**Appendix S1**. Proteins in the reference *Saccharomyces cerevisiae* (S288C) and their corresponding orthologues in investigated yeasts

| *Yarrowia lipolytica* (CLIB122) | | | | *Candida albicans* (WO-1) | | | | *Dekkera bruxelensis* (AWRI 1499) | | | | *Kluyveromyces lactis* (Y707) | | | | *Candida glabrata* (Y475) | | | | *Saccharomyces cerevisiae* (Y706) | | | | *Saccharomyces cerevisiae* (s288c) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genebank ID | E value | Identities | Positives | Genebank ID | E value | Identities | Positives | Genebank ID | E value | Identities | Positives | Genebank ID | E value | Identities | Positives | Genebank ID | E value | Identities | Positives | Genebank ID | E value | Identities | Positives | Protein |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | gi\|392296702 | 6.5e-297 | 525/525 (100%) | 525/525 (100%) | ATF1 (YOR377W) |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | gi\|392299430 | 3.1e-297 | 535/535 (100%) | 535/535 (100%) | ATF2 (YGR177C ) |
| gi\|496650080 | 3.4e-133 | 250/496 (50%) | 334/496 (67%) | gi\|238881848 | 2.3e-143 | 262/497 (52%) | 352/497 (70%) | gi\|385304822 | 5.1e-123 | 224/442 (50%) | 299/442 (67%) | gi\|49644672 | 4.6e-177 | 318/504 (63%) | 388/504 (76%) | gi\|49525724 | 9E-197 | 355/508 (69%) | 419/508 (82%) | gi\|392299549 | 4.3e-277 | 499/500 (99%) | 500/500 (100%) | ARO8 (YGL202W) |
| gi\|49647333 | 2.9e-51 | 132/448 (29%) | 221/448 (49%) | gi\|238881328 | 7.1e-89 | 171/439 (38%) | 260/439 (59%) | gi\|385302174 | 1.2e-52 | 132/362 (36%) | 195/362 (53%) | gi\|49642691 | 9.6e-161 | 292/506 (57%) | 381/506 (75%) | gi\|49525932 | 9.6e-161 | 292/506 (57%) | 381/506 (75%) | gi\|392298944 | 4.6e-280 | 513/513 (100%) | 513/513 (100%) | ARO9 (YHR137W) |
| gi\|49648423 | 6.8e-128 | 243/495 (49%) | 331/495 (66%) | - | - | - | - | - | - | - | - | gi\|49642640 | 2.4e-189 | 340/501 (67%) | 412/501 (82%) | gi\|49525613 | 1.8e-182 | 329/503 (65%) | 400/503 (79%) | - | - | - | - | ALD2 (YMR170C) |
| - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | ALD3 (YMR169C) |
| gi\|49647250 | 1.5e-162 | 294/488 (60%) | 379/488 (77%) | - | - | - | - | gi\|385302426 | 4.6e-177 | 325/524 (62%) | 401/524 (76%) | gi\|49644235 | 2E-222 | 395/512 (77%) | 457/512 (89%) | gi\|49525001 | 1E-234 | 423/514 (82%) | 470/514 (91%) | gi\|392296700 | 1.6e-279 | 519/519 (100%) | 519/519 (100%) | ALD4 (YOR374W) |
| - | - | - | - | gi\|238882092 | 7.8e-175 | 318/499 (63%) | 393/499 (78%) | - | - | - | - | gi\|49641679 | 4E-226 | 398/502 (79%) | 449/502 (89%) | gi\|49527155 | 5.6e-220 | 400/513 (77%) | 449/513 (87%) | gi\|392299771 | 2.8e-280 | 520/520 (100%) | 520/520 (100%) | ALD5 (YER073W) |
| - | - | - | - | - | - | - | - | - | - | - | - | gi\|49644127 | 3E-205 | 364/491 (74%) | 435/491 (88%) | gi\|49526328 | 9.9e-207 | 361/495 (72%) | 434/495 (87%) | gi\|392295949 | 6.9e-270 | 500/500 (100%) | 500/500 (100%) | ALD6 (YPL061W) |
| - | - | - | - | - | - | - | - | gi\|385303323 | 5.3e-105 | 199/378 (52%) | 264/378 (69%) | gi\|49644238 | 1.3e-135 | 240/381 (62%) | 298/381 (78%) | gi\|49524727 | 2.2e-129 | 231/383 (60%) | 291/383 (75%) | gi\|392301243 | 2.7e-211 | 382/382 (100%) | 382/382 (100%) | BDH1 (YAL060W) |
| - | - | - | - | - | - | - | - | - | - | - | - | gi\|49644239 | 2E-128 | 230/377 (61%) | 289/377 (76%) | - | - | - | - | gi\|392301232 | 3.8e-230 | 412/417 (98%) | 412/417 (98%) | BDH2 (YAL061W) |
| gi\|49648146 | 8.6e-137 | 247/390 (63%) | 300/390 (76%) | gi\|238879061 | 2.9e-97 | 181/394 (45%) | 255/394 (64%) | gi\|385302974 | 2.3e-143 | 257/372 (69%) | 305/372 (81%) | gi\|49640582 | 1.1e-173 | 315/383 (82%) | 337/383 (87%) | gi\|49525675 | 4.9e-173 | 308/372 (82%) | 334/372 (89%) | gi\|392299022 | 4.1e-217 | 393/393 (100%) | 393/393 (100%) | BAT1 (YHR208W) |
| - | - | - | - | gi\|238882204 | 5.6e-133 | 248/371 (66%) | 287/371 (77%) | - | - | - | - | - | - | - | - | - | - | - | - | gi\|392298577 | 6.7e-208 | 376/376 (100%) | 376/376 (100%) | BAT2 (YJR148W) |

Orthologs are identified by their unique Genebank ID. The E value indicates the statistical significance of each alignment. The lower the E value, the more significant is the hit, and the less likely it is to have occured by chance. Identities is the ratio (and percentage) of identical aminoacids and the subject length for each alignment. Positives is the ratio (and percentage) of conservative substitutions and the subject length for each alignment, as defined by the substitution matrix (BLOSUM62).