**Glucose metabolic reprogramming and modulation in glycerol biosynthesis regulates drug resistance in clinical isolates of *Candida***

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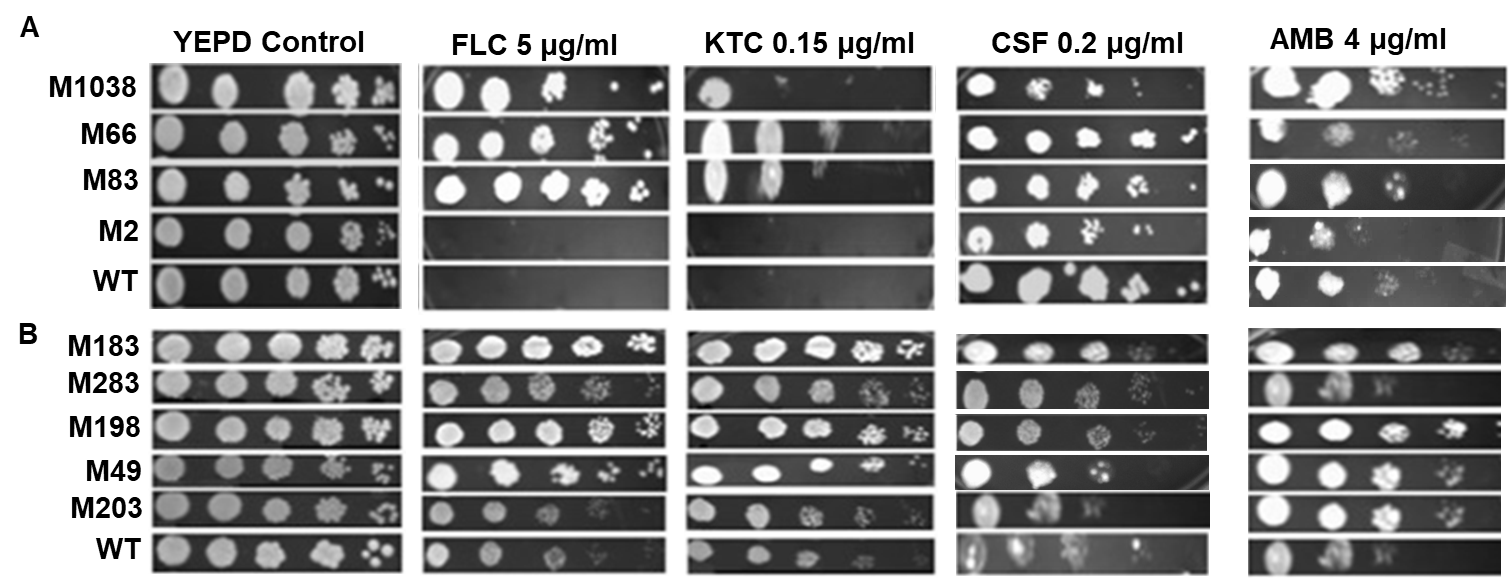
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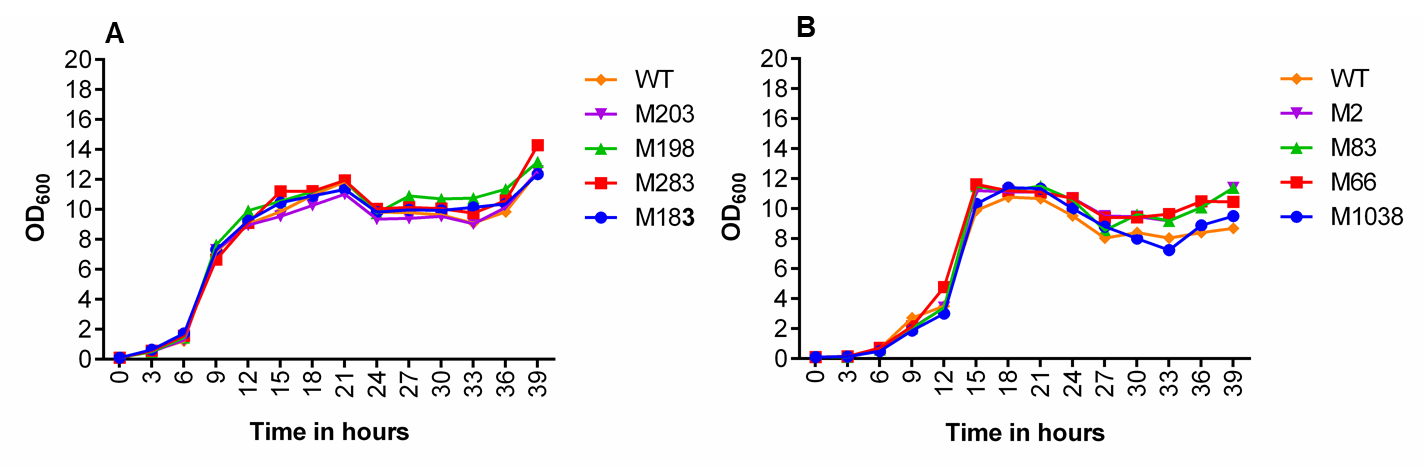
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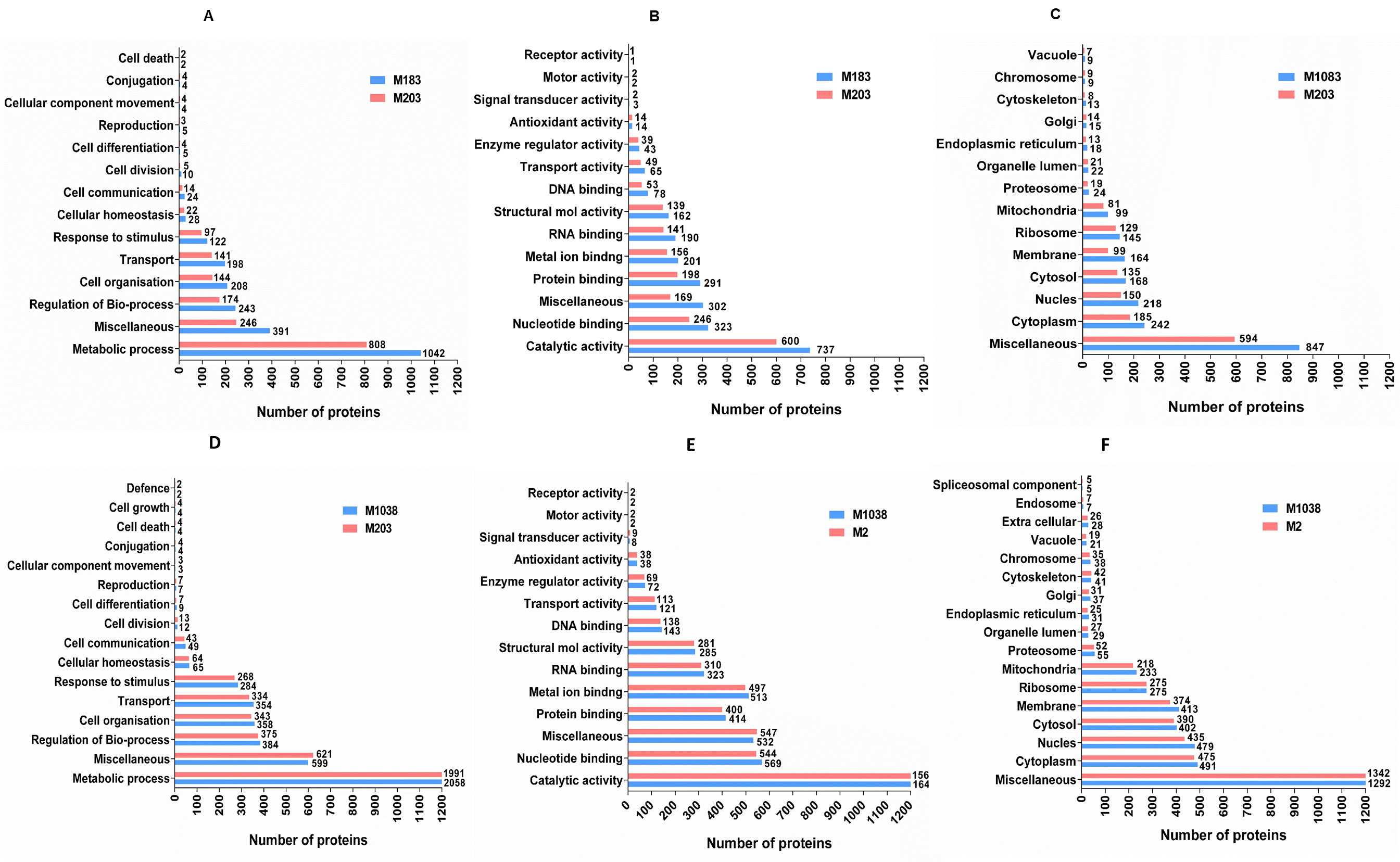
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**Running Title: IM and *Candida* Drug Resistance**

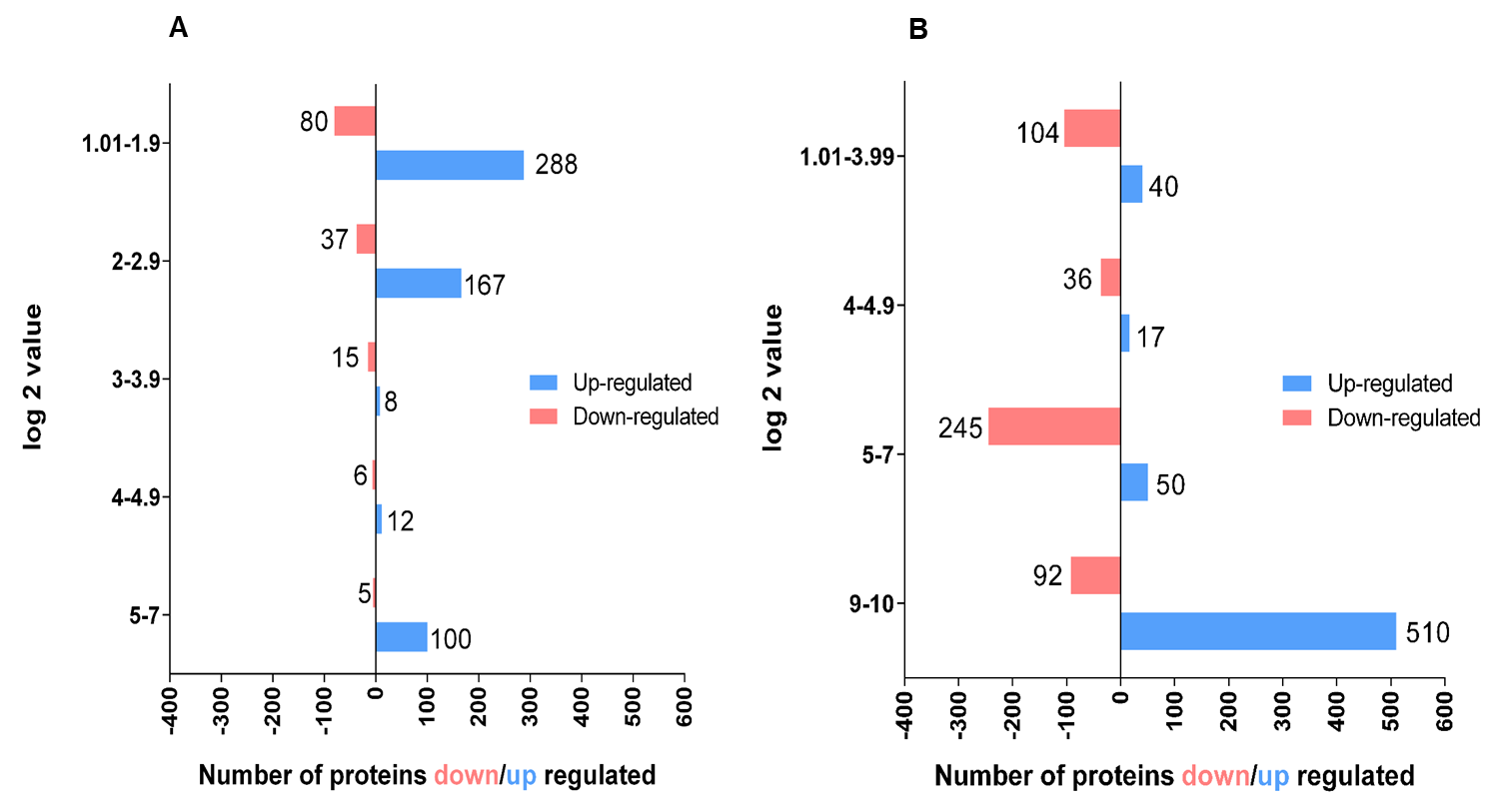
**Supplementary Information:**

** Figure S1: Spot assay-based drug susceptibility analysis of *Candida.* (**A) Spot assay-based drug susceptibility analysis of drug-resistant and drug-susceptible clinical isolates of *C. albicans* along with the corresponding wild-type strain, where M1038, M66, and M83 are the drug-resistant *C. albicans* clinical isolates; M2 is the drug-susceptible *C. albicans* clinical isolates; WT is the corresponding wild type strain (B) Spot assay based drug susceptibility analysis of drug-resistant and drug-susceptible clinical isolates of *C. glabrata* along with the corresponding wild type strain, where M183, M283, and M198 are the drug-resistant *C. glabrata* clinical isolates; M203 is the drug-susceptible *C. glabrata* clinical isolate; WT is the corresponding wild type strain.

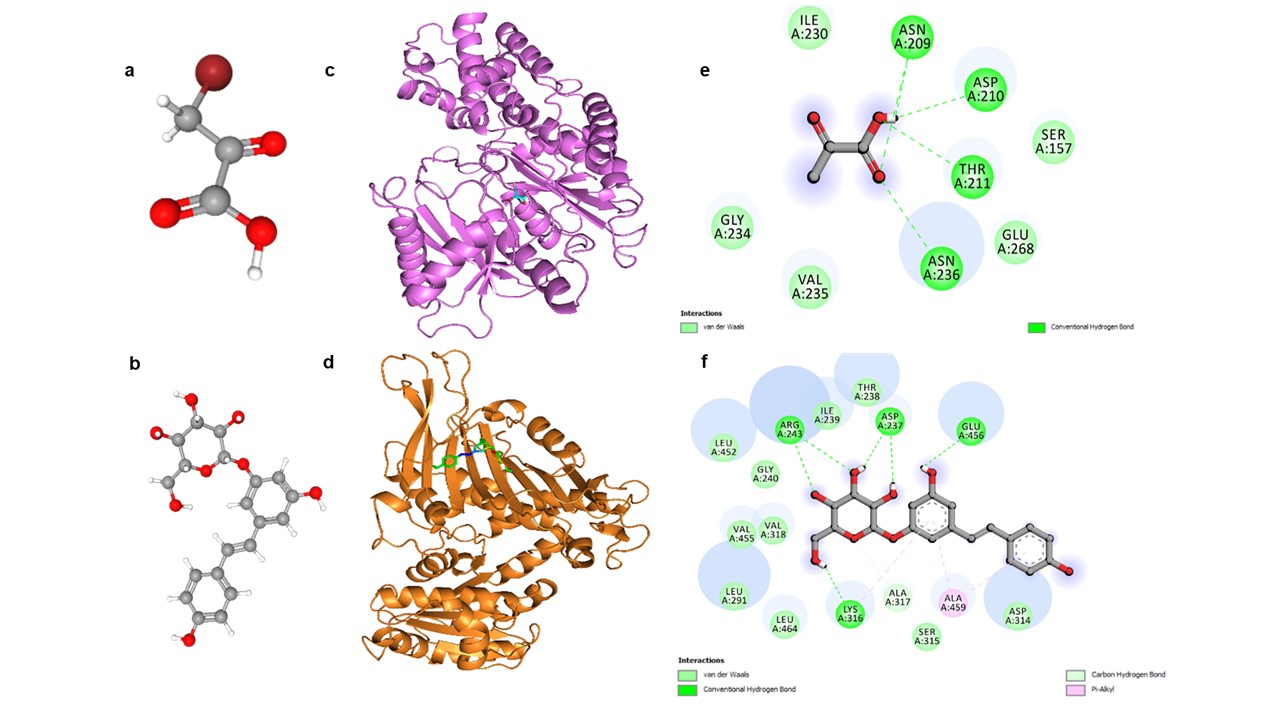
** Figure S2: Growth analysis of *Candida* strains. (**A) Growth analysis of drug-resistant and drug-susceptible clinical isolates of *C. glabrata* and corresponding wild-type strains, where M183, M283, and M198 are the drug-resistant *C. glabrata* clinical isolates; M203 is the drug-susceptible *C. glabrata* clinical isolate; WT is the corresponding wild type strain. (B) Growth analysis of drug-resistant and drug-susceptible clinical isolates of *C. albicans* along with the corresponding wild-type strain, where M1038, M66, and M83 are the drug-resistant *C. albicans* clinical isolates; M2 is the drug-susceptible *C. albicans* clinical isolate; WT is the corresponding wild type strain.

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**Figure S3: Classification of different proteins obtained in mass spectrometry in drug-resistant and drug-susceptible isolates of *C. albicans* and *C. glabrata* based on (**A and D) Biological processes (B and E) Molecular function and (C and F) Cellular component. Further, M183 and M203 represent drug-resistant and drug-susceptible clinical isolates of *C. glabrata*; M1038 and M2 represent drug-resistant and drug-susceptible clinical isolates of *C. albicans*.



**Figure S4: Differential expression profile of proteins in drug-resistant compared to drug-susceptible isolates of *C. albicans* and *C. glabrata*.** (A) Distribution of differentially expressed proteins possessing fold change greater than 1 into different subsets according to abundance (number of proteins) in each subset in drug-resistant *C. glabrata* (M183) compared to respective drug-susceptible (M203) isolate. (B) Distribution of differentially expressed proteins possessing fold changes greater than 1 into different subsets according to abundance (number of proteins) in each subset in drug-resistant *C. albicans* (M1038) compared to respective drug-susceptible (M2) isolate.



**Figure S5: *In-silico* molecular docking analysis of 3-Bromopyruvate and polydatin with *C. albicans* hexokinase 2 and glucose-6-phosphate dehydrogenase, respectively.** (A, B) represent the interaction of 3-Bromopyruvate with amino acids of hexokinase 2; (C, D) represent the interaction of polydatin with the amino acids of glucose-6-phosphate dehydrogenase; (E, F) represent three-dimensional molecular structures of 3-Bromopyruvate and polydatin respectively.

**Table S1: Detailed list of materials and reagents used in the study**

|  |  |  |  |
| --- | --- | --- | --- |
| **Reagent** | **Source & Cat No.** | **Reagent** | **Source & Cat No.** |
| Yeast extract peptone dextrose (YEPD) | HiMedia (*#M1363*) | Sodium Fluoride | Sigma- Aldrich (*#20114*) |
| HiCandidaTM identification kit | HiMedia (#KB006) | Yeast/ Fungal Protease arrest | G Biosciences (*#786-333*) |
| *Msp*I enzyme | New England Biolabs (*#R0106S*) | PhosStop | Roche (*#4906845001*) |
| DNase I | Thermo Scientific EN0521 | Calcofluor white | Sigma- Aldrich 18909 |
| RNase A | Sigma-Aldrich (*#R6148*) | Congo red | Sigma- Aldrich (*#C6277*) |
| RevertAid First Strand cDNA Synthesis Kit | Thermo Scientific (*#K1622*) | Hydrogen peroxide solution | Sigma-Aldrich  *(#7722-84-1*) |
| Q5® High-Fidelity DNA Polymerase | New England Biolabs (*#M0491S*) | DCFDA | Sigma-Aldrich  (*#D6883*) |
| Trizol reagent | Sigma-Aldrich (*#T9424*) | Bromopyruvic acid | Sigma-Aldrich (*#1113-59-3*) |
| Glycerol | Sigma-Aldrich (*#9012*) | Polydatin [Reservatrol-3-β-mono-D-glucoside] | Sigma-Aldrich (*#65914-17-2*) |
| HEPES | Sigma-Aldrich (*#*[*7365-45-9*](https://www.sigmaaldrich.com/IN/en/search/7365-45-9?focus=products&page=1&perpage=30&sort=relevance&term=7365-45-9&type=cas_number)) | PVDF membrane | Amersham (*#GE10600023*) |
| Free Glycerol Reagent | (Sigma-Aldrich *(# MAK117*) | Immobilon Forte Western Substrate | Merck (*#WBLUF0100*) |
| Glucose uptake kit | Eton Bioscience (*#SKU- 1200032002*) | Anti-phospho-p38 antibody | Cell Signaling Technology *#9211* |
| Lactate measurement kit | Eton Bioscience (*#SKU- 1200012002*) | Anti-hexokinase 2 antibody | Rockland antibodies and assays (*#200-4359S*) |
| ATP Colorimetric/Fluorometric Kit | Bio vision *(#K354-100*) | Anti- glucose-6-phosphate dehydrogenase | Sigma-Aldrich (*#A9521-1VL*) |
| Amplite Colorimetric NADPH Assay Kit | AAT Bioquest (*#15272*) | Anti-β-actin antibody | Genetex (*#GTX109639*) |
| PMSF | Thermo Scientific (*#36978*) | Anti-rabbit HRP secondary antibody | CST (*#7074*) |

**Table S2: Detailed list of various clinical isolates procured and used in the study**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S. No** | **Strain** | **Source** | **S. No** | **Strain** | **Source** | **S. No** | **Strain** | **Source** |
| 1 | M15/Ck | Blood | 30 | M1056/Ck | Blood | 59 | M1037/Cg | Urine |
| 2 | M637/Ck | Blood | 31 | M8/Ck | Blood | 60 | M1057/Cg | Urine |
| 3 | M1012/Ck | Urine | 32 | M14/Ck | Blood | 61 | M203/Cg | Urine |
| 4 | M1022/Ck | Urine | 33 | M42/Ck | Blood | 62 | M183/Cg | Urine |
| 5 | M320/Ck | Blood | 34 | M253/Ck | Blood | 63 | M626/Cg | Urine |
| 6 | M321/Ck | Blood | 35 | M280/Ck | Blood | 64 | M283/Cg | Urine |
| 7 | M348/Ck | Blood | 36 | M425/Ck | Blood | 65 | M198/Cg | Urine |
| 8 | M99/Ck | Blood | 37 | M417/Ck | Urine | 66 | M49/Cg | Urine |
| 9 | M116/Ck | Blood | 38 | M745/Ck | Blood | 67 | M717/Cp | Urine |
| 10 | M306/Ck | Sputum | 39 | M586/Ck | Blood | 68 | M463/Cp | Urine |
| 11 | M360/Ck | Blood | 40 | M2/Ca | Blood | 69 | M551/Cp | Blood |
| 12 | M378/Ck | Blood | 41 | M1038/Ca | Blood | 70 | M30/Cp | Blood |
| 13 | M752/Ck | Blood | 42 | M169/Ca | Urine | 71 | M342/Cp | Urine |
| 14 | M357/Ck | Blood | 43 | M100/Ca | Urine | 72 | M742/Cp | Urine |
| 15 | M363/Ck | Blood | 44 | M194/Ca | Sputum | 73 | M336/Cp | Urine |
| 16 | M264/Ck | Blood | 45 | M67/Ca | Urine | 74 | M168/Cp | Urine |
| 17 | M365/Ck | Blood | 46 | M3/Ca | Blood | 75 | M529/Cp | Blood |
| 18 | M366/Ck | Blood | 47 | M66/Ca | Sputum | 76 | M478/Cp | Blood |
| 19 | M377/Ck | Blood | 48 | M295/Ca | Blood | 77 | M276/Cp | Blood |
| 20 | M426/Ck | Blood | 49 | M35/Ca | Blood | 78 | M1068/Cp | Blood |
| 21 | M175/Ck | Blood | 50 | M46/Ca | Urine | 79 | M90/Cr | Urine |
| 22 | M241/Ck | Blood | 51 | M26/Ca | Urine | 80 | M196/Cr | Urine |
| 23 | M1031/Ck | Urine | 52 | M6/Ca | Blood | 81 | M666/Ct | Urine |
| 24 | M403/Ck | Blood | 53 | M83/Ca | Urine | 82 | M729/Ct | Urine |
| 25 | M783/Ck | Blood | 54 | M39/Ca | Urine | 83 | M144/Cg | pus |
| 26 | M615/Ck | Urine | 55 | M738/Ca | Urine | 84 | M328/Cl | pus |
| 27 | M457/Ck | Blood | 56 | M195/Ca | Urine |  |  |  |
| 28 | M462/Ck | Blood | 57 | M54/Ca | pus |  |  |  |
| 29 | M903/Ck | Blood | 58 | M349/Cg | Urine |  |  |  |

**Table S3: Interpretive guidelines for in-vitro susceptibility testing of *C. albicans* and *C. glabrata* against different antifungal drugs used in the study.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Antifungal agent | Species | MIC range (μg/ml) | | |
| S | I | R |
| Fluconazole | *C. albicans* | ≤2 | 4 | ≥8 |
| *C. glabrata* | 1 | ≤32 | ≥64 |
| Caspofungin | *C. albicans* | ≤0.25 | 0.5 | ≥1 |
| *C. glabrata* | ≤0.12 | 0.25 | ≥0.5 |
| Amphotericin B | *C. albicans* | ≤1 | 1-4 | ≥4 |
| *C. glabrata* | ≤1 | 1-4 | ≥4 |
| Ketoconazole | *C. albicans* | ≤0.0625 | 0.0125-0.5 | ≥1 |
| *C. glabrata* | ≤0.0625 | 0.0125-0.5 | ≥1 |
| Miconazole | *C. albicans* | ≤4 | 8-32 | ≥64 |
| *C. glabrata* | ≤4 | 8-32 | ≥64 |

**Table S4: MIC80 (in μg/ml) of different classes of antifungal drugs against clinical isolates of *C. parapsilosis*.(R) represents resistant isolates.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **FLC** | **KTC** | **MICO** | **CSF** | **AMB** |
| M276 | 32 (R) | 0.0625 | 0.5 | 0.0625 | 0.5 |
| M463 | 4 | 0.0039 | 0.125 | 0.8 | 4 |
| M551 | 16 (R) | 0.0039 | 0.5 | 0.8 | 4 |
| M478 | 2 | 0.00097 | 0.5 | 0.8 | 4 |
| M742 | 16 (R) | 0.0078 | 0.5 | 0.8 | 4 |
| M336 | 8 (R) | 0.0039 | 0.5 | 0.8 | 4 |
| M1068 | 8 (R) | 0.0078 | 0.5 | 0.8 | 4 |
| M529 | 16 (R) | 0.0039 | 0.5 | 0.8 | 4 |
| M30 | 1 | 0.0039 | 0.125 | 0.8 | 4 |
| M717 | 0.5 | 0.0039 | 0.125 | 0.8 | 4 |
| M168 | 1 | 0.0039 | 0.125 | 0.4 | 2 |
| M342 | 2 | 0.0078 | 0.125 | 0.8 | 0.5 |
| WT | 4 | 0.00097 | 0.0078 | 0.4 | 0.5 |

**Table S5: MIC80 (in μg/ml) of different classes of antifungal drugs against clinical isolates of C. *krusei***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **FLC** | **KTC** | **MICO** | **CSF** | **AMB** |
| M1022 | 64 | 0.125 | 1 | 0.05 | 4 |
| M425 | 256 | 0.125 | 0.5 | 0.0125 | 4 |
| M360 | 256 | 0.125 | 1 | 0.05 | 4 |
| M403 | 256 | 0.0625 | 0.5 | 0.025 | 4 |
| M426 | 256 | 0.125 | 0.5 | 0.025 | 4 |
| M377 | 256 | 0.125 | 0.25 | 0.05 | 4 |
| M417 | 256 | 0.125 | 0.5 | 0.05 | 4 |
| M378 | 256 | 0.125 | 0.5 | 0.00625 | 4 |
| M783 | >256 | 0.5 | >2 | 0.05 | 2 |
| M745 | >256 | >0.5 | 2 | 1.6 | 2 |
| M752 | 256 | 0.125 | 2 | 0.00625 | 4 |
| M615 | 2 | 0.125 | 0.25 | 0.8 | 16 |
| M586 | 256 | >0.5 | 2 | 0.00625 | 4 |
| M15 | 64 | 0.125 | 1 | 0.05 | 4 |
| M637 | 64 | 0.125 | 1 | 0.05 | 4 |
| M1012 | 64 | 0.125 | 1 | 0.05 | 4 |
| M320 | 64 | 0.125 | 1 | 0.05 | 4 |
| M321 | 64 | 0.125 | 1 | 0.05 | 4 |
| M348 | 64 | 0.125 | 1 | 0.05 | 4 |
| M99 | 64 | 0.125 | 1 | 0.05 | 4 |
| M116 | 64 | 0.125 | 1 | 0.05 | 4 |
| M357 | 64 | 0.125 | 1 | 0.05 | 4 |
| M363 | 256 | 0.125 | 0.5 | 0.025 | 4 |
| M264 | 256 | 0.125 | 0.5 | 0.025 | 4 |
| M365 | 256 | 0.125 | 0.5 | 0.025 | 4 |
| M366 | 256 | 0.125 | 0.5 | 0.025 | 4 |
| M175 | 256 | 0.125 | 0.5 | 0.025 | 4 |
| M241 | 256 | 0.125 | 0.5 | 0.025 | 4 |
| M1031 | 64 | 0.125 | 1 | 0.05 | 4 |
| M457 | 64 | 0.125 | 1 | 0.05 | 4 |
| M462 | 64 | 0.125 | 1 | 0.05 | 4 |
| M903 | 64 | 0.125 | 1 | 0.05 | 4 |
| M1056 | 64 | 0.125 | 1 | 0.05 | 4 |
| M8 | 64 | 0.125 | 1 | 0.05 | 4 |
| M14 | 64 | 0.125 | 1 | 0.05 | 4 |
| M42 | 64 | 0.125 | 1 | 0.05 | 4 |
| M253 | 64 | 0.125 | 1 | 0.05 | 4 |
| M280 | 64 | 0.125 | 1 | 0.05 | 4 |
| M306 | 64 | 0.125 | 1 | 0.05 | 2 |
| WT | 48 | 0.125 | 0.375 | 0.0125 | 2 |

**Table S6: MIC80 (in μg/ml) of different classes of antifungal drugs against clinical isolates of some rare *Candida* species**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **FLC** | **KTC** | **MICO** | **AMB** | **CSF** |
| M196 | 8 | 0.0156 | 0.312 | 0.0125 | 0.5 |
| M90 | 128 | 1 | 0.125 | 8 | 0.0039 |
| M666 | 8 | 0.0156 | 0.312 | 0.0125 | 0.5 |
| M729 | 8 | 0.0156 | 0.312 | 0.0125 | 0.5 |
| M328 | 64 | 0.25 | 0.5 | 16 | 0.5 |
| M144 | 128 | 0.0625 | 4 | 8 | 0.5 |

# (Where M196/M90 = *C. rugosa*; M328= *Yarrowia lipolytica*; M666/M729 = *C. tropicalis*; M144= *Meyerozyma guilliermondii*)

**Table S7: Mass spectrometry-based whole-cell proteome analysis of drug-resistant *Candida* isolates versus corresponding drug-susceptible isolates**

1. Mass spectrometry-based whole cell proteome analysis of drug-resistant *C. albicans* versus corresponding drug susceptible isolate.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Accession** | | **Description** | **Abundance Ratio (log2): (M1038) / (M2)** | |
| **Proteins down-regulated in drug-resistant isolate** | | | | |
| C4YIL8 | Pyruvate kinase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04294 PE=3 SV=1 | | | -9.97 |
| B9WBK1 | Pyruvate kinase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_19920 PE=3 SV=1 | | | -9.97 |
| B9WEW8 | Triosephosphate isomerase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=TPI1 PE=3 SV=1 | | | -9.97 |
| B9WIG8 | Ketol-acid reductoisomerase, mitochondrial OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_60880 PE=3 SV=1 | | | -9.97 |
| B9WCJ1 | Stress response protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_23350 PE=4 SV=1 | | | -9.97 |
| B9W8U1 | Dihydroxyacetone kinase 1, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_08670 PE=4 SV=1 | | | -9.97 |
| A0A1D8PP39 | Aamy domain-containing protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.3982 PE=4 SV=1 | | | -9.97 |
| B9WIR8 | NADH-cytochrome b5 reductase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_62170 PE=3 SV=1 | | | -9.97 |
| B9W9I2 | Vigilin-like protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_11110 PE=4 SV=1 | | | -9.97 |
| Q9P837 | Actin binding protein (Fragment) OS=Candida albicans OX=5476 GN=abp1 PE=2 SV=1 | | | -9.97 |
| B9WI36 | Alpha-glucosidase (Maltase), putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_54540 PE=4 SV=1 | | | -9.97 |
| A0A2R4LN72 | Mannose phosphate isomerase (Fragment) OS=Candida albicans OX=5476 GN=MPIb PE=4 SV=1 | | | -9.97 |
| A0A075MHE7 | Mannose phosphate isomerase (Fragment) OS=Candida albicans OX=5476 GN=MPIb PE=4 SV=1 | | | -9.97 |
| C4YJX9 | Epimerase domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05771 PE=4 SV=1 | | | -9.97 |
| A0A1D8PHQ6 | Gre2p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GRE2 PE=4 SV=1 | | | -9.97 |
| C4YDL6 | GTP-binding protein 128up OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00613 PE=4 SV=1 | | | -9.97 |
| C4YFD6 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01253 PE=4 SV=1 | | | -9.97 |
| B9WJG6 | Uncharacterized protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_70560 PE=4 SV=1 | | | -9.97 |
| C4YDD4 | NADH-ubiquinone oxidoreductase subunit 8 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00527 PE=3 SV=1 | | | -9.97 |
| A0A1D8PEH4 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4758 PE=3 SV=1 | | | -9.97 |
| C4YGB6 | 26S proteasome regulatory subunit RPN2 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00237 PE=3 SV=1 | | | -9.97 |
| Q5A3L0 | 26S proteasome regulatory subunit RPN2 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=RPN2 PE=3 SV=1 | | | -9.97 |
| B9W9J9 | 26S proteasome regulatory subunit RPN2 OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_11280 PE=3 SV=1 | | | -9.97 |
| A0A1D8PN69 | Carboxypeptidase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PRC2 PE=3 SV=1 | | | -9.97 |
| C4YR33 | Carboxypeptidase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04532 PE=3 SV=1 | | | -9.97 |
| C4YES7 | GTP-binding protein YPT1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01035 PE=4 SV=1 | | | -9.97 |
| B9WB78 | Acyl carrier protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_18680 PE=3 SV=1 | | | -9.97 |
| C4YI89 | Acyl carrier protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04161 PE=3 SV=1 | | | -9.97 |
| C4YS91 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04950 PE=4 SV=1 | | | -9.97 |
| Q59Z57 | Prb1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PRB1 PE=3 SV=1 | | | -9.97 |
| C4YJZ5 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05787 PE=3 SV=1 | | | -9.97 |
| B6C801 | Wwm1 OS=Candida albicans OX=5476 PE=4 SV=1 | | | -9.97 |
| O94060 | Hypothetical transmembrane protein OS=Candida albicans OX=5476 GN=Ca49C4.01 PE=4 SV=1 | | | -9.97 |
| C4YL09 | WW domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01523 PE=4 SV=1 | | | -9.97 |
| B9WFG1 | Pentafunctional AROM polypeptide OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=ARO1 PE=3 SV=1 | | | -9.97 |
| A0A1D8PI07 | Serine/threonine protein kinase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=RCK2 PE=4 SV=1 | | | -9.97 |
| B9WC00 | Serine/threonine protein kinase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_21410 PE=4 SV=1 | | | -9.97 |
| C4YK16 | Serine/threonine-protein kinase srk1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05810 PE=4 SV=1 | | | -9.97 |
| O42765 | Elongation-like factor OS=Candida albicans OX=5476 GN=ELF PE=4 SV=1 | | | -9.97 |
| B9WMV0 | [NU+] prion formation protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_34680 PE=4 SV=1 | | | -9.97 |
| C4YMX0 | mRNA export factor elf1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02207 PE=4 SV=1 | | | -9.97 |
| C4YSR5 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05134 PE=4 SV=1 | | | -9.97 |
| B9WDU1 | DNA repair protein rad50 homologue, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_83290 PE=4 SV=1 | | | -9.97 |
| A0A1D8PJR3 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.332.1 PE=4 SV=1 | | | -9.97 |
| Q96W31 | Subtilisin-like protease PRB1 (Fragment) OS=Candida albicans OX=5476 PE=3 SV=1 | | | -9.97 |
| A0A1D8PRY9 | Protein transport protein Sec61 subunit beta OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_CR01490CA PE=3 SV=1 | | | -9.97 |
| A0A1D8PPA8 | 2-aminoadipate transaminase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.1180 PE=4 SV=1 | | | -9.97 |
| B9WF03 | Fructose-1,6-bisphosphatase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_87700 PE=3 SV=1 | | | -9.97 |
| Q9UUZ0 | Putative fructose-1,6-bisphosphatase OS=Candida albicans OX=5476 GN=FBP1 PE=3 SV=1 | | | -9.97 |
| A0A1D8PKC9 | Dynamin-related GTPase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=DNM1 PE=3 SV=1 | | | -9.97 |
| B9WED6 | Dynamin-related protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_85490 PE=3 SV=1 | | | -9.97 |
| C4YNS9 | Dynamin-type G domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02862 PE=3 SV=1 | | | -9.97 |
| A0A1D8PFP3 | 5'-3' exoribonuclease 1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=KEM1 PE=3 SV=1 | | | -9.97 |
| B9W9W4 | 5'-3' exoribonuclease 1 OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_12450 PE=3 SV=1 | | | -9.97 |
| C4YFZ6 | 5'-3' exoribonuclease 1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00109 PE=3 SV=1 | | | -9.97 |
| Q5A7P6 | Mitochondrial 54S ribosomal protein RML2 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.5420 PE=4 SV=1 | | | -9.97 |
| C4YPH9 | 60S ribosomal protein RML2, mitochondrial OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02380 PE=4 SV=1 | | | -9.97 |
| B9WD22 | Ribosomal protein of the large subunit, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_80410 PE=4 SV=1 | | | -9.97 |
| Q5A2U9 | V-type proton ATPase subunit C OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=VMA5 PE=3 SV=1 | | | -9.97 |
| C4YKB3 | V-type proton ATPase subunit C OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05910 PE=3 SV=1 | | | -9.97 |
| B9WC95 | V-type proton ATPase subunit C OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_22370 PE=3 SV=1 | | | -9.97 |
| B9W8S5 | NADH-ubiquinone oxidoreductase 23 subunit, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_08510 PE=3 SV=1 | | | -9.97 |
| C4YMQ6 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02140 PE=4 SV=1 | | | -9.97 |
| C4YSD5 | CS domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04998 PE=4 SV=1 | | | -9.97 |
| Q5AI97 | Mitochondrial genome maintenance protein MGM101 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MGM101 PE=3 SV=2 | | | -9.97 |
| C4YF07 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01117 PE=4 SV=1 | | | -9.97 |
| B9W749 | Mitochondrial-genome maintenance, protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_02480 PE=4 SV=1 | | | -9.97 |
| Q5AHZ4 | Ubiquinone biosynthesis monooxygenase COQ6, mitochondrial OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=COQ6 PE=3 SV=1 | | | -9.97 |
| A0A1D8PLD9 | M20\_dimer domain-containing protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4610 PE=4 SV=1 | | | -9.97 |
| A0A1D8PJ94 | CHCH domain-containing protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.1667.1 PE=4 SV=1 | | | -9.97 |
| Q59MN0 | Vacuolar protein 8 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=VAC8 PE=3 SV=3 | | | -9.97 |
| C4YGW4 | Vacuolar protein 8 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03300 PE=4 SV=1 | | | -9.97 |
| B9WGH4 | Vacuolar inheritance protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=VAC8 PE=4 SV=1 | | | -9.97 |
| C4YSP0 | RRM domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05108 PE=4 SV=1 | | | -9.97 |
| A0A1D8PPX7 | Nab3p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=NAB3 PE=4 SV=1 | | | -9.97 |
| Q9P8Q4 | Fructose 1,6-bisphosphatase OS=Candida albicans OX=5476 GN=FBP1 PE=3 SV=1 | | | -9.97 |
| B9WDB1 | EH domain-containing protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_81330 PE=4 SV=1 | | | -9.97 |
| C4YPS0 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02472 PE=4 SV=1 | | | -9.97 |
| Q5AJ82 | Actin cytoskeleton-regulatory complex protein END3 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=END3 PE=2 SV=1 | | | -9.97 |
| B9WBM9 | Uncharacterized protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_20200 PE=4 SV=1 | | | -9.97 |
| Q59T30 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.6887 PE=4 SV=1 | | | -9.97 |
| Q5A4M2 | Malate dehydrogenase (Oxaloacetate-decarboxylating) OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MAE1 PE=4 SV=1 | | | -9.97 |
| B9WIN4 | NAD-dependent malic enzyme, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_61770 PE=4 SV=1 | | | -9.97 |
| A0A1D8PFU2 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.7210 PE=3 SV=1 | | | -9.97 |
| B9WA20 | Uncharacterized protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_13010 PE=3 SV=1 | | | -9.97 |
| A0A1D8PRU4 | Actin-related protein 2/3 complex subunit 4 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ARC19 PE=3 SV=1 | | | -9.97 |
| Q5A0H8 | Polyubiquitin-binding protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.5833 PE=4 SV=1 | | | -9.97 |
| C4YJM3 | Ubiquitin fusion degradation protein 1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04041 PE=4 SV=1 | | | -9.97 |
| B9WAU0 | Uncharacterized protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_17320 PE=4 SV=1 | | | -9.97 |
| C4YJH9 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03994 PE=4 SV=1 | | | -9.97 |
| Q5ALN3 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.1544 PE=4 SV=1 | | | -9.97 |
| A0A1D8PUB9 | Oligo-1,6-glucosidase IMA1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MAL2 PE=4 SV=1 | | | -6.91 |
| Q02751 | Alpha-glucosidase OS=Candida albicans OX=5476 GN=MAL2 PE=1 SV=4 | | | -6.91 |
| C4YT82 | Superoxide dismutase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05368 PE=3 SV=1 | | | -6.24 |
| B9WJN7 | Superoxide dismutase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=SOD3 PE=3 SV=1 | | | -6.24 |
| C4YR99 | Putative\_PNPOx domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04598 PE=4 SV=1 | | | -6.08 |
| Q5AGF9 | Pyridoxal 5'-phosphate synthase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4220 PE=4 SV=1 | | | -6.08 |
| B9WHD8 | Putative pyridoxamine 5'-phosphate oxidase ylr456w (Ec 1.4.3.5 (Pnp/pmp oxidase ylr456w) (Pnpox ylr456w)) OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_51960 PE=4 SV=1 | | | -6.08 |
| C4YNC6 | Sm domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01385 PE=4 SV=1 | | | -5.86 |
| A0A1D8PRP0 | U4/U6-U5 snRNP complex subunit OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=LSM6 PE=3 SV=1 | | | -5.86 |
| G1UAU6 | Uncharacterized protein CaJ7.0240 OS=Candida albicans OX=5476 GN=CaJ7.0240 PE=4 SV=1 | | | -5.78 |
| C4YJN8 | Oxidored\_FMN domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04056 PE=4 SV=1 | | | -5.78 |
| Q5A0J5 | Ebp7p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=EBP7 PE=4 SV=1 | | | -5.78 |
| C4YKY9 | PPM-type phosphatase domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01502 PE=3 SV=1 | | | -5.67 |
| B9WKY2 | Protein phosphatase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_26490 PE=3 SV=1 | | | -5.67 |
| C4YEG4 | Aldo\_ket\_red domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00921 PE=4 SV=1 | | | -5.63 |
| A0A1D8PDE2 | Aldo-keto reductase superfamily protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=LPG20 PE=4 SV=1 | | | -5.63 |
| Q5A923 | Ifd3p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=IFD3 PE=4 SV=1 | | | -5.63 |
| Q59WT0 | Actin-related protein 2/3 complex subunit 3 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ARC18 PE=3 SV=1 | | | -5.62 |
| B9WIJ3 | Actin-related protein 2/3 complex subunit 3 OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_61250 PE=3 SV=1 | | | -5.62 |
| A0A1D8PC77 | Ubiquitin carboxyl-terminal hydrolase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=UBP6 PE=3 SV=1 | | | -5.54 |
| C4YFL1 | Ubiquitin carboxyl-terminal hydrolase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01329 PE=3 SV=1 | | | -5.54 |
| Q8TGW9 | Putative transcriptional repressor OS=Candida albicans OX=5476 GN=SSN6 PE=4 SV=1 | | | -5.54 |
| Q5ADP3 | Transcription regulator OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SSN6 PE=1 SV=1 | | | -5.54 |
| C4YP67 | TPR\_REGION domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03010 PE=4 SV=1 | | | -5.54 |
| C4YSU5 | ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05164 PE=3 SV=1 | | | -5.51 |
| B9WIR7 | ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_62160 PE=3 SV=1 | | | -5.51 |
| Q59M69 | ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_C602030CA PE=3 SV=2 | | | -5.51 |
| A0A1D8PRL8 | Aminotran\_1\_2 domain-containing protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_CR00130CA PE=4 SV=1 | | | -5.47 |
| B9WKK8 | Aminotransferase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_25150 PE=4 SV=1 | | | -5.47 |
| C4YNB8 | Aminotran\_1\_2 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01374 PE=4 SV=1 | | | -5.47 |
| B9WB98 | Branched-chain-amino-acid aminotransferase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_18880 PE=3 SV=1 | | | -5.46 |
| C4YIA7 | Branched-chain-amino-acid aminotransferase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04179 PE=3 SV=1 | | | -5.46 |
| A0A1D8PH42 | Branched-chain-amino-acid aminotransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=BAT21 PE=3 SV=1 | | | -5.46 |
| B9WIV8 | NADP-dependent alcohol dehydrogenase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_62710 PE=3 SV=1 | | | -5.44 |
| B9WFX5 | T-complex protein 1 subunit delta OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_42650 PE=3 SV=1 | | | -5.43 |
| A0A1D8PTV7 | Putative cystathionine beta-lyase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_CR09010CA PE=3 SV=1 | | | -5.41 |
| A0A1D8PDA4 | Fma1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=FMA1 PE=3 SV=1 | | | -5.41 |
| C4YEJ2 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00949 PE=3 SV=1 | | | -5.41 |
| C4YSP4 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05112 PE=4 SV=1 | | | -5.37 |
| C4YI52 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03760 PE=4 SV=1 | | | -5.36 |
| A0A1D8PKZ4 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.5648 PE=4 SV=1 | | | -5.36 |
| B9WF98 | mRNA export receptor, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_40300 PE=4 SV=1 | | | -5.36 |
| C4YJK7 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04022 PE=4 SV=1 | | | -5.35 |
| A0A1D8PGR5 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.1578 PE=4 SV=1 | | | -5.35 |
| B9WAR4 | rRNA biogenesis protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_17060 PE=4 SV=1 | | | -5.35 |
| A0A1D8PKG5 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.7422 PE=4 SV=1 | | | -5.34 |
| C4YP14 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02949 PE=4 SV=1 | | | -5.34 |
| B9W8Y5 | Uncharacterized protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_09110 PE=4 SV=1 | | | -5.32 |
| Q59ZI8 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.3531 PE=4 SV=1 | | | -5.3 |
| C4YIH7 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04252 PE=4 SV=1 | | | -5.3 |
| B9WBG0 | Mitochondrial morphogenesis protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_19510 PE=4 SV=1 | | | -5.3 |
| A0A1D8PGF0 | Lysophospholipase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PLB4.5 PE=3 SV=1 | | | -5.28 |
| C4YJ98 | Lysophospholipase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03911 PE=3 SV=1 | | | -5.28 |
| A0A1D8PCJ1 | Mitochondrial 54S ribosomal protein YmL41 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MRP20 PE=4 SV=1 | | | -5.27 |
| B9W6V3 | 60S ribosomal protein L41, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_01470 PE=4 SV=1 | | | -5.27 |
| D7RYZ0 | Lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEY6 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| A0A0D5W9L9 | Cytochrome P450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SF10 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEW4 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| A0A0A0Y2M2 | Erg11 OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEV8 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEZ5 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| B2MV50 | Cytochrome P-450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=erg11 PE=3 SV=1 | | | -5.25 |
| C7DRL2 | Cytochrome P450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7DRM5 | Cytochrome P450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| D7RYY7 | Cytochrome P450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| A0A2L0P1A5 | Lanosterol 14-alpha demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| B0LVD9 | Cytochrome P-450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=erg11 PE=3 SV=1 | | | -5.25 |
| A0A2L0P1B2 | Lanosterol 14-alpha demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| A0A0A7RMJ3 | Cytochrome P450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=2 SV=1 | | | -5.25 |
| C7DRM7 | Cytochrome P450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| Q8J2U4 | Cytochrome P-450 lanosterol 14alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=erg11 PE=3 SV=1 | | | -5.25 |
| A0A0M3LD44 | Lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEV2 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| P10613 | Lanosterol 14-alpha demethylase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ERG11 PE=1 SV=2 | | | -5.25 |
| C7SEY1 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C8XRD6 | Cytochrome P-450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| A0A110A0T5 | Lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEW2 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEY9 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEZ4 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7DRL9 | Cytochrome P450 L1A1 OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
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| G1JT15 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| D7RYT6 | Lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| Q9P4V8 | CYP51 variant 3 OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
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| C7SEV7 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
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| A0A0A0Y6Q8 | Erg11 OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| A0A0A0Y6Q6 | Erg11 OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| D7RYY1 | Lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| B5B796 | Cytochrome P-450 lanosterol 14-alpha-demethylase OS=Candida albicans OX=5476 GN=erg11 PE=2 SV=1 | | | -5.25 |
| Q9P4V9 | CYP51 variant 2 OS=Candida albicans OX=5476 PE=3 SV=1 | | | -5.25 |
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| E7BZD9 | Cytochrome P450 L1A1 OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SEZ8 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
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| E2IPI4 | Lanosterol 14-alpha demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=4 SV=1 | | | -5.25 |
| C7SEX9 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
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| C7SEW1 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
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| A0A110A0P8 | Lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
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| A0A2Z3EEB8 | Cytochrome P450 lanosterol 14-alpha demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=4 SV=1 | | | -5.25 |
| C7SF04 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C7SF11 | Cytochrome P-450 lanosterol 14-alpha-demethylase (Fragment) OS=Candida albicans OX=5476 GN=ERG11 PE=3 SV=1 | | | -5.25 |
| C4YR82 | 4Fe-4S ferredoxin-type domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04581 PE=4 SV=1 | | | -5.25 |
| A0A1D8PNB3 | Putative electron-transferring-flavoprotein dehydrogenase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.3175 PE=4 SV=1 | | | -5.25 |
| B9WHC3 | Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_51810 PE=4 SV=1 | | | -5.25 |
| C4YFQ4 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00030 PE=4 SV=1 | | | -5.24 |
| A0A1D8PFW3 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.7234 PE=4 SV=1 | | | -5.24 |
| B9WFR1 | Uncharacterized protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_42000 PE=4 SV=1 | | | -5.22 |
| Q5AMR6 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4580 PE=4 SV=1 | | | -5.22 |
| C4YHN5 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03583 PE=4 SV=1 | | | -5.22 |
| C4YT27 | WD\_REPEATS\_REGION domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05725 PE=4 SV=1 | | | -5.21 |
| B9WJV4 | Histone acetyltransferase subunit, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_73630 PE=4 SV=1 | | | -5.21 |
| Q3MPF4 | Uncharacterized protein CaJ7.s008 OS=Candida albicans OX=5476 GN=CaJ7.s008 PE=4 SV=1 | | | -5.2 |
| C4YTP5 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05540 PE=4 SV=1 | | | -5.2 |
| P87187 | Cysteine desulfurase, mitochondrial OS=Candida maltosa OX=5479 GN=SPL1 PE=3 SV=1 | | | -5.15 |
| B9WLM6 | RNA cytidine acetyltransferase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=NAT10 PE=3 SV=1 | | | -5.14 |
| C4YLP2 | RNA cytidine acetyltransferase OS=Candida albicans (strain WO-1) OX=294748 GN=NAT10 PE=3 SV=1 | | | -5.14 |
| B9WEM8 | Cell wall biogenesis protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_86440 PE=4 SV=1 | | | -5.13 |
| A0A1D8PKH0 | Ecm15p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ECM15 PE=4 SV=1 | | | -5.13 |
| B9WA71 | Meiosis-specific transcription factor, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_15120 PE=4 SV=1 | | | -5.11 |
| Q5ACU9 | Transcription factor OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=NDT80 PE=4 SV=1 | | | -5.11 |
| C4YIY2 | NDT80 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03794 PE=4 SV=1 | | | -5.11 |
| C4YEJ3 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00950 PE=4 SV=1 | | | -5.04 |
| A0A1D8PDA0 | Sepiapterin reductase family protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.5194.1 PE=4 SV=1 | | | -5.04 |
| B9WIT8 | Coatomer subunit beta' OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_62450 PE=3 SV=1 | | | -5.04 |
| A0A1D8PPV5 | Coatomer subunit beta' OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SEC27 PE=3 SV=1 | | | -5.04 |
| C4YSS2 | Coatomer subunit beta' OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05141 PE=3 SV=1 | | | -5.04 |
| C4YIE0 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04213 PE=4 SV=1 | | | -5.02 |
| B9WJU1 | Polyamine acetyltransferase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_73500 PE=4 SV=1 | | | -5 |
| B9WL68 | NADH-ubiquinone oxidoreductase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_27600 PE=3 SV=1 | | | -5 |
| C4YNK3 | Transcription initiation factor TFIID subunit 10 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01465 PE=3 SV=1 | | | -4.98 |
| Q5A886 | Transcription initiation factor TFIID subunit 10 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_CR01120CA PE=3 SV=1 | | | -4.98 |
| B9WKU7 | Transcription initiation factor TFIID subunit 10 OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_26120 PE=3 SV=1 | | | -4.98 |
| B9WDW7 | Glutathione S-transferase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_83610 PE=3 SV=1 | | | -4.97 |
| C4YQD2 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02689 PE=3 SV=1 | | | -4.97 |
| C4YQ80 | GST C-terminal domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02636 PE=4 SV=1 | | | -4.97 |
| B9WDX5 | Glutathione S-transferase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_83710 PE=3 SV=1 | | | -4.97 |
| A0A1D8PJX4 | Bifunctional glutathione transferase/peroxidase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GTT12 PE=3 SV=1 | | | -4.97 |
| B9WJ22 | RNA-binding protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_63610 PE=4 SV=1 | | | -4.95 |
| Q59TS4 | Chorismate mutase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ARO7 PE=4 SV=1 | | | -4.95 |
| B9W9F0 | Chorismate mutase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_10790 PE=4 SV=1 | | | -4.95 |
| Q59RQ4 | Mitochondrial 54S ribosomal protein YmL8 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MRPL8 PE=3 SV=1 | | | -4.93 |
| B9WME0 | Mitochondrial ribosomal protein, large subunit, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_33020 PE=3 SV=1 | | | -4.93 |
| A0A1D8PGA2 | Protein phosphatase regulator OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=REG1 PE=4 SV=1 | | | -4.93 |
| C4YJ82 | DUF1752 domain-containing protein (Fragment) OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03895 PE=4 SV=1 | | | -4.93 |
| B9WCF0 | Eukaryotic initiation factor 4F subunit p150 homologue, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_22930 PE=4 SV=1 | | | -4.9 |
| Q5A8X7 | Protein FYV4, mitochondrial OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=FYV4 PE=3 SV=1 | | | -4.89 |
| C4YF97 | IGR domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01210 PE=4 SV=1 | | | -4.89 |
| Q5APT8 | ATP-dependent RNA helicase DBP3 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=DBP3 PE=3 SV=1 | | | -4.84 |
| C4YD41 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00429 PE=3 SV=1 | | | -4.84 |
| B9WEQ5 | Protein transport protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_86720 PE=3 SV=1 | | | -4.83 |
| C4YDP9 | Amidophosphoribosyltransferase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00646 PE=3 SV=1 | | | -4.77 |
| A0A1D8PE37 | Amidophosphoribosyltransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ADE4 PE=3 SV=1 | | | -4.77 |
| B9W8F8 | Amidophosphoribosyltransferase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_07230 PE=3 SV=1 | | | -4.77 |
| Q5AHG8 | Mitochondrial 54S ribosomal protein YmL24/YmL14 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.828 PE=4 SV=1 | | | -4.75 |
| B9WB70 | Ribosomal protein, large subunit, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_18600 PE=4 SV=1 | | | -4.75 |
| C4YI81 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04153 PE=4 SV=1 | | | -4.75 |
| A0A1D8PNJ2 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4316 PE=4 SV=1 | | | -4.67 |
| C4YRH3 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04673 PE=4 SV=1 | | | -4.67 |
| C4YGI4 | GYF domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03161 PE=4 SV=1 | | | -4.49 |
| A0A1D8PF30 | Tubulin-binding pre folding complex subunit OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.2305 PE=4 SV=1 | | | -4.47 |
| B9W9B7 | Prefoldin subunit, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_10420 PE=4 SV=1 | | | -4.47 |
| A0A1D8PQH5 | Superoxide dismutase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SOD3 PE=3 SV=1 | | | -4.26 |
| Q5A4X7 | Ribose phosphate diphosphokinase subunit OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.969 PE=4 SV=1 | | | -4.19 |
| C4YQG5 | UCR\_hinge domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02723 PE=4 SV=1 | | | -3.4 |
| A0A1D8PJT8 | Ubiquinol--cytochrome-c reductase subunit 6 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.913.2 PE=4 SV=1 | | | -3.4 |
| B9WE04 | Ubiquinol-cytochrome C reductase hinge protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_84010 PE=4 SV=1 | | | -3.4 |
| B9WCE2 | MutS protein homolog, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_22850 PE=4 SV=1 | | | -1.94 |
| B9WC24 | Heat shock protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_21650 PE=3 SV=1 | | | -1.91 |
| O74254 | Glucoamylase 1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GAM1 PE=1 SV=3 | | | -1.64 |
| A0A1D8PEW1 | Gca2p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GCA2 PE=3 SV=1 | | | -1.64 |
| C4YD16 | Glucoamylase 1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00404 PE=3 SV=1 | | | -1.64 |
| C4YTF9 | Alpha-1,4 glucan phosphorylase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05451 PE=3 SV=1 | | | -1.51 |
| B9WJJ6 | Alpha-1,4 glucan phosphorylase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_70860 PE=3 SV=1 | | | -1.51 |
| B9WFY2 | Protein phosphatase regulatory subunit, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_42730 PE=4 SV=1 | | | -1.48 |
| C4YGW5 | Glycogen debranching enzyme (Dextrin 6-alpha-D-glucosidase) OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03301 PE=4 SV=1 | | | -1.48 |
| Q59MN2 | Bifunctional 4-alpha-glucanotransferase/amylo-alpha-1,6-glucosidase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GDB1 PE=4 SV=1 | | | -1.48 |
| B9WGH3 | Uncharacterized protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_44790 PE=4 SV=1 | | | -1.48 |
| A0A1D8PCP6 | Age3p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=AGE3 PE=4 SV=1 | | | -1.47 |
| C4YF46 | ADP-ribosylation factor GTPase-activating protein GCS1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01157 PE=4 SV=1 | | | -1.47 |
| B9W713 | ADP-ribosylation factor GTPase-activating protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_02110 PE=4 SV=1 | | | -1.47 |
| C4YEB9 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00874 PE=3 SV=1 | | | -1.46 |
| B9W7U5 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_05000 PE=3 SV=1 | | | -1.46 |
| Q5A2A1 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SDH1 PE=3 SV=1 | | | -1.46 |
| C4YNC2 | Phosphoenolpyruvate carboxykinase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01381 PE=3 SV=1 | | | -1.45 |
| A0A1D8PRM7 | Phosphoenolpyruvate carboxykinase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PCK1 PE=3 SV=1 | | | -1.45 |
| B9W8S6 | Cytochrome C oxidase polypeptide V, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_08520 PE=4 SV=1 | | | -1.45 |
| C4YDD3 | Cytochrome c oxidase polypeptide Vb, mitochondrial OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00526 PE=4 SV=1 | | | -1.45 |
| C4YS96 | Aminotran\_5 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04957 PE=3 SV=1 | | | -1.44 |
| Q59X49 | Stress protein DDR48 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=DDR48 PE=1 SV=1 | | | -1.41 |
| B2B9P3 | Glutamate decarboxylase (Fragment) OS=Candida albicans OX=5476 PE=4 SV=1 | | | -1.41 |
| C4YPL1 | Delta(24(24(1)))-sterol reductase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02412 PE=4 SV=1 | | | -1.41 |
| B9WBL9 | Peptide-n4-(N-acetyl-beta-d-glucosaminyl) asparaginase amidase n, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_20100 PE=4 SV=1 | | | -1.38 |
| B9WMT0 | Meiotic sister chromatid recombination protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_34540 PE=4 SV=1 | | | -1.36 |
| A0A1D8PLQ3 | Gly-Xaa carboxypeptidase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.2686 PE=4 SV=1 | | | -1.34 |
| C4YHE8 | M20\_dimer domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03494 PE=4 SV=1 | | | -1.34 |
| A0A1D8PF53 | Cta3p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CTA3 PE=4 SV=1 | | | -1.33 |
| C4YCP9 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00283 PE=4 SV=1 | | | -1.33 |
| O93947 | CTA3p (Fragment) OS=Candida albicans OX=5476 GN=cta3 PE=2 SV=1 | | | -1.33 |
| A0A075MGB4 | Aspartate aminotransferase (Fragment) OS=Candida albicans OX=5476 PE=4 SV=1 | | | -1.31 |
| A0A075MM62 | Aspartate aminotransferase (Fragment) OS=Candida albicans OX=5476 PE=4 SV=1 | | | -1.31 |
| A0A075MHV1 | Aspartate aminotransferase (Fragment) OS=Candida albicans OX=5476 PE=4 SV=1 | | | -1.31 |
| O13434 | Phosphoenolpyruvate carboxykinase (ATP) OS=Candida albicans OX=5476 GN=PCK1 PE=3 SV=1 | | | -1.29 |
| C4YHF4 | Tyrosine--tRNA ligase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03500 PE=3 SV=1 | | | -1.29 |
| Q5A8Z9 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.3335 PE=4 SV=1 | | | -1.29 |
| B9WFZ3 | Tyrosine--tRNA ligase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_42850 PE=3 SV=1 | | | -1.29 |
| C4YQE7 | Peptidase A1 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02704 PE=3 SV=1 | | | -1.29 |
| Q59SU1 | Candidapepsin-9 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SAP9 PE=1 SV=2 | | | -1.29 |
| O42779 | Candidapepsin-9 OS=Candida albicans OX=5476 GN=SAP9 PE=3 SV=1 | | | -1.29 |
| B9WDY9 | Aspartyl protease, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=SAP9 PE=3 SV=1 | | | -1.29 |
| C4YRM1 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04722 PE=4 SV=1 | | | -1.28 |
| A0A1D8PNP4 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.6658 PE=4 SV=1 | | | -1.28 |
| C4YSC3 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04986 PE=4 SV=1 | | | -1.26 |
| Q5A8I5 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.5763 PE=4 SV=1 | | | -1.26 |
| B9WJ88 | Peroxisomal 2,4-dienoyl-CoA reductase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_64400 PE=4 SV=1 | | | -1.26 |
| C4YKJ4 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05999 PE=4 SV=1 | | | -1.25 |
| A0A1D8PLN9 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.2710 PE=4 SV=1 | | | -1.24 |
| C4YHG6 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03512 PE=4 SV=1 | | | -1.24 |
| B9WJC5 | Alanine-glyoxylate aminotransferase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_64910 PE=3 SV=1 | | | -1.24 |
| C4YRK4 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04704 PE=4 SV=1 | | | -1.22 |
| A0A1D8PNN8 | Cam1-1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAM1-1 PE=4 SV=1 | | | -1.22 |
| Q5A6M9 | Ribonucleoprotein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=NHP2 PE=3 SV=1 | | | -1.22 |
| A0A1D8PTW2 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_CR09140CA PE=4 SV=1 | | | -1.22 |
| C4YMV0 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02187 PE=4 SV=1 | | | -1.22 |
| B9WCX3 | Trehalose synthase complex regulatory subunit, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_24670 PE=4 SV=1 | | | -1.22 |
| Q59VY8 | Galactokinase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GAL1 PE=4 SV=1 | | | -1.21 |
| C4YF58 | Galactokinase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01170 PE=4 SV=1 | | | -1.21 |
| P56091 | Galactokinase OS=Candida albicans OX=5476 GN=GAL1 PE=3 SV=1 | | | -1.21 |
| C4YF57 | GAL10 bifunctional protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01168 PE=4 SV=1 | | | -1.2 |
| A0A1D8PCN0 | Bifunctional UDP-glucose 4-epimerase/aldose 1-epimerase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GAL10 PE=4 SV=1 | | | -1.2 |
| B9W702 | GAL10 bifunctional protein [includes: UDP-glucose 4-epimerase (Galactowaldenase) aldose 1-epimerase (Mutarotase)], putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_02000 PE=4 SV=1 | | | -1.2 |
| C4YFV8 | Glycine cleavage system H protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00084 PE=3 SV=1 | | | -1.2 |
| C4YF75 | AMPK1\_CBM domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01187 PE=4 SV=1 | | | -1.19 |
| A0A1D8PCL8 | AMPK1\_CBM domain-containing protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4530.1 PE=4 SV=1 | | | -1.19 |
| B9WKL5 | Phosphoenolpyruvate carboxykinase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=PCK1 PE=3 SV=1 | | | -1.18 |
| Q59RR7 | Phosphotransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GLK4 PE=3 SV=1 | | | -1.18 |
| Q8TGC7 | Catalase (Fragment) OS=Candida albicans OX=5476 GN=cta PE=4 SV=1 | | | -1.18 |
| B9WHK9 | NAD(P)H-dependent D-xylose reductase I,II, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=XYRA PE=4 SV=1 | | | -1.18 |
| B9WH24 | Glutathione reductase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=GLR1 PE=3 SV=1 | | | -1.18 |
| Q59PZ4 | 60S ribosomal export protein NMD3 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=NMD3 PE=3 SV=1 | | | -1.17 |
| B9WFZ9 | Carboxypeptidase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_42910 PE=4 SV=1 | | | -1.17 |
| C4YGV0 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03284 PE=4 SV=1 | | | -1.16 |
| B9WGI9 | Xylulokinase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_44960 PE=4 SV=1 | | | -1.16 |
| B9WCD4 | NADH-quinone oxidoreductase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_22770 PE=4 SV=1 | | | -1.15 |
| B9WFW2 | Uncharacterized protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_42520 PE=4 SV=1 | | | -1.14 |
| A5GXM4 | Glycoamidase OS=Candida albicans OX=5476 PE=2 SV=1 | | | -1.13 |
| A5GXM6 | Glycoamidase OS=Candida albicans OX=5476 PE=2 SV=1 | | | -1.13 |
| F8SU65 | Glycomidase OS=Candida albicans OX=5476 GN=PNG2 PE=4 SV=1 | | | -1.13 |
| A5GXM5 | Glycoamidase OS=Candida albicans OX=5476 PE=2 SV=1 | | | -1.13 |
| A0A1D8PHH2 | Png2p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PNG2 PE=4 SV=1 | | | -1.13 |
| F8SU64 | Glycomidase OS=Candida albicans OX=5476 GN=PNG2 PE=4 SV=1 | | | -1.13 |
| Q5AF71 | Putative phosphotransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.2737 PE=4 SV=1 | | | -1.11 |
| C4YHI6 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03533 PE=4 SV=1 | | | -1.11 |
| C4YFV9 | Cytochrome b5 heme-binding domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00085 PE=4 SV=1 | | | -1.11 |
| Q5AKX2 | Fumarate reductase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=OSM2 PE=4 SV=1 | | | -1.11 |
| P87219 | Sorbose reductase SOU1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SOU1 PE=1 SV=1 | | | -1.11 |
| B9W9Y4 | Fumarate reductase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_12650 PE=4 SV=1 | | | -1.11 |
| B9WA05 | Sulfate adenylyltransferase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=MET3 PE=3 SV=1 | | | -1.1 |
| C4YFT9 | Sulfate adenylyltransferase OS=Candida albicans (strain WO-1) OX=294748 GN=MET3 PE=3 SV=1 | | | -1.1 |
| Q9Y872 | Sulfate adenylyltransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MET3 PE=3 SV=2 | | | -1.1 |
| Q59U72 | Ferrochelatase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=HEM15 PE=3 SV=1 | | | -1.1 |
| B9WMG0 | Aspartate aminotransferase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_33240 PE=4 SV=1 | | | -1.09 |
| B9W9Y0 | Cytochrome b2, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_12610 PE=3 SV=1 | | | -1.09 |
| A0A1D8PDN3 | Peroxiredoxin OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=TRP99 PE=3 SV=1 | | | -1.08 |
| C4YEA5 | Peroxiredoxin OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00860 PE=3 SV=1 | | | -1.08 |
| B9WI30 | Multifunctional fusion protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_54480 PE=3 SV=1 | | | -1.08 |
| C4YKX1 | Glyco\_transf\_20 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_06130 PE=4 SV=1 | | | -1.07 |
| A0A1D8PIS4 | Trehalose 6-phosphate synthase/phosphatase complex subunit OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=TPS3 PE=1 SV=1 | | | -1.07 |
| C4YP94 | Aldo\_ket\_red domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03043 PE=4 SV=1 | | | -1.06 |
| Q5ADT4 | Glycerol 2-dehydrogenase (NADP(+)) OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GCY1 PE=4 SV=1 | | | -1.06 |
| C4YFC5 | Eukaryotic initiation factor 4A OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01241 PE=3 SV=1 | | | -1.06 |
| A0A1D8PF79 | Glutamate decarboxylase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GAD1 PE=3 SV=1 | | | -1.05 |
| B9W7V9 | Peroxiredoxin OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_05140 PE=3 SV=1 | | | -1.03 |
| C4YJJ4 | Bap31 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04009 PE=4 SV=1 | | | -1.03 |
| B9WAS6 | Endoplasmic reticulum transmembrane protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_17180 PE=4 SV=1 | | | -1.03 |
| Q59N40 | Aspartate aminotransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=AAT21 PE=4 SV=1 | | | -1.02 |
| B9WMB5 | Phosphotransferase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_32740 PE=3 SV=1 | | | -1.02 |
| Q5AK46 | Multifunctional fusion protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PUT2 PE=3 SV=1 | | | -1.02 |
| C4YRZ6 | Multifunctional fusion protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04854 PE=3 SV=1 | | | -1.02 |
| B9W8Y7 | Malate synthase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_09130 PE=3 SV=1 | | | -1.01 |
| **Proteins up-regulated in drug-resistant isolate** | | | | |
| **Accession** | **Description** | | | **Abundance Ratio (log2): (M1038) / (M2)** |
| C4YRB3 | MHD domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04612 PE=3 SV=1 | | | 1.01 |
| A0A1D8PND9 | Coatomer subunit delta OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=RET2 PE=3 SV=1 | | | 1.01 |
| A0A1D8PPJ1 | Cic1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CIC1 PE=4 SV=1 | | | 1.01 |
| B9WHF3 | Delta subunit of the coatomer complex, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_52110 PE=3 SV=1 | | | 1.01 |
| C4YDJ0 | Hcy-binding domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00585 PE=4 SV=1 | | | 1.01 |
| A0A1D8PEB0 | S-adenosylmethionine-homocysteine S-methyltransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SAM4 PE=4 SV=1 | | | 1.01 |
| C4YG18 | NTP\_transferase domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00133 PE=4 SV=1 | | | 1.04 |
| C4YLZ2 | Protoplast secreted protein 2 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01865 PE=4 SV=1 | | | 1.04 |
| C4YPM1 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02422 PE=4 SV=1 | | | 1.05 |
| A0A1D8PL78 | Crd2p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CRD2 PE=4 SV=1 | | | 1.06 |
| B9W9U1 | Mannose-1-phosphate guanyltransferase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_12220 PE=4 SV=1 | | | 1.07 |
| B9WF25 | GYF domain-containing protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_46150 PE=4 SV=1 | | | 1.09 |
| A0A1D8PQN3 | Long-chain fatty acid transporter OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ACB1 PE=4 SV=1 | | | 1.1 |
| B9WJI0 | Acyl-CoA-binding protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_70690 PE=4 SV=1 | | | 1.1 |
| C4YP33 | Saccharopine dehydrogenase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02969 PE=4 SV=1 | | | 1.1 |
| C4YP91 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03039 PE=4 SV=1 | | | 1.12 |
| G1UA43 | Lysine/glutamic acid-rich protein OS=Candida albicans OX=5476 PE=4 SV=1 | | | 1.12 |
| C4YS55 | Uncharacterized protein (Fragment) OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04914 PE=4 SV=1 | | | 1.15 |
| Q5A397 | Hsp70 family ATPase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SSB1 PE=3 SV=1 | | | 1.16 |
| D2J4C7 | Heat shock protein 70 (Fragment) OS=Candida albicans OX=5476 PE=2 SV=1 | | | 1.16 |
| C4YE07 | Glutamate synthase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00757 PE=4 SV=1 | | | 1.16 |
| A0A1D8PDU9 | Glutamate synthase (NADH) OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GLT1 PE=4 SV=1 | | | 1.16 |
| A0A1D8PSE7 | Ifr2p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=IFR2 PE=4 SV=1 | | | 1.21 |
| B9W853 | Glutamate synthase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_06130 PE=4 SV=1 | | | 1.24 |
| Q59XQ1 | 3'(2'),5'-bisphosphate nucleotidase 2 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=HAL22 PE=3 SV=3 | | | 1.36 |
| Q5AG68 | Nucleoside diphosphate kinase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=YNK1 PE=3 SV=1 | | | 1.36 |
| A0A290GHQ6 | Uncharacterized protein (Fragment) OS=Candida albicans OX=5476 PE=4 SV=1 | | | 1.39 |
| C4YG27 | Ribosomal\_L14e domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00143 PE=4 SV=1 | | | 1.41 |
| B9WA82 | STF2-like protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_15230 PE=4 SV=1 | | | 1.41 |
| B9WFI0 | Metallothionein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=CDR2 PE=4 SV=1 | | | 1.44 |
| Q59MZ5 | Phosphoribosylformylglycinamidine synthase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ADE6 PE=3 SV=1 | | | 1.46 |
| A0A1D8PFV7 | Mdg1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MDG1 PE=4 SV=1 | | | 1.48 |
| C4YFP9 | AMPK1\_CBM domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00025 PE=4 SV=1 | | | 1.48 |
| B9WLC9 | Zinc-binding oxidoreductase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_28420 PE=4 SV=1 | | | 1.48 |
| A0A1D8PND4 | Mitochondrial 37S ribosomal protein YMR31 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4225.1 PE=4 SV=1 | | | 1.55 |
| B9WM32 | Adenylosuccinate lyase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_31680 PE=3 SV=1 | | | 1.6 |
| C4YF82 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01194 PE=4 SV=1 | | | 1.6 |
| P83780 | Glucose-6-phosphate isomerase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PGI1 PE=1 SV=2 | | | 1.6 |
| P46273 | Phosphoglycerate kinase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PGK1 PE=3 SV=1 | | | 1.6 |
| B9W6X4 | Transcription elongation factor SII, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_01700 PE=4 SV=1 | | | 1.6 |
| O74261 | Heat shock protein 60, mitochondrial OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=HSP60 PE=3 SV=1 | | | 1.71 |
| P82612 | Phosphoglycerate mutase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GPM1 PE=1 SV=3 | | | 1.81 |
| B9WM55 | Heat shock protein 60, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_31990 PE=3 SV=1 | | | 1.71 |
| C4YDI1 | Enolase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00576 PE=3 SV=1 | | | 1.81 |
| A0A1D8PFL9 | Ribosomal 60S subunit protein L14B OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=RPL14 PE=4 SV=1 | | | 1.81 |
| A0A1D8PIM0 | Ifr1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=IFR1 PE=4 SV=1 | | | 1.9 |
| B9WCT0 | Zinc-binding dehydrogenase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_24240 PE=4 SV=1 | | | 1.9 |
| C4YKT1 | PKS\_ER domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_06089 PE=4 SV=1 | | | 1.9 |
| A0A1D8PPI6 | Cip1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CIP1 PE=4 SV=1 | | | 2.29 |
| B9WII7 | NmrA-like negative transcriptional regulator, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=CIP1 PE=4 SV=1 | | | 2.29 |
| C4YIV3 | Inosine-5'-monophosphate dehydrogenase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04382 PE=3 SV=1 | | | 2.29 |
| C4YCZ1 | Glucoamylase 1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00378 PE=3 SV=1 | | | 3.94 |
| Q5APF2 | GMP synthase [glutamine-hydrolyzing] OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GUA1 PE=3 SV=1 | | | 3.94 |
| Q5ADM7 | Glyceraldehyde-3-phosphate dehydrogenase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=TDH3 PE=3 SV=1 | | | 3.94 |
| B9W942 | Glucoamylase 1, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_09690 PE=3 SV=1 | | | 3.94 |
| B9W966 | Glucoamylase 1, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_09920 PE=3 SV=1 | | | 3.94 |
| C4YJR4 | Ribonucleoside-diphosphate reductase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04083 PE=3 SV=1 | | | 4.21 |
| A0A1D8PFS4 | 6-phosphogluconate dehydrogenase, decarboxylating OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GND1 PE=3 SV=1 | | | 4.21 |
| G1U9X5 | Ribonucleoside-diphosphate reductase (Fragment) OS=Candida albicans OX=5476 GN=rnr1 PE=2 SV=1 | | | 4.21 |
| B9WAK5 | Cytochrome c oxidase subunit 6A, mitochondrial OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_16440 PE=3 SV=1 | | | 4.53 |
| G1UAZ8 | Uncharacterized protein CaJ7.0058 OS=Candida albicans OX=5476 GN=CaJ7.0058 PE=4 SV=1 | | | 4.69 |
| C4YNB7 | Mitogen-activated protein kinase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01373 PE=4 SV=1 | | | 4.81 |
| Q5AAG6 | Mitogen-activated protein kinase MKC1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=MKC1 PE=1 SV=1 | | | 4.81 |
| P43068 | Mitogen-activated protein kinase MKC1 OS=Candida albicans OX=5476 GN=MKC1 PE=3 SV=1 | | | 4.81 |
| C4YJ38 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03850 PE=4 SV=1 | | | 4.81 |
| A0A1D8PG62 | Npl6p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=NPL6 PE=4 SV=1 | | | 4.81 |
| B9WAC5 | Chromatin structure remodeling complex protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_15650 PE=4 SV=1 | | | 4.81 |
| C4YPT1 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02483 PE=4 SV=1 | | | 4.82 |
| B9WDC2 | Translation machinery-associated protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_81440 PE=4 SV=1 | | | 4.82 |
| A0A1D8PJ76 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.1697 PE=4 SV=1 | | | 4.82 |
| Q59P03 | NADH-cytochrome b5 reductase 1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CBR1 PE=3 SV=1 | | | 4.88 |
| C4YM91 | 6-phosphogluconolactonase-like protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01969 PE=3 SV=1 | | | 4.88 |
| B9WGK3 | NADH-cytochrome b5 reductase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_45110 PE=3 SV=1 | | | 4.88 |
| B9WAT3 | Epsin, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_17250 PE=4 SV=1 | | | 4.95 |
| C4YJI7 | ENTH domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04002 PE=4 SV=1 | | | 4.95 |
| A0A1D8PGL6 | Ent3p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ENT3 PE=4 SV=1 | | | 4.95 |
| A0A075MG50 | Glucose-6-phosphate dehydrogenase (Fragment) OS=Candida albicans OX=5476 GN=ZWF1b PE=4 SV=1 | | | 4.95 |
| C4YHT7 | Periodic tryptophan protein 1 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03639 PE=4 SV=1 | | | 5 |
| B9WFK7 | Periodic tryptophan (W) protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_41460 PE=4 SV=1 | | | 5 |
| A0A1D8PLA3 | rRNA-processing protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PWP1 PE=4 SV=1 | | | 5 |
| -3 | Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=GPD2 PE=3 SV=1 | | | 5.1 |
| Q8NKG1 | Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Candida albicans OX=5476 PE=3 SV=1 | | | 5.1 |
| B9WG21 | Vacuolar transporter chaperone, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_43130 PE=4 SV=1 | | | 5.11 |
| C4YHC6 | Vacuolar transporter chaperone 4 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03472 PE=4 SV=1 | | | 5.11 |
| B9WB76 | SHSP domain-containing protein OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_18660 PE=3 SV=1 | | | 5.12 |
| C4YJA7 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03920 PE=4 SV=1 | | | 5.12 |
| Q5ALX3 | Transcription elongation factor SPT5 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SPT5 PE=3 SV=1 | | | 5.12 |
| B9WAJ5 | Transcription elongation factor, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_16340 PE=4 SV=1 | | | 5.12 |
| B9W9B6 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=ADI1 PE=3 SV=1 | | | 5.13 |
| C4YCU0 | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Candida albicans (strain WO-1) OX=294748 GN=ADI1 PE=3 SV=1 | | | 5.13 |
| G1UAM5 | Potential membrane protein OS=Candida albicans OX=5476 GN=Ca20C1.19 PE=4 SV=1 | | | 5.15 |
| B9WM25 | Type II HSP40 co-chaperone, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_31550 PE=4 SV=1 | | | 5.18 |
| A0A1D8PU75 | Tyrosine-protein phosphatase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PTP3 PE=4 SV=1 | | | 5.22 |
| A0A1D8PNZ4 | Cup1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CUP1 PE=4 SV=1 | | | 5.23 |
| B9WI01 | Copper resistance-associated metallothionein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=CUP1 PE=4 SV=1 | | | 5.23 |
| A0A1D8PT27 | Aconitate hydratase, mitochondrial OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ACO2 PE=3 SV=1 | | | 5.34 |
| C4YM25 | Aconitate hydratase, mitochondrial OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01900 PE=3 SV=1 | | | 5.34 |
| B9WM01 | Aconitate hydratase, mitochondrial OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_31190 PE=3 SV=1 | | | 5.34 |
| B9WJ89 | Antiviral protein Ski8 orthologue, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_64410 PE=4 SV=1 | | | 5.35 |
| Q5A8I4 | SKI complex subunit WD repeat protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SKI8 PE=4 SV=1 | | | 5.35 |
| C4YSC2 | WD\_REPEATS\_REGION domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04985 PE=4 SV=1 | | | 5.35 |
| Q5ABD0 | Vacuolar-sorting protein SNF7 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=SNF7 PE=3 SV=1 | | | 5.38 |
| B9W6L6 | ESCRT-III (Endosomal sorting complex required for transport III) subunit, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_00580 PE=4 SV=1 | | | 5.38 |
| A0A1D8PL85 | Aspartate aminotransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=AAT22 PE=4 SV=1 | | | 5.41 |
| G1UAF6 | Uncharacterized protein CaJ7.0211 OS=Candida albicans OX=5476 GN=CaJ7.0211 PE=4 SV=1 | | | 5.45 |
| B9WK68 | Ras GTPase-activating-like protein, IQGAP family member, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_71670 PE=4 SV=1 | | | 5.45 |
| Q5AH02 | Ras GTPase-activating-like protein IQG1 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=IQG1 PE=1 SV=2 | | | 5.45 |
| C4YTP0 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05535 PE=4 SV=1 | | | 5.45 |
| B9W913 | (Monoglyceride) lipase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_09380 PE=4 SV=1 | | | 5.46 |
| A0A1D8PEQ8 | Acylglycerol lipase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4864 PE=4 SV=1 | | | 5.46 |
| C4YD46 | Hydrolase\_4 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00434 PE=4 SV=1 | | | 5.46 |
| A0A1D8PTW0 | Peroxin OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PEX13 PE=4 SV=1 | | | 5.48 |
| B9WMR2 | Peroxisomal membrane protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_34380 PE=4 SV=1 | | | 5.48 |
| C4YMS8 | SH3 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02165 PE=4 SV=1 | | | 5.48 |
| C4YH33 | WW domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03374 PE=4 SV=1 | | | 5.54 |
| A0A1D8PM15 | WW domain-containing protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.1414 PE=4 SV=1 | | | 5.54 |
| C4YPG8 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02367 PE=4 SV=1 | | | 5.65 |
| B9WD10 | (Dl)-glycerol-3-phosphatase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_80290 PE=4 SV=1 | | | 5.65 |
| A0A1D8PNP6 | Nucleoporin OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.6665 PE=4 SV=1 | | | 5.68 |
| C4YRM6 | RanBD1 domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04728 PE=4 SV=1 | | | 5.68 |
| B9WKN5 | Nicotinamide-nucleotide adenylyltransferase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_25480 PE=3 SV=1 | | | 5.79 |
| C4YND6 | Nicotinamide-nucleotide adenylyltransferase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01395 PE=3 SV=1 | | | 5.79 |
| A0A1D8PRN2 | Nicotinamide-nucleotide adenylyltransferase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_CR00350WA PE=3 SV=1 | | | 5.79 |
| B9WBB7 | Homocitrate synthase, mitochondrial, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_19070 PE=3 SV=1 | | | 6.22 |
| Q59TC4 | Lys22p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=LYS22 PE=3 SV=1 | | | 6.22 |
| C4YLP4 | U6 snRNA-associated Sm-like protein LSm2 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01763 PE=3 SV=1 | | | 6.3 |
| B9WMM0 | Cystathionine gamma-lyase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_33930 PE=3 SV=1 | | | 6.34 |
| C4YMN9 | Cystathionine gamma-lyase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02122 PE=3 SV=1 | | | 6.34 |
| P83776 | Hexokinase-2 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=HXK2 PE=1 SV=2 | | | 9.97 |
| C4YCN7 | Glutamate decarboxylase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00271 PE=3 SV=1 | | | 9.97 |
| Q6YK78 | 29 kDa IgE-binging protein OS=Candida albicans OX=5476 PE=2 SV=1 | | | 9.97 |
| C4YQ30 | Protein SNO4 OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02584 PE=4 SV=1 | | | 9.97 |
| O13289 | Peroxisomal catalase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAT1 PE=2 SV=5 | | | 9.97 |
| Q5AGZ8 | ATP-dependent 6-phosphofructokinase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PFK2 PE=3 SV=1 | | | 9.97 |
| B9W9E8 | Glutamate decarboxylase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_10760 PE=3 SV=1 | | | 9.97 |
| B9W9G7 | Glutamate decarboxylase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_10950 PE=3 SV=1 | | | 9.97 |
| Q5AA01 | Rim1p OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=RIM1 PE=4 SV=1 | | | 9.97 |
| B9WE59 | 60s acidic ribosomal protein, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=RPP2B PE=3 SV=1 | | | 9.97 |
| C4YQM2 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02781 PE=3 SV=1 | | | 9.97 |
| Q9HFQ4 | 60S acidic ribosomal protein P2-B OS=Candida albicans OX=5476 GN=RPP2B PE=1 SV=1 | | | 9.97 |
| Q5ANH5 | Ribosomal protein P2B OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=RPP2B PE=3 SV=1 | | | 9.97 |
| P78594 | Cytosine deaminase OS=Candida albicans OX=5476 GN=FCA1 PE=3 SV=1 | | | 9.97 |
| C4YP60 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_03002 PE=4 SV=1 | | | 9.97 |
| B9WHH2 | UDP-N-acetylglucosamine pyrophosphorylase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=UAP1 PE=4 SV=1 | | | 9.97 |
| O74933 | UDP-N-acetylglucosamine pyrophosphorylase OS=Candida albicans OX=5476 GN=UAP1 PE=1 SV=1 | | | 9.97 |
| C4YRD6 | UDP-N-acetylglucosamine pyrophosphorylase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04635 PE=4 SV=1 | | | 9.97 |
| A0A1D8PNG6 | UDP-N-acetylglucosamine di-phosphorylase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=UAP1 PE=4 SV=1 | | | 9.97 |
| C4YSR4 | Casein kinase I isoform epsilon OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05133 PE=3 SV=1 | | | 9.97 |
| Q59S64 | Serine/threonine protein kinase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=HRR25 PE=3 SV=1 | | | 9.97 |
| C4YD26 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_00414 PE=4 SV=1 | | | 9.97 |
| A0A1D8PET7 | RRM domain-containing protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.4888 PE=4 SV=1 | | | 9.97 |
| A0A1D8PJ80 | Serine/threonine-protein phosphatase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=PPH21 PE=3 SV=1 | | | 9.97 |
| C4YPT9 | Serine/threonine-protein phosphatase OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_02492 PE=3 SV=1 | | | 9.97 |
| B9WDC9 | Serine/threonine-protein phosphatase OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_81510 PE=3 SV=1 | | | 9.97 |
| G1UAD3 | Uncharacterized protein CaJ7.0341 OS=Candida albicans OX=5476 GN=CaJ7.0341 PE=4 SV=1 | | | 9.97 |
| C4YTY6 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05634 PE=4 SV=1 | | | 9.97 |
| A0A1D8PRA1 | Mitochondrial 54S ribosomal protein YmL49 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.5161 PE=4 SV=1 | | | 9.97 |
| P0CU38 | Agglutinin-like protein 2 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=ALS2 PE=2 SV=1 | | | 9.97 |
| Q9URQ0 | Agglutinin-like protein 2 (Fragments) OS=Candida albicans OX=5476 GN=ALS2 PE=3 SV=2 | | | 9.97 |
| C4YS82 | Candida\_ALS\_N domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_04941 PE=4 SV=1 | | | 9.97 |
| A0A1D8PPW7 | NAD(+) diphosphatase OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=orf19.3482 PE=4 SV=1 | | | 9.97 |
| B9WIV1 | NADH diphosphatase (Pyrophosphatase), putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_62620 PE=4 SV=1 | | | 9.97 |
| C4YSQ9 | Nudix hydrolase domain-containing protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_05127 PE=4 SV=1 | | | 9.97 |
| C4YL38 | Uncharacterized protein OS=Candida albicans (strain WO-1) OX=294748 GN=CAWG\_01553 PE=4 SV=1 | | | 9.97 |
| A0A1D8PS44 | Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_CR02060WA PE=4 SV=1 | | | 9.97 |
| B9WL20 | Phosphomutase, putative OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CBS 7987 / NCPF 3949 / NRRL Y-17841) OX=573826 GN=Cd36\_26980 PE=4 SV=1 | | | 9.97 |
| G1UA98 | Uncharacterized protein CA41C10.11 OS=Candida albicans OX=5476 GN=CA41C10.11 PE=4 SV=1 | | | 9.97 |
| O13307 | GAG protein OS=Candida albicans OX=5476 GN=gag PE=4 SV=1 | | | 9.97 |
| Q3MP86 | Uncharacterized protein CaJ7.0303 OS=Candida albicans OX=5476 GN=CaJ7.0303 PE=4 SV=1 | | | 9.97 |
| A0A1D8PR55 | Uncharacterized protein (Fragment) OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=CAALFM\_C702610CA PE=4 SV=1 | | | 9.97 |
| Q5A0I6 | Negative cofactor 2 transcription regulator complex subunit OS=Candida albicans (strain SC5314 / ATCC MYA-2876) OX=237561 GN=NCB2 PE=4 SV=1 | | | 9.97 |

1. Mass spectrometry-based whole cell proteome analysis of drug-resistant *C. glabrata* versus corresponding drug susceptible isolate.

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| --- | --- | --- | --- |
| **Accession** | | **Description** | **Abundance Ratio (log2): (M183) / (M203)** |
| **Proteins down-regulated in drug-resistant isolate** | | | |
| A0A0W0CSJ5 | Lysophospholipase NTE1 OS=Candida glabrata GN=AO440\_004775 PE=3 SV=1 | | -6.64 |
| A0A0W0CM79 | Putative nitroreductase HBN1 OS=Candida glabrata GN=AO440\_000164 PE=4 SV=1 | | -5.58 |
| Q6FP31 | Arginase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J07062g PE=3 SV=1 | | -5.34 |
| A0A0W0CQ29 | RNA polymerase II transcription factor B subunit 4 OS=Candida glabrata GN=AO440\_000679 PE=4 SV=1 | | -5.19 |
| A0A0W0C8F2 | Nuclear transport factor 2 OS=Candida glabrata GN=AO440\_002308 PE=4 SV=1 | | -5.04 |
| Q6FQA1 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I07909g PE=4 SV=1 | | -4.71 |
| A0A0W0CKI8 | Inhibitory regulator protein IRA2 OS=Candida glabrata GN=AO440\_002676 PE=4 SV=1 | | -4.71 |
| Q6FN92 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K01771g PE=4 SV=1 | | -4.68 |
| A0A0W0DK72 | Putative mitochondrial carnitine O-acetyltransferase OS=Candida glabrata GN=AO440\_003327 PE=4 SV=1 | | -4.68 |
| Q6FKK7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L10802g PE=3 SV=1 | | -4.37 |
| Q6FQK6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I05500g PE=4 SV=1 | | -4.18 |
| A0A0W0D7C1 | Glutathione S-transferase omega-like 2 OS=Candida glabrata GN=AO440\_001570 PE=4 SV=1 | | -3.99 |
| Q6FR33 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I01298g PE=3 SV=1 | | -3.95 |
| A0A0W0D1H6 | Aspartyl aminopeptidase 4 OS=Candida glabrata GN=AO440\_002397 PE=3 SV=1 | | -3.95 |
| A0A0W0D8T7 | Phosphoenolpyruvate carboxykinase OS=Candida glabrata GN=AO440\_002176 PE=3 SV=1 | | -3.82 |
| A0A0W0CMV6 | Glyceraldehyde-3-phosphate dehydrogenase OS=Candida glabrata GN=AO440\_002811 PE=3 SV=1 | | -3.78 |
| A0A0W0D703 | 54S ribosomal protein L20, mitochondrial OS=Candida glabrata GN=AO440\_001578 PE=4 SV=1 | | -3.78 |
| Q6FUN7 | Dihydrolipoyl dehydrogenase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=IRC15 PE=3 SV=1 | | -3.65 |
| Q6FRQ3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H06787g PE=3 SV=1 | | -3.57 |
| A0A0W0CWK9 | Glycerol kinase OS=Candida glabrata GN=AO440\_000984 PE=3 SV=1 | | -3.57 |
| A0A0W0CBA8 | Acetyl-coenzyme A synthetase OS=Candida glabrata GN=AO440\_003812 PE=3 SV=1 | | -3.51 |
| A0A0W0DPB6 | Isocitrate dehydrogenase [NADP] OS=Candida glabrata GN=AO440\_000371 PE=3 SV=1 | | -3.5 |
| Q6FXL1 | Isocitrate dehydrogenase [NADP] OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B04917g PE=3 SV=1 | | -3.5 |
| A0A0W0CYE9 | 3-ketoacyl-CoA thiolase, peroxisomal OS=Candida glabrata GN=AO440\_002184 PE=3 SV=1 | | -3.47 |
| A0A0W0E5S2 | Isocitrate lyase OS=Candida glabrata GN=AO440\_002913 PE=3 SV=1 | | -3.36 |
| Q6FPZ7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I10516g PE=4 SV=1 | | -3.32 |
| Q6FM65 | Glycogen [starch] synthase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K10626g PE=3 SV=1 | | -3.13 |
| A0A0W0DHY0 | Replication factor A protein 1 OS=Candida glabrata GN=AO440\_001514 PE=4 SV=1 | | -2.96 |
| Q6FV26 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=GRE2(B) PE=4 SV=1 | | -2.93 |
| A0A0W0CJZ6 | NADPH-dependent methylglyoxal reductase GRE2 OS=Candida glabrata GN=AO440\_001055 PE=4 SV=1 | | -2.93 |
| A0A0W0EHE8 | Heat shock protein SSA3 OS=Candida glabrata GN=AO440\_001621 PE=3 SV=1 | | -2.92 |
| A0A0W0CGY3 | Aspartic proteinase 3 OS=Candida glabrata GN=AO440\_005872 PE=3 SV=1 | | -2.84 |
| Q6FVI0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=YPS3 PE=3 SV=1 | | -2.84 |
| A0A0W0D369 | Actin cytoskeleton-regulatory complex protein SLA1 OS=Candida glabrata GN=AO440\_005579 PE=4 SV=1 | | -2.78 |
| Q6FVD4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E02783g PE=4 SV=1 | | -2.78 |
| A0A0W0DZG1 | Serine/threonine-protein kinase RIM15 OS=Candida glabrata GN=AO440\_003780 PE=4 SV=1 | | -2.73 |
| Q6FLY2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=RIM15 PE=4 SV=1 | | -2.73 |
| A0A0W0DDF2 | Alanine--glyoxylate aminotransferase 1 OS=Candida glabrata GN=AO440\_003778 PE=4 SV=1 | | -2.71 |
| Q6FLY4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K12518g PE=4 SV=1 | | -2.71 |
| Q6FLB9 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L04598g PE=4 SV=1 | | -2.7 |
| Q537W7 | Superoxide dismutase (Fragment) OS=Candida glabrata GN=MnSOD PE=3 SV=1 | | -2.68 |
| Q6FV67 | Superoxide dismutase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E04356g PE=3 SV=1 | | -2.68 |
| A0A0W0CW57 | Superoxide dismutase OS=Candida glabrata GN=AO440\_001003 PE=3 SV=1 | | -2.68 |
| Q9P421 | Carnitine acetyltransferase OS=Candida glabrata PE=3 SV=1 | | -2.59 |
| A0A0W0DAM3 | Carnitine O-acetyltransferase, mitochondrial OS=Candida glabrata GN=AO440\_004904 PE=3 SV=1 | | -2.59 |
| A0A0W0CNT2 | Thioredoxin OS=Candida glabrata GN=AO440\_003284 PE=3 SV=1 | | -2.57 |
| Q6FV31 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=GRE2(A) PE=1 SV=1 | | -2.55 |
| A0A0W0D321 | NADPH-dependent methylglyoxal reductase GRE2 OS=Candida glabrata GN=AO440\_001040 PE=4 SV=1 | | -2.55 |
| Q6FPR8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J01485g PE=4 SV=1 | | -2.55 |
| A0A0W0CRW0 | OTU domain-containing protein 2 OS=Candida glabrata GN=AO440\_002856 PE=4 SV=1 | | -2.55 |
| A0A0W0DMZ3 | Inositol-3-phosphate synthase OS=Candida glabrata GN=AO440\_002598 PE=4 SV=1 | | -2.51 |
| Q6FVI1 | Malate dehydrogenase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E01705g PE=3 SV=1 | | -2.46 |
| Q6FWH2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D00198g PE=3 SV=1 | | -2.26 |
| A0A0W0D6G5 | U1 SNP1-associating protein 1 OS=Candida glabrata GN=AO440\_001783 PE=4 SV=1 | | -2.26 |
| Q5R1Y7 | Catalase OS=Candida glabrata GN=AO440\_003707 PE=3 SV=1 | | -2.23 |
| Q6FVR0 | Aconitate hydratase, mitochondrial OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=ACO1 PE=3 SV=1 | | -2.2 |
| A0A0W0D7M3 | Vacuolar aminopeptidase 1 OS=Candida glabrata GN=APE1 PE=3 SV=1 | | -2.2 |
| Q6FMF2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K08536g PE=3 SV=1 | | -2.2 |
| A0A0W0CEC5 | High mobility group protein 1 OS=Candida glabrata GN=AO440\_000906 PE=4 SV=1 | | -2.19 |
| Q6FP36 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J06952g PE=4 SV=1 | | -2.18 |
| Q6FPF6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=HSP12 PE=4 SV=1 | | -2.12 |
| Q6FQN1 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I04906g PE=4 SV=1 | | -2.12 |
| Q6FUZ5 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E05984g PE=4 SV=1 | | -2.06 |
| A0A0W0E8M2 | Proteasome endopeptidase complex OS=Candida glabrata GN=AO440\_002443 PE=3 SV=1 | | -2.06 |
| Q6FL37 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L06490g PE=4 SV=1 | | -1.98 |
| A0A0W0DEJ1 | DNA-directed RNA polymerases I and III subunit RPAC1 OS=Candida glabrata GN=AO440\_000337 PE=4 SV=1 | | -1.98 |
| A0A0N9M4X0 | Epa1p OS=Candida glabrata GN=EPA1 PE=4 SV=1 | | -1.98 |
| A0A0W0ED39 | Flocculation protein FLO1 OS=Candida glabrata GN=AO440\_001107 PE=4 SV=1 | | -1.98 |
| Q6VBJ0 | Epa1p OS=Candida glabrata GN=EPA1 PE=1 SV=1 | | -1.98 |
| Q6FUW5 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=EPA1 PE=1 SV=1 | | -1.98 |
| A0A0N7FRI7 | Epa1p OS=Candida glabrata GN=EPA1 PE=4 SV=1 | | -1.98 |
| Q6FS01 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H04565g PE=4 SV=1 | | -1.95 |
| Q6FNC3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K01067g PE=3 SV=1 | | -1.94 |
| A0A0W0DKY2 | Aspartic proteinase yapsin-3 (Fragment) OS=Candida glabrata GN=AO440\_005874 PE=3 SV=1 | | -1.94 |
| Q6FVH7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=YPS6 PE=3 SV=1 | | -1.94 |
| A0A0W0CPD1 | ATP synthase subunit H, mitochondrial OS=Candida glabrata GN=AO440\_002366 PE=4 SV=1 | | -1.92 |
| A0A0W0DDT4 | Uncharacterized protein OS=Candida glabrata GN=AO440\_002877 PE=4 SV=1 | | -1.92 |
| B4UN26 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J02128g PE=4 SV=1 | | -1.92 |
| A0A0W0D2T7 | 2-oxoglutarate dehydrogenase, mitochondrial OS=Candida glabrata GN=AO440\_001843 PE=4 SV=1 | | -1.88 |
| A0A0W0CF93 | Cytochrome oxidase assembly factor 4 OS=Candida glabrata GN=AO440\_003150 PE=4 SV=1 | | -1.8 |
| Q6FM13 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K11858g PE=4 SV=1 | | -1.79 |
| A0A0W0CK81 | Succinate dehydrogenase assembly factor 4, mitochondrial OS=Candida glabrata GN=AO440\_002738 PE=4 SV=1 | | -1.78 |
| Q6FTS6 | Branched-chain-amino-acid aminotransferase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=BAT1 PE=3 SV=1 | | -1.77 |
| A0A0W0D9S2 | UV excision repair protein RAD23 OS=Candida glabrata GN=AO440\_005950 PE=4 SV=1 | | -1.75 |
| Q6FTD8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=SSA3 PE=3 SV=1 | | -1.71 |
| Q6FVU0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D05632g PE=4 SV=1 | | -1.7 |
| Q6FW05 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D03982g PE=4 SV=1 | | -1.7 |
| M1RNJ8 | Acid trehalase OS=Candida glabrata PE=4 SV=1 | | -1.69 |
| A0A0W0CJK0 | Vacuolar acid trehalase OS=Candida glabrata GN=AO440\_003472 PE=4 SV=1 | | -1.69 |
| Q6FMU4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K05137g PE=4 SV=1 | | -1.69 |
| A0A0W0CTK3 | Acetyl-CoA carboxylase OS=Candida glabrata GN=AO440\_004758 PE=4 SV=1 | | -1.65 |
| Q6FKK8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L10780g PE=4 SV=1 | | -1.65 |
| A0A0W0CC42 | Acetyl-CoA hydrolase OS=Candida glabrata GN=AO440\_002948 PE=4 SV=1 | | -1.62 |
| Q6FR42 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=GCY1 PE=4 SV=1 | | -1.6 |
| Q5S670 | UTP-glucose-1-phosphate uridylyltransferase (Fragment) OS=Candida glabrata GN=UGP1 PE=4 SV=1 | | -1.56 |
| Q5S657 | UTP-glucose-1-phosphate uridylyltransferase (Fragment) OS=Candida glabrata GN=UGP1 PE=4 SV=1 | | -1.56 |
| Q6FX17 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0C01221g PE=4 SV=1 | | -1.56 |
| A0A0W0CUP4 | Citrate synthase OS=Candida glabrata GN=AO440\_002064 PE=3 SV=1 | | -1.54 |
| Q6FS26 | Citrate synthase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H03993g PE=3 SV=1 | | -1.54 |
| Q6FXI7 | Phosphoacetylglucosamine mutase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B03597g PE=3 SV=1 | | -1.54 |
| A0A0W0DEP0 | Phosphoacetylglucosamine mutase OS=Candida glabrata GN=AO440\_000314 PE=3 SV=1 | | -1.54 |
| Q6FSQ3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G08712g PE=4 SV=1 | | -1.49 |
| A0A0W0CTA5 | Translationally-controlled tumor protein-like protein OS=Candida glabrata GN=AO440\_004850 PE=3 SV=1 | | -1.45 |
| A0A0W0DJ34 | Copper transport protein CTR1 OS=Candida glabrata GN=AO440\_000810 PE=4 SV=1 | | -1.45 |
| A0A0W0D206 | cAMP-dependent protein kinase regulatory subunit OS=Candida glabrata GN=AO440\_002562 PE=3 SV=1 | | -1.44 |
| Q6FLE7 | Malate synthase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L03982g PE=3 SV=1 | | -1.44 |
| A0A0W0E3D0 | Clathrin heavy chain OS=Candida glabrata GN=AO440\_000100 PE=3 SV=1 | | -1.44 |
| A0A0W0C6G0 | Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Candida glabrata GN=AO440\_001595 PE=3 SV=1 | | -1.42 |
| A0A0W0D2B2 | Aspartokinase OS=Candida glabrata GN=AO440\_002906 PE=3 SV=1 | | -1.41 |
| Q6FMM4 | Pyruvate dehydrogenase E1 component subunit beta OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K06831g PE=4 SV=1 | | -1.41 |
| Q6FXW6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0A01045g PE=3 SV=1 | | -1.37 |
| Q6FLP1 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=UGP1 PE=4 SV=1 | | -1.35 |
| A0A0W0CDY8 | Dihydrolipoyllysine-residue succinyltransferase OS=Candida glabrata GN=AO440\_000929 PE=4 SV=1 | | -1.35 |
| A0A0W0CZB0 | Maintenance of telomere capping protein 1 OS=Candida glabrata GN=AO440\_004669 PE=4 SV=1 | | -1.33 |
| Q6FL79 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L05522g PE=4 SV=1 | | -1.33 |
| Q6FJN5 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M04873g PE=4 SV=1 | | -1.29 |
| A4URU0 | Actin (Fragment) OS=Candida glabrata GN=act1 PE=3 SV=1 | | -1.29 |
| A4URU2 | Actin (Fragment) OS=Candida glabrata GN=act1 PE=3 SV=1 | | -1.29 |
| Q6FRB0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H10054g PE=4 SV=1 | | -1.28 |
| Q9P966 | Ugp1 OS=Candida glabrata GN=UGP1 PE=4 SV=1 | | -1.21 |
| Q6FWM0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0C04587g PE=4 SV=1 | | -1.18 |
| A0A0W0CKR3 | Pyruvate decarboxylase OS=Candida glabrata GN=AO440\_004194 PE=3 SV=1 | | -1.17 |
| A0A0W0C7H2 | NAD-specific glutamate dehydrogenase OS=Candida glabrata GN=AO440\_001720 PE=3 SV=1 | | -1.16 |
| Q6FRX5 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H05137g PE=3 SV=1 | | -1.13 |
| A0A0W0CVQ5 | Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial OS=Candida glabrata GN=AO440\_000267 PE=4 SV=1 | | -1.12 |
| A0A0W0CM23 | 60S ribosomal protein L29 OS=Candida glabrata GN=AO440\_000826 PE=3 SV=1 | | -1.12 |
| A0A0W0DNH6 | Uncharacterized protein OS=Candida glabrata GN=AO440\_005893 PE=4 SV=1 | | -1.11 |
| A0A0W0DIT8 | Aspartic proteinase 3 OS=Candida glabrata GN=AO440\_005908 PE=3 SV=1 | | -1.11 |
| Q6FRT4 | Proteasome endopeptidase complex OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H06105g PE=3 SV=1 | | -1.09 |
| Q6FRD8 | Tyrosine--tRNA ligase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H09372g PE=3 SV=1 | | -1.08 |
| A0A0W0D945 | Tyrosine--tRNA ligase OS=Candida glabrata GN=AO440\_002297 PE=3 SV=1 | | -1.08 |
| A0A0W0DLR9 | Riboflavin synthase OS=Candida glabrata GN=AO440\_000830 PE=4 SV=1 | | -1.08 |
| Q6FVV4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D05302g PE=4 SV=1 | | -1.08 |
| A0A0W0DUG0 | NADH-cytochrome b5 reductase OS=Candida glabrata GN=AO440\_001099 PE=3 SV=1 | | -1.06 |
| Q6FMY5 | Transaldolase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K04235g PE=4 SV=1 | | -1.06 |
| A0A0W0C9G7 | Transaldolase OS=Candida glabrata GN=AO440\_003434 PE=4 SV=1 | | -1.06 |
| A0A0W0CCE8 | Diphthamide biosynthesis protein 2 OS=Candida glabrata GN=AO440\_002962 PE=3 SV=1 | | -1.06 |
| A0A0W0CSI4 | Uncharacterized protein OS=Candida glabrata GN=AO440\_003658 PE=4 SV=1 | | -1.05 |
| Q6FPA1 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J05478g PE=3 SV=1 | | -1.05 |
| Q6FXB8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B02167g PE=3 SV=1 | | -1.05 |
| Q6FQD4 | Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I07139g PE=3 SV=1 | | -1.03 |
| Q6FUC8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0F04477g PE=4 SV=1 | | -1.03 |
| Q6FN79 | Serine/threonine-protein phosphatase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=GLC7 PE=3 SV=1 | | -1.02 |
| **Proteins up-regulated in drug-resistant isolate** | | | |
| **Accession** | **Description** | | **Abundance Ratio (log2): (M183) / (M203)** |
| Q6FUX2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E06490g PE=3 SV=1 | | 1.01 |
| A0A0W0DAN8 | Nascent polypeptide-associated complex subunit beta OS=Candida glabrata GN=AO440\_004835 PE=3 SV=1 | | 1.02 |
| Q6FQS9 | DNA-directed RNA polymerase subunit OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=RPB1 PE=3 SV=1 | | 1.02 |
| Q6FPL8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J02816g PE=4 SV=1 | | 1.02 |
| G1BJ41 | Ribosomal protein RPL31 (Fragment) OS=[Candida] nivariensis GN=RPL31 PE=4 SV=1 | | 1.03 |
| G3K1W6 | Ribosomal protein RPL31p (Fragment) OS=Kluyveromyces delphensis GN=RPL31 PE=4 SV=1 | | 1.03 |
| A0A0W0DBC2 | Homocitrate synthase, mitochondrial OS=Candida glabrata GN=AO440\_003039 PE=3 SV=1 | | 1.04 |
| A0A0W0D6G7 | AMP deaminase OS=Candida glabrata GN=AO440\_001788 PE=3 SV=1 | | 1.04 |
| Q6FSW0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G07425g PE=3 SV=1 | | 1.04 |
| Q6FTS3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G00154g PE=4 SV=1 | | 1.05 |
| Q6FND0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K00913g PE=3 SV=1 | | 1.05 |
| A0A0W0CAW2 | C-1-tetrahydrofolate synthase, cytoplasmic OS=Candida glabrata GN=AO440\_003289 PE=3 SV=1 | | 1.05 |
| A0A0W0CQ39 | 60S ribosomal protein L31 OS=Candida glabrata GN=AO440\_000633 PE=4 SV=1 | | 1.05 |
| O93932 | Putative ATP-dependent RNA helicase Ded1p (Fragment) OS=Candida glabrata GN=DED1 PE=4 SV=1 | | 1.05 |
| A0A0W0DE31 | Ribosome biogenesis protein 15 OS=Candida glabrata GN=AO440\_004596 PE=4 SV=1 | | 1.05 |
| Q6FLF5 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L03806g PE=4 SV=1 | | 1.05 |
| A0A0W0C712 | Isoleucine--tRNA ligase, cytoplasmic OS=Candida glabrata GN=AO440\_001622 PE=3 SV=1 | | 1.05 |
| Q6FTD7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G03311g PE=3 SV=1 | | 1.05 |
| Q6FP88 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J05764g PE=4 SV=1 | | 1.06 |
| A0A0W0E7W4 | U6 snRNA-associated Sm-like protein LSm7 OS=Candida glabrata GN=AO440\_003010 PE=4 SV=1 | | 1.06 |
| Q6FXR5 | Coatomer subunit delta OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0A04741g PE=3 SV=1 | | 1.06 |
| A0A0W0E2W2 | Coatomer subunit delta OS=Candida glabrata GN=AO440\_000144 PE=3 SV=1 | | 1.06 |
| A0A0W0DX49 | ATP-dependent molecular chaperone HSC82 OS=Candida glabrata GN=AO440\_000614 PE=4 SV=1 | | 1.07 |
| A0A0W0DKN8 | T-complex protein 1 subunit epsilon OS=Candida glabrata GN=AO440\_001126 PE=3 SV=1 | | 1.08 |
| Q6FUU7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0F00539g PE=3 SV=1 | | 1.08 |
| A0A0W0CZ83 | Ribosome biogenesis protein ERB1 OS=Candida glabrata GN=ERB1 PE=3 SV=1 | | 1.08 |
| A0A0W0ES51 | Proteasome subunit beta type-1 OS=Candida glabrata GN=AO440\_000742 PE=4 SV=1 | | 1.09 |
| A0A0W0DA40 | 40S ribosomal protein S23 OS=Candida glabrata GN=AO440\_004643 PE=3 SV=1 | | 1.1 |
| A0A0W0CKI5 | Fructose-2,6-bisphosphatase OS=Candida glabrata GN=AO440\_002600 PE=4 SV=1 | | 1.1 |
| Q6FQH9 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=FBP26 PE=4 SV=1 | | 1.1 |
| A0A0W0CHC6 | Heat shock protein 42 OS=Candida glabrata GN=AO440\_000909 PE=3 SV=1 | | 1.11 |
| A0A0W0CEL2 | Heat shock protein 42 OS=Candida glabrata GN=AO440\_004704 PE=3 SV=1 | | 1.11 |
| Q6FVM1 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E00803g PE=3 SV=1 | | 1.11 |
| Q8TFL6 | Mitochondrial ribosomal protein MRPL28 OS=Candida glabrata GN=MRPL28 PE=4 SV=1 | | 1.11 |
| Q6FMP3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K06391g PE=4 SV=1 | | 1.11 |
| A0A0W0DM74 | Translocation protein SEC66 OS=Candida glabrata GN=AO440\_004118 PE=4 SV=1 | | 1.11 |
| Q6FLU9 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=HSC82 PE=3 SV=1 | | 1.12 |
| A0A0W0DCE3 | Ubiquitin-activating enzyme E1 1 OS=Candida glabrata GN=AO440\_003263 PE=3 SV=1 | | 1.12 |
| Q6FNF6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K00319g PE=3 SV=1 | | 1.12 |
| Q6FY94 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0A04015g PE=4 SV=1 | | 1.12 |
| A0A0W0E3X3 | Nucleolar protein 56 OS=Candida glabrata GN=AO440\_000112 PE=4 SV=1 | | 1.12 |
| Q6FV21 | Alanine--tRNA ligase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=ALA1 PE=3 SV=1 | | 1.12 |
| A0A0W0CWA9 | Alanine--tRNA ligase OS=Candida glabrata GN=ALA1 PE=3 SV=1 | | 1.12 |
| A0A0W0CSV2 | Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Candida glabrata GN=AO440\_001441 PE=3 SV=1 | | 1.12 |
| A0A0W0CNW7 | Protein phosphatase 1 regulatory subunit SDS22 OS=Candida glabrata GN=AO440\_000763 PE=4 SV=1 | | 1.13 |
| Q6FW24 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D03564g PE=4 SV=1 | | 1.13 |
| Q6FQV0 | Adenylate kinase isoenzyme 6 homolog OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I03366g PE=3 SV=1 | | 1.13 |
| A0A0W0CQE1 | Adenylate kinase isoenzyme 6 homolog OS=Candida glabrata GN=AO440\_002478 PE=3 SV=1 | | 1.13 |
| Q6FJY0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M02695g PE=3 SV=1 | | 1.14 |
| Q6FJV7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M03223g PE=4 SV=1 | | 1.14 |
| A0A0W0DH26 | S-adenosylmethionine synthase OS=Candida glabrata GN=AO440\_003128 PE=3 SV=1 | | 1.14 |
| Q6FNW9 | S-adenosylmethionine synthase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=SAM2 PE=3 SV=1 | | 1.14 |
| Q6FK92 | Branched-chain-amino-acid aminotransferase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=BAT2 PE=3 SV=1 | | 1.15 |
| A0A0W0DVC7 | 60S ribosomal protein L24 OS=Candida glabrata GN=AO440\_000057 PE=4 SV=1 | | 1.16 |
| A0A0W0CGE0 | D-3-phosphoglycerate dehydrogenase 2 OS=Candida glabrata GN=AO440\_004403 PE=3 SV=1 | | 1.16 |
| Q6FX49 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0C00319g PE=4 SV=1 | | 1.16 |
| A0A0W0DQK1 | Carboxypeptidase S OS=Candida glabrata GN=AO440\_000382 PE=4 SV=1 | | 1.16 |
| A0A0W0E336 | 60S ribosomal protein L36 OS=Candida glabrata GN=AO440\_003709 PE=3 SV=1 | | 1.17 |
| A0A0W0CMY9 | Protein URA2 OS=Candida glabrata GN=AO440\_004910 PE=3 SV=1 | | 1.17 |
| Q6FL72 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L05676g PE=3 SV=1 | | 1.17 |
| A0A0W0CLS6 | Superoxide dismutase 1 copper chaperone OS=Candida glabrata GN=AO440\_001353 PE=4 SV=1 | | 1.17 |
| Q6FN35 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K03091g PE=4 SV=1 | | 1.17 |
| A0A0W0D0Z3 | NAD(+) kinase OS=Candida glabrata GN=AO440\_002400 PE=3 SV=1 | | 1.17 |
| Q6FR29 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I01386g PE=3 SV=1 | | 1.17 |
| A0A0W0CAD1 | Uncharacterized protein OS=Candida glabrata GN=AO440\_003384 PE=4 SV=1 | | 1.17 |
| A0A0W0EB87 | 60S ribosomal protein L9-B OS=Candida glabrata GN=AO440\_001844 PE=4 SV=1 | | 1.18 |
| A0A0W0DIQ1 | Histone H2A OS=Candida glabrata GN=AO440\_005895 PE=3 SV=1 | | 1.18 |
| A0A0W0ESL3 | Tryptophan synthase OS=Candida glabrata GN=AO440\_000053 PE=3 SV=1 | | 1.21 |
| Q6FX16 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0C01243g PE=3 SV=1 | | 1.21 |
| A0A0W0CJ07 | Histidinol-phosphate aminotransferase OS=Candida glabrata GN=AO440\_000413 PE=3 SV=1 | | 1.21 |
| A0A0W0DET9 | Exportin-1 OS=Candida glabrata GN=AO440\_000256 PE=4 SV=1 | | 1.23 |
| Q6FXG2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B02189g PE=4 SV=1 | | 1.23 |
| Q6FRK3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H07887g PE=3 SV=1 | | 1.24 |
| A0A0W0C9J4 | Nucleoporin NUP84 OS=Candida glabrata GN=AO440\_002344 PE=4 SV=1 | | 1.24 |
| Q6FR90 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H10494g PE=4 SV=1 | | 1.24 |
| A0A0W0CNM9 | ATP-dependent RNA helicase DBP2 OS=Candida glabrata GN=AO440\_004598 PE=3 SV=1 | | 1.25 |
| A0A0W0DL99 | General transcriptional corepressor TUP1 OS=Candida glabrata GN=AO440\_000547 PE=4 SV=1 | | 1.25 |
| Q6FWR0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=TUP1 PE=4 SV=1 | | 1.25 |
| Q6FSW7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G07271g PE=4 SV=1 | | 1.25 |
| A0A0W0D1C3 | 26S protease regulatory subunit 4-like protein OS=Candida glabrata GN=AO440\_002545 PE=3 SV=1 | | 1.25 |
| A0A0W0DYU6 | Adenylosuccinate synthetase OS=Candida glabrata GN=AO440\_003467 PE=3 SV=1 | | 1.26 |
| A0A0W0EKU7 | DNA-directed RNA polymerase subunit beta OS=Candida glabrata GN=AO440\_004615 PE=3 SV=1 | | 1.26 |
| A0A0W0ELH2 | GPN-loop GTPase 1 OS=Candida glabrata GN=AO440\_003268 PE=4 SV=1 | | 1.26 |
| A0A0W0CSI3 | FACT complex subunit SPT16 OS=Candida glabrata GN=AO440\_000524 PE=4 SV=1 | | 1.27 |
| Q6FVB3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E03267g PE=4 SV=1 | | 1.27 |
| A0A0W0DF74 | Acetyltransferase component of pyruvate dehydrogenase complex OS=Candida glabrata GN=AO440\_003202 PE=3 SV=1 | | 1.28 |
| A0A0W0DDW9 | 26S protease regulatory subunit 6B-like protein OS=Candida glabrata GN=AO440\_003652 PE=3 SV=1 | | 1.28 |
| Q6FTY3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0F07887g PE=3 SV=1 | | 1.28 |
| A0A0W0DKX9 | Nuclear polyadenylated RNA-binding protein NAB2 OS=Candida glabrata GN=AO440\_001398 PE=4 SV=1 | | 1.28 |
| Q6FU17 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0F07095g PE=4 SV=1 | | 1.28 |
| Q6FWA4 | Proliferating cell nuclear antigen OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D01716g PE=3 SV=1 | | 1.28 |
| A0A0W0DNH7 | Plasma membrane ATPase OS=Candida glabrata GN=AO440\_000019 PE=3 SV=1 | | 1.29 |
| A0A0W0D2C6 | Bifunctional purine biosynthetic protein ADE5,7 OS=Candida glabrata GN=AO440\_002234 PE=3 SV=1 | | 1.3 |
| A0A0W0EBT4 | ADP-ribosylation factor GTPase-activating protein GCS1 OS=Candida glabrata GN=AO440\_001709 PE=4 SV=1 | | 1.3 |
| Q707X0 | Putative Gcs1 protein OS=Candida glabrata GN=gcs1 PE=4 SV=1 | | 1.3 |
| A0A0W0EG77 | ATP-dependent RNA helicase DBP5 OS=Candida glabrata GN=AO440\_005240 PE=3 SV=1 | | 1.3 |
| A0A0W0CAZ4 | ATP-dependent RNA helicase SUB2 OS=Candida glabrata GN=AO440\_005117 PE=4 SV=1 | | 1.31 |
| A0A0W0E0T4 | 26S protease regulatory subunit 8-like protein OS=Candida glabrata GN=AO440\_000869 PE=3 SV=1 | | 1.31 |
| Q6FWB2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D01540g PE=4 SV=1 | | 1.31 |
| A0A0W0DIC5 | Inner nuclear membrane protein SRC1 OS=Candida glabrata GN=AO440\_003520 PE=4 SV=1 | | 1.32 |
| A0A0W0DLC3 | ATP-dependent RNA helicase DED1 OS=Candida glabrata GN=AO440\_004557 PE=3 SV=1 | | 1.33 |
| A0A0W0EM67 | Aromatic/aminoadipate aminotransferase 1 OS=Candida glabrata GN=AO440\_001535 PE=4 SV=1 | | 1.34 |
| Q6FMX3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K04499g PE=3 SV=1 | | 1.35 |
| A0A0W0DK52 | Phosphoribosylformylglycinamidine synthase OS=Candida glabrata GN=AO440\_003446 PE=3 SV=1 | | 1.35 |
| Q6FJM9 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M05005g PE=4 SV=1 | | 1.37 |
| Q6FK78 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M00484g PE=4 SV=1 | | 1.38 |
| A0A0W0CY24 | rRNA biogenesis protein RRP5 OS=Candida glabrata GN=AO440\_004064 PE=4 SV=1 | | 1.38 |
| A0A0W0CSB5 | Heterogeneous nuclear rnp K-like protein 2 OS=Candida glabrata GN=AO440\_001276 PE=4 SV=1 | | 1.39 |
| A0A0W0DAB3 | Putative metalloprotease ARX1 OS=Candida glabrata GN=AO440\_005091 PE=4 SV=1 | | 1.39 |
| Q6FR55 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I00814g PE=3 SV=1 | | 1.39 |
| Q6FR05 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=OYE2 PE=4 SV=1 | | 1.39 |
| A0A0W0DMC0 | NADPH dehydrogenase 2 OS=Candida glabrata GN=AO440\_005222 PE=4 SV=1 | | 1.39 |
| Q6FQQ2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I04444g PE=3 SV=1 | | 1.4 |
| Q6FNP8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J10032g PE=3 SV=1 | | 1.4 |
| A0A0W0DF75 | 25S rRNA (Cytosine(2870)-C(5))-methyltransferase OS=Candida glabrata GN=AO440\_003195 PE=3 SV=1 | | 1.4 |
| A0A0W0CCV4 | GrpE protein homolog OS=Candida glabrata GN=AO440\_004873 PE=3 SV=1 | | 1.4 |
| Q6FNI4 | Importin subunit alpha OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J11440g PE=3 SV=1 | | 1.41 |
| A0A0W0D805 | 1,4-alpha-glucan-branching enzyme OS=Candida glabrata GN=AO440\_004002 PE=4 SV=1 | | 1.41 |
| A0A0W0EHY7 | Amidophosphoribosyltransferase OS=Candida glabrata GN=AO440\_004442 PE=3 SV=1 | | 1.41 |
| A0A0W0EQL9 | Protein SIS1 OS=Candida glabrata GN=AO440\_002051 PE=4 SV=1 | | 1.41 |
| Q6FS39 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H03707g PE=4 SV=1 | | 1.41 |
| Q6FTB7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G03751g PE=4 SV=1 | | 1.42 |
| A0A0W0D614 | Uncharacterized protein OS=Candida glabrata GN=AO440\_001642 PE=4 SV=1 | | 1.42 |
| Q6FVB2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E03289g PE=4 SV=1 | | 1.44 |
| Q6FMI7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K07744g PE=4 SV=1 | | 1.44 |
| Q6FRL9 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H07535g PE=3 SV=1 | | 1.44 |
| A0A0W0D8M1 | Cyclin-dependent kinase 1 OS=Candida glabrata GN=AO440\_002218 PE=3 SV=1 | | 1.44 |
| Q6FS64 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H03157g PE=3 SV=1 | | 1.45 |
| Q6FXR3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B03685g PE=4 SV=1 | | 1.46 |
| A0A0W0E891 | NADPH dehydrogenase 2 OS=Candida glabrata GN=AO440\_002449 PE=4 SV=1 | | 1.47 |
| A0A0W0D8P0 | Deoxyhypusine synthase OS=Candida glabrata GN=AO440\_002205 PE=4 SV=1 | | 1.49 |
| A0A0W0D9R2 | Glutamate dehydrogenase OS=Candida glabrata GN=AO440\_003806 PE=3 SV=1 | | 1.5 |
| A0A0W0DEZ0 | Peptidyl-prolyl cis-trans isomerase D OS=Candida glabrata GN=AO440\_003149 PE=4 SV=1 | | 1.5 |
| Q6FW00 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=DOG2 PE=4 SV=1 | | 1.5 |
| A0A0W0CDW4 | 2-deoxyglucose-6-phosphate phosphatase 2 OS=Candida glabrata GN=AO440\_000787 PE=4 SV=1 | | 1.5 |
| Q6FN11 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K03641g PE=4 SV=1 | | 1.5 |
| A0A0W0CA58 | Protein ASI1 OS=Candida glabrata GN=AO440\_003409 PE=4 SV=1 | | 1.5 |
| Q6FX95 | Protein disulfide-isomerase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=PDI1 PE=3 SV=1 | | 1.53 |
| A0A0W0DAS8 | Cysteine--tRNA ligase OS=Candida glabrata GN=AO440\_003098 PE=3 SV=1 | | 1.53 |
| Q6FP00 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J07744g PE=3 SV=1 | | 1.53 |
| A0A0W0DI46 | Histone H3 OS=Candida glabrata GN=AO440\_000446 PE=3 SV=1 | | 1.54 |
| A0A0W0CEV7 | Protein AIM2 OS=Candida glabrata GN=AO440\_003070 PE=4 SV=1 | | 1.54 |
| A0A0W0CHU4 | ATP synthase subunit f, mitochondrial OS=Candida glabrata GN=AO440\_005496 PE=4 SV=1 | | 1.54 |
| Q6FY44 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0A03036g PE=4 SV=1 | | 1.54 |
| Q6FIS4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M12144g PE=4 SV=1 | | 1.55 |
| A0A0W0E8A1 | 13 kDa ribonucleoprotein-associated protein OS=Candida glabrata GN=AO440\_002473 PE=4 SV=1 | | 1.57 |
| Q6FLN6 | Malic enzyme OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L02035g PE=3 SV=1 | | 1.58 |
| A0A0W0DDH4 | Malic enzyme OS=Candida glabrata GN=AO440\_004490 PE=3 SV=1 | | 1.58 |
| Q6FR32 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I01320g PE=4 SV=1 | | 1.59 |
| Q6FSK9 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G09779g PE=4 SV=1 | | 1.59 |
| Q6FUB4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0F04807g PE=4 SV=1 | | 1.6 |
| A0A0W0E3C3 | Mitochondrial outer membrane protein OM45 OS=Candida glabrata GN=AO440\_001299 PE=4 SV=1 | | 1.6 |
| A0A0W0CRU6 | ARS-binding factor 1 OS=Candida glabrata GN=AO440\_002842 PE=4 SV=1 | | 1.6 |
| Q6FPT2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J01177g PE=4 SV=1 | | 1.6 |
| A0A0W0CLH5 | Inhibitor of glycogen debranching 1 OS=Candida glabrata GN=AO440\_000074 PE=4 SV=1 | | 1.61 |
| Q6FTE7 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G03091g PE=3 SV=1 | | 1.63 |
| A0A0W0D5W0 | Valine--tRNA ligase, mitochondrial OS=Candida glabrata GN=AO440\_001612 PE=3 SV=1 | | 1.63 |
| F2Z629 | Ribosomal protein L37 OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B01203g PE=3 SV=1 | | 1.65 |
| A0A0W0CNU1 | T-complex protein 1 subunit theta OS=Candida glabrata GN=AO440\_000740 PE=3 SV=1 | | 1.66 |
| Q6FY14 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0A01848g PE=4 SV=1 | | 1.66 |
| A0A0W0DB38 | Suppressor of mar1-1 protein OS=Candida glabrata GN=AO440\_003234 PE=4 SV=1 | | 1.68 |
| Q6FNK6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=SUM1 PE=4 SV=1 | | 1.68 |
| A0A0W0DHJ3 | DNA-directed RNA polymerase I subunit RPA49 OS=Candida glabrata GN=AO440\_003099 PE=4 SV=1 | | 1.7 |
| Q6FXP9 | Peptidyl-prolyl cis-trans isomerase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B04037g PE=4 SV=1 | | 1.71 |
| A0A0W0EFK7 | Peptidyl-prolyl cis-trans isomerase OS=Candida glabrata GN=AO440\_000334 PE=4 SV=1 | | 1.71 |
| A0A0W0DCP1 | Eukaryotic translation initiation factor 6 OS=Candida glabrata GN=TIF6 PE=3 SV=1 | | 1.74 |
| A0A0W0DJH2 | Nucleolar GTP-binding protein 1 OS=Candida glabrata GN=AO440\_002137 PE=3 SV=1 | | 1.75 |
| A0A0W0DG11 | Transcription factor IIIB 70 kDa subunit OS=Candida glabrata GN=AO440\_001443 PE=4 SV=1 | | 1.76 |
| Q6FTD1 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G03443g PE=4 SV=1 | | 1.77 |
| A0A0W0EB88 | Importin subunit beta-4 OS=Candida glabrata GN=AO440\_001628 PE=4 SV=1 | | 1.77 |
| Q874M8 | Ribosomal protein L37 OS=Kluyveromyces delphensis GN=RPL37A PE=3 SV=1 | | 1.78 |
| A0A0W0DBT9 | Phosphorelay intermediate protein YPD1 OS=Candida glabrata GN=AO440\_003464 PE=4 SV=1 | | 1.78 |
| Q6FVS0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D06160g PE=4 SV=1 | | 1.79 |
| Q6FUG2 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0F03729g PE=4 SV=1 | | 1.79 |
| A0A0W0CD45 | 40S ribosomal protein S27 OS=Candida glabrata GN=AO440\_002824 PE=3 SV=1 | | 1.81 |
| Q6FPV0 | 40S ribosomal protein S27 OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J00737g PE=3 SV=1 | | 1.81 |
| A0A0W0EQC9 | Glycerol-1-phosphate phosphohydrolase 1 OS=Candida glabrata GN=AO440\_004388 PE=4 SV=1 | | 1.82 |
| Q6FS94 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H02409g PE=3 SV=1 | | 1.83 |
| A0A0W0CFG6 | Eukaryotic translation initiation factor eIF-1 OS=Candida glabrata GN=AO440\_003095 PE=4 SV=1 | | 1.84 |
| A0A0W0EI29 | Ceramide synthase subunit LIP1 OS=Candida glabrata GN=AO440\_004440 PE=4 SV=1 | | 1.84 |
| A0A0W0EI07 | Eukaryotic translation initiation factor 3 subunit C OS=Candida glabrata GN=NIP1 PE=3 SV=1 | | 1.85 |
| Q6FJ86 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M08338g PE=3 SV=1 | | 1.85 |
| Q6FUP9 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0F01683g PE=4 SV=2 | | 1.86 |
| A0A0W0CLR3 | RuvB-like helicase OS=Candida glabrata GN=AO440\_001336 PE=3 SV=1 | | 1.86 |
| A0A0W0CSA5 | Uncharacterized protein OS=Candida glabrata GN=AO440\_004749 PE=4 SV=1 | | 1.87 |
| A0A0W0CP72 | 78 kDa glucose-regulated protein-like protein OS=Candida glabrata GN=AO440\_000737 PE=4 SV=1 | | 1.88 |
| A0A0W0CK14 | Glycerol-3-phosphate dehydrogenase [NAD(+)] OS=Candida glabrata GN=AO440\_003323 PE=3 SV=1 | | 1.89 |
| Q6FR86 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H10582g PE=3 SV=1 | | 1.89 |
| A0A0W0CDK0 | Ubiquitin carboxyl-terminal hydrolase 1 OS=Candida glabrata GN=AO440\_002348 PE=3 SV=1 | | 1.89 |
| Q6FUU0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=PRO2 PE=3 SV=1 | | 1.91 |
| A0A0W0DGA5 | CTP synthase OS=Candida glabrata GN=AO440\_001284 PE=3 SV=1 | | 1.92 |
| A0A0W0CUV0 | Protein transport protein SEC23-2 OS=Candida glabrata GN=AO440\_001908 PE=4 SV=1 | | 1.93 |
| A0A0W0D1Y3 | 54S ribosomal protein L33, mitochondrial OS=Candida glabrata GN=AO440\_002453 PE=4 SV=1 | | 1.93 |
| A0A0W0DCH4 | Twinfilin-1 OS=Candida glabrata GN=AO440\_003298 PE=4 SV=1 | | 1.95 |
| Q6FIS2 | Glycine cleavage system H protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M12188g PE=3 SV=1 | | 1.96 |
| Q6FPH4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J03806g PE=4 SV=1 | | 1.97 |
| Q6FQI8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=YAK1 PE=4 SV=1 | | 2 |
| A0A0W0DG18 | Uncharacterized protein OS=Candida glabrata GN=AO440\_000707 PE=4 SV=1 | | 2 |
| Q6FRQ6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H06721g PE=3 SV=1 | | 2 |
| A0A0W0D956 | Ubiquitin carboxyl-terminal hydrolase 7 OS=Candida glabrata GN=AO440\_002180 PE=3 SV=1 | | 2 |
| A0A0W0DED9 | 54S ribosomal protein L19, mitochondrial OS=Candida glabrata GN=AO440\_003251 PE=3 SV=1 | | 2.02 |
| A0A0W0DNG3 | Mannose-1-phosphate guanyltransferase 2 OS=Candida glabrata GN=AO440\_002105 PE=4 SV=1 | | 2.04 |
| Q6FX67 | MICOS complex subunit MIC10 OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B00396g PE=3 SV=2 | | 2.05 |
| Q6FXI6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0B03619g PE=3 SV=1 | | 2.07 |
| A0A0W0DF97 | Cerevisin OS=Candida glabrata GN=AO440\_000315 PE=3 SV=1 | | 2.07 |
| A0A0W0DD20 | Mitochondrial intermembrane space cysteine motif-containing protein MIX17 OS=Candida glabrata GN=AO440\_004898 PE=4 SV=1 | | 2.07 |
| A0A0W0E3D5 | DNA-directed RNA polymerases I, II, and III subunit RPABC2 OS=Candida glabrata GN=AO440\_001897 PE=3 SV=1 | | 2.11 |
| A0A0W0C6Z4 | Nuclear localization sequence-binding protein (Fragment) OS=Candida glabrata GN=AO440\_005598 PE=4 SV=1 | | 2.12 |
| Q6FNA0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K01595g PE=3 SV=1 | | 2.14 |
| A0A0W0D7R8 | Phosphoribosylaminoimidazole carboxylase OS=Candida glabrata GN=AO440\_003688 PE=3 SV=1 | | 2.15 |
| A0A0W0EMY7 | PAB-dependent poly(A)-specific ribonuclease subunit PAN3 OS=Candida glabrata GN=PAN3 PE=3 SV=1 | | 2.15 |
| Q6FRI1 | Uroporphyrinogen decarboxylase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0H08371g PE=3 SV=1 | | 2.16 |
| Q6FN19 | Acetolactate synthase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K03465g PE=3 SV=1 | | 2.17 |
| A0A0W0DUS0 | 4-nitrophenylphosphatase OS=Candida glabrata GN=AO440\_000597 PE=4 SV=1 | | 2.17 |
| A0A0W0CEP6 | Putative trans-2-enoyl-CoA reductase, mitochondrial OS=Candida glabrata GN=AO440\_000346 PE=4 SV=1 | | 2.21 |
| A0A0W0CUY5 | RuvB-like helicase OS=Candida glabrata GN=AO440\_001942 PE=3 SV=1 | | 2.22 |
| A0A0W0C7W9 | D-arabinono-1,4-lactone oxidase OS=Candida glabrata GN=AO440\_002069 PE=4 SV=1 | | 2.25 |
| Q6FJF8 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M06633g PE=4 SV=1 | | 2.25 |
| A0A0W0EC96 | Putative electron transfer flavoprotein subunit beta OS=Candida glabrata GN=AO440\_003286 PE=4 SV=1 | | 2.27 |
| Q6FIJ0 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M14025g PE=4 SV=1 | | 2.27 |
| A0A0W0E2U0 | Eukaryotic translation initiation factor 3 subunit J OS=Candida glabrata GN=HCR1 PE=3 SV=1 | | 2.27 |
| A0A0W0D357 | Putative oxidoreductase TDA3 OS=Candida glabrata GN=AO440\_001004 PE=4 SV=1 | | 2.31 |
| A0A0W0D4W8 | Eukaryotic translation initiation factor 3 subunit I OS=Candida glabrata GN=TIF34 PE=3 SV=1 | | 2.31 |
| Q6FP91 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J05698g PE=4 SV=1 | | 2.34 |
| A0A0W0DHG8 | DNA-directed RNA polymerase III subunit RPC7 OS=Candida glabrata GN=AO440\_003007 PE=4 SV=1 | | 2.34 |
| A0A0W0DQN9 | Ribosome-interacting GTPase 1 OS=Candida glabrata GN=AO440\_004375 PE=4 SV=1 | | 2.38 |
| Q6FIS5 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M12122g PE=4 SV=1 | | 2.38 |
| Q6FN37 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K03047g PE=4 SV=1 | | 2.4 |
| A0A0W0D2Q3 | Protein HRI1 OS=Candida glabrata GN=AO440\_002361 PE=4 SV=1 | | 2.41 |
| A0A0W0DL61 | Protein SSO1 OS=Candida glabrata GN=AO440\_001088 PE=3 SV=1 | | 2.41 |
| A0A0W0CS10 | Nuclear and cytoplasmic polyadenylated RNA-binding protein PUB1 OS=Candida glabrata GN=AO440\_002349 PE=4 SV=1 | | 2.42 |
| Q6FR85 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=PUB1 PE=4 SV=1 | | 2.42 |
| Q6FUL3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=HPT1 PE=4 SV=1 | | 2.43 |
| A0A0W0DG60 | Enolase-phosphatase E1 OS=Candida glabrata GN=UTR4 PE=3 SV=1 | | 2.45 |
| A0A0W0CIH3 | Delta-aminolevulinic acid dehydratase OS=Candida glabrata GN=AO440\_000862 PE=3 SV=1 | | 2.46 |
| Q6FSY3 | T-complex protein 1 subunit gamma OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G06908g PE=3 SV=1 | | 2.48 |
| Q6FQ58 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0I08965g PE=4 SV=1 | | 2.49 |
| Q6FVK3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E01221g PE=4 SV=1 | | 2.5 |
| A0A0W0C669 | Protein GIR2 OS=Candida glabrata GN=AO440\_000949 PE=4 SV=1 | | 2.5 |
| Q6FN51 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K02717g PE=3 SV=1 | | 2.5 |
| A0A0W0EA32 | Protein SSP120 OS=Candida glabrata GN=AO440\_002046 PE=4 SV=1 | | 2.51 |
| A0A0W0CAR6 | Acetolactate synthase OS=Candida glabrata GN=AO440\_003401 PE=3 SV=1 | | 2.53 |
| A0A0W0DLE8 | Diphthine methyl ester synthase OS=Candida glabrata GN=AO440\_000373 PE=3 SV=1 | | 2.55 |
| Q6FMH6 | Signal recognition particle 54 kDa protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K07986g PE=3 SV=1 | | 2.57 |
| A0A0W0EPF3 | Signal recognition particle 54 kDa protein OS=Candida glabrata GN=AO440\_003588 PE=3 SV=1 | | 2.57 |
| Q6FMP6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K06325g PE=4 SV=1 | | 2.57 |
| Q6FKZ6 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L07370g PE=4 SV=1 | | 2.59 |
| A0A0W0D577 | UDP-N-acetylglucosamine pyrophosphorylase OS=Candida glabrata GN=AO440\_005137 PE=4 SV=1 | | 2.59 |
| A0A0W0DLK5 | Actin cytoskeleton-regulatory complex protein PAN1 OS=Candida glabrata GN=AO440\_002867 PE=4 SV=1 | | 2.61 |
| A0A0W0ES33 | Glucosamine 6-phosphate N-acetyltransferase OS=Candida glabrata GN=AO440\_000702 PE=4 SV=1 | | 2.63 |
| A0A0W0CMH2 | Chromatin structure-remodeling complex protein RSC6 OS=Candida glabrata GN=AO440\_000523 PE=4 SV=1 | | 2.64 |
| Q6FWT5 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0C03025g PE=4 SV=1 | | 2.64 |
| Q6FQ81 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=TIF3 PE=4 SV=1 | | 2.65 |
| A0A0W0DNE2 | Uridylate kinase OS=Candida glabrata GN=URA6 PE=3 SV=1 | | 2.65 |
| Q6FKP3 | Uridylate kinase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=URA6 PE=3 SV=1 | | 2.65 |
| A0A0W0DQ88 | Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Candida glabrata GN=AO440\_004405 PE=3 SV=1 | | 2.67 |
| B4UN30 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0J06374g PE=3 SV=1 | | 2.68 |
| A0A0W0CKR7 | Eukaryotic translation initiation factor 4B OS=Candida glabrata GN=AO440\_002697 PE=4 SV=1 | | 2.87 |
| A0A0W0CJ05 | Diphosphomevalonate decarboxylase OS=Candida glabrata GN=AO440\_000548 PE=3 SV=1 | | 2.87 |
| Q6FWQ9 | Diphosphomevalonate decarboxylase OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0C03630g PE=3 SV=1 | | 2.87 |
| Q6FUD3 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0F04367g PE=3 SV=1 | | 2.93 |
| A0A0W0DGA1 | UPF0001 protein OS=Candida glabrata GN=AO440\_001281 PE=3 SV=1 | | 2.93 |
| Q6FY93 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0A04037g PE=4 SV=1 | | 2.95 |
| A0A0W0CMX8 | Periodic tryptophan protein 1 OS=Candida glabrata GN=AO440\_000113 PE=4 SV=1 | | 2.95 |
| A0A0W0CWP1 | SWI/SNF complex subunit SWI3 OS=Candida glabrata GN=AO440\_004344 PE=4 SV=1 | | 2.96 |
| Q6FWM5 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=ATP16 PE=3 SV=1 | | 3.02 |
| Q6FM25 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0K11572g PE=4 SV=1 | | 3.03 |
| A0A0W0CRC0 | Co-chaperone protein SBA1 OS=Candida glabrata GN=AO440\_003738 PE=4 SV=1 | | 3.03 |
| Q6FVB4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0E03245g PE=4 SV=1 | | 3.05 |
| A0A0W0EDH0 | Nuclear localization sequence-binding protein OS=Candida glabrata GN=AO440\_005637 PE=4 SV=1 | | 3.05 |
| Q6FLV4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L00385g PE=4 SV=1 | | 3.08 |
| A0A0W0CM44 | mRNA 3'-end-processing protein RNA15 OS=Candida glabrata GN=AO440\_000865 PE=4 SV=1 | | 3.08 |
| Q6FVR9 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0D06182g PE=4 SV=1 | | 3.08 |
| A0A0W0CA45 | Transcription elongation factor SPT5 (Fragment) OS=Candida glabrata GN=AO440\_002092 PE=4 SV=1 | | 3.22 |
| A0A0W0CED5 | Ribonucleotide reductase inhibitor protein SML1 OS=Candida glabrata GN=AO440\_004774 PE=4 SV=1 | | 3.23 |
| A0A0W0EBU1 | Prefoldin subunit 1 OS=Candida glabrata GN=AO440\_001793 PE=4 SV=1 | | 3.33 |
| A0A0W0EE15 | Mitochondrial phosphate carrier protein OS=Candida glabrata GN=AO440\_001113 PE=3 SV=1 | | 3.41 |
| A0A0W0D8Y0 | Reduced viability upon starvation protein 167 OS=Candida glabrata GN=AO440\_003927 PE=4 SV=1 | | 3.64 |
| Q6FK28 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0M01650g PE=4 SV=1 | | 3.64 |
| Q6FSY4 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0G06886g PE=4 SV=1 | | 3.65 |
| A0A0W0DQ40 | Cell wall mannoprotein CIS3 OS=Candida glabrata GN=AO440\_004218 PE=4 SV=1 | | 3.79 |
| Q6FJ79 | Uncharacterized protein OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=PIR5 PE=4 SV=1 | | 3.79 |
| A0A0W0DHD0 | Translation machinery-associated protein 46 OS=Candida glabrata GN=AO440\_003138 PE=4 SV=1 | | 4.01 |

**Table S8: Antifungal activity of A) 3-BP B) Polydatin alone and in combination with FLC against the representative drug-resistant and drug-susceptible clinical isolates of *C. albicans* and *C. glabrata***

**A)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **FLC mM (MIC80)** | **FLC Comb mM** | **BP mM (MIC80)** | **BP Comb mM** | **FICI value** |
| M1038 | 0.208 | 0.013 | 1.56 | 0.39 | 0.31 |
| M2 | 0.013 | 0.0032 | 1.56 | 0.195 | 0.4 |
| M183 | 0.208 | 0.104 | 3.12 | 0.78 | 0.75 |
| M203 | 0.0033 | 0.00165 | 3.12 | 0.39 | 0.63 |

**B)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **FLC**  **(mM) (MIC80)** | **FLC Comb**  **(mM)** | **Pd**  **(mM) (MIC80)** | **Pd Comb**  **(mM)** | **FICI value** |
| M1038 | 0.208 | 0.026 | 1.25 | 0.078 | 0.187 |
| M2 | 0.013 | 0.00325 | 2.5 | 0.0195 | 0.35 |
| M183 | 0.208 | 0.052 | 5 | 0.625 | 0.375 |
| M203 | 0.0033 | 0.0008 | 5 | 0.312 | 0.303 |

**Table S9: Molecular docking showing affinity energies of A) 3-Bromopyruvate interactions with hexokinase 2 of *C. albicans* B) Polydatin interactions with glucose-6-phosphate dehydrogenase of *C. albicans***

**A)**

|  |  |  |  |
| --- | --- | --- | --- |
| **S. No.** | **Affinity (kcal mol-1)** | **Distance from RMSD l.b** | **Best mode RMSD u.b.** |
| 1 | -4.0 | 0.000 | 0.000 |
| 2 | -3.8 | 17.655 | 18.227 |
| 3 | -3.8 | 9.635 | 9.823 |
| 4 | -3.7 | 9.181 | 9.338 |
| 5 | -3.7 | 2.536 | 3.252 |
| 6 | -3.7 | 18.470 | 19.004 |
| 7 | -3.7 | 13.340 | 13.664 |
| 8 | -3.7 | 8.769 | 8.937 |
| 9 | -3.7 | 37.337 | 37.538 |

**B)**

|  |  |  |  |
| --- | --- | --- | --- |
| **S. No.** | **Affinity (kcal mol-1)** | **Distance from RMSD l.b** | **Best mode RMSD u.b.** |
| 1 | -8.6 | 0.000 | 0.000 |
| 2 | -8.5 | 1.969 | 3.016 |
| 3 | -7.9 | 1.412 | 2.386 |
| 4 | -7.8 | 1.911 | 2.367 |
| 5 | -7.4 | 28.548 | 34.347 |
| 6 | -7.3 | 18.965 | 20.592 |
| 7 | -7.2 | 3.904 | 8.049 |
| 8 | -7.0 | 25.768 | 28.764 |
| 9 | -7.0 | 25.672 | 29.023 |

**Supplementary Methodology:**

**Identification & drug susceptibility testing of clinical isolates:** Initially, clinical isolates were identified by conventional phenotypic assays such as colony color on Hi-Crome *Candida* agar and cornmeal agar (CMA) and Vitek 2 compact (bioMe'rieux, Inc., France). Preliminary antifungal susceptibility testing of clinical isolates was done by Vitek 2 compact (bioMe'rieux, Inc., France) and by minimum inhibitory concentration (MIC80) determinations [1].

**Molecular identification of clinical isolates:** The drug-resistant isolates obtained by preliminary drug susceptibility testing were further identified by the HiCandidaTM identification kit, procured from HiMedia (KB006) and molecular identification of *Candida* species was performed by polymerase chain reaction-based restriction fragment length polymorphism (RFLP) of amplicons. For kit-based identification, one kit was used for each strain. Briefly, 50 µl of the cells (OD630= 0.5) of each strain were poured into all the 12 wells of the kit and the color change of wells was monitored according to the manufacturer's instructions. For PCR-RFLP-based molecular identification, the phenol-chloroform-based method was used to isolate the genomic DNA of drug-resistant and control strains (reference strains). PCR amplification of internal transcribed spacer 1 (ITS1)-5.8S-ITS4 rDNA regions was achieved by thermocycler using the ITS1 (forward, 5'-TCC GTA GGT GAA CCT GCG G-3') and ITS4 (reverse, 5'TCC TCC GCT TAT TGA TAT GC-3') primer pairs. The size of PCR- and digestion products of RFLP (using *Msp*I enzyme) was determined by comparison with two different DNA ladders [2, 3].

**Growth curve analysis:**An overnight primary culture was incubated with constant shaking at 30oC. Secondary culture, 1x106 cells/ml (OD600 =0.1) was set up in conical flasks in 50 ml culture media. The growth was calculated by measuring OD600 at different time points.

**References:**

1. Shah, A.H., et al., *Mutational analysis of intracellular loops identify cross talk with nucleotide binding domains of yeast ABC transporter Cdr1p.* Scientific reports, 2015. **5**(1): p. 1-17.

2. Mirhendi, H., et al., *A one-enzyme PCR-RFLP assay for identification of six medically important Candida species.* Nippon Ishinkin Gakkai Zasshi, 2006. **47**(3): p. 225-229.

3. Fatima, A., et al., *Molecular identification of Candida species isolated from cases of neonatal candidemia using polymerase chain reaction-restriction fragment length polymorphism in a tertiary care hospital.* Indian Journal of Pathology and Microbiology, 2017. **60**(1): p. 61.

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