IMG1, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85041 3 IMG1; YCR046C cell organization and biogenesis;metabolic process mitochondrion,ribosome structural molecule activity 1.031 0.705 0.68

Mitochondrial peculiar membrane protein 1 [Os=Saccharomyces cerevisiae S288c]

85337 9 MMP1; YIL066C membrane;mitochondrion catalytic activity;protein binding 0.848 0.585 0.69

Tryptophan–tRNA ligase, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85186 1 MTW1; YDR268W metabolic process cytosol,mitochondrion;organellar lumen catalytic activity;nucleotide binding 0.668 0.468 0.70

Mitochondrial carrier protein [Os=Saccharomyces cerevisiae S288c]

85426 7 CRE1; YOR10 0C metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 1.994 1.404 0.70

Mitochondrial protein ZEO1 [Os=Saccharomyces cerevisiae S288c]

85404 0 ZEO1; YOL109W cell organization and biogenesis membrane;mitochondrion catalytic activity;protein binding 2.981 2.162 0.73

cytochrome c peroxidase, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85394 0 CCP1; YKR066C metabolic process;response to stimulus mitochondrion;organellar lumen antioxidant activity;catalytic activity;metal ion binding;protein binding 0.557 0.425 0.76

Kynurenine 3-monooxygenase [Os=Saccharomyces cerevisiae S288c]

85217 9 BNA4; YBL098W metabolic process membrane;mitochondrion catalytic activity;protein binding 0.487 0.374 0.77

ATP-dependent clpX-like chaperone, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85252 8 MCK1; YBR227C metabolic process membrane;mitochondrion;organellar lumen catalytic activity;protein binding 0.403 0.311 0.77

Mitochondrial ribosomal protein L22, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85554 4 MRPL22 2; YNL177C cell organization and biogenesis;metabolic process mitochondrion,ribosome RNA binding;structural molecule activity 0.931 0.73 0.78

Mitochondrial ribosomal protein L3, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85033 9 MRPL3; YMR024W cell organization and biogenesis;metabolic process;response to stimulus mitochondrion;nucleus;ribosome catalytic activity;RNA binding;structural molecule activity 0.61 0.487 0.80

Mitochondrial ribosomal protein mrx4, mitochondrial [Os=Saccharomyces cerevisiae S288c]

85281 6 MRX4; YGL054 cell organization and biogenesis;metabolic process mitochondrion;organellar lumen catalytic activity;protein binding 0.501 0.409 0.80
| Gene Name | Description                                                                 | Genes                                                                 | GO Terms                                                                 | Binding Type          | Binding Specificity |
|-----------|------------------------------------------------------------------------------|------------------------------------------------------------------------|--------------------------------------------------------------------------|-----------------------|--------------------|
| P36517    | 54S ribosomal protein L4, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S116 0 MRPL4; 1YR439 W                                               | cell organization and biogenesis;metabolic process                       | mitochondrion;ribosome | 1.081 0.874 0.81  |
| P29038    | Translation initiation factor IF-2, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S413 5 IFM1; 1YD223 W                                               | cell organization and biogenesis;metabolic process                       | mitochondrion;nucleus | 0.369 0.299 0.81  |
| P38088    | Glycine–tRNA ligase 1, mitochondrial [OS=Saccharomyces cerevisiae 5288c]      | 8S247 7 FZD1; 1YBR179 C                                               | cell organization and biogenesis;protein binding                        | catalytic activity;nucleotide binding;RNA binding | 0.334 0.271 0.81  |
| P38297    | Mitofusin Fzo1 [OS=Saccharomyces cerevisiae 5288c]                           | 8S543 6 MRPL11 0; YNL284 C                                           | cell organization and biogenesis;protein binding                        | structural molecule activity | 1.404 1.154 0.82  |
| P36520    | 54S ribosomal protein L10, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S432 9 PET123; YOR15 BW                                              | cell organization and biogenesis;metabolic process                       | mitochondrion;ribosome | 2.162 1.783 0.82  |
| P17558    | 37S ribosomal protein PET123, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S274 8 RSM23; YGL129 C                                              | cell organization and biogenesis;metabolic process                       | mitochondrion;ribosome | 2.065 1.707 0.83  |
| P28817    | 3-hydroxysterolubonyl-CoA hydrolase, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S160 6 EHD3; YDR03 IC                                               | protein binding                                                          | mitochondrial         | 0.887 0.743 0.84  |
| P36567    | ABC1 family protein MCF2 [OS=Saccharomyces cerevisiae 5288c]                 | 8S091 5 YLP253 W; MCP2; YLS253 W                                     | cell organization and biogenesis;protein binding                        | catalytic activity;nucleotide binding;RNA binding | 0.693 0.585 0.84  |
| P40098    | uncharacterized mitochondrial membrane protein FMP10 [OS=Saccharomyces cerevisiae 5288c] | 8S693 1 FMP10; YER182 W                                              | membrane;mitochondrion                                                  | structural molecule activity | 2.793 2.36 0.84  |
| P30327    | Mitochondrial fusion and transport protein Ugo1 [OS=Saccharomyces cerevisiae 5288c] | 8S208 1 UGO1; YDR47 IC                                              | cell organization and biogenesis;protein binding                        | membrane;mitochondrion | 1.424 1.219 0.86  |
| P32332    | Mitochondrial oxaloacetate transport protein [OS=Saccharomyces cerevisiae 5288c] | 8S373 9 DAC1; YKL120 W                                              | protein binding                                                          | membrane;mitochondrion | 5.813 4.995 0.86  |
| P21801    | Succinate dehydrogenase (ubiquinone) iron-sulfur subunit, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S068 5 SHD2; YLD041 C                                              | membrane;transport                                                       | mitochondrial         | 2.85 2.480 0.87  |
| P27929    | 37S ribosomal protein NAM9, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S558 5 NAM9; YNL137 C                                               | cell organization and biogenesis;protein binding                        | catalytic activity;metal ion binding | 1.865 1.683 0.90  |
| P15424    | ATP-dependent RNA helicase Mss116, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S177 5 MSS116 6 YDR19 1C                                           | DNA helicase                                                             | membrane;mitochondrion | 1.387 1.268 0.91  |
| Q12031    | Mitochondrial 2-methylisocitrinate lyase [OS=Saccharomyces cerevisiae 5288c] | 8S611 4 IC2; YPR006 C                                               | ATP binding                                                              | structural molecule activity | 2.793 2.793 1.00  |
| P43635    | Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae 5288c]        | 8S610 7 CT3; YPR001 W                                               | cell organization and biogenesis;protein binding                        | mitochondrial         | 2.914 2.914 1.00  |
| P35087    | Sterol 24-C-methyltransferase [OS=Saccharomyces cerevisiae 5288c]            | 8S550 3 ERG6; YML00 BC                                              | metabolic process                                                        | endoplasmic reticulum;membrane;mitochondrion | 1.894 1.894 1.00  |
| P39952    | Mitochondrial inner membrane protein Oxa1 [OS=Saccharomyces cerevisiae 5288c] | 8S689 8 OXA1; YER154 W                                              | cell organization and biogenesis;transport                              | membrane;mitochondrion | 3.87 3.87 1.00  |
| Q40138    | Citrate:exoglutarate carrier protein [OS=Saccharomyces cerevisiae 5288c]    | 8S528 2 YHM2; YMR241Y 1W                                          | cell organization and biogenesis;protein binding                        | mitochondrial         | 4.623 4.623 1.00  |
| P53266    | Cytochrome oxidase assembly protein Shy1 [OS=Saccharomyces cerevisiae 5288c] | 8S300 9 SHY1; YGR11 2W                                             | cell organization and biogenesis;protein binding                        | mitochondrial         | 1.555 1.555 1.00  |
| Q17029    | Probable mitochondrial transport protein fts1 [OS=Saccharomyces cerevisiae 5288c] | 8S444 5 YOR27 1C                                                  | transport                                                                | mitochondrial         | 2.36 2.36 1.00  |
| P35721    | Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae 5288c] | 8S575 2 RCP2; YMR01 BW                                            | cell organization and biogenesis;transport                              | mitochondrial         | 9 9 1.00  |
| P38079    | protein Yro2 [OS=Saccharomyces cerevisiae 5288c]                            | 8S234 3 YRO2; YBR054 W                                             | transport                                                                | endoplasmic reticulum;membrane;mitochondrion | 3.125 3.125 1.00  |
| Q0668 | Methyltransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85191 | OMS1; YDR31 W | metabolic process | membrane, mitochondrion | catalytic activity | 0.484 | 0.484 | 1.00 |

| P00447 | Superoxide dismutase [Mn], mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85639 | SOD2; YHR008C | metabolic process;response to stimulus | mitochondrion, organelle lumen | antioxidant activity; catalytic activity; metal ion binding | 2.455 | 2.455 | 1.00 |

| P00444 | Cytochrome c iso-1 [OS=Saccharomyces cerevisiae S288c] | 85350 | CYC1; YIR048 W | metabolic process; transport | mitochondrion | metal ion binding; protein binding | 3.217 | 3.217 | 1.00 |

| P40508 | Uncharacterised protein YIL077C [OS=Saccharomyces cerevisiae S288c] | 85473 | YIL077C; YIL077C | | mitochondrion | | 0.896 | 0.896 | 1.00 |

| P3969 | Sorting assembly machinery 50 kDa subunit [OS=Saccharomyces cerevisiae S288c] | 85570 | SAM50; YNL026 W | cell organization and biogenesis; transport | membrane, mitochondrion | protein binding; transporter activity | 0.487 | 0.487 | 1.00 |

| P23331 | Carrier protein YM1C, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85617 | YM1C; YPR058 W | metabolic process; transport | membrane, mitochondrion; vacuole | structural molecular activity; transporter activity | 1.581 | 1.581 | 1.00 |

| P33330 | Phosphatidylethanolamine transferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85293 | TAM41; YGR048 W | metabolic process | membrane, mitochondrion, organelle lumen | catalytic activity | 0.668 | 0.668 | 1.00 |

| P0950 | Phosphoglycerate mutase 1 [OS=Saccharomyces cerevisiae S288c] | 85370 | GPM1; YKL152 | metabolic process; regulation of biological process | cytoplasm, cytosol, membrane, mitochondrion | catalytic activity | 1.929 | 1.929 | 1.00 |

| Q0143 | Mitochondrial dicarboxylate transporter [OS=Saccharomyces cerevisiae S288c] | 85108 | DCL1; YLR348C | metabolic process; transport | membrane, mitochondrion | structural molecular activity; transporter activity | 0.931 | 0.931 | 1.00 |

| P40416 | Iron-sulfur clusters transporter ATM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85534 | ATM1; YMR330C | cellular homeostasis; metabolic process; transport | membrane, mitochondrion | catalytic activity; nucleotide binding; transporter activity | 0.453 | 0.453 | 1.00 |

| P28737 | Protein MSF1 [OS=Saccharomyces cerevisiae S288c] | 85291 | MSF1; YGR028W | cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport | membrane, mitochondrion; nucleus | catalytic activity; nucleotide binding; protein binding; RNA binding; structural molecular activity | 0.778 | 0.778 | 1.00 |

| P40709 | Probable lysine--oxoglutarate transaminase [OS=Saccharomyces cerevisiae S288c] | 85338 | BNA3; YIL060W | metabolic process; regulation of biological process | cytoplasm; mitochondrion | catalytic activity | 0.468 | 0.468 | 1.00 |

| Q12251 | Uncharacterised mitochondrial carrier YPR011C [OS=Saccharomyces cerevisiae S288c] | 85612 | YPR011C; YPR011C | metabolic process; transport | membrane, mitochondrion | structural molecular activity; transporter activity | 0.73 | 0.73 | 1.00 |

| P23837 | 545 ribosomal protein L41, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85201 | MRP20; YDR40W | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | nucleotide binding; protein binding; RNA binding; structural molecular activity | 0.501 | 0.501 | 1.00 |

| P36101 | Immunoantwort [OS=Saccharomyces cerevisiae S288c] | 85384 | TCD2; YKL027W; YKL027W | metabolic process | cytoplasm; membrane; mitochondrion | catalytic activity; nucleotide binding | 0.334 | 0.334 | 1.00 |

| P37299 | Cytochrome b-1 complex subunit 10 [OS=Saccharomyces cerevisiae S288c] | 85639 | OCR10; YHR000W | metabolic process; transport | membrane, mitochondrion | catalytic activity; transporter activity | 2.981 | 2.981 | 1.00 |

| P53889 | Uncharacterised mitochondrial hydroxylase [OS=Saccharomyces cerevisiae S288c] | 85555 | FMP41; YNL168C | metabolic process | mitochondrion | catalytic activity; metal ion binding | 0.501 | 0.501 | 1.00 |

| Q04172 | Sensitive to high expression protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85200 | SHE8; YDR39W | cell organization and biogenesis | membrane, mitochondrion | | 0.269 | 0.269 | 1.00 |

| P21771 | 375 ribosomal protein S28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85193 | MRP52; YDR337W | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | RNA binding; structural molecular activity | 0.624 | 0.624 | 1.00 |

| P50945 | MICOS complex subunit MIC27 [OS=Saccharomyces cerevisiae S288c] | 85562 | AIM37; MIC27; YNL100W | cell organization and biogenesis | membrane, mitochondrion | | 0.719 | 0.719 | 1.00 |

| P42900 | Sigma-like sequence protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85083 | SL5; YLR139C | cell organization and biogenesis; metabolic process | membrane, mitochondrion | protein binding | 0.266 | 0.266 | 1.00 |

| Q58824 | Uncharacterised protein YOR020W-A [OS=Saccharomyces cerevisiae S288c] | 14664 | YOR020W-A; YOR020W-A | metabolic process; transport | membrane, mitochondrion | | 2.162 | 2.162 | 1.00 |

| P36521 | 545 ribosomal protein L11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85132 | MRP1; YDL202W | cell organization and biogenesis; metabolic process | mitochondrion, ribosome | structural molecular activity | 0.833 | 0.833 | 1.00 |
Mitochondrial ATPase complex subunit ATP10 [OS=Saccharomyces cerevisiae S288c]

| Q12233 | P25372 | Q05779 | P36519 | P40159 | P48525 | P40015 | P10849 |
|--------|--------|--------|--------|--------|--------|--------|--------|
| 85110  | 9      | ATP10; YLR393 W | cell organization and biogenesis, cytoplasm, membrane, mitochondrion | protein binding | 0.585 | 0.585 | 1.00 |

Putative ATP-dependent RNA helicase YLR419W [OS=Saccharomyces cerevisiae S288c]

| Q0698 | P32839 | Q12247 |
|-------|--------|--------|
| 85113 | 7      | YLR419 W; YLR419 W | metabolic process, cytoplasm, mitochondrion, nucleus | catalytic activity, nucleotide binding, protein binding | 0.11 | 0.11 | 1.00 |

MIOREX complex component 4 [OS=Saccharomyces cerevisiae S288c]

| P32839 | Q2904 | P10834 |
|--------|-------|--------|
| 85593  | 5     | YPL168 W | membrane, mitochondrion | 0.318 | 0.318 | 1.00 |

Mitochondrial chaperone BCS1 [OS=Saccharomyces cerevisiae S288c]

| P32839 | Q2904 | P10834 |
|--------|-------|--------|
| 85198  | 1     | BCS1; YDR37 SC | cell organization and biogenesis, cytoplasm, membrane, mitochondrion | catalytic activity, nucleotide binding, RNA binding | 0.194 | 0.194 | 1.00 |

54S ribosomal protein L6, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| P32839 | Q2904 | P10834 |
|--------|-------|--------|
| 85655  | 2     | MRPL6; YHR14 7C | cell organization and biogenesis, mitochondrial process | mitochondrion, ribosome, RNA binding, structural molecule activity | 1.054 | 1.054 | 1.00 |

protein PETS4 [OS=Saccharomyces cerevisiae S288c]

| P32839 | Q2904 | P10834 |
|--------|-------|--------|
| 85313  | 7     | PETS4; YGR22 2W | metabolic process, regulation of biological process | membrane, mitochondrion, organelle lumen, nucleotide binding, RNA binding, translation regulator activity | 0.369 | 0.369 | 1.00 |

Mitochondrial ornithine transporter 1 [OS=Saccharomyces cerevisiae S288c]

| Q12375 | Q01522-1 |
|--------|----------|
| 85429  | 7     | ORT1; YDR13 SC | metabolic process, transport | membrane, mitochondrion, structural molecule activity, transporter activity | 0.54 | 0.54 | 1.00 |

Cysteine proteinase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Q01522-1 | P39677 | P33759 |
|----------|-------|-------|
| 85334   | 2     | MEP2; YIL102 W | cell organization and biogenesis, mitochondrial process | cytoplasm, mitochondrion, catalytic activity, RNA binding | 0.116 | 0.116 | 1.00 |

Ribosome-releasing factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Q39677 | P33759 |
|--------|-------|
| 85255  | 3     | MRPP5; YBR251 W | cell organization and biogenesis, mitochondrial process | mitochondrion, ribosome, RNA binding, structural molecule activity | 0.413 | 0.413 | 1.00 |

37S ribosomal protein S55, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| P33759 | P41911 |
|--------|-------|
| 85409  | 5     | GPD2; YOL059 W | metabolic process | cytoplasm, cytosol, mitochondrial catalytic activity, nucleotide binding, protein binding | 0.186 | 0.186 | 1.00 |

Glycerol-3-phosphate dehydrogenase [NAD+] [OS=Saccharomyces cerevisiae S288c]

| P41911 | P40496 |
|--------|-------|
| 85471  | 5     | RSM25; YIL093 C | cell organization and biogenesis, mitochondrial process | mitochondrion, ribosome, structural molecule activity | 0.668 | 0.668 | 1.00 |

Ribonucleic acid-ribonuclease A [OS=Saccharomyces cerevisiae S288c]

| P40496 | P10849 |
|--------|-------|
| 85151  | 7     | MTP2; YDL044 C | metabolic process, mitochondrion, organelle lumen, protein binding, RNA binding | 0.166 | 0.166 | 1.00 |

mitochondrial transcription factor 2 [OS=Saccharomyces cerevisiae S288c]

| P10849 | P40115 |
|--------|-------|
| 85673  | 9     | ISC1; YER019 W | metabolic process, response to stimulus | endoplasmic reticulum, membrane, mitochondrion, catalytic activity, metal ion binding | 0.334 | 0.334 | 1.00 |

Mitochondrial group I intron splicing factor CCMI [OS=Saccharomyces cerevisiae S288c]

| P40115 |
|--------|
| 85305  | 3     | CCM1; YGR15 SC | cell organization and biogenesis, mitochondrial process | mitochondrion, RNA binding | 0.089 | 0.089 | 1.00 |

Glutamate-RNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| P4825 |
|-------|
| 85412  | 4     | MSE1; YDL033 W | cell organization and biogenesis, mitochondrial process | cytoplasm, mitochondrion, organelle lumen, catalytic activity, nucleotide binding, RNA binding | 0.145 | 0.145 | 1.00 |

Uncharacterized protein YNL208W [OS=Saccharomyces cerevisiae S288c]

| P40159 |
|--------|
| 85551  | 3     | YNL208 W; YNL208 W | membrane, mitochondrion, ribosome | 0.292 | 0.292 | 1.00 |

Abhydrolase domain-containing protein IMQ032 [OS=Saccharomyces cerevisiae S288c]

| P53219 |
|--------|
| 85291  | 9     | IMQ032; YGR03 1W | metabolic process, transport | mitochondrion, catalytic activity | 0.245 | 0.245 | 1.00 |

Mitochondrial distribution and morphology protein 10 [OS=Saccharomyces cerevisiae S288c]

| P81409 |
|--------|
| 85122  | 3     | MDM1; YAL010 C | cell organization and biogenesis, transport | membrane, mitochondrion, protein binding | 0.16 | 0.16 | 1.00 |

Mitochondrial ATPase complex subunit ATP10 [OS=Saccharomyces cerevisiae S288c]

| P82159 |
|--------|
| 85182  | 3     | MRPL7; YDR23 7W | cell organization and biogenesis, mitochondrial process | mitochondrion, ribosome, RNA binding, structural molecule activity | 0.136 | 0.136 | 1.00 |

Iron-sulfur assembly protein 1 [OS=Saccharomyces cerevisiae S288c]

| Q07281 |
|--------|
| 85063  | 2     | IS11; YLL027 W | cell organization and biogenesis, mitochondrial process | mitochondrion, organelle lumen, metal ion binding, structural molecule activity | 0.136 | 0.136 | 1.00 |

Ubiquinone biosynthesis protein COQ9, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Q0779 |
|--------|
| 85089  | 8     | COQ9; YLR201 C | metabolic process | membrane, mitochondrion | 0.166 | 0.166 | 1.00 |

Thioredoxin-3, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| P25372 |
|--------|
| 85044  | 4     | TRX3; YCM083 W | cellular homeostasis, metabolic process, regulation of biological process, response to stimulus, transport | cytoplasm, mitochondrion, catalytic activity | 0.52 | 0.52 | 1.00 |

ATP synthase subunit g, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| P21306 |
|--------|
| 85613  | 1     | ATP20; YPR020 W | cell organization and biogenesis, metabolic process, transport | membrane, mitochondrion, catalytic activity, transporter activity | 0.778 | 0.778 | 1.00 |

ATP synthase subunit epsilon, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| P21306 |
|--------|
| 85585  | 7     | ATP15; YPL271 W | metabolic process, transport | membrane, mitochondrion, catalytic activity, transporter activity | 0.778 | 0.778 | 1.00 |
| P19516 | Cytochrome c oxidase assembly protein COX11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85597 | COX11; YPL132 W | cell organization and biogenesis;metabolic process | membrane;mitochondrion;ribosome | metal ion binding | 0.274 | 0.274 | 1.00 |
| Q06336 | Mitochondrial inner membrane protein SHIM4 [OS=Saccharomyces cerevisiae S288c] | 85086 | SHIM4; YLR164 W | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding | 0.778 | 0.778 | 1.00 |
| P39515 | mitochondrial import inner membrane translocase subunit Tim17 [OS=Saccharomyces cerevisiae S288c] | 85329 | TIM17; YIL143 W | cell organization and biogenesis;transport | membrane;mitochondrion | protein binding;transporter activity | 0.778 | 0.778 | 1.00 |
| P03875 | Putative COXII/OX3 intron 1 protein [OS=Saccharomyces cerevisiae S288c] | 85459 | A01; Q0050 | metabolic process;transport | mitochondrion | catalytic activity;RNA binding;transporter activity | 0.081 | 0.081 | 1.00 |
| P36523 | 54S ribosomal protein L15, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85102 | MRPL1 5; YLR132 W-A | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | catalytic activity;RNA binding;structural molecule activity | 0.155 | 0.155 | 1.00 |
| P38909 | cytochrome c mitochondrial import factor CYC2 [OS=Saccharomyces cerevisiae S288c] | 85420 | CYC2; YDR037 W | cell organization and biogenesis;metabolic process | membrane;mitochondrion | catalytic activity | 0.194 | 0.194 | 1.00 |
| P08525 | Cytochrome b-c complex subunit 8 [OS=Saccharomyces cerevisiae S288c] | 85327 | YER088 W; YIL166 W | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 0.585 | 0.585 | 1.00 |
| P34263 | Acyl Carrier protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85364 | ALCL2; YEL192 C | metabolic process;transport | mitochondrion | catalytic activity | 0.259 | 0.259 | 1.00 |
| P35270 | rRNA methyltransferase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85437 | MRMM1; YOR20 W-C | metabolic process | mitochondrion | catalytic activity;RNA binding | 0.274 | 0.274 | 1.00 |
| P14151 | ATP synthase subunit 8, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85407 | ATP19; YKL077 W-A | cell organization and biogenesis;metabolic process | membrane;mitochondrion | catalytic activity;transporter activity | 1.154 | 1.154 | 1.00 |
| P33305 | Mitochondrial 37S ribosomal protein S27 [OS=Saccharomyces cerevisiae S288c] | 85312 | RSM27; YDR215 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.468 | 0.468 | 1.00 |
| P36531 | 54S ribosomal protein L36, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85241 | MRPL3 6; YBR122 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.292 | 0.292 | 1.00 |
| P24923 | ATPase expression protein 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85508 | AEP1; YMR006 4W | regulation of biological process | mitochondrion | translation regulator activity | 0.15 | 0.15 | 1.00 |
| P23254 | 54S ribosomal protein L20, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85396 | MRPL2 0; YKR085 C | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | structural molecule activity | 0.389 | 0.389 | 1.00 |
| Q2V99 | Uncharacterized protein YDR119W-A [OS=Saccharomyces cerevisiae S288c] | 37999 | COX26; YOR119W-A | | membrane;mitochondrion | | 1.154 | 1.154 | 1.00 |
| P08379 | Intron-encoded RNA maturase b14 [OS=Saccharomyces cerevisiae S288c] | 85458 | B4; Q0120 | metabolic process | membrane;mitochondrion | catalytic activity;RNA binding | 0.179 | 0.179 | 1.00 |
| P38341 | MICOS complex subunit MIC12 [OS=Saccharomyces cerevisiae S288c] | 85256 | AIM5; MIC12; YBR862 C | cell organization and biogenesis | membrane;mitochondrion | | 0.292 | 0.292 | 1.00 |
| P38816 | thioredoxin reductase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85650 | TRK2; YHR10 6W | cellular homeostasis;metabolic process;response to stimulus | cytoplasm;mitochondrion | antioxidant activity;catalytic activity | 0.156 | 0.156 | 1.00 |
| Q03218 | Mitochondrial metal transporter 1 [OS=Saccharomyces cerevisiae S288c] | 85521 | MMT1; YMR177 W | cellular homeostasis;regulation of biological process;response to stimulus | membrane;mitochondrion | transporter activity | 0.096 | 0.096 | 1.00 |
| P04039 | Cytochrome c oxidase polypeptide VIII, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85111 | COX8; YKR395 C | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 0.778 | 0.778 | 1.00 |
| P04748 | Protein S0V1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85508 | S0V1; YMR006 6W | | mitochondrion | | 0.041 | 0.041 | 1.00 |
| P04487 | Mitochondrial inner membrane protein SHIM3 [OS=Saccharomyces cerevisiae S288c] | 85514 | SHIM3; YMR11 8C | metabolic process | membrane;mitochondrion | catalytic activity;metal ion binding | 0.194 | 0.194 | 1.00 |
| P40858 | 54S ribosomal protein L49, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85334 | MRPL4 9; YIL096 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.212 | 0.212 | 1.00 |
| P10174 | cytochrome c oxidase subunit 7 [OS=Saccharomyces cerevisiae S288c] | 85529 | COX7; YMR25 6C | metabolic process;transport | membrane;mitochondrion | catalytic activity;transporter activity | 1.155 | 1.155 | 1.00 |
| P06476 | Tricarbin 3 [OS=Saccharomyces cerevisiae S288c] | 85490 | TC3; YML077 2C | cell organization and biogenesis;regulation of biological process | endoplasmic reticulum;membrane;mitochondrion | metal ion binding;protein binding | 0.806 | 0.863 | 1.07 |
| P05660 | Phosphoglycerate kinase [OS=Saccharomyces cerevisiae S288c] | 85037 | PGK1; YCR012 W | metabolic process;regulation of biological process | cytoplasm;membrane;mitochondrion | catalytic activity;nucleotide binding | 2.981 | 3.299 | 1.11 |
| P07806 | Valine-tRNA ligase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85298 | VA1; YGR09 4W | metabolic process;regulation of biological process | cytoplasm;cytosol;mitochondrion | catalytic activity;nucleotide binding | 0.422 | 0.468 | 1.11 |
Glycerol-3-phosphate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P32191  | GUT2; YIL155 C | metabolic process, mitochondrial | catalytic activity |

Endoplasmic reticulum-membrane, mitochondrial

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| Q07349  | TDG27 C; MRK9; YDL277 C | endoplasmic reticulum, mitochondrial | catalytic activity |

RNA binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P22136  | YEP2; YMR282 C | metabolic process, regulation of biological process | mitochodrion |

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| Q08023  | YMR275 W | cell organization and biogenesis | membrane, mitochondrial |

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P35918  | YER015 W | metabolic process, transport | cytoplasm, mitochondrial |

activity, nucleotide binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P53292  | YGR16 5W | cell organization and biogenesis, metabolic process | mitochondrial, ribosome |

structural molecule activity

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| G12482  | YP021 C | metabolic process, transport | membrane, mitochondrial |

structural molecule activity, transporter activity

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P46881  | DLD2; YDL178 W | metabolic process | mitochondrial, organelle lumen |

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P40086  | COX15; YER141 W | cell organization and biogenesis, metabolic process, transport | membrane, mitochondrial |

activity, catalytic activity, protein binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P43616  | DUG1; YPR044 C | metabolic process | cytoplasm, mitochondrial, ribosome |

activity, metal ion binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P51179  | MID1; YPL104 W | metabolic process | cytoplasm, mitochondrial, organelle lumen |

activity, nucleotide binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P51194  | Msd2; Yhr024 C | metabolic process, transport | membrane, mitochondrial, organelle lumen |

activity, metal ion binding, protein binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P38626  | Cbr1; Yil043 C | metabolic process | endoplasmic reticulum, membrane, mitochondrial, nucleus |

activity, nucleotide binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| Q08968  | Fmp40; Ypl222 W | mitochodrion | protein binding |

transport activity

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P40745  | TIM54; YIL054 W | cell organization and biogenesis, transport | cytoplasm, membrane, mitochondrial |

reticulum, membrane, mitochondrial, nucle

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P8869  | Pnt1; Ydr26 5W | cell organization and biogenesis, response to stimulus | membrane, mitochondrial |

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P40012  | HEM14 ; YER014 | metabolic process | membrane, mitochondrial |

catalytic activity

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| Q03976  | Rsm24; Ydr17 5C | cell organization and biogenesis, metabolic process | mitochondrial, ribosome |

structural molecule activity

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P40047  | Ald15; Yer073 3W | metabolic process | mitochondrial, organelle lumen |

activity, catalytic activity |

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| Q12117  | Mrh1; Ydr03 5W | transport | endoplasmic reticulum, membrane, mitochondrial |

transporter activity

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P48527  | Msp1; Ypl097 W | metabolic process | cytoplasm, cytosol, mitochondrial, organelle lumen |

activity, nucleotide binding, RNA binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P46066  | Ykl133 C; Ykl133 C | metabolic process | membrane, mitochondrial |

protein binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P21375  | Dsm4; Yih051 W | metabolic process | endoplasmic reticulum, mitochondrial |

catalytic activity, nucleotide binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P95440  | Msi1; Ybh084 W | metabolic process | cytoplasm, mitochondrial |

activity, nucleotide binding

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P93006  | Psd1; Ynl169 C | metabolic process, regulation of biological process | membrane, mitochondrial |

catalytic activity

| Gene ID | Description | Localization | Functional Category |
|---------|-------------|--------------|---------------------|
| P32611  | Rml2; Yel050 C | cell organization and biogenesis, metabolic process | mitochondrial, ribosome |

activity, RNA binding, structural
| Gene ID | Name | Function | Location | Molecular Activity | Protein Domain | GO Terms |
|--------|------|----------|----------|--------------------|----------------|-----------|
| P10507 | mitochondrial processing peptidase subunit beta | [OS=Saccharomyces cerevisiae S288c] | 85086 0 | Metabolic process;transport | Mitochondrion,organelle lumen | Catalytic activity;metal ion binding;protein binding |
| P48526 | Isoenzyme--RNA ligase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85060 7 | Cellular organization and biogenesis;metabolic process;regulation of biological process | Cytoplasm;cytosol;mitochondrion,organelle lumen | Catalytic activity;nucleotide binding |
| P11998 | S45 ribosomal protein ym6, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85498 3 | Cell organization and biogenesis;metabolic process | Mitochondrion,ribosome | RNA binding;structural molecular activity |
| P24533 | Protein ATP11, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85540 1 | Cell organization and biogenesis | Mitochondrion | Protein binding |
| P49095 | Glutamate dehydrogenase (Decarboxylating), mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85522 7 | Metabolic process | Cytosol;mitochondrion | Catalytic activity |
| P28241 | Isocitrate dehydrogenase (NAD) subunit 2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85430 3 | Metabolic process | Mitochondrion,organelle lumen | Catalytic activity;metal ion binding;protein binding |
| P38771 | Ribosome-recycling factor, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85463 3 | Cell organization and biogenesis;metabolic process | Mitochondrion | RNA binding |
| P43660 | Probable NADPH:adenodoxin oxidoreductase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85198 2 | Cellular homeostasis;metabolic process;transport | Cytoplasm;membrane;mitochondrion,organelle lumen | Catalytic activity |
| P28834 | Isocitrate dehydrogenase (NAD) subunit 1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85569 1 | Metabolic process;transport | Cytosol;mitochondrion,organelle lumen | Catalytic activity;metal ion binding;protein binding;RNA binding |
| P04710 | ADP,ATP carrier protein 1 | [OS=Saccharomyces cerevisiae S288c] | 85507 8 | Metabolic process;transport | Cytosol;membrane;mitochondrion | Structural molecule activity;transporter activity |
| P39676 | Flavohemoprotein | [OS=Saccharomyces cerevisiae S288c] | 85314 9 | Metabolic process;response to stimulus | Cytoplasm;cytosol;mitochondrion;organelle lumen | Catalytic activity;metal ion binding;protein binding |
| P37923 | N-terminal acetyltransferase 2 | [OS=Saccharomyces cerevisiae S288c] | 85305 0 | Metabolic process | Cytoplasm;mitochondrion | Catalytic activity |
| P88072 | Protein SCO2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85231 2 | Cell organization and biogenesis;cellular homeostasis;metabolic process;transport | Membrane;mitochondrion | Antioxidant activity;catalytic activity;metal ion binding |
| P50110 | Sorting assembly machinery 37 kDa subunit | [OS=Saccharomyces cerevisiae S288c] | 85508 2 | Cell organization and biogenesis;transport | Membrane;mitochondrion | Protein binding |
| P09457 | ATP synthase subunit 5, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85189 2 | Metabolic process;transport | Membrane;mitochondrion | Catalytic activity;transporter activity |
| Q29801 | ABC1 family protein YPL109C, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85599 5 | | | 7.799 10.36 |
| P40471 | NADPH-dependent 3-acetylhydroxysaccharone phosphate reductase | [OS=Saccharomyces cerevisiae S288c] | 85468 2 | Metabolic process | Cytoplasm;endoplasmic reticulum;membrane;mitochondrion | Catalytic activity |
| P32335 | Protein MSS51, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85090 0 | Metabolic process;regulation of biological process | Membrane;mitochondrion | Protein binding;translation regulator activity |
| P16603 | NADPH--cyclochrome P450 reductase | [OS=Saccharomyces cerevisiae S288c] | 85643 8 | Metabolic process | Cytoplasm;cytosol;endoplasmic reticulum;membrane;mitochondrion | Catalytic activity;metal ion binding;protein binding;RNA binding |
| Q10028 | Mitochondrial 2-oxidolcarboxylate carrier 1 | [OS=Saccharomyces cerevisiae S288c] | 85596 9 | | | Structural molecule activity;transporter activity |
| P53206 | Putative cysteine synthase | [OS=Saccharomyces cerevisiae S288c] | 85289 5 | Metabolic process | Mitochondrion | Catalytic activity |
| P33111 | ATP-dependent permease MOL2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85385 8 | Response to stimulus;transport | Membrane;mitochondrion | Catalytic activity;nucleotide binding;transporter activity |
| P00175 | Cytochrome b2, mitochondrial | [OS=Saccharomyces cerevisiae S288c] | 85495 0 | Metabolic process;transport | Cytosol;membrane;mitochondrion;organelle lumen | Catalytic activity;metal ion binding |

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| S288c | AC | binding; nucleotide binding | antioxidant activity; catalytic activity; protein binding | metabolic process | cell organization and biogenesis | membrane; mitochondrial |
|-------|----|-----------------------------|----------------------------------------------------------|------------------|---------------------------------|------------------------|
| P40582 | Glutathione S-transferase 1  | 85485 6  | GTT1; YBR038 C  | metabolic process | endoplasmic reticulum; membrane; mitochondrial; nucleus | membrane; mitochondrial |
| P5087 | MICOS subunit MIC26  | 85315 0  | M052; MIC26; YGR23 SC  | cell organization and biogenesis | membrane; mitochondrial | 0.931 1.276 1.37 |
| P3310 | ATP-dependent permease MOL1, mitochondrial | 85088 5  | MDL1; YKL88 W  | transport | membrane; mitochondrial | catalytic activity; nucleotide binding; transporter activity | 0.528 0.725 1.37 |
| P02360 | glyceroldehyde-3-phosphate dehydrogenase 1  | 85339 5  | TDM1; YGL052 W  | metabolic process | cytoplasm; cytosol; membrane; mitochondrial | catalytic activity; nucleotide binding | 1.462 2.008 1.37 |
| P23574 | Cytochrome desulfurase, mitochondrial | 85034 3  | NFS1; YCL017 C  | cell organization and biogenesis; cellular homeostasis; metabolic process | mitochondrial; nucleus | catalytic activity; metal binding; protein binding | 0.978 1.346 1.38 |
| Q12374 | Nuclear control of ATPase protein 2  | 85627 8  | NCA2; YPR155  | metabolic process | membrane; mitochondrial | 0.565 0.778 1.38 |
| P33112 | Succinyl-CoA ligase (ADP-forming) subunit beta, mitochondrial | 85315 9  | UGC2; YGR24 4C  | metabolic process | mitochondrial | catalytic activity; nucleotide binding | 9 12.46 1.38 |
| P3170 | Pyruvate dehydrogenase (acetyl-transferring) kinase 2, mitochondrial | 85282 1  | PP2; YGL059 W  | metabolic process; regulation of biological process | mitochondrial; organelle lumen | catalytic activity; nucleotide binding; protein binding | 0.28 0.389 1.39 |
| P32898 | Mitochondrial presucrose protease  | 85204 1  | CYM1; YDR43 C  | metabolic process | mitochondrial | catalytic activity; metal ion binding | 0.682 0.951 1.39 |
| Q08222 | Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial | 85453 8  | CIR2; YOR35 6W  | metabolic process; transport | membrane; mitochondrial | catalytic activity; metal ion binding; nucleotide binding | 2.162 3.019 1.40 |
| P32902 | 37s ribosomal protein MRP4, mitochondrial | 85638 4  | YRP4; YHL004 W  | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | 0.334 0.468 1.40 |
| P48015 | Aminomethyltransferase, mitochondrial | 85158 2  | GCV2; YDR01 9C  | metabolic process | mitochondrial | catalytic activity; protein binding | 6.406 9 1.40 |
| P32454 | Aminopeptidase 2, mitochondrial | 85389 9  | APE2; YKL157 W  | metabolic process | cytoplasm; extracellular; membrane; mitochondrial; nucleus | catalytic activity; metal ion binding | 1.688 2.346 1.41 |
| Q08922 | NADH kinase PD55, mitochondrial | 85591 3  | PDS5; YPL188 W  | metabolic process; response to stimulus | mitochondrial; organelle lumen | catalytic activity; nucleotide binding | 0.369 0.52 1.41 |
| P2950 | 37s ribosomal protein MRPS1, mitochondrial | 85598 5  | MRPS1 1; YPL118 W  | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | 0.817 1.154 1.41 |
| P40035 | Mitochondrial phosphate carrier protein 2  | 85677 9  | PIC2; YER003 C  | cellular homeostasis; metabolic process; transport | membrane; mitochondrial | structural molecule activity; transporter activity | 1.976 2.793 1.41 |
| P01822 | Mitochondrial import inner membrane translocase subunit TIM44  | 85479 0  | TIM44; YIL022 W  | transport | membrane; mitochondrial | nucleotide binding; protein binding | 4.946 7.003 1.42 |
| P36163 | mitochondrial metalloendopeptidase OMA1, mitochondrial | 85396 2  | OMA1; YKR087 C  | metabolic process | membrane; mitochondrial | catalytic activity; metal ion binding | 0.389 0.551 1.42 |
| P48176 | Uncharacterized mitochondrial carrier YFR045W  | 85060 6  | YFR045 W; YFR045 W  | metabolic process; transport | membrane; mitochondrial | structural molecule activity; transporter activity | 0.413 0.585 1.42 |
| P63534 | 54s ribosomal protein L40, mitochondrial | 85593 0  | MRPL4 0; YPL173 W  | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | protein binding; structural molecule activity | 0.413 0.585 1.42 |
| Q12186 | 2-kisopropylimidazole synthase 2, mitochondrial | 85427 5  | LEU9; YOR10 RW  | metabolic process | mitochondrial | catalytic activity; protein binding | 2.065 2.932 1.42 |
| Q03798 | Altered inheritance of mitochondria protein 36, mitochondrial | 85518 9  | AIM36; YMK15 7C  | membrane; mitochondrial | 0.438 0.624 1.42 |
| P06168 | Kinetochore ubiquitin ligase, mitochondrial | 85106 9  | ILV5; YLR355 C  | cell organization and biogenesis; metabolic process | mitochondrial | catalytic activity; DNA binding; metal ion binding | 10.78 15.37 1.43 |
| P05626 | ATP synthase subunit 4, mitochondrial | 85602 7  | ATP4; YPL078 | cell organization and biogenesis; metabolic process | mitochondrial | catalytic activity; transporter activity | 2.162 3.084 1.43 |
| Protein | Description | C 1 | C 2 | Process/Transport | Activity |
|---------|-------------|-----|-----|------------------|----------|
| P32795  | Mitochondrial inner membrane + AAA protease supercomplex subunit | YME1 | YPR024 | metabolic process;response to stimulus | membrane/mitochondrion catalytic activity;metal ion binding;nucleotide binding;protein binding | 0.986 | 1.415 | 1.44 |
| P05359  | Glyceroldehyde-3-phosphate dehydrogenase 3 | TDH3 | YGR19 | cell death;metabolic process | cytoplasm;cytosol;membrane/mitochondrion/nucleus catalytic activity | 3.962 | 5.7 | 1.44 |
| P08417  | Fumarate hydratase, mitochondrial | FUM1 | YPL262 | cell organization and biogenesis;metabolic process | cytoplasm;cytosol;mitochondrion;organellar lumen catalytic activity | 5.21 | 7.532 | 1.45 |
| P42940  | Probable electron transfer flavoprotein subunit beta | CPR1 | YGR20 | metabolic process;transport | mitochondrion;organellar lumen | 2.652 | 3.87 | 1.46 |
| P33146  | Heat shock protein 78, mitochondrial | MDH7 | YDR25 | cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus | mitochondrion;organellar lumen catalytic activity;nucleotide binding;protein binding | 3.042 | 4.466 | 1.47 |
| P52893  | Probable alanine aminotransferase, mitochondrial | ALT1 | YLR089 | metabolic process | mitochondrion;organellar lumen catalytic activity | 1.102 | 1.626 | 1.48 |
| P36046  | Mitochondrial intermembrane space import and assembly protein 40 | MIA40 | YKL195 | cellular component movement;metabolic process;response to stimulus;transport | membrane/mitochondrion catalytic activity | 1.555 | 2.3 | 1.48 |
| P37292  | Serine hydroxymethyltransferase, mitochondrial | SHM1 | YBR263 | metabolic process | mitochondrion catalytic activity | 6.565 | 9.723 | 1.48 |
| P33511  | Mitochondrial pyruvate carrier 3 | FMP43 | YPC24 | transport | membrane/mitochondrion transporter activity | 0.778 | 1.154 | 1.48 |
| P25039  | Elongation factor G, mitochondrial | MF1 | YLR069 | cell organization and biogenesis;metabolic process | cytosol;mitochondrion catalytic activity | 0.456 | 0.677 | 1.48 |
| P16387  | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial | PDA1 | YER178 | cell growth;metabolic process | mitochondrion;organellar lumen catalytic activity | 12.46 | 18.51 | 3.149 |
| Q07651  | SUR7 family protein FMP45 | FMP45 | YDL222 | cell differentiation;cell organization and biogenesis | membrane/mitochondrion | 6.017 | 9 | 1.5 |
| P33003  | Succinate:fumarate mitochondrial transporter | SFC1 | YHR095 | metabolic process;transport | membrane/mitochondrion structural molecule activity;transporter activity | 11.91 | 17.95 | 7 | 1.51 |
| Q04728  | Arginine biosynthesis bifunctional protein Arg5, mitochondrial | ARG67 | YMR006 | metabolic process | mitochondrion;organellar lumen catalytic activity | 0.417 | 0.63 | 1.51 |
| P06208-1| 3-hydroxyisovalerate synthase | LEU4 | YNL104 | metabolic process | cytoplasm/mitochondrion catalytic activity;protein binding | 4.878 | 7.377 | 1.51 |
| P38988  | Mitochondrial GTP/GDP carrier protein 1 | GGC1 | YDL198 | cell organization and biogenesis;cellular homeostasis;metabolic process;transport | membrane/mitochondrion structural molecule activity;transporter activity | 3.16 | 4.78 | 1.51 |
| P10662  | 37S ribosomal protein MRP1 | MRP1 | YDR34 | cell organization and biogenesis;metabolic process;response to stimulus | mitochondrion;ribosome antioxidant activity;catalytic activity;metal ion binding;structural molecule activity | 0.995 | 1.512 | 1.52 |
| P03558  | Glyceroldehyde-3-phosphate dehydrogenase 2 | TTD2 | YHR009 | cell death;metabolic process | cytoplasm;cytosol;membrane/mitochondrion/nucleus catalytic activity;protein binding | 2.008 | 3.062 | 1.52 |
| P02117  | Protein AR65.6, mitochondrial | ARG5 | YER069 | metabolic process;regulation of biological process | cytoplasm/mitochondrion;organellar lumen catalytic activity;protein binding | 0.087 | 0.134 | 1.54 |
| P36775  | Len protease homolog, mitochondrial | PM1 | YBL022 | cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus | cytoplasm;mitochondrion;organellar lumen catalytic activity;DNA binding;nucleotide binding;RNA binding | 0.792 | 1.222 | 1.54 |
| P32445  | Single-stranded DNA-binding protein RIM1, mitochondrial | RIM1 | YCR028 | cell organization and biogenesis;metabolic process;regulation of biological process | mitochondrion DNA binding | 1.154 | 1.783 | 1.55 |
| P17298  | Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial | SDH4 | YDR17 | metabolic process;transport | membrane/mitochondrion catalytic activity | 1.154 | 1.783 | 1.55 |
| P39533  | Homocitrate dehydrogenase, | ACO2 | YLR002 | metabolic process | mitochondrion catalytic activity | 0.11 | 0.17 | 1.55 |
| XNL   | Gene Name                                                                 | YNL   | Description                                                                 | Type                          | Activity/Metal Ion Binding                      | Binding                      |
|-------|---------------------------------------------------------------------------|-------|----------------------------------------------------------------------------|-------------------------------|------------------------------------------------|-------------------------------|
| P37922| Mitochondrial Rho GTPase 1 [Saccharomyces cerevisiae 5288c]               | P39754| Probable oxidoreductase A/M17 [Saccharomyces cerevisiae 5288c]              | mitochondrial                 | catalytic activity, metal ion binding, nucleotide binding | 2.981 15.68 1 1.55          |
| P36112| Microsomal complex subunit Mic60 [Saccharomyces cerevisiae 5288c]         | P38756| tRNA thymidylate deaminase 1 [Saccharomyces cerevisiae 5288c]              | mitochondrial                 | catalytic activity, metal ion binding, nucleotide binding | 0.194 0.304 1.57           |
| Q0648 | Mitorex complex component 10 [Saccharomyces cerevisiae 5288c]             |       |                                                                            |                               |                                                |                               |
| P02381| Ribosomal protein VAR1, mitochondrial [Saccharomyces cerevisiae 5288c]    |       |                                                                            |                               |                                                |                               |
| P07256| Cytochrome b-c1 complex subunit 1, mitochondrial [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| P40530| Pyruvate dehydrogenase (acetyltransfering) kinase 1, mitochondrial [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| P38127| Mitochondrial carrier protein Rim2 [Saccharomyces cerevisiae 5288c]       |       |                                                                            |                               |                                                |                               |
| Q12466| Tricarboxylic acid [Saccharomyces cerevisiae 5288c]                      |       |                                                                            |                               |                                                |                               |
| Q08926| ULP1-interacting protein 4 [Saccharomyces cerevisiae 5288c]              |       |                                                                            |                               |                                                |                               |
| Q12283| Malonyl CoA-acyl carrier protein transacylase, mitochondrial [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| Q09297| Mitochondrial 2-oxoacid decarboxylase carrier 2 [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| Q12106| MDM10 complementing protein 2 [Saccharomyces cerevisiae 5288c]           |       |                                                                            |                               |                                                |                               |
| P07342| Acetolactate synthase catalytic subunit, mitochondrial [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| P35982| Isocitrate dehydrogenase [NADP] [Saccharomyces cerevisiae 5288c]         |       |                                                                            |                               |                                                |                               |
| P16451| Pyruvate dehydrogenase complex protein X component, mitochondrial [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| Q03246| 37S ribosomal protein 37S1, mitochondrial [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| P05931| Heat shock protein 40S, mitochondrial [Saccharomyces cerevisiae 5288c]   |       |                                                                            |                               |                                                |                               |
| P39987| Heat shock protein 40S, mitochondrial [Saccharomyces cerevisiae 5288c]   |       |                                                                            |                               |                                                |                               |
| Q03104| Meiotic sister chromatid recombination protein 1 [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| Q39525| 3-oxoacyl (acyl-carrier protein) synthase homolog [Saccharomyces cerevisiae 5288c] |       |                                                                            |                               |                                                |                               |
| Gene ID | Description                                                                 | Organism (strain)                      | Localization                          | Molecular Function                                      | Interactions                | Gene Ontology Terms                                                                 |
|---------|------------------------------------------------------------------------------|----------------------------------------|----------------------------------------|----------------------------------------------------------|-----------------------------|--------------------------------------------------------------------------------------|
| P32843  | Mitochondrial escape protein 2 (S. cerevisiae)                                |                                           |                                        | membrane, mitochondrial                                  |                              | cell organization and biogenesis, metabolic process                                  |
| P0890   | Citrate synthase, mitochondrial                                             | (S. cerevisiae)                        |                                        | cytoplasm, mitochondrial, organelle lumen                | catalytic activity           | metabolic process, transport                                                          |
| P37396  | Uncharacterized protein YNR040W (S. cerevisiae)                              |                                         |                                        | mitochondrion                                            |                              | cell death, metabolic process, transport                                               |
| P18239  | ADP-ATP carrier protein 2 (S. cerevisiae)                                    |                                         |                                        | membrane, mitochondrial                                  | structural molecule activity | ATP binding, RNA binding                                                              |
| P0927   | Threonine dehydratase, mitochondrial                                         | (S. cerevisiae)                        |                                        | cytoplasm, mitochondrial                                 | catalytic activity           | metabolic process, cytoplasm                                                          |
| Q08179  | Mitochondrial distribution and morphology protein 38 (S. cerevisiae)          |                                         |                                        | mitochondrion, organelle lumen                           | catalytic activity           | metal ion binding                                                                     |
| P0685   | Prohibitin-2 (S. cerevisiae)                                                  |                                         |                                        | membrane, mitochondrial                                  | protein binding              | cell organization and biogenesis, metabolic process, regulation of biological process |
| P3140   | Protein RMD9, mitochondrial                                                 | (S. cerevisiae)                        |                                        | membrane, mitochondrial                                  | RNA binding                  | membrane, mitochondrial                                                              |
| Q0784   | Monothiol glutaredoxin-5, mitochondrial                                       | (S. cerevisiae)                        |                                        | mitochondrion, organelle lumen                           | catalytic activity           | metal ion binding                                                                     |
| Q0560   | Protein isd1 (S. cerevisiae)                                                  |                                         |                                        | mitochondrion, organelle lumen                           | catalytic activity           | protein binding, protein binding                                                      |
| P3598   | Succinyl-CoA ligase (ADP-forming) subunit alpha, mitochondrial                | (S. cerevisiae)                        |                                        | cytoplasm, mitochondrial                                 | catalytic activity, nucleotide binding | cytoplasm, mitochondrial                                                             |
| P11325  | Leucine--tRNA ligase, mitochondrial                                          | (S. cerevisiae)                        |                                        | cytoplasm, mitochondrion, organelle lumen                | catalytic activity           | cytoplasm, mitochondrial                                                             |
| P3326   | Uncharacterized protein YGR266W (S. cerevisiae)                               |                                         |                                        | membrane, mitochondrion                                  |                              | cytoplasm, mitochondrial                                                             |
| P3220   | Mitochondrial import inner membrane translocase subunit TIM2 (S. cerevisiae)  |                                         |                                        | membrane, mitochondrion                                  | protein binding              | cell organization and biogenesis, transport                                           |
| P34227  | Mitochondrial prexiredoxin PRX1 (S. cerevisiae)                              |                                         |                                        | mitochondrion                                            | antioxidant activity         | cell organization and biogenesis, transport                                           |
| P00410  | Cystochrome c oxidase subunit 2 (S. cerevisiae)                               |                                         |                                        | membrane, mitochondrion                                  | catalytic activity, metal ion binding | catalytic activity, protein binding, protein binding, transport                      |
| Q0204   | S45 ribosomal protein L13, mitochondrial                                     | (S. cerevisiae)                        |                                        | mitochondrion, ribosome                                  | structural molecule activity | cell organization and biogenesis, metabolic process                                  |
| P36147  | Presequence translocated-associated motor subunit pam1 (S. cerevisiae)       |                                         |                                        | membrane, mitochondrion                                  |                              | transport                                                                            |
| P32473  | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial              | (S. cerevisiae)                        |                                        | mitochondrion, organelle lumen                           | catalytic activity           | metabolic process                                                                     |
| P38077  | ATP synthase subunit gamma, mitochondrial                                      | (S. cerevisiae)                        |                                        | membrane, mitochondrion                                  | catalytic activity, transporter activity | metabolic process, transport                                                         |
| Q2298   | Uncharacterized ABC transporter ATP-binding protein YDR061W (S. cerevisiae)    |                                         |                                        | mitochondrial                                            | catalytic activity, nucleotide binding | mitochondrial, organelle lumen                                                      |
| P12695  | Dihydrolipoamide-residue acetyltransferase component of pyruvate dehydrogenase | (S. cerevisiae)                        |                                        | mitochondrial, organelle lumen                           | catalytic activity           | metabolic process                                                                     |
| P3092   | ATP synthase subunit d, mitochondrial                                        | (S. cerevisiae)                        |                                        | membrane, mitochondrion                                  | catalytic activity, transporter activity | metabolic process, transport                                                         |
| Q06VH5  | MICOS complex subunit Mic10 (S. cerevisiae)                                  |                                         |                                        | membrane, mitochondrion                                  |                              | cell organization and biogenesis                                                       |
| Q06493 | LETM1 domain-containing protein YLH47, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85624 | 3 | YLM47; YPR125 W | cell organization and biogenesis;transport | membrane/mitochondrion | 0.487 | 0.887 | 1.82 |
| P47127 | Altered inheritance of mitochondria protein 24, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85354 | 3 | AIM24; YIR080 C | cell organization and biogenesis | mitochondrion | 2.857 | 5.21 | 1.82 |
| Q04548 | Fatty aldehyde dehydrogenase HFD1 [OS=Saccharomyces cerevisiae S288c] | 85513 | 7 | HFD1; YMR111 C | metabolic process | endoplasmic reticulum;endosome;membrane/mitochondrion | 1.783 | 3.262 | 1.83 |
| P08607 | cytochrome b-c1 complex subunit Rieske, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85668 | 9 | RIF1; YEL024 W | metabolic process;transport | membrane/mitochondrion | catalytic activity;metal ion binding;transporter activity | 11.11 | 20.54 | 1.85 |
| P40185 | Protein mmm1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85476 | 0 | MMF1; YIL051 C | cell organization and biogenesis;metabolic process | mitochondrion;organelle lumen | 2.162 | 4.012 | 1.86 |
| P40053 | Altered inheritance of mitochondria protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85681 | 3 | AIP9; YER080 B | catalytic activity | mitochondrion | 1.798 | 3.348 | 1.86 |
| P87897 | Protein phosphatase 2C homolog 7, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85647 | 5 | PTC7; YHR078 W | catalytic activity | mitochondrion | RNA binding | 0.369 | 0.688 | 1.86 |
| P88188 | Meiotic sister chromatid recombination protein 6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85453 | 6 | MRC6; YOR135 C | metabolic process | mitochondrial;organelle lumen | catalytic activity | 0.506 | 0.945 | 1.87 |
| P32796-1 | Carotene D-acetyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85496 | 5 | CAT2; YML042 W | metabolic process;transport | membrane/mitochondrion | catalytic activity | 5.749 | 10.83 | 1.88 |
| P07257 | Cytochrome b-c1 complex subunit 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85632 | 1 | GCV1; YPR191 W | metabolic process;transport | membrane/mitochondrion | catalytic activity;metal ion binding;protein binding;transporter activity | 25.49 | 48.23 | 1.89 |
| P07275 | Delta-1-pyruvly-5-carboxylate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85643 | 2 | PUT2; YHR037 W | metabolic process | membrane/mitochondrion;organelle lumen | catalytic activity | 5.136 | 9.723 | 1.89 |
| P36151 | Uncharacterized protein YKR070W [OS=Saccharomyces cerevisiae S288c] | 85394 | 4 | YKR070 W; YKR070 W | metabolic process | mitochondrion | 0.438 | 0.833 | 1.90 |
| P23833 | Protein SCD1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85232 | 5 | SCO1; YBR037 C | cell organization and biogenesis;cellular homeostasis;response to stimuli;transport | membrane/mitochondrion | antioxidant activity;catalytic activity;metal ion binding | 0.468 | 0.896 | 1.91 |
| P07000 | External NADH:ubiquinone oxidoreductase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85147 | 4 | NDE2; YDL085 W | metabolic process | mitochondrion | catalytic activity;nucleotide binding | 3.299 | 6.356 | 1.93 |
| P38172 | MIOREX complex component 3 [OS=Saccharomyces cerevisiae S288c] | 85218 | 1 | YBL095 W; YBL095 W | metabolic process | mitochondrial | catalytic activity;nucleotide binding | 0.501 | 0.968 | 1.93 |
| P32860 | NFIU-like protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85382 | 6 | NFIU2; YKL050 C | cell organization and biogenesis;cellular homeostasis;metabolic process | mitochondrion;organelle lumen | metal ion binding | 1.371 | 2.652 | 1.93 |
| Q00711 | Succinate dehydrogenase [ubiquitously] flavoprotein subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85370 | 9 | SDH1; YKL148 C | metabolic process;transport | membrane/mitochondrion | catalytic activity;nucleotide binding;protein binding;transporter activity | 9.578 | 18.61 | 1.94 |
| P45921 | glutathione reductase [OS=Saccharomyces cerevisiae S288c] | 85601 | 4 | GSR1; YPL291 W | cellular homeostasis;metabolic process;regulation of biological process;response to stimulus | cytoplasm;cytosol;mitochondrion;nucleus | antioxidant activity;catalytic activity;metal ion binding | 0.334 | 0.655 | 1.96 |
| P23841 | mitochondrial phosphate carrier protein [OS=Saccharomyces cerevisiae S288c] | 85354 | 0 | MIR1; YIR077 C | metabolic process;transport | membrane/mitochondrion | protein binding;structural molecule binding | 13.67 | 26.82 | 1.96 |
| P46013 | NAD-dependent malic enzyme, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85383 | 9 | MACE1; YKL029 C | metabolic process | mitochondrion;organelle lumen | catalytic activity;metal ion binding;nucleotide binding | 1.512 | 2.981 | 1.97 |
| P32317 | Protein AF62 [OS=Saccharomyces cerevisiae S288c] | 85669 | 8 | AF61; YEL052 W | cell organization and biogenesis;metabolic process;response to stimuli;transport | membrane/mitochondrion | catalytic activity;nucleotide binding | 0.585 | 1.154 | 1.97 |
| P36525 | 5S ribosomal protein L24, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85533 | 1 | MRP12 4; YMR191 W | cell organization and biogenesis;metabolic process | mitochondrion;ribosome | RNA binding;structural molecule activity | 0.585 | 1.154 | 1.97 |
| P47052 | succinate dehydrogenase | 85340 | 5 | YIL045 | metabolic process;transport | membrane/mitochondrion | catalytic activity | 1.88 | 3.739 | 1.99 |
| Protein | GO Terms | Description | Gene ID | GO Terms | Description | Gene ID | GO Terms | Description | Gene ID | GO Terms | Description |
|---------|----------|-------------|---------|----------|-------------|---------|----------|-------------|---------|----------|-------------|
| TOM71   | transport| protein binding, transport activity | P38825  | transport| membrane, mitochondrial | P00427  | transport| membrane, mitochondrial | P38285  | transport| membrane, mitochondrial |
| Cytochrome c oxidase protein 20 | cell organization and biogenesis; metabolic process | Q04935  | cell organization and biogenesis; metabolic process | Q38071  | cell organization and biogenesis; cellular homeostasis | Q12171  | cell organization and biogenesis; cellular homeostasis | P36206  | cell organization and biogenesis; cellular homeostasis | P39925  | cell organization and biogenesis; metabolic process | P20967  | cell organization and biogenesis; cellular homeostasis | P00427  | cell organization and biogenesis; cellular homeostasis | P3874  | cell organization and biogenesis; cellular homeostasis |
| Protein FMP52 | endoplasmic reticulum; membrane, mitochondrial | P40008  | endoplasmic reticulum; membrane, mitochondrial | P42606  | endoplasmic reticulum; membrane, mitochondrial | P09925  | endoplasmic reticulum; membrane, mitochondrial | P3874  | endoplasmic reticulum; membrane, mitochondrial | P40008  | endoplasmic reticulum; membrane, mitochondrial | P09925  | endoplasmic reticulum; membrane, mitochondrial | P3874  | endoplasmic reticulum; membrane, mitochondrial |
| Mitochondrial respiratory chain complexes assembly protein AFG3 | cell organization and biogenesis; metabolic process | P20967  | cell organization and biogenesis; cellular homeostasis | P00427  | cell organization and biogenesis; cellular homeostasis | P3874  | cell organization and biogenesis; cellular homeostasis | P40008  | cell organization and biogenesis; cellular homeostasis | P09925  | cell organization and biogenesis; cellular homeostasis | P3874  | cell organization and biogenesis; cellular homeostasis | P40008  | cell organization and biogenesis; cellular homeostasis | P09925  | cell organization and biogenesis; cellular homeostasis |
| Q04472 | Mitochondrial inner membrane + AAA protease supercomplex subunit MGR3 [OS=Saccharomyces cerevisiae S288c] | 85514 | 2 | MGR3; YMR111 C | metabolic process | membrane; mitochondrion | protein binding | 0.15 | 0.322 | 2.15 |
| P09624 | Dihydrolipoyl dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85052 | 7 | LPD1; YFG018 C | cellular homeostasis; metabolic process; regulation of biological process | mitochondrion; organelle lumen | catalytic activity; nucleotide binding | 23.11 | 9 | 49.80 | 2 | 2.15 |
| P42847 | 37S ribosomal protein S18, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85541 | 0 | RPS51 B; YNL306 W | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | RNA binding; structural molecule activity | 0.155 | 0.334 | 2.15 |
| P14693 | Sorting assembly machinery 35 kDa subunit [OS=Saccharomyces cerevisiae S288c] | 85648 | 3 | SAM35; YHR08 C | cell organization and biogenesis; transport | membrane; mitochondrion | protein binding | 0.155 | 0.334 | 2.15 |
| P32799 | Cytochrome c oxidase subunit 6A, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85268 | 4 | COX13; YGL191 W | cell organization and biogenesis; metabolic process; regulation of biological process | membrane; mitochondrion | catalytic activity; enzyme regulator activity; transporter activity | 0.995 | 7 | 2.162 | 2.17 |
| P40961 | prohibitin 1 [OS=Saccharomyces cerevisiae S288c] | 85303 | 3 | PHB1; YKL187 C; YKL187 C | cell organization and biogenesis; transport | membrane; mitochondrion | protein binding | 2.36 | 3.158 | 2.19 |
| P34231 | Uncharacterized protein YKL187C [OS=Saccharomyces cerevisiae S288c] | 85364 | 8 | FAT1; YKL187 C; YKL187 C | cell organization and biogenesis; transport | membrane; mitochondrion | catalytic activity; metal ion binding | 0.194 | 0.425 | 2.19 |
| P01976 | ADP-ribose pyrophosphatase [OS=Saccharomyces cerevisiae S288c] | 85240 | 8 | YSA1; YBR111 C | metabolic process | cytoplasm; mitochondrion; nucleus | catalytic activity; metal ion binding | 0.194 | 0.425 | 2.19 |
| P02010 | 37S ribosomal protein S10, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85161 | 1 | RSM10; YDR041 W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | structural molecule activity | 0.194 | 0.425 | 2.19 |
| P34222 | Peptidyl-tRNA hydrolase 2 [OS=Saccharomyces cerevisiae S288c] | 85222 | 3 | PTH2; YBL057 C | regulation of biological process | cytoplasm; cytosol; membrane; mitochondrion | catalytic activity; protein binding | 0.194 | 0.425 | 2.19 |
| P07251 | ATP synthase subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85217 | 7 | ATP1; YBL099 W | metabolic process; transport | cytoplasm; membrane; mitochondrion | catalytic activity; nucleotide binding; transporter activity | 26.82 | 6 | 58.94 | 8 | 2.20 |
| P00830 | ATP synthase subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85358 | 5 | ATP2; YHR121 W | metabolic process; transport | cytoplasm; membrane; mitochondrion | catalytic activity; nucleotide binding; protein binding; transporter activity | 24.11 | 9 | 53.11 | 7 | 2.20 |
| P04165 | NAD(P)H-dehydrogenase [OS=Saccharomyces cerevisiae S288c] | 85552 | 1 | YNL200 C; YNL200 C | metabolic process | cytoplasm; mitochondrion | catalytic activity; metal ion binding; nucleotide binding | 0.212 | 0.468 | 2.21 |
| P34224 | Uncharacterized protein YBL059W [OS=Saccharomyces cerevisiae S288c] | 85222 | 1 | YBL059 W; YBL059 W | membrane | membrane; mitochondrion | 0.212 | 0.468 | 2.21 |
| P47015 | Altered inheritance of mitochondria protein 23, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85331 | 0 | AIM23; YIL131 C | metabolic process | mitochondrion | RNA binding | 0.222 | 0.492 | 2.22 |
| P32792 | UFD704 protein YSC83 [OS=Saccharomyces cerevisiae S288c] | 85641 | 0 | YSC83; YMR017 W | membrane; mitochondrion | 0.233 | 0.52 | 2.23 |
| P54857 | Lipase 2 [OS=Saccharomyces cerevisiae S288c] | 85162 | 8 | TGL12; YDR058 C | metabolic process; transport | mitochondrion | catalytic activity | 0.233 | 0.52 | 2.23 |
| P41832 | peptidyl-prolyl cis-trans isomerase [OS=Saccharomyces cerevisiae S288c] | 85173 | 3 | CPR1; YDR15 SC | cell differentiation; cell organization and biogenesis; metabolic process; regulation of biological process; transport | cytoplasm; mitochondrion; nucleus | catalytic activity; RNA binding | 0.233 | 0.52 | 2.23 |
| P19955 | 37S ribosomal protein YMR31, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85061 | 0 | YMR31 ; YFR049 W | cell organization and biogenesis; metabolic process | mitochondrion; ribosome | catalytic activity; protein binding; structural molecule activity | 1.154 | 2.504 | 2.25 |
| P40502 | Altered inheritance of mitochondria protein 19, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85472 | 2 | AIM19; YIL087 C | membrane; mitochondrion | 0.259 | 0.585 | 2.26 |
| P04341 | Mitochondrial respiratory chain complexes assembly protein YTA12 [OS=Saccharomyces cerevisiae S288c] | 85511 | 4 | YTA12; YMR08 RC | cell organization and biogenesis; metabolic process; response to stimulus; transport | cytoplasm; membrane; mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | 1.276 | 1.284 | 2.26 |
| P40513 | Mitochondrial acidic protein MAM33 [OS=Saccharomyces cerevisiae S288c] | 85474 | 0 | MAM3 3; YIL070 W | metabolic process; regulation of biological process | mitochondrion; organelle lumen | transmembrane regulator activity | 1.61 | 3.642 | 2.26 |
| P39522 | Dihydroxy-acid dehydratase, | 85347 | 7 | ILV8; | metabolic process | mitochondrion | catalytic | 9.723 | 22.10 | 2.27 |
| Entry | Symbol | Gene Name | Function | Subcellular Location | Taxonomy | Activity | Metal Ion Binding |
|-------|--------|-----------|----------|---------------------|----------|----------|------------------|
| 20141 | Aconitate hydratase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 1 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 20162 | Alcohol dehydrogenase 3, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 2 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | 1.637 | 3.833 | 2.34 |
| 20178 | Mitochondrial genome maintenance protein | [OS=Saccharomyces cerevisiae S288c] 3 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 201622 | Ferrochelatase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 4 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | 3.806 | 9 | 2.36 |
| 201941 | Aconitate hydratase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 5 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 201862 | 375 ribosomal protein MRFP13, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 6 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 201840 | Mitochondrial outer membrane protein | [OS=Saccharomyces cerevisiae S288c] 7 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 201755 | Malate dehydrogenase, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 8 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 201897 | Mitochondrial import inner membrane translocase subunit tim23 | [OS=Saccharomyces cerevisiae S288c] 9 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 201762 | Dynamin-like GTase Mgm1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 10 | cell organization and biogenesis | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200424 | Cytochrome c oxidase subunit 5a, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 11 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200363 | 545 ribosomal protein L12, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 12 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200321 | monocytoplasmic | [OS=Saccharomyces cerevisiae S288c] 13 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200713 | Mitochondrial import receptor submit TOM70 | [OS=Saccharomyces cerevisiae S288c] 14 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200042 | Nuclear migration protein Num1 | [OS=Saccharomyces cerevisiae S288c] 15 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200415 | External NADH-ubiquinone oxidoreductase 1, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 16 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 2003120 | 375 ribosomal protein S9, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 17 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200742 | Alcohol dehydrogenase 3, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 18 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200600 | NADH-cytochrome c reductase 2 | [OS=Saccharomyces cerevisiae S288c] 19 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 2006485 | Autophagy-related protein 33 | [OS=Saccharomyces cerevisiae S288c] 20 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 200727 | Mitochondrial import inner membrane translocase subunit Tim10 | [OS=Saccharomyces cerevisiae S288c] 21 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
| 2009726 | Glycine cleavage system II protein, mitochondrial | [OS=Saccharomyces cerevisiae S288c] 22 | catalytic activity | membrane;mitochondrion;organelle lumen | catalytic activity | DNA binding |
Peptidyl-prolyl cis-trans isomerase C, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85489 7 CPR3; YML072W cell death, metabolic process mitochondrion, organelle lumen catalytic activity 0.848 2.415 2.85
Mitochondrial inner membrane ATP-AAA protease supercomplex subunit MGP1 [OS=Saccharomyces cerevisiae S288c] 85031 3 MGR1; YCL044C metabolic process membrane, mitochondrion protein binding 0.425 1.219 2.87
N-acetyl-phosphodiethanolamine-hydrolyzing phospholipase D, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85600 1 FMP30; YPL103C metabolic process membrane, mitochondrion catalytic activity, metal ion binding 0.194 0.557 2.87
Probable 2-methylisocitrinate dehydratase [OS=Saccharomyces cerevisiae S288c] 85610 8 PDH1; YPR002W metabolic process cytoplasm, membrane, mitochondrion catalytic activity 4.623 13.33 2.88
Long chain fatty-acid-CoA ligase 1 [OS=Saccharomyces cerevisiae S288c] 85449 5 FAA1; YOR31C metabolic process, transport endoplasmic reticulum, membrane, mitochondrion catalytic activity, nucleotide binding 3.725 10.74 3 2.88
Rotenone-insensitive NADH ubiquinone oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85491 9 ND1; YML123C metabolic process, regulation of biological process membrane, mitochondrion, organelle lumen catalytic activity, nucleotide binding 12.73 8 37.56 6 2.95
Protein CBP3, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85588 6 CBP3; YPL215W cell organization and biogenesis, regulation of biological process membrane, mitochondrion, ribosome 0.557 1.649 2.96
Homosorbitate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85471 4 LYS12; YIL094C metabolic process mitochondrion catalytic activity, metal ion binding, nucleotide binding 2.162 6.499 3.01
Sphingolipid long chain base-responsive protein PIL1 [OS=Saccharomyces cerevisiae S288c] 85297 7 PIL1; YGR086C cell organization and biogenesis, regulation of biological process, response to stimulus, transport cytoplasm, membrane, mitochondrion protein binding 24.80 9 75.27 3.03
Cytochrome c homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85440 7 MTR1; YDR232W metabolic process, regulation of biological process, transport membrane, mitochondrion, organelle lumen enzyme regulator activity, nucleotide binding, protein binding 0.274 0.833 3.04
Alanine-glyoxylate aminotransferase 1 [OS=Saccharomyces cerevisiae S288c] 85051 4 AGX1; YFL030W metabolic process cytosol, mitochondrion catalytic activity 0.616 1.873 3.04
Dihydroxypropylene residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85172 6 KGD2; YDR148C cell organization and biogenesis, metabolic process mitochondrion catalytic activity, protein binding 4.484 13.92 5 3.11
Elongation factor Tu, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85435 9 TUF1; YOR187W cell organization and biogenesis, metabolic process mitochondrion catalytic activity, nucleotide binding, RNA binding 6.017 19.30 9 3.21
MIOREX complex component 2 [OS=Saccharomyces cerevisiae S288c] 85099 7 YLR290C; YCO11; YJR290C metabolic process mitochondrion catalytic activity 0.54 1.738 3.22
Cytochrome c oxidase subunit 4, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85268 8 COX4; YGL187C cell organization and biogenesis, metabolic process, transport membrane, mitochondrion catalytic activity, metal ion binding, transporter activity 4.337 14.19 9 3.27
Protein SUR7 [OS=Saccharomyces cerevisiae S288c] 85495 3 SUR7; YML052W cell differentiation, transport membrane, mitochondrion 0.585 1.929 3.30
Mitochondrial outer membrane protein OM14 [OS=Saccharomyces cerevisiae S288c] 85253 1 OM14; YBR230C transport membrane, mitochondrion 2.728 9 3.30
Mitochondrial import receptor subunit Tom20 [OS=Saccharomyces cerevisiae S288c] 85297 3 TOM20; YGR082W cell organization and biogenesis, transport membrane, mitochondrion protein binding, transporter activity 0.425 1.424 3.35
Altered inheritance of mitochondria protein 32 [OS=Saccharomyces cerevisiae S288c] 85495 5 AIM32; YML050W cell differentiation, transport membrane, mitochondrion 0.11 0.369 3.35
Malate dehydrogenase, peroxisomal [OS=Saccharomyces cerevisiae S288c] 85148 1 MDH1; YGL078C metabolic process organelle lumen catalytic activity, nucleotide binding, RNA binding 2.162 7.254 3.36
Cytochrome c oxidase subunit 1 [OS=Saccharomyces cerevisiae S288c] 85459 8 COX1; QOD045 metabolic process, transport membrane, mitochondrion catalytic activity, metal ion binding, transporter activity 0.468 1.61 3.44
Glutaryl-β-NAD (Gln) amidotransferase subunit A, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85533 8 HER2; YMR293C cell organization and biogenesis, metabolic process mitochondrion catalytic activity, nucleotide binding 0.166 0.585 3.52
Acetyl-CoA hydrolase [OS=Saccharomyces cerevisiae S288c] 85226 6 ACH1; YBL015W metabolic process cytoplasm, cytosol, mitochondrion catalytic activity 8.326 29.53 9 3.55
Potassium-activated aldehyde dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] 85455 6 ALD4; YOR374W metabolic process mitochondrion, organelle lumen catalytic activity 19.62 70.96 9 3.62
| Gene ID | Description | Process/Type | Location | Activity | Categories |
|--------|-------------|--------------|----------|----------|-------------|
| P00128 | Cytochrome b-c1 complex subunit 7 | cell organization and biogenesis; metabolic process | membrane; mitochondrial | catalytic activity; transporter activity | [OS=Saccharomyces cerevisiae S288c] |
| P23459 | Flavoprotein-like protein YCP4 | metabolic process; regulation of biological process | cytoplasm; membrane; mitochondrial | catalytic activity; nucleotide binding; protein binding | [OS=Saccharomyces cerevisiae S288c] |
| P25605 | Acetolactate synthase small subunit, mitochondrial | metabolic process; regulation of biological process | mitochondrion | catalytic activity; enzyme regulator activity | [OS=Saccharomyces cerevisiae S288c] |
| P32891 | D-lactate dehydrogenase (cytochrome) 1, mitochondrial | metabolic process; transport | membrane; mitochondrial | catalytic activity; nucleotide binding | [OS=Saccharomyces cerevisiae S288c] |
| Q07914 | Mitochondrial import inner membrane translocase subunit TIM14 | regulation of biological process; transport | membrane; mitochondrial | enzyme regulator activity; protein binding; transporter activity | [OS=Saccharomyces cerevisiae S288c] |
| Q21265 | ATP synthase subunit delta, mitochondrial | metabolic process; transport | membrane; mitochondrial | catalytic activity; transporter activity | [OS=Saccharomyces cerevisiae S288c] |
| P19546 | Isocitrate dehydrogenase (NADP), mitochondrial | metabolic process | mitochondrion | catalytic activity; metal ion binding; nucleotide binding; protein binding | [OS=Saccharomyces cerevisiae S288c] |
| P19546 | Hexaprenyl-pyrophosphate synthase, mitochondrial | metabolic process | membrane; mitochondrial | catalytic activity; metal ion binding; protein binding | [OS=Saccharomyces cerevisiae S288c] |
| Q06510 | Lysophosphatidylcholine acyltransferase | cell organization and biogenesis; metabolic process | membrane; mitochondrial | catalytic activity | [OS=Saccharomyces cerevisiae S288c] |
| P38885 | Altered inheritance of mitochondria protein 46, mitochondrial | - | mitochondrial | catalytic activity | [OS=Saccharomyces cerevisiae S288c] |
| P00128 | S45 ribosomal protein L35, mitochondrial | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | [OS=Saccharomyces cerevisiae S288c] |
| P23536 | Threonine–tRNA ligase, mitochondrial | metabolic process | cytoplasm; mitochondrial; organelle lumen | catalytic activity; nucleotide binding; RNA binding | [OS=Saccharomyces cerevisiae S288c] |
| P81444 | ATP synthase subunit e, mitochondrial | cell organization and biogenesis; metabolic process; transport | membrane; mitochondrial | catalytic activity; structural molecule activity; transporter activity | [OS=Saccharomyces cerevisiae S288c] |
| P23536 | S45 ribosomal protein L8, mitochondrial | cell organization and biogenesis; metabolic process | mitochondrial; ribosome | structural molecule activity | [OS=Saccharomyces cerevisiae S288c] |
| P16547 | Mitochondrial outer membrane protein OM45 | - | membrane; mitochondrial | - | [OS=Saccharomyces cerevisiae S288c] |
### Supplemental Table S15. The relative concentrations of proteins in mitochondria purified from ups2Δ cells cultured with or without LCA.

Mitochondria were purified from ups2Δ cells recovered on day 7 of cell culturing with or without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between specified datasets. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Accession | Description                  | Entrez Gene ID | Gene ID | Biological Process                                                                 | Cellular Component                  | Molecular Function                                | emP AI ups2 | emP AI ups2 / LCA | Ratio ups2 / ups2 + LCA |
|-----------|------------------------------|----------------|---------|-----------------------------------------------------------------------------------|-------------------------------------|---------------------------------------------------|------------|-------------------|------------------------|
| Q0163     | 375 ribosomal protein S23, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85274          | 8       | RNS2; YGL129 C                                                                       | mitochondrion; ribosome            | catalytic activity; nucleotide binding; RNA binding; structural molecule activity | 0.751      | 0.131             | 0.18                   |
| P00447    | Superoxide dismutase [Mn], mitochondrial [OS=Saccharomyces cerevisiae S288c] | 8569            | 9       | SOD2; YHR008 C                                                                       | mitochondrion; mitochondrial       | metabolic process; response to stimulus           | 1.894      | 0.701             | 0.37                   |
| Q12031    | Mitochondrial 2-methylisocitrinate lyase [OS=Saccharomyces cerevisiae S288c] | 85611          | 4       | ICL2; YPR006 C                                                                       | mitochondrion; mitochondrial       | metabolic process                                | 1.976      | 0.833             | 0.42                   |
| P40035    | Mitochondrial phosphate carrier protein 2 [OS=Saccharomyces cerevisiae S288c] | 85677          | 9       | PCC2; YER053 C                                                                       | membrane; mitochondrion            | structural molecule activity; transporter activity | 1.976      | 0.833             | 0.42                   |
| Q09297    | Mitochondrial 2-oxocarboxylate carrier 2 [OS=Saccharomyces cerevisiae S288c] | 85439          | 7       | ODC2; YDR222 C                                                                       | membrane; mitochondrion            | metabolic process; transport                      | 0.778      | 0.334             | 0.43                   |
| P12904    | 545 ribosomal protein L6, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85655          | 2       | MRPL6; YHR147 C                                                                     | mitochondrion; mitochondrial       | RNA binding; structural molecule activity         | 0.778      | 0.334             | 0.43                   |
| P17558    | 375 ribosomal protein PET123, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85432          | 9       | PET123; YDR158 W                                                                    | mitochondrion; mitochondrial       | cell organization and biogenesis; metabolite process | 0.668      | 0.292             | 0.44                   |
| P49334    | Mitochondrial import receptor subunit tom22 [OS=Saccharomyces cerevisiae S288c] | 85559          | 8       | TOM22; YNL131 W                                                                      | membrane; mitochondrion            | protein binding; transport                        | 0.668      | 0.292             | 0.44                   |
| P33759    | 375 ribosomal protein S5, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85555          | 3       | MRPS5; YBR215 W                                                                      | mitochondrion; ribosome            | RNA binding; structural molecule activity         | 0.385      | 0.259             | 0.44                   |
| P54857    | Ipase 2 [OS=Saccharomyces cerevisiae S288c] | 85162          | 8       | TGL2; YDR058 C                                                                       | mitochondrion                     | catalytic activity                                | 0.52       | 0.233             | 0.45                   |
| Q06892    | NADH kinase PO55, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85591          | 3       | PO55; YPL188 W                                                                       | mitochondrial; mitochondrial       | metabolic process; response to stimulus           | 0.52       | 0.233             | 0.45                   |
| P61441    | Putative redox protein fmp46, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85392          | 3       | FMP46; YDR049 C                                                                      | mitochondrial                     | catalytic activity; protein binding                | 0.52       | 0.233             | 0.45                   |
| P04542    | Cytochrome c oxidase assembly factor 1 [OS=Saccharomyces cerevisiae S288c] | 85464          | 9       | COA1; YIL157 C                                                                       | membrane; mitochondrion            | protein binding                                   | 0.52       | 0.233             | 0.45                   |
| P34224    | Uncharacterized protein YBL059W [OS=Saccharomyces cerevisiae S288c] | 85222          | 1       | YBL059 W                                                                           | membrane; mitochondrion            | catalytic activity; metabolic activity            | 0.468      | 0.212             | 0.45                   |
| P65166    | 545 ribosomal protein L3, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85503          | 9       | MRPL3; YMR024 W                                                                      | mitochondrion; nucleus; ribosome   | catalytic activity; RNA binding; structural molecule activity | 0.374      | 0.172             | 0.46                   |
| P32611    | 545 ribosomal protein RML2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85666          | 9       | RML2; YEL050 C                                                                       | mitochondrion; ribosome            | catalytic activity; RNA binding; structural molecule activity | 0.389      | 0.179             | 0.46                   |
| Q12298    | uncharacterized ABC transporter ATP-binding protein YDR0616W [OS=Saccharomyces cerevisiae S288c] | 85163          | 3       | YDR0616W; YDR0617W                                                                 | mitochondrial                     | catalytic activity; nucleotide binding            | 0.266      | 0.125             | 0.47                   |
| P81122    | 3-methyl-1-oxobutanoate hydroxymethyltransferase [OS=Saccharomyces cerevisiae S288c] | 85247          | 4       | ECM31; YBR176 W                                                                      | mitochondrial                     | metabolic process                                | 0.259      | 0.122             | 0.47                   |
| P65628    | 545 ribosomal protein L17, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85464          | 9       | MRPL1; YNL252 C                                                                     | mitochondrial; ribosome            | structural molecule activity                      | 0.233      | 0.11              | 0.47                   |
| P51998    | 545 ribosomal protein yml8, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85498          | 3       | YML16; YML02 W                                                                       | mitochondrial; ribosome            | RNA binding; structural molecule activity         | 0.245      | 0.116             | 0.47                   |
| Q06610    | Lysophosphatidylcholine acyltransferase [OS=Saccharomyces cerevisiae S288c] | 85626          | 2       | TAZ1; YPR140                                                                        | mitochondrial; ribosome            | catalytic activity                                | 0.194      | 0.093             | 0.48                   |
| Entry | Description                                                                 | W   | Process/Transport | ProteinMotif | Localization                      | MolecularFunction                  | GO Terms                                                                 | GeneID |
|-------|------------------------------------------------------------------------------|-----|-------------------|--------------|-----------------------------------|------------------------------------|--------------------------------------------------------------------------------|--------|
| P03879| Intron-encoded RNA maturase b4                                               | 85458| 2                 | B4; Q0120    | metabolic process                  | membrane/mitochondrion            | catalytic activity, RNA binding                                             |        |
| P40309| K(t)(H+) antipporter 1                                                       | 85383| 1                 | KHA1; YNL094C| transport                          | endoplasmic reticulum, Golgi, membrane, mitochondrion | transporter activity                                                        |        |
| P25338| Translation initiation factor IF-2, mitochondrial                           | 85413| 5                 | IFM1; YDL023W| cell organization and biogenesis; metabolic process | mitochondrion; nucleus             | catalytic activity, nucleotide binding, RNA binding                         |        |
| P09440| C-1-tetrahydrofolate-synthase, mitochondrial                               | 85237| 8                 | M51; YBR084W | metabolic process                  | cytosol/mitochondrion              | catalytic activity, nucleotide binding                                      |        |
| Q03976| 37S ribosomal protein 524, mitochondrial                                     | 85175| 5                 | RMD24; YDR17SC| cell organization and biogenesis; metabolic process | mitochondrion; ribosome            | structural molecule activity                                                |        |
| P39369| Sorting assembly machinery 50 kDa subunit                                    | 85570| 5                 | SAM50; YNL026W| cell organization and biogenesis; transport | membrane/mitochondrion             | protein binding, transporter activity                                        |        |
| P27929| 37S ribosomal protein NAA9, mitochondrial                                    | 85558| 5                 | NAM9; YNL137C| cell organization and biogenesis; metabolic process; regulation of biological process | mitochondrion; ribosome            | RNA binding, structural molecule activity                                     |        |
| P40364| Mitochondrial peculiar membrane protein 1                                    | 85337| 9                 | MPM1; YL066C | mitochondrial                      | membrane/mitochondrion             | 1.512; 0.848; 0.56                                                            |        |
| P51739| Aspartate–RNA ligase, mitochondrial                                          | 85600| 0                 | MS01; YPL104W| metabolic process                  | cytoplasm/mitochondrion, organelle lumen | catalytic activity, nucleotide binding                                       |        |
| P21449| ATP synthase subunit e, mitochondrial                                         | 85192| 2                 | YMR11; YDR322C-A| cell organization and biogenesis; metabolic process| membrane/mitochondrion             | catalytic activity, structural molecule, transporter activity                |        |
| P18898| Mitochondrial GTP/KDP carrier protein 1                                      | 85132| 9                 | GGC1; YDL198C| cell organization and biogenesis;cellular homeostasis;metabolic process;transport | membrane/mitochondrion             | structural molecule activity, transporter activity                           |        |
| P49767| Flavohemoprotein                                                              | 85314| 9                 | YHB1; YDR234W| metabolic process;response to stimulus | cytoplasm/mitochondrion; nucleos;organelle lumen | catalytic activity, metal ion binding, protein binding                      |        |
| P04840| Mitochondrial outer membrane protein pent 1                                  | 85666| 0                 | POR1; YNL05C | cell death; cell organization and biogenesis;cellular homeostasis;regulation of biological process;transport | cytoplasm; membrane/mitochondrion | transporter activity, mitochondrial protein binding                          |        |
| P40015| Aminomethyltransferase, mitochondrial                                         | 85158| 5                 | GCV1; YDR019C| metabolic process                  | mitochondrial                      | catalytic activity, protein binding                                         |        |
| P00431| cytochrome c peroxidase, mitochondrial                                         | 85394| 0                 | CPP1; YKR066C| metabolic process;response to stimulus | mitochondrial;organelle lumen      | antioxidant activity, catalytic activity, metal ion binding, protein binding |        |
| P09492| Triosephosphate isomerase                                                     | 85162| 0                 | TPH1; YDR05OC| metabolic process                  | cytoplasm; cytosol; membrane, mitochondrion | catalytic activity                                                          |        |
| P40084| Cytochrome c oxidase assembly protein cox1                                    | 85888| 4                 | COX15; YER141 | cell organization and biogenesis;cellular homeostasis;metabolic process;transport | mitochondrion                      | catalytic activity, transporter activity                                     |        |
| P43616| Cys-Gly metalloepitidase dgl                                                   | 85060| 5                 | DUG1; YFR044C| metabolic process                  | cytoplasm/mitochondrion, ribosome  | catalytic activity, metal ion binding                                       |        |
| P46325| S45 ribosomal protein L24, mitochondrial                                       | 85231| 1                 | MRPL2; YMR193W| cell organization and biogenesis; metabolic process | mitochondrion; ribosome            | RNA binding, structural molecule activity                                   |        |
| Q09190| Very-long-chain enoyl-CoA reductase                                            | 85154| 7                 | TSC13; YDL015C| metabolic process                  | cytoplasm; endoplasmic reticulum, membrane, mitochondrion | catalytic activity, protein binding                                         |        |
| P36151| Uncharacterized protein YKR070W                                               | 85394| 4                 | YKR070W; YKR070W| metabolic process                  | mitochondrial                      | 0.438; 0.274; 0.63                                                            |        |
| Q12480| Probable electron transfer flavoprotein subunit alpha, mitochondrial         | 85611| 2                 | AIM45; YPR004C| metabolic process;transport        | mitochondrial;organelle lumen     | catalytic activity, nucleotide binding                                      |        |
| P32795| Mitochondrial inner membrane l-AAA protease supercomplex subunit YME1        | 85613| 5                 | YME1; YBR024W| metabolic process;response to stimulus;transport | membrane/mitochondrion             | catalytic activity, metal ion binding, protein binding                      |        |
| P88910| 10 kDa heat shock protein, mitochondrial                                       | 85418| 5                 | HSP10; YDR02OC| cell organization and biogenesis; metabolic process;response to stimulus;transport | cytoplasm/mitochondrion,organelle lumen | metal ion binding, nucleotide binding, protein binding                       |        |
| identifier | description | gene | protein | cellular component | biological process | molecular function | subcellular localization | GO ID | PMID |
|------------|-------------|------|---------|-------------------|-------------------|--------------------|------------------------|-------|------|
| Q03430     | 375 ribosomal protein RSM28, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85210 | YSR28; YDR49 | mitochondrion; ribosome | structural molecular activity | 0.35 | 0.222 | 0.63 |
| P12902     | 375 ribosomal protein MRP4, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85638 | YMR4; YHL004 | mitochondrion; ribosome | structural molecular activity | 0.334 | 0.322 | 0.63 |
| P32473     | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85252 | YPRB1; YBR221 | mitochondrial; organelle lumen | catalytic activity | 5.158 | 3.281 | 0.64 |
| P4783      | D-arabinono-1,4-lactone oxidase [OS=Saccharomyces cerevisiae S288c] | 85488 | ALO1; YML08 | membrane; mitochondrion | catalytic activity; nucleotide binding | 2.981 | 1.929 | 0.65 |
| P33110     | ATP-dependent permease MDL1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85088 | MDL1; YLR188 | membrane; mitochondrion | catalytic activity; nucleotide binding; transporter activity | 0.528 | 0.354 | 0.67 |
| P39952     | Mitochondrial inner membrane protein OXAA1 [OS=Saccharomyces cerevisiae S288c] | 85689 | OXAA1; YER154 | membrane; mitochondrion | transporter activity | 3.217 | 2.162 | 0.67 |
| P38325     | Mitochondrial outer membrane protein OXM14 [OS=Saccharomyces cerevisiae S288c] | 85253 | OXM14; YBR230 | membrane; mitochondrion | transporter activity | 6.197 | 4.179 | 0.67 |
| P00950     | Phosphoglycerate mutase 1 [OS=Saccharomyces cerevisiae S288c] | 85370 | GPM1; YKL152 | cytoplasm; cytosol; membrane; mitochondrial | catalytic activity | 4.412 | 2.981 | 0.68 |
| P00640     | Phosphoglycerate kinase [OS=Saccharomyces cerevisiae S288c] | 85037 | PKA1; YCR012 | cytoplasm; membrane; mitochondrial | catalytic activity; nucleotide binding; protein binding | 4.484 | 3.062 | 0.68 |
| P00358     | glycerol-dehyde-3-phosphate dehydrogenase 2 [OS=Saccharomyces cerevisiae S288c] | 85366 | TDH2; YIR009 | cytoplasm; cytosol; mitochondrion | catalytic activity; nucleotide binding; protein binding | 9.391 | 6.038 | 0.69 |
| P34321     | Succinate dehydrogenase [ubiquitine] cytochrome b subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85371 | SDH3; YKL141 | membrane; mitochondrion | catalytic activity; metal ion binding | 0.931 | 0.638 | 0.69 |
| P32332     | Mitochondrial oxaloacetate transport protein [OS=Saccharomyces cerevisiae S288c] | 85373 | OAC1; YKL120 | membrane; mitochondrion | structural molecular activity; transporter activity | 2.594 | 1.783 | 0.69 |
| P39726     | Glycine cleavage system H protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85125 | GCVC3; YAL044 | mitochondrion | catalytic activity | 2.594 | 1.783 | 0.69 |
| P25719     | Peptide-prollys-trans-sorusamase C, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85489 | CPR3; YLM07 | mitochondrion; organelle lumen | catalytic activity | 0.848 | 0.585 | 0.69 |
| Q01879     | Mitochondrial distribution and morphology protein 38 [OS=Saccharomyces cerevisiae S288c] | 85413 | MDM3; YOL027 | membrane; mitochondrion | catalytic activity | 5.31 | 3.732 | 0.70 |
| P46637     | Potassium-activated aldehyde dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85455 | ALD4; YDR37 | mitochondrion; organelle lumen | catalytic activity | 19.62 | 13.84 | 0.71 |
| P65314     | 454 ribosomal protein L40, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85593 | MRPL40 | mitochondrion; ribosome | protein binding; structural molecular activity | 0.585 | 0.413 | 0.71 |
| P85618     | Uncharacterized protein YNR040W [OS=Saccharomyces cerevisiae S288c] | 85577 | YNR04 0W; YNR04 0W | mitochondrion | structural molecular activity | 0.551 | 0.389 | 0.71 |
| P49095     | Glycine dehydrogenase (Decarboxylating), mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85522 | GCV2; YMR18 | cytosol; mitochondrial | catalytic activity | 1.096 | 0.778 | 0.71 |
| P17505     | Malate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85377 | MDH1; YKL085 | mitochondrion; organelle lumen | catalytic activity; protein binding; RNA binding | 32.40 | 32.40 | 0.71 |
| P11914     | Mitochondrial-processing peptidase subunit alpha [OS=Saccharomyces cerevisiae S288c] | 85641 | MAS2; YHR02 4C | membrane; mitochondrion; organelle lumen | catalytic activity; metal ion binding; protein binding | 0.445 | 0.318 | 0.71 |
| Q04772     | Sensitive to high expression protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85200 | SHX9; YDR39 | cell organization and biogenesis | membrane; mitochondrion | 0.374 | 0.269 | 0.72 |
| P32286     | DHM2 inner membrane protein MIM1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85438 | MIM1; YDR21 | mitochondrion; organelle lumen | catalytic activity; nucleotide binding; protein binding | 0.389 | 0.28 | 0.72 |
| P40185     | Protein mmf1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85476 | MFM1; YIO51 | mitochondrion; organelle lumen | catalytic activity | 2.981 | 2.162 | 0.73 |
| P32191     | Glycerol-3-phosphate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85465 | GUT2; YIL155 | mitochondrion; organelle lumen | catalytic activity | 4.289 | 3.14 | 0.73 |
| P54003     | Protein SUR7 [OS=Saccharomyces cerevisiae S288c] | 85495 | SUR7; YLM05 | mitochondrion; organelle lumen | catalytic activity | 1.154 | 0.848 | 0.73 |
| P32860     | Nfu1-like protein, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85382 | NZF1; YKL040 | mitochondrion; organelle lumen | metal ion binding | 1.054 | 0.778 | 0.74 |
| GO028 | Mitochondrial 2-oxoisocarboxylic acid carrier | C | homeostasis/metabolic process | membrane/mitochondrion | structural molecule activity;transporter activity | 6.743 | 4.995 | 0.74 |
| P00410 | Cytochrome c oxidase subunit 2 | 85462 | 2 | COR2; Q0921 | metabolic process;transport | membrane/mitochondrion | catalytic activity;metal ion binding;protein binding;transporter activity | 2.162 | 1.61 | 0.74 |
| P03798 | Altered inheritance of mitochondria protein 36, mitochondrial | 85118 | 9 | AIM36; YMR157C | | membrane/mitochondrion | | 0.833 | 0.624 | 0.75 |
| P06168 | Ketol-acid reductoisomerase, mitochondrial | 85106 | 9 | ILV5; YLR355C | cell organization and biogenesis;metabolic process | mitochondrial | catalytic activity;DNA binding;metal ion binding | 8.211 | 6.197 | 0.75 |
| P37293 | N-terminal acetyltransferase 2 | 85305 | 0 | NAT2; YGR142C | | cytoplasm;mitochondrion | catalytic activity | 0.73 | 0.551 | 0.75 |
| P28241 | Isocitrate dehydrogenase (NAD) subunit 2, mitochondrial | 85430 | 3 | IDH1; YOR136W | metabolic process | mitochondrial;organelle lumen | catalytic activity;metal ion binding;nucleotide binding;protein binding;RNA binding | 4.179 | 3.16 | 0.76 |
| P31598 | Succinyl-CoA ligase (ADP-forming) subunit alpha, mitochondrial | 85411 | 0 | LSC1; YDR142W | metabolic process | cytosol;mitochondrion | catalytic activity;nucleotide binding | 7.859 | 5.952 | 0.76 |
| P40047 | Aldehyde dehydrogenase 9, mitochondrial | 85680 | 4 | AUD5; YER073W | metabolic process | mitochondrial;organelle lumen | catalytic activity | 1.106 | 0.84 | 0.76 |
| P36101 | RNA binding carbamoylase/deaminase dehydrogenase 2 | 85384 | 1 | YCL021Y; YKL027W; YLL027W | metabolic process | cytosol;membrane;mitochondrion | catalytic activity;nucleotide binding | 0.616 | 0.468 | 0.76 |
| P36230 | Phosphatidate cytidylyltransferase, mitochondrial | 85293 | 7 | TAM41; YGR048W | metabolic process | membrane;mitochondrion;organelle lumen | catalytic activity | 0.532 | 0.407 | 0.77 |
| P50910 | Heat shock protein SSC1, mitochondrial | 85350 | 3 | SSC1; YJR045C | cell organization and biogenesis;metabolic process;regulation of biological process;transport | membrane;mitochondrion;nucleus;organelle lumen | catalytic activity;enzyme regulator activity;DNA binding;protein binding | 25.10 | 19.20 | 9 | 0.77 |
| P32331 | Carrier protein YMC1, mitochondrial | 85617 | 1 | YMC1; YPR058W | metabolic process;transport | membrane;mitochondrion | structural molecule activity;transporter activity | 1.254 | 0.968 | 0.77 |
| P47127 | Altered inheritance of mitochondria protein 24, mitochondrial | 85354 | 3 | AIM24; YIR080B | cell organization and biogenesis | mitochondrial | | 1.807 | 1.395 | 0.77 |
| P38071 | Enoyl-(acyl-carrier protein) reductase (NADPH, B-specific), mitochondrial | 85231 | 4 | ETR1; YBR026C | metabolic process | mitochondrial;organelle lumen | catalytic activity;DNA binding;metal ion binding | 5.579 | 4.337 | 0.78 |
| P38127 | mitochondrial carrier protein RIM2 | 85249 | 1 | RIM2; YBR192W | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | structural molecule activity;transporter activity | 0.995 | 0.778 | 0.78 |
| P39522 | Dehydroxy-acid dehydratase, mitochondrial | 85347 | 1 | ILV3; YIR016C | metabolic process | mitochondrial | catalytic activity;metal ion binding | 6.565 | 5.136 | 0.78 |
| Q04458 | Fatty alcohol dehydrogenase FHD1 | 85513 | 7 | FHD1; YMR11OC | metabolic process | endoplasmic reticulum;endosome;membrane;mitochondrion | catalytic activity | 2.594 | 2.03 | 0.78 |
| P16387 | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial | 85682 | 5 | PAO1; YER178W | cell growth;metabolic process | mitochondrial;organelle lumen | catalytic activity | 11.49 | 6 | 9 | 0.78 |
| P40495 | Homoserine dehydrogenase, mitochondrial | 85471 | 4 | LYS12; YLR094C | metabolic process | mitochondrial | catalytic activity;metal ion binding;nucleotide binding | 4.623 | 3.642 | 0.79 |
| Q08968 | UPT0061 protein | 85587 | 9 | FMP40; YPL222W | | mitochondrial | protein binding | 0.823 | 0.65 | 0.79 |
| P00359 | Glyceroldehyde-3-phosphate dehydrogenase 3 | 85130 | 6 | TDM5; YGR192C | cell death;metabolic process | cytosol;membrane;mitochondrion | catalytic activity;nucleotide binding;RNA binding | 6.406 | 5.062 | 0.79 |
| P43567 | alanine-glyoxylate aminotransferase 1 | 85051 | 4 | AGX1; YFL030W | metabolic process | cytosol;mitochondrion | catalytic activity | 0.778 | 0.616 | 0.79 |
Acetolactate synthase small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85094  8  ILV6; YCL009 C  metabolic process;regulation of biological process mitochondrion catalytic activity;enzyme regulator activity  1.336  1.069  0.80

D-lactate dehydrogenase (cytochrome) 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85137  6  OLD2; YDL178 W  metabolic process mitochondrion;organellar lumen catalytic activity;protein binding  0.562  0.45  0.80

mitochondrial import inner membrane translocase subunit TIM54 [OS=Saccharomyces cerevisiae S288c]  85339  2  TIM54; YIL054 W  cell organization and biogenesis;transport cytosol;membrane;mitochondrion transporter activity  0.54  0.433  0.80

Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85453  8  CIR2; YDR353 W  metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding;protein binding  2.481  2.014  0.81

cytochrome b-6 complex subunit Raske, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85668  9  RIP1; YEL024 W  metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding;transporter activity  16.78  3.14  0.81

375 ribosomal protein S35, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85307  5  MPF53; YGR165 C  cell organization and biogenesis;membrane;mitochondrion ribosome structural molecular activity  0.905  0.738  0.82

heat shock protein 60, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85096  5  HIS560; YUR259 C  cell organization and biogenesis;metabolic process mitochondrion;ribosome catalytic activity  5.404  4.52  0.84

Mitochondrial fusion and transport protein Ugo1 [OS=Saccharomyces cerevisiae S288c]  85208  1  UGO1; YDR470 OC  cell organization and biogenesis;membrane;mitochondrion protein binding;structural molecular activity  1.031  0.859  0.83

Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85655  3  LAT1; YNL071 W  metabolic process mitochondrion;organellar lumen catalytic activity  5.404  4.52  0.84

uncharacterized mitochondrial membrane protein FMP10 [OS=Saccharomyces cerevisiae S288c]  85683  1  FMP10; YER182 W  membrane;mitochondrion catalytic activity  2.36  1.97  0.84

glyceroldehyde-3-phosphate dehydrogenase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85339  5  TDP1; YIL052 W  metabolic process cytoplasm;cytosol;membrane;mitochondrion catalytic activity;protein binding  1.462  1.228  0.84

Probable 2-methylisocitrade dehydratase [OS=Saccharomyces cerevisiae S288c]  85610  8  PDH1; YPR002 W  metabolic process cytoplasm;membrane;mitochondrion catalytic activity  7.058  5.978  0.85

putative cysteine synthase [OS=Saccharomyces cerevisiae S288c]  85289  5  YGR017W; YGR01 W  metabolic process mitochondrion catalytic activity  1.154  0.978  0.85

Mitochondrial import receptor subunit TDH70 [OS=Saccharomyces cerevisiae S288c]  85600  2  TDH70; YNL121 C  cell organization and biogenesis;transport membrane;mitochondrion protein binding;transporter activity  3.125  2.665  0.85

ATPase expression protein 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85352  5  AEP2; YMR282 C  metabolic process;regulation of biological process mitochondrial RNA binding  0.585  0.506  0.86

ATP-dependent RNA helicase Mss51, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85177  6  M5511; YDR19 W  metabolic process;regulation of biological process mitochondrial;organellar lumen catalytic activity;protein binding;RNA binding  0.585  0.506  0.86

Sucinate/fumarate mitochondrial transporter [OS=Saccharomyces cerevisiae S288c]  83355  8  SFC1; YJR095 W  metabolic process;transport membrane;mitochondrion structural molecular activity;transporter activity  9  7.799  0.87

Citrate synthase 3, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85610  7  CSI3; YPR001 W  metabolic process mitochondrion catalytic activity  1.783  1.555  0.87

Homoaconitate, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85382  0  LYS4; YDR234 W  metabolic process mitochondrion catalytic activity;metal ion binding;protein binding  0.73  0.638  0.87

Carotene D-acetyltransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85496  5  CAT2; YML04 W  metabolic process;transport membrane;mitochondrion catalytic activity  6.552  5.74  0.88

Long-chain fatty-acid-CoA ligase 2 [OS=Saccharomyces cerevisiae S288c]  85673  4  FAA2; YER015 W  metabolic process;transport cytoplasm;mitochondrion catalytic activity;protein binding  0.802  0.708  0.88

Lpn protease homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85325  9  PHM4; YBL022 C  cell organization and biogenesis;membrane;mitochondrion catalytic activity;DNA binding;RNA binding  0.402  0.359  0.89

Aconitate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85101  3  ACO1; HXX304 W  cell organization and biogenesis;membrane;mitochondrion catalytic activity;DNA binding;metal ion binding  18.16  9.16  3.90

External NADH-ubiquinone oxidoreductase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85147  4  NDE2; YDL085 W  metabolic process mitochondrion catalytic activity;protein binding  4.012  3.642  0.91

Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c]  85643  2  PUT2; YHR037 W  metabolic process mitochondrion;organellar lumen catalytic activity  2.765  2.511  0.91
catalytic activity

P37292
Serine hydroxymethyltransferase, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85256 5 SHM1; YBR263 W
metabolic process
mitochondrion
catalytic activity
3.037 2.765 0.91

P08890
citrate synthase, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85757 2 CIT1; YNR001C
metabolic process;transport
cytoplasm;mitochondrion;organelle lumen
catalytic activity
14.08 6 12.89 5 0.92

P53312
Succinyl-CoA ligase (ADP-forming) subunit beta, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85315 9 LSC2; YGR242C
metabolic process
mitochondrion
catalytic activity
5.898 5.404 0.92

P31216
acetyl-CoA hydratase (OS=Saccharomyces cerevisiae S288c)
85236 6 ACH1; YBL015 W
metabolic process
cytoplasm;cytosol;mitochondrion
catalytic activity
8.326 7.697 0.92

P07342
Acetolactate synthase catalytic subunit, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85513 5 ILV2; YMR10 W
metabolic process
mitochondrion
catalytic activity
3.642 3.375 0.93

Q00711
Succinate dehydrogenase [ubiquinone] flavoprotein subunit
mitochondrial (OS=Saccharomyces cerevisiae S288c)
85370 9 SDH1; YKL148C
metabolic process;transport
membrane;mitochondrion
catalytic activity
5.381 5.032 0.94

P20967
2-oxoglutarate dehydrogenase, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85468 1 KG01; YIL125 C
metabolic process
cytoplasm;mitochondrion;organelle lumen
catalytic activity
9.908 9.444 0.95

P16547
Mitochondrial outer membrane protein OM45 (OS=Saccharomyces cerevisiae S288c)
85467 0 OM45; YIL136 W
membrane;mitochondrion
330.1 31 330.1 31 1.00

P08308
ATP synthase subunit beta, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85358 5 ATP2; YJR121 W
metabolic process;transport
cytoplasm;membrane;mitochondrion
catalytic activity
28.12 3 26.12 3 1.00

Q12230
Sphingolipid long chain base-responsive protein LSP1 (OS=Saccharomyces cerevisiae S288c)
85610 3 LSP1; YPL004 C
regulation of biological process;response to stimulus;transport
cytoplasm;membrane;mitochondrion
62.09 6 62.09 6 1.00

P23641
mitochondrial phosphate carrier protein (OS=Saccharomyces cerevisiae S288c)
85354 0 MR11; YMR077 C
metabolic process;transport
membrane;mitochondrion
catalytic activity
13.67 8 13.67 8 1.00

P18077
ATP synthase subunit gamma, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85232 7 ATP3; YBR039 W
metabolic process;transport
membrane;mitochondrion
catalytic activity
12.68 9 12.68 9 1.00

P07143
Cytochrome c1, heme protein, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85423 1 CYT1; YDR065 W
metabolic process;transport
cytoplasm;membrane;mitochondrion
metal ion binding
16.01 3 16.01 3 1.00

P06208-1
2-keto-3-(pyridin-2-yl)malate synthase (OS=Saccharomyces cerevisiae S288c)
85661 9 LEU4; YNL104 C
metabolic process
cytoplasm;mitochondrion
catalytic activity;protein binding
3.125 3.125 1.00

P25349
Flavoprotein-like protein YCP4 (OS=Saccharomyces cerevisiae S288c)
85036 0 YCP4; YCR004 C
metabolic process;regulation of biological process
cytoplasm;membrane;mitochondrion
catalytic activity;protein binding;transporter activity
9 9 1.00

P36860
NADH-cytochrome b5 reductase 1 (OS=Saccharomyces cerevisiae S288c)
85370 7 MCR1; YKL150 W
metabolic process;response to stimulus
membrane;mitochondrion
catalytic activity;protein binding
10.28 8 10.28 8 1.00

P47052
succinate dehydrogenase [ubiquinone] flavoprotein subunit 2, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85340 5 YL045 W; YL045 W
metabolic process;transport
membrane;mitochondrion
catalytic activity;protein binding
2.065 2.065 1.00

P28834
Isocitrate dehydrogenase (NAD) subunit 1, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85669 1 IDH1; YNL037 C
metabolic process;transport
cytoplasm;mitochondrion;organelle lumen
catalytic activity
3.833 3.833 1.00

P15108
ATP-dependent molecular chaperone HSC82 (OS=Saccharomyces cerevisiae S288c)
85252 4 HSC82; YMR18 W
cell organization and biogenesis;metabolic process;response to stimulus
cytoplasm;membrane;mitochondrion
catalytic activity
1.081 1.081 1.00

P04710
ADP,ATP carrier protein 1 (OS=Saccharomyces cerevisiae S288c)
85507 8 AAC1; YMR058C
metabolic process;transport
cytoplasm;membrane;mitochondrion
structural molecule activity;transporter activity
6.848 6.848 1.00

P07246
Alcohol dehydrogenase 3, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85510 7 ADH3; YMR088C
metabolic process
mitochondrion;organelle lumen
catalytic activity
4.179 4.179 1.00

P36046
Mitochondrial intermembrane space import and assembly protein 40 (OS=Saccharomyces cerevisiae S288c)
85363 9 MIA40; YKL195 W
cellular component movement;metabolic process;response to stimulus
membrane;mitochondrion
catalytic activity
2.03 2.03 1.00

P04377
cytochrome c oxidase subunit 4, mitochondrial (OS=Saccharomyces cerevisiae S288c)
85268 8 COX4; YGL187C
cell organization and biogenesis;metabolic process;transport
membrane;mitochondrion
catalytic activity
9 9 1.00

P40012
protoporphyrinogen oxidase (OS=Saccharomyces cerevisiae S288c)
85673 3 HEM14; YER014 W
metabolic process
membrane;mitochondrion
catalytic activity
0.947 0.947 1.00

P40961
prohibitin 1 (OS=Saccharomyces cerevisiae S288c)
85303 3 PHB1; YOR132C
cell organization and biogenesis;metabolic process;regulation of biological function
membrane;mitochondrion
protein binding
2.793 2.793 1.00
| P0088 | Stationary phase gene 1 protein [OS=Saccharomyces cerevisiae S288c] | 85315 | 1 | SPG1; YER233C | endoplasmic reticulum;membrane;mitochondrion | 62.09 | 62.09 | 1.00 |
| P3140 | Protein RMD9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85277 | 1 | RMD9; YGL107C | cell differentiation;metabolic process;regulation of biological process | membrane;mitochondrion | RNA binding | 0.585 | 0.585 | 1.00 |
| P23180 | Probable oxidoreductase AIM17 [OS=Saccharomyces cerevisiae S288c] | 85636 | 5 | AIM17; YHL021C | cell organization and biogenesis;metabolic process | mitochondrial | catalytic activity;metal ion binding | 1.818 | 1.818 | 1.00 |
| P34271 | Respiratory supercomplex factor 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85375 | 2 | RCF2; YMR021W | cell organization and biogenesis | membrane;mitochondrion | 7.111 | 7.111 | 1.00 |
| Q2289 | mitochondrial carnitine carrier [OS=Saccharomyces cerevisiae S288c] | 85426 | 7 | CRC1; YDR100C | metabolic process;transport | membrane;mitochondrion | structural molecule activity;transporter activity | 1.683 | 1.683 | 1.00 |
| P08466 | mitochondrial nuclease [OS=Saccharomyces cerevisiae S288c] | 85322 | 2 | NUC1; YIL208W | cell death;metabolic process | membrane;mitochondrion;nucleus | catalytic activity;metal ion binding | 1.976 | 1.976 | 1.00 |
| P38826 | NADH-cytochrome b5 reductase 1 [OS=Saccharomyces cerevisiae S288c] | 85476 | 8 | CBR1; YIL043C | metabolic process | endoplasmic reticulum;membrane;mitochondrion | catalytic activity | 1.61 | 1.61 | 1.00 |
| P23574 | Cysteine desulfurase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85094 | 3 | NFS1; YCL017C | cell organization and biogenesis;cellular homeostasis;metabolic process | mitochondrial;nucleus | catalytic activity;metal ion binding;protein binding | 0.817 | 0.817 | 1.00 |
| Q08245 | protein ZEO1 [OS=Saccharomyces cerevisiae S288c] | 85404 | 0 | ZEO1; YOL109W | cell organization and biogenesis | membrane;mitochondrion | protein binding | 5.31 | 5.31 | 1.00 |
| P40416 | Iron-sulfur clusters transporter AMT1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85334 | 7 | AMT1; YMR30C | cellular homeostasis;metabolic process;transport | membrane;mitochondrion | catalytic activity;nucleotide binding;transporter activity | 0.546 | 0.546 | 1.00 |
| P38298 | Mitochondrial pressequence protease [OS=Saccharomyces cerevisiae S288c] | 85204 | 1 | CYM1; YHR433C | metabolic process | mitochondrial | catalytic activity;metal ion binding | 0.297 | 0.297 | 1.00 |
| Q04093 | LET1 domain-containing protein YLH47, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85624 | 3 | YLH47; YHR125W | cell organization and biogenesis;transport | membrane;mitochondrion | 0.61 | 0.61 | 1.00 |
| P40508 | Uncharacterized protein YIL077C [OS=Saccharomyces cerevisiae S288c] | 85473 | 7 | YIL077C; YIL077C | metabolic process;transport | mitochondrial | 0.896 | 0.896 | 1.00 |
| P40008 | Protein FMFS2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85672 | 1 | FMP52; YER004W | endoplasmic reticulum;membrane;mitochondrion | catalytic activity | 1.371 | 1.371 | 1.00 |
| P32317 | Protein AFG1 [OS=Saccharomyces cerevisiae S288c] | 85665 | 8 | AFG1; YEL052W | cell organization and biogenesis;metabolic process;response to stimulus;transport | membrane;mitochondrion | catalytic activity;metal ion binding | 0.585 | 0.585 | 1.00 |
| P28072 | Protein SCD2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85231 | 2 | SCD2; YBR204W | cell organization and biogenesis;metabolic process;transport | membrane;mitochondrion | antioxidant activity;metal ion binding | 0.73 | 0.73 | 1.00 |
| P28377 | Protein MSP2 [OS=Saccharomyces cerevisiae S288c] | 85291 | 5 | MSP1; YGR027W | cell organization and biogenesis;metabolic process;regulation of biological process;response to stimulus;transport | membrane;mitochondrion;nucleus | catalytic activity;nucleotide binding;protein binding;RNA binding | 0.778 | 0.778 | 1.00 |
| P10507 | mitochondrial processing peptidase subunit beta [OS=Saccharomyces cerevisiae S288c] | 85086 | 17 | YAB1; YLR163C | metabolic process;transport | mitochondrial;organelle lumen | catalytic activity;metal ion binding;protein binding | 0.616 | 0.616 | 1.00 |
| P2453 | Protein ATP11, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85540 | 1 | ATP11; YNL315C | cell organization and biogenesis | mitochondrial | protein binding | 0.585 | 0.585 | 1.00 |
| P37928 | Succinate dehydrogenase (ubiquitone) cytochrome b small subunit, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85175 | 8 | SDH4; YDR174W | metabolic process;transport | membrane;mitochondrion | catalytic activity;metal ion binding | 1.154 | 1.154 | 1.00 |
| P19595 | 37S ribosomal protein YMR31, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85061 | 0 | YMR31; YFR049W | cell organization and biogenesis;metabolic process | mitochondrial;ribosome | catalytic activity;protein binding;structural molecule activity | 2.594 | 2.594 | 1.00 |
| Q0223 | Altered inheritance of mitochondria protein 39, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85410 | 3 | AIM30; YOL053C | cytosol;membrane;mitochondrion | 0.468 | 0.468 | 1.00 |
| P38523 | Gp10 protein homolog, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85440 | 7 | MG1; YDR232W | metabolic process;regulation of biological process;transport | membrane;mitochondrion;organelle lumen | enzyme regulator activity;metal ion binding | 0.624 | 0.624 | 1.00 |
| Q0067 | ABC1 family protein MCF2 [OS=Saccharomyces cerevisiae S288c] | 85095 | 5 | YLR253W; MCP2; YLR253W | cell organization and biogenesis | membrane;mitochondrion | 0.218 | 0.218 | 1.00 |
| Q09591 | Heat shock protein SSQ1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85108 | 4 | SSQ1; YLR369W | cell organization and biogenesis;metabolic process | mitochondrial;organelle lumen | nucleotide binding;protein binding | 0.413 | 0.413 | 1.00 |
| P36520 | 54S ribosomal protein L10, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.116 | 1.00 |
|--------|------------------------------------------------------------------------------|-------|------|
| P38300 | Inner membrane mitobiosomal receptor MA1, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.259 | 1.00 |
| P24874 | 37S ribosomal protein S18, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.155 | 1.00 |
| P36562 | 54S ribosomal protein L27, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.259 | 1.00 |
| P32463 | Acy carrier protein, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.259 | 1.00 |
| P40165 | NADP(H)-hydrate epimerase (OS=Saccharomyces cerevisiae S288c) | 0.212 | 1.00 |
| P36523 | 54S ribosomal protein L15, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.155 | 1.00 |
| P48526 | Isoleucine--tRNA ligase, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.04 | 1.00 |
| Q00689 | Uncharacterized mitochondrial outer membrane protein YPR098C (OS=Saccharomyces cerevisiae S288c) | 2.162 | 2.162 |
| P33220 | Mitochondrial carrier protein MTM1 (OS=Saccharomyces cerevisiae S288c) | 0.11 | 1.00 |
| P21306 | ATP synthase subunit epsilon, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.778 | 1.00 |
| P38809 | Cytochrome c mitochondrial import factor CYC2 (OS=Saccharomyces cerevisiae S288c) | 0.194 | 1.00 |
| P21771 | 37S ribosomal protein S28, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.129 | 1.00 |
| P40039 | Cytochrome c oxidase polypeptide VIII, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.778 | 1.00 |
| P40623 | Protein ECM18 (OS=Saccharomyces cerevisiae S288c) | 0.08 | 0.08 |
| P50045 | Cytochrome c iso-2 (OS=Saccharomyces cerevisiae S288c) | 0.259 | 1.00 |
| P38797 | Protein phosphatase 2C homolog 7, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.11 | 1.00 |
| P36064 | COX assembly mitochondrial protein (OS=Saccharomyces cerevisiae S288c) | 0.389 | 1.00 |
| Q02863 | Ubiquitin carboxy-terminal hydrolase 16 (OS=Saccharomyces cerevisiae S288c) | 0.072 | 1.00 |
| Q3776 | Uncharacterized protein YBR255C-A (OS=Saccharomyces cerevisiae S288c) | 0.389 | 1.00 |
| P39103 | Cytochrome c oxidase assembly protein COX14 (OS=Saccharomyces cerevisiae S288c) | 0.585 | 1.00 |
| P21687 | 54S ribosomal protein L2, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.11 | 1.00 |
| P36521 | 54S ribosomal protein L11, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.129 | 1.00 |
| P08456 | CDP-diacylglycerol--serine O-phosphotransferase (OS=Saccharomyces cerevisiae S288c) | 0.212 | 1.00 |
| P38120 | 37S ribosomal protein S9, mitochondrial (OS=Saccharomyces cerevisiae S288c) | 0.145 | 1.00 |
| P07259 | Protein URA2 (OS=Saccharomyces cerevisiae S288c) | 0.016 | 1.00 |
| P07251 | ATP-synthase subunit alpha, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85217 | C | ATP1; YBL099 W | metabolic process;transport cytosol;membrane;mitochondrion catalytic activity;protein binding 20.54 4.37 1.07 |
| P40341 | Mitochondrial respiratory chain complexes assembly protein YTA12 [OS=Saccharomyces cerevisiae S288c] | 85511 | 4 | YTA12; YMR088 C | cell organization and biogenesis;metabolic process;response to stimulus;transport cytoplasm;membrane;mitochondrion catalytic activity;protein binding 1.276 1.371 1.07 |
| P40215 | External NADH-ubiquinone oxidoreductase 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85517 | 6 | NDE1; YMR14 SC | metabolic process mitochondrion catalytic activity;protein binding 3.739 4.043 1.08 |
| P32454 | Aminopeptidase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85369 | 9 | APE2; YKL157 W | metabolic process cytoplasm;extracellular;membrane;mitochondrion catalytic activity;protein binding 0.696 0.762 1.09 |
| P07256 | Cytochrome b-c1 complex subunit 1, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85223 | 5 | COR1; YBL045 C | metabolic process;transport membrane;mitochondrion catalytic activity;metal ion binding;protein binding 7.432 8.138 1.10 |
| P02992 | elongation factor Tu, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85433 | 9 | TUF1; YDR18 7W | cell organization and biogenesis;metabolic process mitochondrion catalytic activity;protein binding 4.38 4.878 1.11 |
| P21266 | 2-ketopropylate synthase 2, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85427 | 5 | LEU9; YDR10 8W | metabolic process mitochondrion catalytic activity;protein binding 1.246 1.39 1.12 |
| P36013 | NAD-dependent malic enzyme, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85383 | 9 | MAL1; YKL029 C | metabolic process mitochondrion;organelle lumen catalytic activity;protein binding 0.995 1.113 1.12 |
| P19262 | Dihydropolyamine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85172 | 6 | KG02; YDR14 8C | cell organization and biogenesis;metabolic process mitochondrion catalytic activity;protein binding 3.062 4.489 1.14 |
| P38891 | Branched-chain amino-acid aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85661 | 5 | BAT1; YHR20 8W | metabolic process;regulation of biological process;response to stimulus mitochondrion;organelle lumen catalytic activity 3.806 4.337 1.14 |
| Q12482 | Mitochondrial aspartate-glutamate transporter AGC1 [OS=Saccharomyces cerevisiae S288c] | 85613 | 2 | AGC1; YPR021 W | metabolic process;transport membrane;mitochondrion structural molecule activity;transporter activity 0.407 0.468 1.15 |
| Q00823 | Protein FMP25, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85076 | 6 | FMP25; YLR077 W | cell organization and biogenesis membrane;mitochondrion 0.84 0.968 1.15 |
| P09624 | Dihydroxycoenzyme dehydrogenase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85052 | 7 | LPD01; YFL018 C | cellular homeostasis;metabolic process;regulation of biological process mitochondrion;organelle lumen catalytic activity;protein binding 13.03 5.05 1.16 |
| Q04013 | Citrate/oxoglutarate carrier protein [OS=Saccharomyces cerevisiae S288c] | 85528 | 2 | YHM2; YMR24 1W | cell organization and biogenesis;metabolic process;transport membrane;mitochondrion DNA binding;structural molecule activity;transporter activity 2.981 3.467 1.16 |
| Q07349 | MIOREX complex component 9 [OS=Saccharomyces cerevisiae S288c] | 85513 | 3 | YDL027 C; MKX9; YDL027 W | endoplasmic reticulum;membrane;mitochondrion 1.096 1.276 1.16 |
| P40053 | Altered inheritance of mitochondria protein 9, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85681 | 3 | AIM9; YER080 W | mitochondrial 1.537 1.798 1.17 |
| P16451 | Pyruvate dehydrogenase complex protein X component, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85310 | 7 | PDX1; YGR19 3C | metabolic process mitochondrion;organelle lumen catalytic activity;structural molecule activity 0.978 1.154 1.18 |
| P36112 | MICOS complex subunit Mid60 [OS=Saccharomyces cerevisiae S288c] | 85388 | 6 | FCJ1; MIC60; YKM016 W | cell organization and biogenesis;transport membrane;mitochondrion 11.79 14.08 1.19 |
| P25573 | Mitochondrial inner membrane i-AAA protease supercomplex subunit MGI2 [OS=Saccharomyces cerevisiae S288c] | 85031 | 3 | MGI2; YCL044 C | metabolic process membrane;mitochondrion protein binding 0.859 1.031 1.20 |
| Q07651 | SUR7 family protein FMP45 [OS=Saccharomyces cerevisiae S288c] | 85130 | 4 | FMP45; YDL222 W | cell differentiation;cell organization and biogenesis membrane;mitochondrion 6.017 7.377 1.23 |
| P08417 | fumarate hydratase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85586 | 6 | FUM1; YPL262 C | cell organization and biogenesis;metabolic process cytoplasm;cytosol;mitochondrion;organelle lumen catalytic activity 3.175 3.894 1.23 |
| Q12374 | Nuclear control of ATPase protein 2 [OS=Saccharomyces cerevisiae S288c] | 85627 | 8 | NCA2; YPR155 W | metabolic process membrane;mitochondrion 0.377 0.468 1.24 |
| P58293 | probable alanine aminotransferase, mitochondrial [OS=Saccharomyces cerevisiae S288c] | 85077 | 8 | ALT1; YLR089 C | metabolic process mitochondrion;organelle lumen catalytic activity 0.45 0.562 1.25 |
| P39925 | Mitochondrial respiratory chain complexes assembly protein AFG3 [OS=Saccharomyces cerevisiae S288c] | 85673 | 7 | AFG3; YER017 C | cell organization and biogenesis;metabolic process;response to stimulus;transport membrane;mitochondrion catalytic activity;metal ion binding;protein binding 0.734 0.917 1.25 |
Mitochondrial genome maintenance protein MGM1 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial import inner membrane translocase subunit TIM50 [OS=Saccharomyces cerevisiae S288c]

Prohibitin flavoprotein subunit beta [OS=Saccharomyces cerevisiae S288c]

Cytochrome c iso 3 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial inner membrane i membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial peroxiredoxin PRX1 [OS=Saccharomyces cerevisiae S288c]

Nuclear migration protein NUM1 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial genome maintenance -dependent permease MDL2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

Methyltransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

Prohibitin-2 [OS=Saccharomyces cerevisiae S288c]

Methytransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

Mitochondrial import inner membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial peroxiredoxin PRX1 [OS=Saccharomyces cerevisiae S288c]

Nuclear migration protein NUM1 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial import inner membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial peroxiredoxin PRX1 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial genome maintenance -dependent permease MDL2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

Methyltransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

Mitochondrial import inner membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial peroxiredoxin PRX1 [OS=Saccharomyces cerevisiae S288c]

Nuclear migration protein NUM1 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial import inner membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial peroxiredoxin PRX1 [OS=Saccharomyces cerevisiae S288c]

Nuclear migration protein NUM1 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial genome maintenance -dependent permease MDL2, mitochondrial [OS=Saccharomyces cerevisiae S288c]

Methyltransferase OMS1, mitochondrial [OS=Saccharomyces cerevisiae S288c]

Mitochondrial import inner membrane translocase subunit TIM44 [OS=Saccharomyces cerevisiae S288c]

Mitochondrial peroxiredoxin PRX1 [OS=Saccharomyces cerevisiae S288c]
| P31801 | Succinate dehydrogenase | OS=Saccharomyces cerevisiae S288c | 85068 | SDH2; YLL041 | C | metabolic process, transport | membrane, mitochondrion | catalytic activity, metal ion binding | 16.19 | 1 | 24.80 | 9 | 1.53 |
| P42900 | Sigma-like sequence protein 1, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85083 | CSL3; YLR139 C | | cell organization and biogenesis, metabolic process | membrane, mitochondrion | protein binding | 0.125 | 0.194 | 1.55 |
| Q04728 | Arginine biosynthesis bifunctional protein ArgJ, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85050 | ARG7; YMR066 C | | metabolic process | mitochondrion, organellar lumen | catalytic activity | 0.15 | 0.233 | 1.55 |
| P07236 | Threonine–mRNA ligase, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85364 | MST1; YKL194 C | | metabolic process | cytoplasm, mitochondrion, organellar lumen | catalytic activity, nucleotide binding, RNA binding | 0.15 | 0.233 | 1.55 |
| P41921 | glutathione reductase | OS=Saccharomyces cerevisiae S288c | 85601 | GLR1; YPL091 W | | cellular homeostasis, metabolic process, regulation of biological process, response to stimulus | cytoplasm, cytosol, mitochondrion | antioxidant activity, catalytic activity, nucleotide binding | 0.155 | 0.241 | 1.55 |
| P54115 | Magnesium-activated aldehyde dehydrogenase, cystolic | OS=Saccharomyces cerevisiae S288c | 85604 | ALO6; YPL061 W | | metabolic process, response to stimulus | cytoplasm, cytosol, mitochondrion | catalytic activity | 0.16 | 0.25 | 1.56 |
| P05626 | ATP synthase subunit 4, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85602 | ATP4; YPL078 C | | cell organization and biogenesis, metabolic process, transport | membrane, mitochondrion | catalytic activity, transporter activity | 4.275 | 6.743 | 1.58 |
| P32792 | UTF0744 protein YSC83 | OS=Saccharomyces cerevisiae S288c | 85641 | YSC83; HMR01 | 7W | | membrane, mitochondrion | | 0.233 | 0.369 | 1.58 |
| P12686 | 37S ribosomal protein MRP13, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85297 | MRPL13; YGR084C | | cell organization and biogenesis, metabolic process | mitochondrion, ribosome | structural molecule activity | 0.259 | 0.413 | 1.59 |
| P53889 | uncharacterized mitochondrial hydrodrolase FMP41 | OS=Saccharomyces cerevisiae S288c | 85555 | FMP41; YNL168 C | | metabolic process | mitochondrion | catalytic activity, metal ion binding | 0.311 | 0.501 | 1.61 |
| P18172 | MIOREX complex component 3 | OS=Saccharomyces cerevisiae S288c | 85218 | YBL095 W; YIR043 X; YBL095 W | | | membrane, mitochondrion | | 0.311 | 0.501 | 1.61 |
| P35220 | Mitochondrial import inner membrane translocase subunit TIM21 | OS=Saccharomyces cerevisiae S288c | 85292 | TIM21; YGR031 C | | cell organization and biogenesis, transport | membrane, mitochondrion | protein binding | 0.311 | 0.501 | 1.61 |
| Q02375 | mitochondrial outer mitochondrial transporter 1 | OS=Saccharomyces cerevisiae S288c | 85429 | ORT71; YDR130C | | metabolic process, transport | membrane, mitochondrion | structural molecule activity, transporter activity | 0.334 | 0.54 | 1.62 |
| P16622 | Ferrochelatase, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85434 | HEM15; YDR176W | | metabolic process | membrane, mitochondrion | catalytic activity | 4.926 | 8.006 | 1.63 |
| P23939 | GTP-binding protein Pp7 | OS=Saccharomyces cerevisiae S288c | 85501 | TPT7; YML001 W | | cell communication, cell organization and biogenesis, metabolic process, regulation of biological process, response to stimulus, transport | cytosol, endosome, membrane, mitochondrion, vacuole | catalytic activity, nucleotide binding, protein binding | 0.359 | 0.585 | 1.64 |
| P32340 | Retinosine-insensitive NADH-ubiquinone oxidoreductase, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85491 | ND11; YML112 OC | | metabolic process, regulation of biological process | membrane, mitochondrion, organellar lumen | catalytic activity, nucleotide binding | 10.72 | 17.87 | 4 | 1.67 |
| P23335 | Protein MTSAS1, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85090 | MTSAS1; YLR203 C | | metabolic process, regulation of biological process | membrane, mitochondrion | protein binding, translation regulator activity | 1.154 | 1.929 | 1.67 |
| Q06143 | mitochondrial dicarboxylate transporter | OS=Saccharomyces cerevisiae S288c | 85106 | DCC1; YUR348C | | metabolic process, transport | membrane, mitochondrion | structural molecule activity, transporter activity | 0.551 | 0.931 | 1.69 |
| P18339 | ATP carrier protein 2 | OS=Saccharomyces cerevisiae S288c | 85325 | PEP7; YBL030C | | cell death, metabolic process, transport | membrane, mitochondrion | structural molecule activity, transporter activity | 88.06 | 150.9 | 91 | 1.70 |
| P30713 | Respiratory supercomplex factor 1, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85497 | MCT1; YML034 W | | cell organization and biogenesis | membrane, mitochondrion | | 0.585 | 0.995 | 1.70 |
| P36444 | Mitochondrial import receptor subunit TOM40 | OS=Saccharomyces cerevisiae S288c | 85244 | TOM40; YMR203 W | | transport | cytosol, membrane, mitochondrion | protein binding, transporter activity | 0.688 | 1.154 | 1.73 |
| P32445 | Single-stranded DNA-binding protein RIM1, mitochondrial | OS=Saccharomyces cerevisiae S288c | 85059 | RIM1; YCR028C A | | cell organization and biogenesis, metabolic process, regulation of biological process | mitochondrion | DNA binding | 0.668 | 1.154 | 1.73 |
| P32843 | Mitochondrial escape protein 2 | OS=Saccharomyces cerevisiae S288c | 85354 | YME2; YMR302C | | cell organization and biogenesis, metabolic process | membrane, mitochondrion | nucleotide binding, RNA binding | 2.099 | 3.642 | 1.74 |
| P53326 | Uncharacterized protein YGR176W | OS=Saccharomyces cerevisiae S288c | 85318 | YGR176W; YGR264W | | | membrane, mitochondrion | | 0.299 | 0.52 | 1.74 |
| P38825 | Protein TOM71 | OS=Saccharomyces cerevisiae S288c | 86651 | TOM71; YMR117W | | transport | membrane, mitochondrion | protein binding, transporter activity | 0.343 | 0.604 | 1.76 |
| P36139 | protein PET10 (OS=Saccharomyces cerevisiae S288c) | 65392 | PET10; YKR046C | metabolic process | membrane | 0.122 | 0.995 | 8.16 |
Supplemental Table S16. Proteins that are downregulated by the ups2Δ mutation (but not by the ups1Δ mutation) in cells cultured without LCA are involved in various biological processes.

Mitochondria were purified from cells recovered on day 2, 4 or 7 of cell culturing without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the "Proteome Discoverer" software was used to calculate the relative abundance of mitochondrial proteins between ups2Δ and WT. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Protein | Ratio ups2Δ/WT | Biological process |
|---------|----------------|--------------------|
| Mgi55   | 0.07           | Ribosome assembly (mitochondrial ribosomal protein) |
| Ins3.22 | 0.08           | Unknown            |
| Tim11   | 0.09           | ATP synthesis (a subunit of mitochondrial FIVOS-ATPase) |
| Ybh1   | 0.09           | Stress response (a flavohemoglobin that plays role in oxidative and nitrosative stress responses) |
| Ami2   | 0.11           | mtdNA replication/combinitary repair (mitochondrial DNA-binding protein) |
| Qcr5   | 0.11           | Electron transport chain/aerobic respiration (subunit 8 of ubiquinol-cytochrome-c reductase [Complex III]) |
| Qcr7   | 0.11           | Electron transport chain/aerobic respiration (subunit 7 of ubiquinol-cytochrome-c reductase [Complex III]) |
| Rhl1   | 0.12           | Protein synthesis (mitochondrial ribosome recycling factor) |
| Idp1   | 0.12           | Amino acid synthesis or degradation (mitochondrial NADP-specific isocitrate dehydrogenase) |
| Gcv3   | 0.13           | Metabolism (H subunit of the glycine decarboxylase complex required for folate synthesis) |
| Gcv2   | 0.13           | Metabolism (I subunit of the glycine decarboxylase complex required for folate synthesis) |
| Mrp1   | 0.14           | Protein import (component of the TOM (translocase of outer membrane) complex; responsible for recognition and initial import of preprotein) |
| Mst1   | 0.14           | Cytoskeleton/microtubule (non-prototrophic NTFase of the AAA family ATPase) |
| Mst2   | 0.14           | Lipid metabolism/oxidative stress (NADH-cytochrome b5 reductase involved in ergosteryl biosynthesis) |
| Mss116 | 0.14           | mRNA synthesis/processing (transcription elongation factor required for splicing of introns) |
| Fkh1   | 0.15           | Proteostasis (subset of the proteome complex that stabilizes newly synthesized proteins) |
| Mip48  | 0.15           | Ribosome assembly (mitochondrial ribosomal protein) |
| Aci1   | 0.15           | TCA cycle (aconitate) |
| Mrp4   | 0.15           | TCA cycle (subunit of mitochondrial NADP-c-dependent isocitrate dehydrogenase) |
| Bar1   | 0.16           | Amino acid synthesis or degradation (mitochondrial branched-chain amino acid (BCAA) aminoaminotransferase) |
| Cox4   | 0.16           | Electron transport chain/aerobic respiration (subunit IV of cytochrome c oxidase) |
| Sdh1   | 0.16           | TCA cycle/Electron transport chain/aerobic respiration (tacox). |
| Ptd4   | 0.17           | Lipid metabolism (phosphatidylethanolamine decarboxylase that converts PS to PE) |
| Lsc2   | 0.17           | TCA cycle (β-subunit of succinyl-CoA ligase involved in conversion of succinyl-CoA to succinate) |
| Aci1   | 0.17           | Carbohydrate metabolism (catalyzes CoA-SH transfer from succinyl-CoA to acetate) |
| Aim66  | 0.17           | Unknown            |
| Cpr1   | 0.18           | Proteostasis (catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline) |
| Rim9   | 0.18           | Aerobic respiration (mitochondrial protein required for respiratory growth) |
| Mip4   | 0.18           | Ribosome assembly (mitochondrial ribosomal protein) |
| Fum1   | 0.18           | TCA cycle (fumarase) |
| Mgm10f | 0.19           | mRNA replication/recombination/repair (protein involved in mitochondrial DNA recombinational repair) |
| Aox1   | 0.19           | Amino acid synthesis or degradation (alanine glyoxlate amonitrasferase; catalyzes the synthesis of Alanine from glyoxlate) |
| YlaO5W | 0.19           | Electron transport chain/aerobic respiration (aminosuccinate dehydrogenase; regulates the oxidation of succinate and transfer of electrons to ubiquinone) |
| Spar   | 0.19           | Proteostasis (mitochondrial hsp70-type molecular chaperone; required for assembly of all cellular chaperones into a protein), a step after cluster synthesis) |
| Lus4   | 0.19           | Amino acid synthesis or degradation (2-isopropylmalate synthase, the main isozyme responsible for the first step in the leucine biosynthesis) |
| Cpr2   | 0.20           | Proteostasis (catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline) |
| Mac1   | 0.21           | Carbohydrate metabolism (mitochondrial malate dehydrogenase; catalyzes the decarboxylation of malate to pyruvate, a key intermediate in gluconeogenesis and a precursor for synthesis of amino acids) |
| Maa33  | 0.21           | Protein synthesis (specific translational activator for the mitochondrial CDX1 mRNA) |
| Tbh1   | 0.22           | Carbohydrate metabolism (major D-lactate dehydrogenase oxidizing D-lactate to pyruvate) |
| Ehd3   | 0.22           | Carbohydrate metabolism (3-hydroxyacyl-CoA dehydrogenase) |
| Rnm24  | 0.22           | Ribosome assembly (mitochondrial ribosomal protein) |
| Ahd8h  | 0.23           | Amino acid metabolism (mitochondrial alcohol dehydrogenase isozyme III) |
| Sdh4   | 0.23           | TCA cycle (electron transport chain/aerobic respiration (membrane anchor subunit of succinate dehydrogenase)) |
| Pld4   | 0.23           | Carbohydrate metabolism (E1 alpha subunit of the pyruvate dehydrogenase complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA) |
| Pev1   | 0.24           | Redox homeostasis (mitochondrial pentatricopeptide repeat-containing protein that regulates NADPH- oxidase activity) |
| Akr1   | 0.24           | Amino acid synthesis or degradation (alanine transaminase; involved in alanine biosynthesis and catalysis) |
| Nad4   | 0.25           | Electron transport chain/aerobic respiration (NADH-ubiquinone oxidoreductase; transfers electrons from NADH to ubiquinone in respiratory chain) |
| Cco6   | 0.25           | Electron transport chain/aerobic respiration (Subunit VI of cytochrome c oxidase [Complex IV]) |
| Mnpl2  | 0.25           | Ribosome assembly (mitochondrial ribosomal protein) |
| Mip11  | 0.26           | Ribosome assembly (mitochondrial ribosomal protein) |
| Aim19  | 0.26           | Unknown            |
| Mfh4   | 0.26           | Protein synthesis (membrane-associated mitochondrial ribosome receptor, forms a complex with Mdm36p that may facilitate recruitment of mRNA-specific translational activators to ribosomes) |
| Mip1   | 0.26           | Ribosome assembly (mitochondrial ribosomal protein) |
| Yne6   | 0.26           | Ribosome assembly (mitochondrial ribosomal protein) |
| Ylh6   | 0.26           | Ribosome assembly (mitochondrial ribosomal protein) |
| Gap2   | 0.27           | Carbohydrate metabolism (E1 alpha subunit of the pyruvate dehydrogenase complex, catalyzes the direct oxidative decarboxylation of pyruvate to acetyl-CoA) |
| Ada4   | 0.27           | Carbohydrate metabolism (mitochondrial glycerol-3-phosphate dehydrogenase involved in glycerol degradation) |
| Mct20  | 0.27           | Protein import (presequence translocase of outer membrane complex, responsible for recognition and initial import steps for all mitochondrionally directed proteins) |
| Scl   | 0.28           | Metabolite transport (mitochondrial malate-fumarate transporter; transports succinate into and fumarate out of the mitochondrion) |
| Arg7   | 0.28           | Amino acid synthesis or degradation (mitochondrial malate acyltransferase; catalyzes the fifth step in arginine biosynthesis) |
| Pm2   | 0.28           | Amino acid synthesis or degradation (delta-1-pyrroline-5-carboxylate dehydrogenase; mitochondrial protein involved in utilization of pyrroline as sole nitrogen source) |
| Cpr1   | 0.28           | Unknown            |
| Ypt7   | 0.28           | Contact sites between mitochondria and vacuoles (Rab family GTPase) |
| Cat5   | 0.29           | Metabolite synthesis (is involved in ubiquinone synthesis) |
| Ysa4   | 0.29           | Protein synthesis (NADH-dependent RNA synthase that performs amino-14N synthase activity) |
| Msn1   | 0.29           | Electron transport chain/aerobic respiration (core subunit of the ubiquinol-cytochrome-c reductase complex) |
| Hgd10  | 0.30           | Proteostasis (mitochondrial matrix co-chaperonin; inhibits the ATPase activity of Hsp60, a mitochondrial chaperonin) |
| Udk    | 0.30           | Unknown            |
| Kgd2   | 0.30           | TCA cycle (f-andropoyltransacetylase; component of the mitochondrial α-ketoglutarate dehydrogenase complex, which catalyzes the oxidative decarboxylation of alpha-ketoglutarate to succinyl-CoA) |
| Mip24  | 0.30           | Ribosome assembly (mitochondrial ribosomal protein) |
| Akr1h   | 0.30           | Carbohydrate metabolism (mitochondrial aldehyde dehydrogenase; involved in aldehyde formation) |
| Bma4   | 0.31           | Metabolite synthesis (kynurenine-3-monooxygenase; required for the de novo biosynthesis of NAD from tryptophan via kynurenine) |
| Gcv1   | 0.31           | Metabolite synthesis (Γ subunit of the glycine decarboxylase complex required for folate synthesis) |
| Gct4   | 0.31           | Redox homeostasis (glutathione oxidoreductase; converts oxidized glutathione to reduced glutathione) |
| Msp2   | 0.31           | Lipid metabolism/oxidative stress (integral membrane protein that localizes to the mitochondrial inner membrane; associates with mitochondrial ribosome) |
| Protein | Function |
|---------|----------|
| Acs1 | Yeast protein synthesis (cysteine desulfurase; involved in thiocarboxylation of mitochondrial cysteine and cytoplasmic tRNAs) |
| Lpd2 | Yeast protein synthesis (cysteine desulfurase) |
| Msx3 | Unknown |
| Nm9 | Ribosome assembly (mitochondrial ribosomal protein) |
| Md9 | TCA cycle (mitochondrial malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate) |
| Cso1 | Metabolism synthesis (involved in ubiquinone synthesis) |
| Apj | ATP synthesis (a subunit of mitochondrial F1-ATPase) |
| YFCG0355W | Unknown |
| YGR026W | Unknown |
| Stc1 | Protein import and proteostasis (Hsp70 family ATPase; involved in protein translocation and folding) |
| Spg4 | Unknown |
| Apj5 | ATP synthesis (a subunit of mitochondrial F1-ATPase) |
| Sed2 | TCA cycle (electron transport chain/substrate degradation respiration (iso-sulfur protein subunit of succinate dehydrogenase); catalyzes the oxidation of succinate to the transfer of electrons to ubiquinone as part of the respiratory chain) |
| YOR020W-A | Unknown |
| YOL001W | Ribonucleotide metabolism (E1 beta subunit of the pyruvate dehydrogenase complex) |
| Shy1 | Electron transport chain/substrate degradation respiration (mitochondrial inner membrane protein required for complex IV assembly) |
| Cyc1 | Electron transport chain/substrate degradation respiration (cytochrome c, isoform 1) |
| Nca1 | ATP synthesis (protein that regulates expression of Fe-S ATP synthase subunits) |
| Ke1 | TCA cycle (subunit of the mitochondrial a-ketoglutarate dehydrogenase complex) |
| Id2 | TCA cycle (subunit of mitochondrial NAD+ and NADP+ dependent isocitrate dehydrogenase) |
| Mmi1 | Metabolite synthesis (mitochondrial C1-tetrahydrofolate synthase) |
| Vly2 | Amino acid synthesis or degradation threo-tocatate dehydrogenase; an NAD-linked mitochondrial enzyme required for the fourth step in the biosynthesis of lysine) |
| Cyl1 | Electron transport chain/substrate degradation respiration (Cytochrome c1) |
| Mti1 | Metabolite transport (mitochondrial phosphate carrier; imports inorganic phosphate into mitochondria) |
| Hemi5 | Metabolite transport (proteolysin involved in the biosynthesis of hom) |
| Ap3 | ATP synthesis (a subunit of the F1 sector of mitochondrial F1-ATP synthase) |
| Spg1 | Unknown |
| Fup41 | Unknown |
| AumS7 | Contact sites/contacts maintenance (Component of the MICOS [Mitochondrial contact site and cristae organizing system] complex) |
| Afg1 | Protein import and proteostasis (non-ribosomal ATPase of the AAA family) |
| Tum40 | Protein import (component of the TIM23 translocase of outer membrane) complex; responsible for recognition and initial import steps for all mitochondrially directed proteins) |
| Ymc1 | Protein import and proteostasis (catalytic subunit of f-AAA protease complex) |
| Pum18 | Protein import and proteostasis (subunit of the PAM [Presenilin translocase-associated motor] complex) |
| Tim17 | Protein transport (essential component of the TIM23 complex; contributes to the architecture and function of the import channel) |
| Lys4 | Amino acid synthesis or degradation (homoarginine; catalyzes the conversion of homocitrulline to homoarginine, which is a step in the lysine biosynthesis pathway) |
| Yia2 | Protein import and proteostasis (mitochondrial inner membrane m-AAA protease complex) |
| Ysh2 | Metabolite transport (citrate and oxoglutarate carrier protein; exports citrate from and imports oxoglutarate into the mitochondrion, causing net export of NADPH reducing equivalents) |
| Yfl1 | Contact sites/contacts maintenance (Component of the MICOS [Mitochondrial contact site and cristae organizing system] complex) |
| Aum24 | Contact sites/contacts maintenance (inner membrane protein that interacts with the MICOS [Mitochondrial contact site and cristae organizing system] complex and is required for its integrity) |
| Muf1 | Amino acid synthesis or degradation (mitochondrial protein required for transamination of isoleucine) |
| Osh1 | Protein import and proteostasis (mitochondrial inner membrane insertion; mediates the insertion of both mitochondrial- and nuclear-encoded proteins from the matrix into the inner membrane) |
| Fip10 | Unknown |
| She9 | Contact sites/contacts maintenance (mitochondrial inner membrane protein required for the inner membrane organization and normal mitochondrial morphology) |
| Apg8 | Ribonucleotide metabolism (NLR family pyrin domain-containing protein) |
| Apf3 | Proteostasis (ATPase and metallopeptidase of the inner mitochondrial membrane; subunit of the m-AAA complex involved in assembly of mitochondrial membrane protein complexes, degradation of processing of proteins imported into mitochondria) |
| Emr7 | Lipid metabolism/threonine metabolism (2-ethyl threonine dehydrogenase; member of the medium chain dehydrogenase/reductase family; has a probable role in fatty acid synthesis) |
| Mcs51 | Protein synthesis (specific translational activator for the mitochondrial COX1 mRNA) |
| Mcy1 | Amino acid synthesis or degradation (putative cysteine synthase) |
| Mcs9 | Unknown |
| Fip32 | Unknown |
| Migs35 | Ribosome assembly (mitochondrial ribosomal protein) |
| Cks1 | Unknown |
| Hsp90 | Proteostasis (mitochondrial chaperone; required for ATP-dependent folding of precursor polypeptides and complex assembly, prevents aggregation and mediates protein refolding after heat shock) |
| Aim13 | Contact sites/contacts maintenance (Component of the MICOS [Mitochondrial contact site and cristae organizing system] complex) |
| YNL200C | Metabolite synthesis (NADH epimerase; catalyzes isomerization of (R)- and (S)-NADH) |
| Cox5A | Electron transport chain/substrate degradation respiration (subunit Va of cytochrome c oxidase) |
| Aim32 | Unknown |
| Mm52 | Metabolite transport (putative metal transporter involved in mitochondrial iron accumulation) |
| Mips16 | Ribosome assembly (mitochondrial ribosomal protein) |
| Per54 | Protein synthesis (mitochondrial inner membrane protein; binds to the 5' UTR of the COX3 mRNA to activate its translation) |
| Qcr6 | Electron transport chain/substrate degradation respiration (subunit 6 of the ubiquinol cytochrome c reductase complex) |
| Rmt10 | Ribosome assembly (mitochondrial ribosomal protein) |
| Cpr5 | Proteostasis (mitochondrial peptidyl-prolyl cis-trans isomerase; cyclophilin; catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues) |
| Aox1 | Amino acid synthesis or degradation (alcoholic amine aminotransferase (AGT); catalyzes the synthesis of glycine from glyoxylate) |
| Cox20 | Proteostasis (inner mitochondrial membrane protein; required for proteolysis processing of Cox2p and its assembly into cytochrome c oxidase) |
| Mips18 | Ribosome assembly (mitochondrial ribosomal protein) |
| Idp1 | Amino acid synthesis or degradation (mitochondrial NADP-specific isocitrate dehydrogenase; catalyzes the oxidation of isocitrate to alpha-ketoglutarate; diverts alpha-ketoglutarate to glutamine synthesis) |
| Mss9 | Ribonucleotide metabolism (ribonucleotide reductase subunit) |
| Hem1 | Metabolite synthesis (5-aminoimidazole-4-carboxamide synthase; catalyzes the first step in the heme biosynthetic pathway) |
| Mit20 | Protein synthesis (mitochondrial threonyl-tRNA synthetase) |
| Ocs2 | Metabolite transport (mitochondrial inner membrane transporter: 2-oxoacid transporter, exports 2-oxoacids and 2-oxoglutarate from the mitochondrial matrix to the cytosol) |
| Mcs7 | Lipid metabolism/threonine metabolism (Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid synthase that produces intermediates for phospholipid remodeling) |
| Ycp8 | Unknown |
| Fup30 | Metabolite transport (involving maintenance of normal cytidine levels) |
| Gcv3 | Metabolite synthesis (H subunit of the glycine decarboxylase complex required for folate synthesis) |
| Cyc2 | Electron transport chain/substrate degradation respiration (cytochrome b, isoform 1) |
| Rnh1 | Unknown |
| YOR020W-A | Unknown |
| Isd11 | Metabolite synthesis (essential for the formation of the peroxisome intermediate at the desulfurase active site during pyridoxal phosphate-dependent desulfuration of cysteine; required for mitochondrial desulfuration) |
| Pum4 | TCA cycle (thiamine pyrophosphate-dependent transketolase) |
| Nn1 | Protein synthesis (cysteine desulfurase; involved in thiocarboxylation of mitochondrial and cytoplasmic tRNAs) |
| Dkh1 | Carbohydrate metabolism (major D-lactate dehydrogenase oxidizing D-lactate to pyruvate) |
| Mgs24 | Ribonucleotide metabolism (ribonucleotide reductase) |
| Cep1 | Redox homeostasis (mitochondrial cytochrome c oxidase; degrades reactive oxygen species in mitochondria, involved in the response to oxidative stress) |
| Nat2 | Unknown |
| YL0085W | Electron transport chain/substrate degradation respiration (putative succinate dehydrogenase isoform; participates in oxidation of succinate and transfer of electrons to ubiquinone) |
| Aca1 | Carbohydrate metabolism (Acetyl-CoA carboxylase) |
| Gene   | Function                                                                                   |
|--------|-------------------------------------------------------------------------------------------|
| Msd1   | Amino acid synthesis or degradation (mitochondrial protein required for transmission of isoleucine) |
| Mgs8   | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Afl3   | Carbohydrate metabolism (mitochondrial citrate cycle isocitrate dehydrogenase involved in aerobic respiration) |
| Car2   | Metabolite transport (carboxylic acid-CoA transferase; transfers activated carboxylic groups to carboxylic acid which can be shuttled across membranes) |
| Pam18  | Protein import/proteostasis (subunit of the PAM [Presequence translocase-associated motor] complex) |
| Aip2   | ATP synthesis (subunit b of the F1 sector of mitochondrial ATP synthase)                    |
| Mip16  | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Omi14  | Protein import (mitochondrial outer membrane protein that binds to the nascent chain-associated complex to dock cytosolic ribosomes at the mitochondrion and facilitate co-translational import of mitochondrial proteins) |
| Adj1   | Protein import/proteostasis (non-processed A TPase of the AAA family)                       |
| Mri49  | Metabolite transport (mitochondrial phosphate carrier; imports inorganic phosphate into mitochondria) |
| Gcv3   | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Yfr2   | Metabolite synthesis (performs a scaffolding function during assembly of iron-sulfur clusters) |
| Ygr266w| Protein import (one of two mitochondrial-localized peptidyl-tRNA hydrolases, negatively regulates the ubiquitin-proteasome pathway via interactions with ubiquitin-like ubiquitin-associated proteins) |
| Tuf1   | ATP synthesis (a subunit of mitochondrial ATP synthase)                                     |
| Atp15  | Metabolite transport (mitochondrial phosphate carrier; imports inorganic phosphate into mitochondria) |
| Idp1   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Pos5   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Ykr070w| Metabolite transport (mitochondrial ribosomal protein)                                     |
| Mgm101 | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Nam9   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Her2   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Bna4   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Gtt1   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Sod1   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Cox6   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Mam33  | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Cbp4   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Ilv6   | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Mrp7   | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Rnl28  | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Pcl3   | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Mrp22  | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Mrp27  | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Mrp38  | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Nam28  | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Vari   | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Ybi8   | Stress response (a flavohemoglobin that plays role in oxidative and intrusive stress responses) |
| Mrp22  | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Hdh3   | Carbohydrate metabolism (3-hydroxybutyryl-CoA dehydrogenase)                               |
| Arg7   | Amino acid synthesis or degradation (mitochondrial protein containing arginine)            |
| Lr1   | Protein import (essential component of the TMC complex, involved in protein import into mitochondrial matrix and inner membrane) |
| Brl3   | Protein synthesis (ribosome recycling factors)                                             |
| Per123 | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Ge22   | Redox homeostasis (glutathione S-transferase, glutathione-dependent disulfide oxidoreductase involved in maintaining redox state of target proteins, also exhibits glutathione peroxidase activity) |
| IhV1   | Amino acid synthesis or degradation (threonine dehydratase, catalyzes first step in isocitric acid biosynthesis) |
| Nla4   | Protein import (essential component of the TMC complex, involved in protein import into mitochondrial matrix and inner membrane) |
| Cox11  | Metabolite synthesis involved in ubiquinone synthesis                                       |
| Man33  | Protein synthesis (specific, translational activator for the mitochondrial COX1 mRNA)      |
| Cis6   | Electron transport chain/aerobic respiration (Subunit VI of cytochrome c oxidase)          |
| Yso4   | Stress response (a flavohemoglobin that plays role in oxidative and intrusive stress responses) |
| Bha4   | Metabolite synthesis (kynurenine 3-monooxygenase; required for the de novo biosynthesis of NAD from tryptophan via kynurenine) |
| Hez2   | Unknown                                                                                    |
| Sdb4   | TCA cycle/Electron transport chain/aerobic respiration (membrane anchor subunit of succinate dehydrogenase) |
| Aitm33  | Contact sites/organ maintenance (Component of the Miro2 [Mitochondrial contact site and constraining organization] complex) |
| Nam9   | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Mgm101 | Unknown                                                                                    |
| Yko107w| Unknown                                                                                    |
| Mne16  | mRNA synthesis/processing (transcription elongation factor required for splicing of introns) |
| Pse3   | Metabolite synthesis (NAD-dependent glycerol 3-phosphate dehydrogenase, involved in glycerol biosynthesis) |
| Mip33  | Metabolite synthesis (kynurenine 3-monooxygenase; required for the de novo biosynthesis of NAD from tryptophan via kynurenine) |
| Mbi1   | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Cern1l  | Carbohydrate metabolism (mitochondrial beta-ketoacyl synthase, possible role in fatty acid synthesis) |
| Pcr15S | Metabolite transport (mitochondrial ribosomal protein)                                     |
| Mrp4   | Ribosome assembly (mitochondrial ribosomal protein)                                        |
| Idp1   | Amino acid synthesis or degradation (mitochondrial protein containing arginine)            |
| Cpp4   | Protein synthesis (mitochondrial precursors of protein-protein-translocase activity (cytoplasm), catalyzes the co-translocation of peptide bonds N-terminal to proximal residues) |
| Nfl   | Protein synthesis (cytosolic desifluorase; involved in the modification of mitochondrial and cytoplasmic RNA) |
| Akgx   | Amino acid synthesis or degradation (Alanine and Glycine ammonia transferase (AGT), catalyzes the synthesis of glycine from glycine) |
| Aip15   | ATP synthesis (a subunit of mitochondrial ATP synthase)                                     |
| Tcil   | Protein synthesis (mitochondrial translation elongation factor 1)                          |
| Ptr1   | Protein synthesis (mitochondrial integral inner membrane protein, involved in membrane insertion of C-terminus of Cox2p) |
| Cym1   | Protein synthesis (lysine-specific metalloproteinase of the pih/fel family; metalloproteinase of the integran membrane space, degrades proteins and presence peptides cleaved from imported proteins) |
| Pnt1   | Protein synthesis (mitochondrial translation elongation factor 2)                          |
| Hap73   | Protein synthesis (mitochondrial matrix chaperone; able to prevent the aggregation of misfolded proteins as well as resolubilize protein aggregates) |
| Run1   | ATP synthesis (mitochondrial ribosomal protein essential for mitochondrial genome maintenance; involved in mitochondrial DNA replication) |
| Yar1   | Protein synthesis (valyl-tRNA synthetase that synthesizes valyl-tRNA aminoacylation by coupling valine to valyl-tRNA) |
| Fip40   | Unknown                                                                                    |
| Aitm9  | Unknown                                                                                    |
| Yor256w| Unknown                                                                                    |
| Ycv6   | Metabolite synthesis (kynurenine 3-monooxygenase; required for the de novo biosynthesis of NAD from tryptophan via kynurenine) |
| Fum1   | TCA cycle (fumarase)                                                                       |
| Rcl1   | Protein import (cytosol c oxalate subunit; required for assembly of the Complex III-Complex IV supercomplex, and for assembly of Cox3p and Rcl2p into cytochrome c oxidase) |

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| Gene  | Score | Function Description                                                                                                                                 |
|-------|-------|------------------------------------------------------------------------------------------------------------------------------------------------------|
| Shm1  | 0.39  | Metabolite synthesis (mitochondrial serine hydroxymethyltransferase; converts serine to glycine plus 5,10 methylentetrahydrofolate; involved in generating precursors for purine, pyrimidine, amino acid, and lipid biosynthesis; reverse reaction generates serine) |
| lh3   | 0.40  | Metabolite synthesis (dihydroxyacid dehydratase; catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids)            |
| Fh4a3 | 0.41  | Metabolite transport (highly conserved subunit of the mitochondrial pyruvate carrier)                                                                     |
| Mips17| 0.42  | Ribosome assembly (mitochondrial ribosomal protein)                                                                                                        |
| Ccp1  | 0.43  | Redox homeostasis (mitochondrial cytochrome-c peroxidase; degrades reactive oxygen species in mitochondria, involved in the response to oxidative stress)   |
| Fh4a3 | 0.43  | Carbohydrate metabolism (L3-binding protein of the mitochondrial pyruvate dehydrogenase complex)                                                         |
| Mrp13 | 0.43  | Ribosome assembly (mitochondrial ribosomal protein)                                                                                                        |
| Pami8 | 0.43  | Protein import/proteostasis (subunit of the PAM [Presequence translocase-associated motor] complex)                                                    |
| Mrp14 | 0.43  | Amino acid synthesis or degradation (mitochondrial protein required for transamination of isoleucine)                                                   |
| Mce3  | 0.43  | Unknown                                                                                                                                                 |
| Tim21 | 0.43  | Protein import (component of the TIM23 complex, interacts with the Translocase of the Outer Mitochondrial membrane (TOM complex))                     |
| Wsd1  | 0.43  | Protein synthesis (mitochondrial aspartyl-tRNA synthetase; required for acylation of asparyl-tRNA)                                                   |
| Amf1  | 0.44  | ATP synthesis (a subunit of mitochondrial F1F0-ATPase)                                                                                                   |
| Dkm2  | 0.44  | Carbohydrate metabolism (D-2-hydroxyglutarate dehydrogenase, and minor D-lactate dehydrogenase; mitochondrial matrix protein that oxidizes D-2-hydroxyglutarate to α-ketoglutarate) |
| Mdx9  | 0.45  | Unknown                                                                                                                                                 |
| Ysa1  | 0.46  | Metabolite synthesis (nudix hydrolase family member with ADP-ribose pyrophosphatase activity; metabolizes O-acetyl-ADP-ribose to AMP and acetylated ribose 5-phosphate) |
| Usq1  | 0.47  | Mitochondrial fusion (mitohuman, integral membrane protein involved in mitochondrial outer membrane tethering and fission)                           |
| Mrp1  | 0.47  | Ribosome assembly (mitochondrial ribosomal protein)                                                                                                        |
| Fzo1  | 0.47  | Mitochondrial fusion (mitofusin; integral membrane protein involved in mitochondrial outer membrane tethering and fusion)                           |
| Mrp1  | 0.47  | Ribosome assembly (mitochondrial ribosomal protein)                                                                                                        |
| Mrp1  | 0.47  | Ribosome assembly (mitochondrial ribosomal protein)                                                                                                        |
| Mdr1  | 0.47  | Amino acid synthesis or degradation (alanine transaminase (glutamic pyruvic transaminase); involved in alanine biosynthesis and catabolism)           |
| Mdp1  | 0.47  | Protein synthesis (gamma subunit of translational elongation factor eEF1B)                                                                                |
| Mrx9  | 0.47  | Unknown                                                                                                                                                 |
| Mdm10 | 0.49  | Metabolite transport (component of ERMES complex which acts as a molecular tether between the mitochondria and the ER, necessary for efficient phospholipid exchange between organelles and for mitophagy) |
| Sod2  | 0.49  | Stress response (mitochondrial manganese superoxide dismutase; protects cells against oxygen toxicity and oxidative stress)                           |
| Cdx1  | 0.49  | Electron transport chain/oxidative phosphorylation (ubiquinol cytochrome c oxidoreductase [Complex III])                                                 |
| Ams5  | 0.49  | Unknown                                                                                                                                                 |
| Srt1  | 0.49  | Protein synthesis (mitochondrial arginyl-tRNA synthetase)                                                                                                |
| Toc711| 0.49  | Protein import (component of the TOM (translocase of outer membrane) complex responsible for recognition and import of mitochrondrally directed proteins) |
| Cht3  | 0.49  | TCA cycle (dual specificity mitochondrial citrate and methylcitrate synthase; catalyzes the condensation of acetyl-CoA and oxaloacetate to form citrate)   |
Supplemental Table S17. Proteins that are upregulated by the ups2Δ mutation (but not by the ups1Δ mutation) in cells cultured without LCA are involved in various biological processes. Mitochondria were purified from cells recovered on day 2, 4 or 7 of cell culturing without LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the "Proteome Discoverer" software was used to calculate the relative abundance of mitochondrial proteins between ups2Δ and WT. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Day | Protein | Ratio ups2/WT | Biological processes |
|-----|---------|--------------|---------------------|
| 2   | Cys2    | 1.60         | Metabolite synthesis is involved in ubiquinone synthesis |
|     | Cvc1    | 1.81         | Metabolite transport is required for carnitine-dependent transport of acetyl-CoA |
|     | Zo1     | 1.86         | Unknown |
|     | Cyt2    | 2.16         | Electron transport chain/cytochrome c1 |
| 4   | Pe18    | 1.52         | Metabolite transport (major ADP/ATP carrier of the mitochondrial inner membrane; exchanges cytosolic ADP for mitochondrial-synthetized ATP, also imports heme and ATP) |
|     | Muc1    | 1.55         | mRNA syntheses/processing (proteins involved in spliceosome Group I intron from COX1 mRNA) |
|     | Msm1    | 1.56         | Protein synthesis (mitochondrial methionyl-tRNA synthetase) |
|     | Rgl2    | 1.61         | Electron transport chain/respiration (cytochrome c oxidase subunit; has a role in assembly of respiratory supercomplexes) |
|     | Fba1    | 1.62         | Carbohydrate metabolism (Fructose 1,6-bisphosphate aldolase; required for glycolysis and gluconeogenesis; catalyzes conversion of fructose 1,6-bisphosphate to glyceraldehyde-3-P and dihydroxyacetone-P in oxidative stress) |
|     | Mip2D2  | 1.70         | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Rsm18   | 1.70         | Ribosome assembly (mitochondrial ribosomal protein) |
|     | YPL109C | 1.75         | Unknown |
|     | Nam9    | 1.76         | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Ncp1    | 1.76         | Lipid metabolism (NADP-acceptor of fatty acid-CoA carboxylase, biotin containing enzyme; catalyzes carboxylation of acetyl-CoA to form malonyl-CoA, required for de novo biosynthesis) |
|     | Out1    | 1.80         | Metabolite synthesis (fumarate reductase with a role in oxidation of FAD) |
|     | Mip7    | 1.85         | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Ccm1    | 2.02         | mRNA syntheses/processing (mitochondrial JS RNA-binding protein; required for intron removal of COB and COX1 pre-mRNA) |
|     | Aar1    | 2.07         | Amino acid metabolism (mitochondrial aspartate aminotransferase; catalyzes conversion of aspartate to glutamate and asparagine biosynthesis) |
|     | Gpd2    | 2.09         | Carbohydrate metabolism (NADP-dependent glycerol 3-phosphate dehydrogenase; is involved in glycerol metabolism) |
|     | Rsm23   | 2.10         | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Nla3    | 2.12         | Unknown |
|     | Pgil    | 2.16         | Carbohydrate metabolism (phosphoglucoisomerase; catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate in glycolysis and gluconeogenesis) |
|     | Mtb4    | 2.23         | Ribosome assembly (mitochondrial ATP-dependent RNA helicase of the DEAD-box family; required for assembly of the large subunit of mitochondrial ribosomes) |
|     | Aep2    | 2.29         | Protein synthesis (is involved in translation of the mitochondrial OLJ1 mRNA) |
|     | Misc1   | 2.29         | Protein synthesis (mitochondrial tryptophanyl-tRNA synthetase) |
|     | Rsm28   | 2.39         | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Mip6101 | 2.55         | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Efs1    | 2.70         | Unknown |
|     | Ota1    | 2.82         | Protein import/proteostasis (mitochondrial inner membrane insertase; mediates the insertion of both mitochondrial- and nuclear-encoded proteins from the matrix into the inner membrane; also has a role in inner membrane) |
|     | Bna4    | 2.83         | Metabolite synthesis (kynurenine-3-monooxygenase; required for de novo biosynthesis of NAD from tryptophan via kynurenine) |
|     | Tcb3    | 2.85         | Unknown |
|     | Mip94   | 2.93         | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Liu1    | 3.55         | Protein synthesis (Mitochondrial translation initiation factor 2) |
|     | Mtb1    | 3.56         | Unknown |
|     | Pgn1    | 4.51         | Lipid metabolism (Phosphatidylglycerophosphate synthase; catalyzes the synthesis of phosphatidyglycerophosphate from CDP-diacylglycerol and sn-glycerol 3-phosphate in the first committed and rate-limiting step of cardiolipin biosynthesis) |
|     | Tsc13   | 1.61         | Lipid metabolism (enoyl reductase; catalyzes last step in each cycle of very long chain fatty acid elongation) |
|     | Aep2    | 1.63         | Protein synthesis (is involved in translation of the mitochondrial OLJ1 mRNA) |
|     | Efs1    | 1.66         | Unknown |
| 7   | Gic1    | 1.72         | Metabolite transport (mitochondrial GTP/GDP transporter) |
|     | Hip26   | 1.85         | Protection against stress by chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation) |
|     | Ugd1    | 1.85         | Mitochondrial fusion (outer membrane component of the mitochondrial fusion machinery) |
|     | Ady2    | 2.03         | Metabolite transport (acetate transporter) |
|     | Fat3    | 2.09         | Metabolite transport (protein required for fatty acid uptake) |
|     | Pal1    | 2.09         | Amino acid metabolism (promote endoplasmic reticulum; nuclear encoded mitochondrial protein involved in utilization of proline as sole nitrogen source) |
|     | Tg2     | 2.23         | Lipid metabolism (Triglyceride; that is localized to the mitochondria) |
|     | San37   | 3.35         | Protein synthesis (component of the Sorting and Assembly Machinery (SAM) complex; the SAM complex is located in the mitochondrial outer membrane; binds precursors of beta-barrel proteins and facilitates the SAM complex stability) |
|     | Acc1    | 8.47         | Lipid metabolism (acetyl-CoA carboxylase, biont containing enzyme; catalyzes carboxylation of acetyl-CoA to form malonyl-CoA, required for de novo biosynthesis of long-chain fatty acids) |
Supplemental Table S18. Proteins that are downregulated by LCA only in ups2Δ cells (but not in WT or ups1Δ cells) are involved in several biological processes. Mitochondria were purified from cells recovered on day 2, 4 or 7 of cell culturing with LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between ups2Δ cells cultured with or without LCA. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Day | Protein | Ratio ups2+ / LCA/ups2 | Biological process |
|-----|---------|------------------------|-------------------|
| 2   | Mgpa28  | 0.47                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Pr7     | 0.47                   | Metabolite synthesis (type 2C sterol gene) |
|     | Mth1    | 0.48                   | Protein synthesis (mitochondrial thiol-tRNA synthetase) |
|     | Oae1    | 0.49                   | Metabolite transport (mitochondrial inner membrane transporter) |
| 4   | Pr40    | 0.22                   | Lipid metabolism (phosphatidylglycerolphosphate synthase) |
|     | Muc27   | 0.26                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Muc1    | 0.31                   | mRNA synthesis/processing (protein involved in splicing Group Ia5-beta intron from COX1 mRNA) |
|     | Acsl    | 0.37                   | Carbohydrate metabolism (acyl-CoA synthetase isoform) |
|     | Mgrs28  | 0.45                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Mpg7    | 0.45                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Mpg5    | 0.46                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Mth1    | 0.46                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Adh6    | 0.46                   | Carbohydrate metabolism (aldehyde dehydrogenase; required for conversion of acetaldehyde to acetate) |
|     | Coo2    | 0.47                   | Metabolite synthesis (Parahydroxybenzoate polypropyltransferase) |
|     | Nt5     | 0.47                   | Unknown |
|     | Ybl2    | 0.48                   | Unknown |
|     | Dss4    | 0.48                   | Protein synthesis (mitochondrial ser-1-trNA synthetase that performs ser-1-trNA aminocylating in the mitochondria) |
|     | Rrom22  | 0.49                   | Ribosome assembly (mitochondrial ribosomal protein) |
| 7   | Mgr6    | 0.43                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Perl259 | 0.44                   | Protein import (Component of the TOM [Translocase of Outer Membrane] complex; responsible for initial import of mitochondrially directed proteins) |
|     | Toms22  | 0.44                   | Protein import (Component of the TOM [Translocase of Outer Membrane] complex; responsible for initial import of mitochondrially directed proteins) |
|     | Mgr5    | 0.44                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Tgl2    | 0.45                   | Lipid metabolism (triacylglycerol lipase that is localized to the mitochondria) |
|     | Fmp46   | 0.45                   | Unknown |
|     | Rmt2    | 0.46                   | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Bi6     | 0.47                   | mRNA synthesis/processing (Mitochondrial mRNA matutenase; forms a complex with Nam2p to initiate splicing of the M4 intron of the COB gene) |
|     | Kha1    | 0.48                   | Metabolite transport (putative K+/H+ antiporter) |
|     | Rim1    | 0.49                   | Protein synthesis (mitochondrial translation initiation factor 2) |
Supplemental Table S19. Proteins that are upregulated by LCA only in ups2Δ cells (but not in WT or ups1Δ cells) are involved in various biological processes. Mitochondria were purified from cells recovered on day 2, 4 or 7 of cell culturing with LCA. Mass spectrometry-based identification and quantitation of proteins recovered in purified mitochondria were performed as described in Materials and methods. The exponentially modified protein abundance index (emPAI) provided by the “Proteome Discoverer” software was used to calculate the relative abundance of mitochondrial proteins between ups2Δ cells cultured with or without LCA. Data on the relative concentrations of mitochondrial proteins are presented as means of 2 independent experiments.

| Day | Protein | Ratio ups2Δ / LCA | Biological process |
|-----|---------|------------------|-------------------|
| 2   | Aac1    | 1.63             | Metabolism (transport mitochondrial inner membrane ADP/ATP translocator; exchanges cytosolic ADP for mitochondrially synthesized ATP) |
|     | Aum17   | 1.52             | Unknown           |
|     | Per1    | 1.52             | Metabolism (transport major ADP/ATP carrier of the mitochondrial inner membrane; exchanges cytosolic ADP for mitochondrially synthesized ATP, also imports heme and ATP) |
|     | Hem154  | 1.54             | Metabolism (ferrochelatase; a mitochondrial inner membrane protein, catalyzes assimilation of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic pathway) |
|     | Sdh4    | 1.55             | TCA cycle and ETC/respiration (membrane anchor subunit of succinate dehydrogenase; involved in coupling the oxidation of succinate to the transfer of electrons to ubiquinone as part of the TCA cycle and the ETC) |
|     | Chp3    | 1.55             | Proteostasis and protein synthesis (mitochondrial protein required for assembly of cytochrome bcl complex; forms a complex with Chp6p that binds to mitroosomes near the polypyrrole tunnel exit and promotes assembly of the cytochrome bcl complex) |
|     | Tcb1    | 1.56             | Lipid metabolism (lipid-bounding protein) |
|     | Idh2    | 1.56             | TCA cycle (substrate of mitochondrial NAD(+) dependent isocitrate dehydrogenase; complex catalyzes the oxidation of isocitrate to alpha-ketoglutarate in the TCA cycle) |
|     | Mip68   | 1.56             | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Leu4    | 1.57             | Lipid metabolism (farnesyl-diphosphate farnesyl transferase (squalene synthase); joins two farnesyl pyrophosphate moieties to form squalene in the sterol biosynthesis pathway) |
|     | Aum16   | 1.59             | Unknown           |
|     | YFR6045 W | 1.59         | Unknown           |
|     | Mip440  | 1.59             | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Mdh1    | 1.59             | Proteostasis (membrane-associated mitochondrial ribosome receptor, forms a complex with Mdm10p that may facilitate recruitment of mRNA-specific translational activators to ribosomes) |
|     | Op11    | 1.60             | Unknown           |
|     | Mipl1   | 1.60             | Ribosome assembly (mitochondrial ribosomal protein) |
|     | Cyt1    | 1.60             | Lipid metabolism (membrane protein involved in lipid transport) |
|     | Aco1    | 1.60             | Proteostasis (mitochondrial mitochondrial inner membrane protein) |
|     | Fv1x    | 1.60             | Unknown           |
|     | Leu4    | 1.60             | Amino acid metabolism (α-amino acid dehydrogenase; catalyzes first step in isoleucine biosynthesis) |
|     | Leu4    | 1.61             | Unknown           |
|     | Lsm4    | 1.61             | Amino acid metabolism (α-isoaspartylproteinase synthetase, the main enzyme responsible for the first step in the leucine biosynthesis pathway) |
|     | Prx1    | 1.61             | Redox homeostasis (mitochondrial peroxiredoxin with thioareoxid peroxidase activity, has a role in reduction of hydroperoxides) |
|     | Rsm3    | 1.61             | TCA cycle (acyl-CoA oxidase) |
|     | Lsm4    | 1.61             | mRNA replication/compression/repair (mRNA-binding protein essential for mitochondrial genome maintenance; involved in mitochondrial DNA replication) |
|     | Faa1    | 1.61             | Lipid metabolism (long chain fatty acyl-CoA synthetase; activates fatty acids with a preference for C12:0-C16:0 chain lengths) |
|     | Arg3    | 1.76             | Mitophagy (mitophagic ATPase-specific protein; required primarily for mitophagy induced at post-log phase) |
|     | Tim11   | 1.76             | ATP synthesis (subunit epsilon of mitochondrial ATP synthase) |
|     | Qcr10   | 1.78             | ETC/respiration (ubiquinol-cytochrome c oxidoreductase complex; this complex comprises part of the mitochondrial respiratory chain) |
|     | Apr17   | 1.78             | ATP synthesis (ubiquinol-CoQ reductase) |
|     | Apl1    | 1.78             | ATP synthesis (ubiquinol-CoQ reductase) |
|     | Apr17   | 1.78             | ATP synthesis (ubiquinol-CoQ reductase) |
|     | Afg1    | 1.81             | Proteostasis and protein import (ubiquitination) |
|     | Na2     | 1.88             | Unknown           |
|     | YN8040 W | 1.88         | Unknown           |
|     | Ou65    | 1.92             | Unknown           |
|     | Fsc1    | 1.92             | Contact sites/cristae maintenance (component of the MICOS [Mitochondrial contact site and cristae organizing system] complex; MICOS is a mitochondrial inner membrane complex that extends into the inner membrane of cristae junctions, inner membrane architecture, and formation of contact sites to the outer membrane) |
|     | Aum37   | 1.93             | Contact sites/cristae maintenance (component of the MICOS [Mitochondrial contact site and cristae organizing system] complex; MICOS is a mitochondrial inner membrane complex that extends into the inner membrane of cristae junctions, inner membrane architecture, and formation of contact sites to the outer membrane) |
|     | YKL13L C | 1.96             | Unknown           |
|     | Yml2    | 1.97             | Metabolite transport (carrier and chaperonin carrier protein, exports cytosol and imports oxoglutarate into the mitochondrion, causing net export of NADPH reducing equivalents) |
|     | Sdh3    | 2.00             | TCA cycle and ETC/respiration (mitochondrial protein involved in the TCA cycle and the mitochondrial respiratory chain) |
|     | Inv5    | 2.00             | Amino acid metabolism and mitochondrial replication (ubiquinol-cytochrome c oxidoreductase complex; this complex comprises part of the mitochondrial respiratory chain) |
|     | Shy1    | 2.01             | Proteostasis (mitochondrial inner membrane protein required for complex IV assembly; associates with complex IV and is involved in the assembly of the bc1 complex) |
|     | Bra1    | 2.01             | Lipid metabolism (mitochondrial inner membrane protein) |
|     | Fkh1    | 2.09             | Proteostasis (ubiquitin-like protein, catalyzes the degradation of ubiquitinated proteins) |
|     | Isc1    | 2.10             | Lipid metabolism (reguluted phospholipid/lipid-phospholipid C; hydrolyzes complex phospholipids to produce ceramides) |
|     | Ami18   | 2.14             | Unknown           |
|     | Ycp1    | 2.14             | Mitochondria/vacuolar contact site (Rab family ATPase; localizes to sites of contact between the vacuole and mitochondria) |
|     | Cyt1    | 2.17             | ETC/respiration (cytochrome c 1 component of the mitochondrial respiratory chain) |
|     | She9    | 2.17             | Unknown           |
|     | Tom20   | 2.19             | Proteostasis (component of the TOM translocator of outer membrane complex, responsible for recognition and insertion into the outer membrane proteins, acts as a receptor for incoming proteins) |
|     | Ynm3    | 2.25             | TCA cycle (substrate of the mitochondrial NAD(+) dependent dehydrogenase) |
|     | Apil2   | 2.26             | Proteostasis and ATP synthesis (assembly factor for the F1 sector of mitochondrial ATP synthase) |
|     | Yml1    | 2.28             | Unknown           |
|     | Rpi1    | 2.28             | ETC/respiration (ubiquinol-cytochrome c reductase, a Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex; transfers electrons from ubiquinol to cytochrome c1 during respiration) |
|     | Flp45   | 2.28             | Unknown           |
|     | Ugo1    | 2.31             | Mitochondrial fusion (outer membrane component of the mitochondrial fusion machinery) |
|     | Mxi1    | 2.35             | Lipid metabolism (mitochondrial NAD-dependent dehydrogenase, involved in the biogenesis of the mitochondrial inner membrane) |
|     | Chp4    | 2.52             | Proteostasis and ETC/respiration (mitochondrial protein required for assembly of cytochrome bcl complex; interacts with the Chp3p-Chp6p complex and newly synthesized cytochrome b (Chb) to promote assembly of the complex) |
|     | Fru1    | 2.62             | Unknown           |
|     | Apr17   | 2.63             | ATP synthesis (ubiquinol subunit of the F1 sector of mitochondrial ATP synthase) |
|     | Idp1    | 2.85             | Amino acid metabolism (mitochondrial NADP-specific isocitrate dehydrogenase; catalyzes the oxidation of isocitrate to α-ketoglutarate and NADPH production; involved in mitochondrial respiration; diverts α-ketoglutarate to glutamate) |
|     | Mip32   | 3.02             | Lipid metabolism (mitochondrial protein involved in lipid transport) |
|     | Pdh1    | 3.24             | Lipid metabolism (phosphatidylethanolamine deacylase of the mitochondrial inner membrane, converts phosphatidylethanolamine to phosphatidylethanolamine) |
|     | Bsc1    | 3.27             | Proteostasis and ETC/respiration (ubiquitin required for Complex III assembly; member of the AAA ATPase family; also required for assembly of the Qcr10p subunit) |
|     | Mip435  | 3.27             | Ribosome assembly (mitochondrial ribosomal protein) |
Aim19
Cpr1
Atp2
Cyt1
Hsp60
Nuc1
Ubp16
Mdm32
Tom71
Bat1
Alo1
YJL045
Mir1
Sdh1
Nde2
Msc6
Rip1
Aim24
Atp7
W
YDR061
Atp3
Cox2
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Rmd9
Mdm38
Pet9
Tcb1
Cor1
Pim1
Tdh2
Ggc1
Arg7
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Unknown
ATP synthesis (β subunit of the F1 sector of mitochondrial F1F0 ATP synthase)
ETC/respiration (cytochrome c1; complex III is a component of the mitochondrial inner membrane electron transport chain)
Proteostasis (deubiquitinating enzyme attached to the outer mitochondrial membrane)
Carbohydrate metabolism (gliceraldehyde-3-phosphate dehydrogenase, enzyme 2; involved in glycolysis and gluconeogenesis)
Proteostasis (ATP-dependent Lon protease; involved in degradation of misfolded proteins in mitochondria)
TCR (mitochondrial acetylase needed, similarity to Alc6; an acetylase required for the TCA cycle)
Ribosomal assembly (ribosomal ribonucleic protein)
Carbohydrate metabolism (glycoldehyde-3-phosphate dehydrogenase, enzyme 2; involved in glycolysis and gluconeogenesis)
Amino acid metabolism (homoaconitase; similarity to Aco1, an aconitase required for the TCA cycle)
Proteostasis (mitochondrial inner membrane protein; required for proteolytic processing of Cox2p and it's end processing of mitochondrial RNAs)
Lipid metabolism (3-ketoacyl-CoA thiolase; involved in mitochondrial fatty acid beta oxidation)
Amino acid metabolism (mitochondrial ornithine acetyltransferase; catalyzes the fifth step in arginine biosynthesis)
Amino acid metabolism (mitochondrial branched chain amino acid CoA transferase; transfers activated acetyl groups to carnitine to form acetylcarnitine which can be shuttled across membranes)
Amino acid metabolism (α-ketoglutarate dehydrogenase complex; catalyzes a key step in the tricarboxylic acid (TCA) cycle; the oxidative decarboxylation of alpha-ketoglutarate to form succinyl-CoA)
Lipid metabolism (dehydrogenase involved in ubiquinone and sphingolipid metabolism; oxidizes 4-hydroxybenzaldehyde into 4-hydroxybenzoic acid in ubiquinone biosynthesis; catalyzes the first step in the leucine biosynthesis pathway)
Protein synthesis (mutant phenotype and genetic interactions suggest a role in delivering mt mRNAs to the mitochondrial ribosome)
Unknown
Protein synthesis (mutant phenotype and genetic interactions suggest a role in delivering mt mRNAs to the mitochondrial ribosome)
Protein import (essential component of the TIM23 complex; with Tim23p, contributes to the architecture and function of the inner mitochondrial membrane)
Protein import (component of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps of mitochondrial proteins)
Proteostasis (mitochondrial aconitase isozyme; similarity to Aco1, an aconitase required for the TCA cycle)
Proteostasis (mitochondrial protein involved in lipid homeostasis; interacts genetically with MDM10 and other members of the ERMD6 complex)
Protein synthesis (mutant phenotype and genetic interactions suggest a role in delivering mt mRNAs to the mitochondrial ribosome)
Protein synthesis (mutant phenotype and genetic interactions suggest a role in delivering mt mRNAs to the mitochondrial ribosome)
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Protein synthesis (mutant phenotype and genetic interactions suggest a role in delivering mt mRNAs to the mitochondrial ribosome)
| Gene | Function |
|------|----------|
| YDR183c | Amino acid metabolism (tryptophan biosynthesis) |
| Aum45 | Unknown |
| Yce1 | Protein import and Preprotein (Hsp70 family ATPase; constituent of the import motor component of the Translocase of the Outer Mitochondrial membrane (TIM23 complex); involved in protein translocation) |
| Mgm110 | mRNA replication/recombination/repair (protein with a role in mitochondrial DNA recombinational repair; also involved in transcription-cross link repair; component of the mitochondrial nucleoid, required for mitochondrial genome organization) |
| Hem15 | Mitochondrial synthesis (terrestrial; a mitochondrial inner membrane protein, catalyzes insertion of ferrous iron into protoporphyrin IX, the eighth and final step in the heme biosynthetic pathway) |
| Pef1 | Mitochondrial transport (membrane-bound RNA; required for maintenance of mitochondrial membrane permeability) |
| Mrp1 | mRNA translation ( mitochondrial RNA; encoded by the mitochondrial DNA) |
| Cox15A1 | ETC/respiration (cytochrome c oxidase 5A; also involved in the respiratory complex) |
| Yja1 | Lipid metabolism (glycerol-3-phosphate dehydrogenase involved in glycerol biosynthesis) |
| Yme2 | Mitochondria (cytochrome c oxidase; subunit of the mitochondrial inner membrane electron transport chain) |
| Fmp30 | Protein import (component of the TOM (translocase of outer membrane) complex; involved in the recognition and initial import steps for all mitochondrially directed proteins) |
| Num1 | Mitochondria (ER contact site component of mitochondria-ER-cortex-anchor (Meca); required for the association of mitochondria with the cell cortex; interacts with Mdm36p to form the ER and mitotic machinery) |
| Nde1 | ETC/respiration (external mitochondrial matrix dehydrogenase; provides cytosolic NADH to the mitochondrial respiratory chain) |
| Cyp9 | Ribosome assembly (mitochondrial ribosomal protein) |
| Adh3 | Carbohydrate metabolism (inositol phosphosphingolipid phospholipase C; hydrolyzes complex sphingolipids to produce ceramide) |
| Sox1 | Lipid metabolism (bifunctional triacylglycerol lipase and 1-acyl 2-acyl dihydroxyacetone phosphatase) |
| Mrx3 | Lipid metabolism (involved in maintaining normal cardiolipin levels) |
| Mus51 | ETC/respiration (ubiquinol cytochrome c reductase subunit IV; homodimeric complex) |
| Mrp1 | mRNA translation ( mitochondrial RNA; encoded by the mitochondrial DNA) |
| Mrx3 | Lipid metabolism (involved in maintaining normal cardiolipin levels) |
| Ysc83 | Unknown |
| Ald6 | Carbohydrate metabolism (aldehyde dehydrogenase; required for conversion of acetaldehyde to acetate) |
| Mst1 | Mitochondria (mitochondrial ribosomal protein) |
| Arg7 | Unknown |
| Sdh2 | Unknown |
| Om45 | Amino acid metabolism (homoarginine dehydrogenase; involved in homocitrulline metabolism) |
| Aim46 | Unknown |
| Lipid metabolism (inositol phosphosphingolipid phospholipase C; hydrolyzes complex sphingolipids to produce ceramide) |
| Carbohydrate metabolism (NADH-ubiquinone oxidoreductase; transfers electrons from NADH to ubiquinone in respiratory chain) |
| Mitophagy (mitochondrial mitophagy, cytochrome c oxidase 5A; also involved in the respiratory complex) |
| mtDNA replication/recombination/repair (role in maintaining mitochondrial nucleoid structure and number; mutants exhibit an increased rate of mitochondrial DNA escape) |
| Gene  | pAim  | Function and Location | Note |
|-------|-------|-----------------------|------|
| Pnt1  | 2.26  | Proteostasis (mitochondrial integral inner membrane protein; involved in membrane insertion of C-terminus of Cox2p) | |
| Aim19 | 2.26  | Unknown               | |
| Yim1  | 2.28  | Unknown               | |
| Aim37 | 2.31  | Contact sites/cristae maintenance (component of the MICOS [Mitochondrial contact site and cristae organizing system] complex. MICOS is a mitochondrial inner membrane complex that extends into the intermembrane space and has a role in the maintenance of cristas, inner membrane architecture, and formation of contact sites to the outer membrane) | |
| Pam18 | 2.33  | Protein import (subset of the import motor (PAM complex); the PAM complex is a component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); essential 3-protein co-chaperone that promotes import) | |
| Chp3  | 2.35  | Proteostasis and protein synthesis (mitochondrial protein required for assembly of cytochrome b1 complex; forms complex with Chp6p that binds to mt ribosomes near the polypeptide tunnel exit and promotes Chp3p-Chp6p complex also interacts with newly synthesized cytochrome b (Chop) and Chp6p to promote assembly of Chop into the cytochrome b1 complex) | |
| Mic1  | 2.37  | Unknown               | |
| Aip54 | 2.39  | ATP synthesis (subset b of the F1 sector of mitochondrial F1F0 ATP synthase) | |
| Cox13 | 2.46  | ETC/respiration and Proteostasis (subset VIa of cytochrome c oxidase; present in a subclass of cytochrome c oxidase complexes that may have a role in minimizing generation of reactive oxygen species; not yet but may modulate activity in response to ATP; required for assembly of RCe2p into cytochrome c oxidase - cytochrome bc1 supercomplexes) | |
| Fum43 | 2.47  | Metabolite transport (subset of the mitochondrial pyruvate carrier (MPC); MPC localizes to the mitochondrial inner membrane and mediates pyruvate uptake) | |
| Qcr8  | 2.58  | ETC/respiration (subset b of ubiquinol cytochrome-c reductase (Complex III); Complex III is a component of the mitochondrial inner membrane electron transport chain) | |
| YFL106K | 2.65 | Unknown               | |
| Ysc1  | 2.78  | Proteostasis (non-proteolytic ATPase of the AAA family; stimulates incorporation of the pyridoxal phosphate cofactor into Hem1p (5-aminolevulinic acid synthase)) | |
| Cox11 | 3.04  | Proteostasis (protein required for delivery of copper to Cox1p) | |
| Aca1  | 3.06  | Carbohydrate metabolism (acyl-CoA synthetase isoform) | |
| Her1  | 3.06  | Unknown               | |
| Ssc1  | 3.07  | Proteostasis and ETC/respiration (copper-binding protein of mitochondrial inner membrane; required for cytochrome c oxidase activity and respiration; may function to deliver copper to cytochrome c oxidase supercomplexes) | |
| Bna4  | 3.24  | Metabolite synthesis (kynurenine 3-monooxygenase; required for the de novo biosynthesis of NAD from tryptophan via kynurenine) | |
| Idg3  | 3.34  | Amino acid metabolism (NADP-dependent isocitrate dehydrogenase; catalyzes oxidation of isocitrate to alpha-ketoisocitrate with the formation of NADPH+; involved in glutamate biosynthesis) | |
| Grl1  | 3.39  | Redox homeostasis (glutathione S-transferase; involved in glutathione-glutaredoxin redox reactions) | |
| Aim46 | 3.80  | Unknown               | |
| Aip57 | 3.95  | ATP synthesis (subset d of the stator stalk of mitochondrial F1F0 ATP synthase) | |
| Tim23 | 4.03  | Protein import (essential component of the TIM23 [translocase of the inner mitochondrial membrane] complex; involved in protein import into mitochondrial matrix and inner membrane) | |
| YLR419W | 4.31 | Unknown               | |
| Chp4  | 4.33  | Proteostasis (required for assembly of cytochrome b1 complex; interacts with the Chp3p-Chp6p complex and newly synthesized cytochrome b (Chop) to promote assembly of Chop into the cytochrome b1 complex) | |
| Tol20 | 5.31  | Protein import (component of the TOM [translocase of outer membrane] complex; responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming proteins) | |
| Lrt1  | 5.51  | Unknown               | |
| Glc2  | 5.62  | Redox homeostasis (glutaredoxin/thioredoxin, glutathione-dependent dithiol oxidoreductase involved in maintaining redox state of target proteins, also exhibits glutathione peroxidase activity) | |
| Pet10 | 8.16  | Unknown               | |