|  | accession | descriptior | score | cover | # pro | # unique p | #pep | #PSM | AA |
|---|---|---|---|---|---|---|---|---|---|
| 1 | P02994 | Elongation factor 1-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TEF1 PE=1 SV=1 - [EF1A_YEAST] | 490.84 | 59.83% | 4 | 16 | 23 | 138 | 458 |
| 2 | P00359 | Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH3 PE=1 SV=3 - [G3P3_YEAST] | 495.95 | 80.42% | 2 | 7 | 20 | 131 | 332 |

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|---|---|---|---|---|---|---|---|---|---|
| 3 | P00549 | Pyruvate kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC19 PE=1 SV=2 - [KPYK1_YEAST] | 426.19 | 81.20% | 5 | 41 | 41 | 121 | 500 |
| 4 | P32324 | Elongation factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EFT1 PE=1 SV=1 - [EF2_YEAST] | 424.91 | 46.08% | 4 | 36 | 36 | 121 | 842 |

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| 5 | P10664 | 60S ribosomal protein L4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL4A PE=1 SV=4 - [RL4A_YEAST] | 419.06 | 51.38% | 2 | 16 | 16 | 107 | 362 |
| 6 | P14126 | 60S ribosomal protein L3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL3 PE=1 SV=4 - [RL3_YEAST] | 361.05 | 48.58% | 2 | 21 | 21 | 97 | 387 |

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| 7 | P41752 | Elongation factor 1-alpha OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=TEF PE=3 SV=1 - [EF1A_ASHGO] | 296.84 | 34.06% | 3 | 1 | 12 | 94 | 458 |
| 8 | P05030 | Plasma membrane ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMA1 PE=1 SV=2 - [PMA1_YEAST] | 295.7 | 32.68% | 2 | 29 | 29 | 78 | 918 |

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| 9 | P00358 | Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH2 PE=1 SV=3 - [G3P2_YEAST] | 229.76 | 67.77% | 2 | 4 | 18 | 66 | 332 |
| 10 | P00560 | Phosphoglycerate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGK1 PE=1 SV=2 - [PGK_YEAST] | 245.25 | 71.63% | 2 | 31 | 31 | 64 | 416 |

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| 11 | P16521 | Elongation factor 3A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YEF3 PE=1 SV=4 - [EF3A_YEAST] | 219.65 | 47.51% | 4 | 35 | 35 | 60 | 1044 |
| 12 | P07259 | Protein URA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA2 PE=1 SV=5 - [PYR1_YEAST] | 167.74 | 26.29% | 2 | 38 | 38 | 49 | 2214 |

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| 13 | P0CX50 | 60S ribosomal protein L18-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL18B PE=1 SV=1 - [RL18B_YEAST] | 161.5 | 38.17% | 1 | 7 | 7 | 47 | 186 |
| 14 | P14120 | 60S ribosomal protein L30 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL30 PE=1 SV=3 - [RL30_YEAST] | 136.58 | 67.62% | 2 | 8 | 8 | 43 | 105 |

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| 15 | P40150 | Ribosome-associated molecular chaperone SSB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSB2 PE=1 SV=2 - [SSB2_YEAST] | 168.08 | 55.14% | 1 | 1 | 28 | 42 | 613 |
| 16 | P11484 | Ribosome-associated molecular chaperone SSB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSB1 PE=1 SV=3 - [SSB1_YEAST] | 166.55 | 57.26% | 2 | 2 | 29 | 42 | 613 |

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| 17 | P00360 | Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TDH1 PE=1 SV=3 - [G3P1_YEAST] | 135.37 | 37.65% | 1 | 4 | 9 | 39 | 332 |
| 18 | P26321 | 60S ribosomal protein L5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL5 PE=1 SV=4 - [RL5_YEAST] | 151.42 | 43.77% | 2 | 11 | 11 | 38 | 297 |

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| 19 | P05740 | 60S ribosomal protein L17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL17A PE=1 SV=4 - [RL17A_YEAST] | 142.13 | 41.30% | 1 | 1 | 6 | 37 | 184 |
| 20 | P0CX35 | 40S ribosomal protein S4-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS4A PE=1 SV=1 - [RS4A_YEAST] | 136.78 | 54.79% | 1 | 17 | 17 | 37 | 261 |

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| 21 | P06169 | Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDC1 PE=1 SV=7 - [PDC1_YEAST] | 144.19 | 45.29% | 2 | 15 | 16 | 36 | 563 |
| 22 | P46990 | 60S ribosomal protein L17-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL17B PE=1 SV=2 - [RL17B_YEAST] | 140.04 | 41.30% | 1 | 1 | 6 | 36 | 184 |

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| 23 | P0CX45 | 60S ribosomal protein L2-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL2A PE=1 SV=1 - [RL2A_YEAST] | 124.18 | 53.54% | 2 | 15 | 15 | 36 | 254 |
| 24 | P05750 | 40S ribosomal protein S3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS3 PE=1 SV=5 - [RS3_YEAST] | 122.51 | 62.92% | 1 | 16 | 16 | 35 | 240 |

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| 25 | P07149 | Fatty acid synthase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAS1 PE=1 SV=2 - [FAS1_YEAST] | 114.63 | 23.65% | 1 | 31 | 31 | 35 | 2051 |
| 26 | P0CX43 | 60S ribosomal protein L1-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL1A PE=1 SV=1 - [RL1A_YEAST] | 115.33 | 46.08% | 2 | 12 | 12 | 31 | 217 |

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| 27 | P00950 | Phosphoglycerate mutase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPM1 PE=1 SV=3 - [PMG1_YEAST] | 107.22 | 69.64% | 1 | 16 | 16 | 31 | 247 |
| 28 | P19097 | Fatty acid synthase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAS2 PE=1 SV=2 - [FAS2_YEAST] | 106.12 | 20.19% | 2 | 25 | 25 | 31 | 1887 |

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| 29 | P26783 | 40S ribosomal protein S5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS5 PE=1 SV=3 - [RS5_YEAST] | 98.99 | 36.44% | 1 | 10 | 10 | 31 | 225 |
| 30 | P16861 | ATP-dependent 6-phosphofructokinase subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PFK1 PE=1 SV=1 - [PFKA1_YEAST] | 109.87 | 34.55% | 1 | 25 | 25 | 30 | 987 |

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| 31 | P0CX41 | 60S ribosomal protein L23-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL23A PE=1 SV=1 - [RL23A_YEAST] | 95.91 | 41.61% | 1 | 7 | 7 | 30 | 137 |
| 32 | P00925 | Enolase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ENO2 PE=1 SV=2 - [ENO2_YEAST] | 106.7 | 52.86% | 3 | 16 | 16 | 29 | 437 |

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| 33 | P0CX37 | 40S ribosomal protein S6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS6A PE=1 SV=1 - [RS6A_YEAST] | 101.65 | 52.12% | 1 | 15 | 15 | 29 | 236 |
| 34 | P06168 | Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV5 PE=1 SV=1 - [ILV5_YEAST] | 97.68 | 54.18% | 1 | 18 | 18 | 29 | 395 |

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| 35 | Q00955 | Acetyl-CoA carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACC1 PE=1 SV=2 - [ACAC_YEAST] | 93.65 | 19.84% | 6 | 28 | 28 | 29 | 2233 |
| 36 | P41805 | 60S ribosomal protein L10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL10 PE=1 SV=1 - [RL10_YEAST] | 93.09 | 65.61% | 1 | 16 | 16 | 27 | 221 |

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| 37 | B3RHV0 | 40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS1A PE=3 SV=1 - [RS3A1_YEAS1] | 86.47 | 54.51% | 1 | 5 | 15 | 27 | 255 |
| 38 | B3LLJ2 | 40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS1B PE=3 SV=1 - [RS3A2_YEAS1] | 85.79 | 54.90% | 3 | 5 | 15 | 27 | 255 |

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| 39 | P26786 | 40S ribosomal protein S7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS7A PE=1 SV=4 - [RS7A_YEAST] | 98.78 | 71.58% | 1 | 9 | 16 | 26 | 190 |
| 40 | P38788 | Ribosome-associated complex subunit SSZ1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSZ1 PE=1 SV=2 - [SSZ1_YEAST] | 98.07 | 52.23% | 1 | 19 | 19 | 26 | 538 |

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| 41 | P23254 | Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TKL1 PE=1 SV=4 - [TKT1_YEAST] | 91.98 | 33.97% | 2 | 19 | 19 | 26 | 680 |
| 42 | P0CX53 | 60S ribosomal protein L12-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL12A PE=1 SV=1 - [RL12A_YEAST] | 87.14 | 44.85% | 1 | 6 | 6 | 26 | 165 |

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| 43 | P0CX39 | 40S ribosomal protein S8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS8A PE=1 SV=1 - [RS8A_YEAST] | 84.5 | 41.00% | 1 | 7 | 7 | 26 | 200 |
| 44 | P06367 | 40S ribosomal protein S14-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS14A PE=1 SV=5 - [RS14A_YEAST] | 92.22 | 58.39% | 3 | 11 | 11 | 25 | 137 |

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| 45 | P0CX23 | 60S ribosomal protein L20-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL20A PE=1 SV=1 - [RL20A_YEAST] | 87.97 | 47.09% | 1 | 13 | 13 | 25 | 172 |
| 46 | P48164 | 40S ribosomal protein S7-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS7B PE=1 SV=1 - [RS7B_YEAST] | 85.91 | 60.53% | 1 | 5 | 12 | 23 | 190 |

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| 47 | P37291 | Serine hydroxymethyltransferase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SHM2 PE=1 SV=2 - [GLYC_YEAST] | 81.73 | 42.22% | 2 | 17 | 17 | 23 | 469 |
| 48 | P02407 | 40S ribosomal protein S17-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS17A PE=1 SV=1 - [RS17A_YEAST] | 76.94 | 62.50% | 2 | 14 | 14 | 22 | 136 |

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| 49 | P38720 | 6-phosphogluconate dehydrogenase, decarboxylating 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GND1 PE=1 SV=1 - [6PGD1_YEAST] | 76.53 | 30.06% | 2 | 14 | 14 | 22 | 489 |
| 50 | Q01855 | 40S ribosomal protein S15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS15 PE=1 SV=1 - [RS15_YEAST] | 69.5 | 42.25% | 1 | 5 | 5 | 22 | 142 |

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| 51 | Q02326 | 60S ribosomal protein L6-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL6A PE=1 SV=2 - [RL6A_YEAST] | 68.16 | 43.18% | 1 | 5 | 11 | 22 | 176 |
| 52 | P05739 | 60S ribosomal protein L6-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL6B PE=1 SV=4 - [RL6B_YEAST] | 68.09 | 47.73% | 1 | 7 | 12 | 22 | 176 |

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| 53 | P0CX26 | 60S ribosomal protein L43-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL43B PE=1 SV=1 - [RL43B_YEAST] | 82.19 | 20.65% | 1 | 2 | 2 | 21 | 92 |
| 54 | P38219 | Obg-like ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OLA1 PE=1 SV=1 - [OLA1_YEAST] | 71.25 | 44.16% | 1 | 14 | 14 | 20 | 394 |

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| 55 | P29453 | 60S ribosomal protein L8-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL8B PE=1 SV=3 - [RL8B_YEAST] | 70.37 | 32.42% | 1 | 2 | 10 | 20 | 256 |
| 56 | P14742 | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GFA1 PE=1 SV=4 - [GFA1_YEAST] | 64.47 | 31.66% | 1 | 16 | 16 | 20 | 717 |

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| 57 | P25443 | 40S ribosomal protein S2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS2 PE=1 SV=3 - [RS2_YEAST] | 79.47 | 40.16% | 1 | 7 | 7 | 19 | 254 |
| 58 | P16862 | ATP-dependent 6-phosphofructokinase subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PFK2 PE=1 SV=4 - [PFKA2_YEAST] | 72.51 | 25.34% | 1 | 14 | 14 | 19 | 959 |

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| 59 | P41940 | Mannose-1-phosphate guanyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PSA1 PE=1 SV=2 - [MPG1_YEAST] | 70.14 | 42.94% | 2 | 12 | 12 | 19 | 361 |
| 60 | P10592 | Heat shock protein SSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSA2 PE=1 SV=3 - [HSP72_YEAST] | 67.06 | 38.97% | 3 | 16 | 17 | 19 | 639 |

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| 61 | P40024 | ABC transporter ATP-binding protein ARB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARB1 PE=1 SV=1 - [ARB1_YEAST] | 65.61 | 37.70% | 1 | 16 | 16 | 19 | 610 |
| 62 | A6ZP47 | ATP-dependent RNA helicase DED1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DED1 PE=3 SV=1 - [DED1_YEAS7] | 63.65 | 36.92% | 7 | 14 | 15 | 19 | 604 |

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| 63 | P17076 | 60S ribosomal protein L8-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL8A PE=1 SV=4 - [RL8A_YEAST] | 63.42 | 35.94% | 1 | 3 | 11 | 19 | 256 |
| 64 | P38934 | Nuclear segregation protein BFR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BFR1 PE=1 SV=1 - [BFR1_YE | 60.59 | 28.72% | 1 | 11 | 11 | 19 | 470 |

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| 65 | A6ZY89 | Pentafunctional AROM polypeptide OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ARO1 PE=3 SV=1 - [ARO1_YEAS7] | 59.02 | 14.48% | 5 | 16 | 16 | 19 | 1588 |
| 66 | P0CX32 | 40S ribosomal protein S24-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS24B PE=1 SV=1 - [RS24B_YEAST] | 56.43 | 47.41% | 1 | 7 | 7 | 19 | 135 |

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| 67 | P07342 | Acetolactate synthase catalytic subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV2 PE=1 SV=1 - [ILVB_YEAST] | 67.08 | 30.42% | 1 | 13 | 13 | 18 | 687 |
| 68 | Q3E754 | 40S ribosomal protein S21-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS21B PE=1 SV=1 - [RS21B_YEAST] | 66.08 | 54.02% | 1 | 1 | 6 | 18 | 87 |

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| 69 | P0C0V8 | 40S ribosomal protein S21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS21A PE=1 SV=1 - [RS21A_YEAST] | 64.98 | 54.02% | 1 | 1 | 6 | 18 | 87 |
| 70 | P38701 | 40S ribosomal protein S20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS20 PE=1 SV=3 - [RS20_YEAST] | 64.12 | 71.90% | 1 | 9 | 9 | 18 | 121 |

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| 71 | P38011 | Guanine nucleotide-binding protein subunit beta-like protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ASC1 PE=1 SV=4 - [GBLP_YEAST] | 61.96 | 38.24% | 1 | 7 | 7 | 18 | 319 |
| 72 | P15108 | ATP-dependent molecular chaperone HSC82 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSC82 PE=1 SV=4 - [HSC82_YEAST] | 61.94 | 27.09% | 5 | 15 | 15 | 18 | 705 |

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| 73 | P53221 | 60S ribosomal protein L26-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL26B PE=1 SV=2 - [RL26B_YEAST] | 55.74 | 53.54% | 2 | 12 | 12 | 18 | 127 |
| 74 | P25491 | Mitochondrial protein import protein MAS5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YDJ1 PE=1 SV=1 - [MAS5_YEAST] | 52.24 | 31.78% | 1 | 12 | 12 | 18 | 409 |

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| 75 | P38625 | GMP synthase [glutamine-hydrolyzing] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GUA1 PE=1 SV=4 - [GUAA_YEAST] | 69.19 | 29.90% | 2 | 11 | 11 | 17 | 525 |
| 76 | P05737 | 60S ribosomal protein L7-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL7A PE=1 SV=3 - [RL7A_YEAST] | 57.49 | 40.57% | 3 | 9 | 9 | 17 | 244 |

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| 77 | P38631 | 1,3-beta-glucan synthase component FKS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FKS1 PE=1 SV=2 - [FKS1_YEAST] | 57.07 | 14.13% | 3 | 14 | 14 | 17 | 1876 |
| 78 | O14467 | Multiprotein-bridging factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MBF1 PE=1 SV=2 - [MBF1_YEAST] | 53.74 | 26.49% | 1 | 4 | 4 | 17 | 151 |

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| 79 | P06105 | Protein SCP160 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCP160 PE=1 SV=3 - [SC160_YEAST] | 46.03 | 14.98% | 1 | 15 | 15 | 17 | 1222 |
| 80 | P07280 | 40S ribosomal protein S19-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS19A PE=1 SV=2 - [RS19A_YEAST] | 63.53 | 37.50% | 2 | 5 | 5 | 16 | 144 |

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| 81 | P02400 | 60S acidic ribosomal protein P2-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP2B PE=1 SV=2 - [RLA4_YEAST] | 57.41 | 100.00% | 1 | 9 | 9 | 16 | 110 |
| 82 | P05317 | 60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP0 PE=1 SV=2 - [RLA0_YE | 56.91 | 31.73% | 1 | 8 | 8 | 16 | 312 |

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| 83 | P0CX83 | 60S ribosomal protein L19-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL19B PE=1 SV=1 - [RL19B_YEAST] | 56.52 | 29.10% | 1 | 10 | 10 | 16 | 189 |
| 84 | Q12460 | Nucleolar protein 56 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP56 PE=1 SV=1 - [NOP56_Y | 56.1 | 29.56% | 1 | 12 | 12 | 16 | 504 |

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| 85 | P32527 | Zuotin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZUO1 PE=1 SV=1 - [ZUO1_YEAST] | 53.78 | 32.10% | 1 | 9 | 9 | 16 | 433 |
| 86 | P17255 | V-type proton ATPase catalytic subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA1 PE=1 SV=3 - [VATA_YEAST] | 50.49 | 19.05% | 2 | 15 | 15 | 16 | 1071 |

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| 87 | P0CX47 | 40S ribosomal protein S11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS11A PE=1 SV=1 - [RS11A_YEAST] | 48.49 | 68.59% | 1 | 11 | 11 | 16 | 156 |
| 88 | P38249 | Eukaryotic translation initiation factor 3 subunit A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPG1 PE=1 SV=1 - [EIF3A_YEAST] | 46.29 | 17.84% | 1 | 12 | 12 | 16 | 964 |

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| 89 | P0CX84 | 60S ribosomal protein L35-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL35A PE=1 SV=1 - [RL35A_YEAST] | 55.08 | 42.50% | 1 | 9 | 9 | 15 | 120 |
| 90 | P52910 | Acetyl-coenzyme A synthetase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACS2 PE=1 SV=1 - [ACS2_YEAST] | 49.71 | 21.82% | 2 | 11 | 11 | 15 | 683 |

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| 91 | O14455 | 60S ribosomal protein L36-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL36B PE=1 SV=3 - [RL36B_YEAST] | 49.44 | 42.00% | 2 | 8 | 8 | 15 | 100 |
| 92 | P04456 | 60S ribosomal protein L25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL25 PE=1 SV=4 - [RL25_YEAST] | 48.15 | 45.77% | 1 | 9 | 9 | 15 | 142 |

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| 93 | Q12672 | 60S ribosomal protein L21-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL21B PE=1 SV=1 - [RL21B_YEAST] | 43.14 | 44.38% | 1 | 3 | 8 | 15 | 160 |
| 94 | P05759 | Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS31 PE=1 SV=3 - [RS31_YEAST] | 50.68 | 39.47% | 3 | 8 | 8 | 14 | 152 |

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| 95 | P07251 | ATP synthase subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP1 PE=1 SV=5 - [ATPA_YEAST] | 47.13 | 30.28% | 1 | 13 | 13 | 14 | 545 |
| 96 | P02406 | 60S ribosomal protein L28 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL28 PE=1 SV=3 - [RL28_YEAST] | 46.53 | 35.57% | 1 | 7 | 7 | 14 | 149 |

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| 97 | Q02753 | 60S ribosomal protein L21-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL21A PE=1 SV=1 - [RL21A_YEAST] | 43.35 | 44.38% | 1 | 3 | 8 | 14 | 160 |
| 98 | P05755 | 40S ribosomal protein S9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS9B PE=1 SV=4 - [RS9B_YEAST] | 41.15 | 47.18% | 2 | 12 | 12 | 14 | 195 |

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| 99 | P26785 | 60S ribosomal protein L16-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL16B PE=1 SV=3 - [RL16B_YEAST] | 37.77 | 25.76% | 1 | 3 | 7 | 14 | 198 |
| 100 | P14540 | Fructose-bisphosphate aldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FBA1 PE=1 SV=3 - [ALF_YEAST] | 52.26 | 41.78% | 1 | 8 | 8 | 13 | 359 |

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| 101 | P46784 | 40S ribosomal protein S10-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS10B PE=1 SV=1 - [RS10B_YEAST] | 51.74 | 33.33% | 2 | 5 | 5 | 13 | 105 |
| 102 | P10659 | S-adenosylmethionine synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAM1 PE=1 SV=2 - [METK1_YEAST] | 45.95 | 38.74% | 1 | 5 | 13 | 13 | 382 |

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| 103 | B3LT19 | 40S ribosomal protein S0-B OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=RPS0B PE=3 SV=1 - [RSSA2_YEAS1] | 45.35 | 37.30% | 4 | 5 | 5 | 13 | 252 |
| 104 | P0C0T4 | 40S ribosomal protein S25-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS25B PE=1 SV=1 - [RS25B_YEAST] | 45.04 | 46.30% | 3 | 8 | 8 | 13 | 108 |

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| 105 | P47079 | T-complex protein 1 subunit theta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT8 PE=1 SV=1 - [TCPQ_YEAST] | 38.79 | 23.59% | 2 | 9 | 9 | 13 | 568 |
| 106 | P39522 | Dihydroxy-acid dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV3 PE=1 SV=2 - [ILV3_YEAST] | 43.42 | 23.59% | 1 | 8 | 8 | 12 | 585 |

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| 107 | P28777 | Chorismate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO2 PE=1 SV=1 - [AROC_YEAST] | 43.01 | 45.48% | 1 | 10 | 10 | 12 | 376 |
| 108 | P00927 | Threonine dehydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV1 PE=1 SV=2 - [THDH_YEAST] | 41.87 | 24.65% | 1 | 9 | 9 | 12 | 576 |

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| 109 | P00330 | Alcohol dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH1 PE=1 SV=5 - [ADH1_YEAST] | 41.69 | 35.34% | 4 | 10 | 10 | 12 | 348 |
| 110 | P25087 | Sterol 24-C-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG6 PE=1 SV=4 - [ERG6_YEAST] | 41.01 | 32.11% | 1 | 10 | 10 | 12 | 383 |

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| 111 | P0CX51 | 40S ribosomal protein S16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS16A PE=1 SV=1 - [RS16A_YEAST] | 40.6 | 41.96% | 3 | 6 | 6 | 12 | 143 |
| 112 | P38754 | 60S ribosomal protein L14-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL14B PE=1 SV=1 - [RL14B_YEAST] | 39.88 | 22.46% | 2 | 5 | 5 | 12 | 138 |

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| 113 | P0CY39 | 40S ribosomal protein S23-A OS=Naumovozyma castellii (strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) OX=1064592 GN=RPS23A PE=1 SV=1 - [RS23A_NAUCC] | 38.53 | 20.00% | 1 | 3 | 4 | 12 | 145 |
| 114 | P15646 | rRNA 2'-O-methyltransferase fibrillarin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP1 PE=1 SV=1 - [FBRL_YEAST] | 36.89 | 29.66% | 2 | 7 | 7 | 12 | 327 |

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| 115 | A6ZRX0 | ATP-dependent RNA helicase DBP2 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP2 PE=3 SV=1 - [DBP2_YEAS7] | 36.34 | 29.85% | 5 | 11 | 12 | 12 | 546 |
| 116 | Q03195 | Translation initiation factor RLI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLI1 PE=1 SV=1 - [RLI1_YEAST] | 34.45 | 23.52% | 1 | 11 | 11 | 12 | 608 |

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| 117 | P0C0W1 | 40S ribosomal protein S22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS22A PE=1 SV=2 - [RS22A_YEAST] | 46.08 | 43.85% | 3 | 6 | 6 | 11 | 130 |
| 118 | P40212 | 60S ribosomal protein L13-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL13B PE=1 SV=1 - [RL13B_YEAST] | 45.48 | 29.65% | 2 | 1 | 5 | 11 | 199 |

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| 119 | P50094 | Inosine-5'-monophosphate dehydrogenase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD4 PE=1 SV=1 - [IMDH4_YEAST] | 43.53 | 29.96% | 2 | 4 | 9 | 11 | 524 |
| 120 | P51401 | 60S ribosomal protein L9-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL9B PE=1 SV=1 - [RL9B_YEAST] | 42.61 | 31.94% | 1 | 1 | 6 | 11 | 191 |

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| 121 | P32481 | Eukaryotic translation initiation factor 2 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCD11 PE=1 SV=1 - [IF2G_YEAST] | 40.79 | 30.36% | 1 | 9 | 9 | 11 | 527 |
| 122 | P05738 | 60S ribosomal protein L9-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL9A PE=1 SV=2 - [RL9A_YEAST] | 39.43 | 25.65% | 1 | 1 | 6 | 11 | 191 |

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| 123 | P04147 | Polyadenylate-binding protein, cytoplasmic and nuclear OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAB1 PE=1 SV=4 - [PABP_YEAST] | 38.75 | 21.32% | 3 | 8 | 8 | 11 | 577 |
| 124 | P10081 | ATP-dependent RNA helicase eIF4A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF1 PE=1 SV=3 - [IF4A_YEAST] | 38.58 | 33.92% | 3 | 9 | 9 | 11 | 395 |

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| 125 | P28274 | CTP synthase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=URA7 PE=1 SV=2 - [URA7_YEAST] | 37.4 | 24.87% | 4 | 10 | 10 | 11 | 579 |
| 126 | P19358 | S-adenosylmethionine synthase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAM2 PE=1 SV=3 - [METK2_YEAST] | 37.13 | 26.04% | 1 | 2 | 10 | 11 | 384 |

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| 127 | P19882 | Heat shock protein 60, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP60 PE=1 SV=1 - [HSP60_YEAST] | 36.52 | 23.60% | 1 | 10 | 10 | 11 | 572 |
| 128 | P27476 | Nuclear localization sequence-binding protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NSR1 PE=1 SV=1 - [NSR1_YEAST] | 36.02 | 23.91% | 1 | 8 | 8 | 11 | 414 |

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| 129 | P48589 | 40S ribosomal protein S12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS12 PE=1 SV=1 - [RS12_YEAST] | 34.16 | 46.85% | 1 | 6 | 6 | 11 | 143 |
| 130 | P16140 | V-type proton ATPase subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA2 PE=1 SV=2 - [VATB_YEAST] | 33.59 | 32.50% | 1 | 11 | 11 | 11 | 517 |

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| 131 | P0C2H8 | 60S ribosomal protein L31-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL31A PE=1 SV=1 - [RL31A_YEAST] | 41.2 | 45.13% | 3 | 6 | 6 | 10 | 113 |
| 132 | A6ZPE5 | Nucleolar protein 58 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP58 PE=3 SV=1 - [NOP58_Y | 37.98 | 22.50% | 3 | 7 | 7 | 10 | 511 |

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| 133 | P48570 | Homocitrate synthase, cytosolic isozyme OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS20 PE=1 SV=1 - [HOSC_YEAST] | 37.85 | 36.21% | 2 | 10 | 10 | 10 | 428 |
| 134 | P0C0X0 | 40S ribosomal protein S28-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS28B PE=1 SV=1 - [RS28B_YEAST] | 36.64 | 52.24% | 3 | 5 | 5 | 10 | 67 |

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| 135 | P32861 | UTP--glucose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UGP1 PE=1 SV=1 - [UGPA1_YEAST] | 35.41 | 24.25% | 1 | 8 | 8 | 10 | 499 |
| 136 | P09440 | C-1-tetrahydrofolate synthase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIS1 PE=1 SV=1 - [C1TM_YEAST] | 33.41 | 16.62% | 1 | 10 | 10 | 10 | 975 |

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| 137 | P36013 | NAD-dependent malic enzyme, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAE1 PE=1 SV=1 - [MAOM_YEAST] | 33.23 | 25.56% | 1 | 9 | 9 | 10 | 669 |
| 138 | P10964 | DNA-directed RNA polymerase I subunit RPA190 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA190 PE=1 SV=2 - [RPA1_YEAST] | 33.17 | 9.19% | 1 | 9 | 9 | 10 | 1664 |

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| 139 | P12612 | T-complex protein 1 subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TCP1 PE=1 SV=2 - [TCPA_YEAST] | 31.29 | 24.87% | 1 | 8 | 8 | 10 | 559 |
| 140 | P23301 | Eukaryotic translation initiation factor 5A-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HYP2 PE=1 SV=3 - [IF5A1_YEAST] | 30.79 | 24.84% | 2 | 5 | 5 | 10 | 157 |

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| 141 | P05744 | 60S ribosomal protein L33-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL33A PE=1 SV=3 - [RL33A_YEAST] | 30.78 | 35.51% | 1 | 4 | 8 | 10 | 107 |
| 142 | Q05022 | rRNA biogenesis protein RRP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP5 PE=1 SV=1 - [RRP5_YEAST] | 30.02 | 9.08% | 1 | 9 | 9 | 10 | 1729 |

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| 143 | P0CX27 | 60S ribosomal protein L42-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL42A PE=1 SV=1 - [RL44A_YEAST] | 28.09 | 19.81% | 2 | 3 | 3 | 10 | 106 |
| 144 | Q12690 | 60S ribosomal protein L13-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL13A PE=1 SV=1 - [RL13A_YEAST] | 35.59 | 29.65% | 2 | 1 | 5 | 9 | 199 |

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| 145 | P50095 | Inosine-5'-monophosphate dehydrogenase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IMD3 PE=1 SV=1 - [IMDH3_YEAST] | 34.64 | 29.45% | 4 | 3 | 8 | 9 | 523 |
| 146 | P0C2H6 | 60S ribosomal protein L27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL27A PE=1 SV=1 - [RL27A_YEAST] | 31.69 | 44.85% | 2 | 8 | 8 | 9 | 136 |

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| 147 | P39938 | 40S ribosomal protein S26-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS26A PE=1 SV=1 - [RS26A_YEAST] | 31.65 | 33.61% | 2 | 4 | 4 | 9 | 119 |
| 148 | P05756 | 40S ribosomal protein S13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS13 PE=1 SV=3 - [RS13_YEAST] | 29.9 | 41.72% | 1 | 6 | 6 | 9 | 151 |

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| 149 | Q03690 | Clustered mitochondria protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CLU1 PE=1 SV=1 - [CLU_YEAST] | 29.37 | 11.12% | 1 | 8 | 8 | 9 | 1277 |
| 150 | P32563 | V-type proton ATPase subunit a, vacuolar isoform OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VPH1 PE=1 SV=3 - [VPH1_YEAST] | 28.78 | 16.19% | 1 | 8 | 8 | 9 | 840 |

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| 151 | P0CX55 | 40S ribosomal protein S18-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS18A PE=1 SV=1 - [RS18A_YEAST] | 27.86 | 49.32% | 1 | 8 | 8 | 9 | 146 |
| 152 | P0C0W9 | 60S ribosomal protein L11-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL11A PE=1 SV=2 - [RL11A_YEAST] | 27.54 | 39.66% | 3 | 8 | 8 | 9 | 174 |

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| 153 | P38061 | 60S ribosomal protein L32 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL32 PE=1 SV=1 - [RL32_YEAST] | 27.31 | 39.23% | 2 | 5 | 5 | 9 | 130 |
| 154 | P07283 | Phosphomannomutase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC53 PE=1 SV=1 - [PMM_YEAST] | 24.93 | 34.65% | 2 | 7 | 7 | 9 | 254 |

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| 155 | P04449 | 60S ribosomal protein L24-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL24A PE=1 SV=1 - [RL24A_YEAST] | 28.96 | 18.06% | 2 | 2 | 4 | 8 | 155 |
| 156 | P24000 | 60S ribosomal protein L24-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL24B PE=1 SV=1 - [RL24B_YEAST] | 28.66 | 18.06% | 1 | 2 | 4 | 8 | 155 |

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| 157 | Q08972 | [NU+] prion formation protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NEW1 PE=1 SV=1 - [NEW1_YEAST] | 27.92 | 11.96% | 1 | 8 | 8 | 8 | 1196 |
| 158 | P15303 | Protein transport protein SEC23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC23 PE=1 SV=1 - [SEC23_YEAST] | 27.49 | 14.45% | 1 | 6 | 6 | 8 | 768 |

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| 159 | P05748 | 60S ribosomal protein L15-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL15A PE=1 SV=3 - [RL15A_YEAST] | 26.79 | 29.90% | 2 | 6 | 6 | 8 | 204 |
| 160 | P26784 | 60S ribosomal protein L16-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL16A PE=1 SV=3 - [RL16A_YEAST] | 26.14 | 25.63% | 1 | 3 | 7 | 8 | 199 |

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| 161 | P38708 | Putative proline--tRNA ligase YHR020W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHR020W PE=1 SV=1 - [YHI0_YEAST] | 25.13 | 16.42% | 1 | 7 | 7 | 8 | 688 |
| 162 | P40069 | Importin subunit beta-4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAP123 PE=1 SV=1 - [IMB4_YEAST] | 25.12 | 10.06% | 1 | 7 | 7 | 8 | 1113 |

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| 163 | P21954 | Isocitrate dehydrogenase [NADP], mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IDP1 PE=1 SV=1 - [IDHP_YEAST] | 24.49 | 23.13% | 3 | 7 | 7 | 8 | 428 |
| 164 | P39076 | T-complex protein 1 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT2 PE=1 SV=1 - [TCPB_YEAST] | 24.28 | 20.49% | 1 | 7 | 7 | 8 | 527 |

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| 165 | P18239 | ADP,ATP carrier protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PET9 PE=1 SV=2 - [ADT2_YEAST] | 23.96 | 22.64% | 3 | 6 | 6 | 8 | 318 |
| 166 | A6ZN26 | Eukaryotic translation initiation factor 3 subunit C OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NIP1 PE=3 SV=1 - [EIF3C_YEAS7] | 27.95 | 10.84% | 2 | 6 | 6 | 7 | 812 |

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| 167 | P06103 | Eukaryotic translation initiation factor 3 subunit B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRT1 PE=1 SV=1 - [EIF3B_YEAST] | 24.5 | 11.53% | 2 | 5 | 5 | 7 | 763 |
| 168 | P28007 | H/ACA ribonucleoprotein complex subunit GAR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GAR1 PE=1 SV=1 - [GAR1_YEAST] | 23.44 | 38.05% | 3 | 5 | 5 | 7 | 205 |

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| 169 | P00830 | ATP synthase subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP2 PE=1 SV=2 - [ATPB_YEAST] | 23.27 | 20.16% | 1 | 7 | 7 | 7 | 511 |
| 170 | P40185 | Protein MMF1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MMF1 PE=1 SV=1 - [MMF1_YEAST] | 22.43 | 65.52% | 1 | 5 | 5 | 7 | 145 |

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| 171 | P15019 | Transaldolase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TAL1 PE=1 SV=4 - [TAL1_YEAST] | 22.22 | 25.67% | 1 | 7 | 7 | 7 | 335 |
| 172 | P54115 | Magnesium-activated aldehyde dehydrogenase, cytosolic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALD6 PE=1 SV=4 - [ALDH6_YEAST] | 22.06 | 11.20% | 1 | 4 | 4 | 7 | 500 |

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| 173 | P49167 | 60S ribosomal protein L38 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL38 PE=1 SV=1 - [RL38_YEAST] | 21.39 | 50.00% | 1 | 3 | 3 | 7 | 78 |
| 174 | P07245 | C-1-tetrahydrofolate synthase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE3 PE=1 SV=1 - [C1TC_YEAST] | 21.11 | 12.47% | 1 | 7 | 7 | 7 | 946 |

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| 175 | Q03532 | ATP-dependent RNA helicase HAS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HAS1 PE=1 SV=1 - [HAS1_YEAST] | 20.81 | 16.83% | 3 | 7 | 7 | 7 | 505 |
| 176 | P39015 | Suppressor protein STM1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STM1 PE=1 SV=3 - [STM1_YEAST] | 25.49 | 32.23% | 1 | 5 | 5 | 6 | 273 |

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| 177 | P07262 | NADP-specific glutamate dehydrogenase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GDH1 PE=1 SV=2 - [DHE4_YEAST] | 24.28 | 17.40% | 2 | 4 | 4 | 6 | 454 |
| 178 | P39079 | T-complex protein 1 subunit zeta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT6 PE=1 SV=1 - [TCPZ_YEAST] | 23.78 | 17.40% | 1 | 6 | 6 | 6 | 546 |

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| 179 | P38879 | Nascent polypeptide-associated complex subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EGD2 PE=1 SV=3 - [NACA_YEAST] | 23.76 | 29.31% | 1 | 3 | 3 | 6 | 174 |
| 180 | P39078 | T-complex protein 1 subunit delta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT4 PE=1 SV=2 - [TCPD_YEAST] | 23.13 | 16.48% | 1 | 5 | 5 | 6 | 528 |

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| 181 | A6ZWL1 | Nascent polypeptide-associated complex subunit beta-1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=EGD1 PE=3 SV=1 - [NACB1_YEAS7] | 22.89 | 42.68% | 1 | 4 | 4 | 6 | 157 |
| 182 | Q05911 | Adenylosuccinate lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE13 PE=1 SV=1 - [PUR8_YEAST] | 22.55 | 11.00% | 1 | 4 | 4 | 6 | 482 |

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| 183 | P40217 | Eukaryotic translation initiation factor 3 subunit I OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF34 PE=1 SV=1 - [EIF3I_YEAST] | 22.05 | 28.82% | 2 | 6 | 6 | 6 | 347 |
| 184 | P16474 | Endoplasmic reticulum chaperone BiP OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KAR2 PE=1 SV=1 - [BIP_YEAST] | 21.48 | 12.02% | 2 | 4 | 5 | 6 | 682 |

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| 185 | P39986 | Manganese-transporting ATPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPF1 PE=1 SV=1 - [ATC6_YEAST] | 21.28 | 8.15% | 1 | 5 | 5 | 6 | 1215 |
| 186 | P07213 | Mitochondrial import receptor subunit TOM70 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM70 PE=1 SV=2 - [TOM70_YEAST] | 21.14 | 14.42% | 1 | 5 | 5 | 6 | 617 |

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| 187 | P41921 | Glutathione reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLR1 PE=1 SV=2 - [GSHR_YEAST] | 20.68 | 22.57% | 2 | 6 | 6 | 6 | 483 |
| 188 | P47912 | Long-chain-fatty-acid--CoA ligase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAA4 PE=1 SV=1 - [LCF4_YEAST] | 20.66 | 11.53% | 1 | 6 | 6 | 6 | 694 |

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| 189 | P23542 | Aspartate aminotransferase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AAT2 PE=1 SV=3 - [AATC_YEAST] | 20.34 | 19.14% | 1 | 4 | 4 | 6 | 418 |
| 190 | Q02892 | Nucleolar GTP-binding protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOG1 PE=1 SV=1 - [NOG1_YEAST] | 20.1 | 11.59% | 1 | 5 | 5 | 6 | 647 |

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| 191 | P39729 | Ribosome-interacting GTPase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RBG1 PE=1 SV=1 - [RBG1_YEAST] | 19.9 | 21.14% | 1 | 5 | 5 | 6 | 369 |
| 192 | P19414 | Aconitate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ACO1 PE=1 SV=2 - [ACON_YEAST] | 19.08 | 13.24% | 1 | 6 | 6 | 6 | 778 |

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| 193 | P40010 | Nuclear GTP-binding protein NUG1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUG1 PE=1 SV=1 - [NUG1_YEAST] | 19.06 | 14.04% | 1 | 6 | 6 | 6 | 520 |
| 194 | P32473 | Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDB1 PE=1 SV=2 - [ODPB_YEAST] | 16.56 | 22.40% | 1 | 5 | 5 | 6 | 366 |

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| 195 | P46655 | Glutamate--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GUS1 PE=1 SV=3 - [SYEC_YEAST] | 16.36 | 9.60% | 1 | 6 | 6 | 6 | 708 |
| 196 | P05319 | 60S acidic ribosomal protein P2-alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP2A PE=1 SV=1 - [RLA2_YEAST] | 21.77 | 74.53% | 1 | 4 | 4 | 5 | 106 |

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| 197 | P07991 | Ornithine aminotransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAR2 PE=1 SV=2 - [OAT_YEAST] | 19.67 | 18.16% | 1 | 4 | 4 | 5 | 424 |
| 198 | P16467 | Pyruvate decarboxylase isozyme 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDC5 PE=1 SV=4 - [PDC5_YEAST] | 19.53 | 9.77% | 2 | 3 | 4 | 5 | 563 |

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| 199 | P25294 | Protein SIS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SIS1 PE=1 SV=1 - [SIS1_YEAST] | 19.46 | 20.45% | 1 | 4 | 4 | 5 | 352 |
| 200 | P38998 | Saccharopine dehydrogenase [NAD(+), L-lysine-forming] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS1 PE=1 SV=3 - [LYS1_YEAST] | 19.1 | 24.66% | 2 | 4 | 4 | 5 | 373 |

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| 201 | P53252 | Sphingolipid long chain base-responsive protein PIL1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PIL1 PE=1 SV=1 - [PIL1_YEAST] | 18.95 | 15.93% | 1 | 3 | 3 | 5 | 339 |
| 202 | P38891 | Branched-chain-amino-acid aminotransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BAT1 PE=1 SV=1 - [BCA1_YEAST] | 18.78 | 12.98% | 2 | 3 | 3 | 5 | 393 |

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| 203 | P40482 | Protein transport protein SEC24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC24 PE=1 SV=1 - [SEC24_YEAST] | 18.75 | 8.53% | 2 | 5 | 5 | 5 | 926 |
| 204 | P39730 | Eukaryotic translation initiation factor 5B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUN12 PE=1 SV=2 - [IF2P_YEAST] | 18 | 8.68% | 1 | 5 | 5 | 5 | 1002 |

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| 205 | Q02931 | NET1-associated nuclear protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAN1 PE=1 SV=1 - [UTP17_YEAST] | 17.96 | 9.38% | 1 | 4 | 4 | 5 | 896 |
| 206 | P12385 | Eukaryotic peptide chain release factor subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUP45 PE=1 SV=2 - [ERF1_YEAST] | 17.4 | 15.79% | 1 | 5 | 5 | 5 | 437 |

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| 207 | P38009 | Bifunctional purine biosynthesis protein ADE17 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE17 PE=1 SV=2 - [PUR92_YEAST] | 17.33 | 17.57% | 1 | 5 | 5 | 5 | 592 |
| 208 | A6ZMA9 | Ribosome biogenesis protein ERB1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ERB1 PE=3 SV=1 - [ERB1_YEAS7] | 17.05 | 8.67% | 4 | 5 | 5 | 5 | 807 |

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| 209 | P13663 | Aspartate-semialdehyde dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM2 PE=1 SV=1 - [DHAS_YEAST] | 17.03 | 16.71% | 1 | 4 | 4 | 5 | 365 |
| 210 | P10869 | Aspartokinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM3 PE=1 SV=2 - [AK_YEAST] | 16.8 | 19.73% | 1 | 5 | 5 | 5 | 527 |

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| 211 | P40991 | 25S rRNA (cytosine(2870)-C(5))-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP2 PE=1 SV=1 - [NOP2_YEAST] | 16.68 | 13.27% | 1 | 5 | 5 | 5 | 618 |
| 212 | P37292 | Serine hydroxymethyltransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SHM1 PE=1 SV=2 - [GLYM_YEAST] | 16.62 | 13.67% | 1 | 4 | 4 | 5 | 490 |

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| 213 | P10614 | Lanosterol 14-alpha demethylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG11 PE=1 SV=1 - [CP51_YEAST] | 16.58 | 11.89% | 3 | 4 | 4 | 5 | 530 |
| 214 | P04840 | Mitochondrial outer membrane protein porin 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=POR1 PE=1 SV=4 - [VDAC1_YEAST] | 16.39 | 28.98% | 1 | 5 | 5 | 5 | 283 |

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| 215 | P07246 | Alcohol dehydrogenase 3, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADH3 PE=1 SV=2 - [ADH3_YEAST] | 16.2 | 18.40% | 1 | 5 | 5 | 5 | 375 |
| 216 | P17128 | Actin OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) OX=284590 GN=ACT PE=3 SV=2 - [ACT_KLULA] | 14.96 | 12.00% | 3 | 3 | 3 | 5 | 375 |

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| 217 | P02992 | Elongation factor Tu, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUF1 PE=1 SV=1 - [EFTU_YEAST] | 14.92 | 11.67% | 1 | 3 | 3 | 5 | 437 |
| 218 | P27809 | Glycolipid 2-alpha-mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE2 PE=1 SV=1 - [KRE2_YEAST] | 14.7 | 16.97% | 1 | 5 | 5 | 5 | 442 |

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| 219 | P12695 | Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LAT1 PE=1 SV=1 - [ODP2_YEAST] | 14.67 | 9.34% | 1 | 4 | 4 | 5 | 482 |

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| 220 | P22138 | DNA-directed RNA polymerase I subunit RPA135 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA135 PE=1 SV=1 - [RPA2_YEAST] | 13.88 | 6.23% | 1 | 5 | 5 | 5 | 1203 |
| 221 | P21147 | Acyl-CoA desaturase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OLE1 PE=1 SV=2 - [ACO1_YEAST] | 13.82 | 8.43% | 1 | 3 | 4 | 5 | 510 |

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| 222 | P38264 | SRP-independent targeting protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PHO88 PE=1 SV=1 - [PHO88_YEAST] | 13.63 | 25.53% | 1 | 3 | 3 | 5 | 188 |
| 223 | P41056 | 60S ribosomal protein L33-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL33B PE=1 SV=2 - [RL33B_YEAST] | 13.22 | 34.58% | 1 | 1 | 5 | 5 | 107 |

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| 224 | P41057 | 40S ribosomal protein S29-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS29A PE=1 SV=3 - [RS29A_YEAST] | 13.06 | 35.71% | 2 | 3 | 3 | 5 | 56 |
| 225 | Q04947 | Reticulon-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RTN1 PE=1 SV=1 - [RTN1_YEAST] | 12.57 | 22.37% | 1 | 4 | 4 | 5 | 295 |

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| 226 | P49367 | Homoaconitase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS4 PE=1 SV=1 - [LYS4_YEAST] | 16.21 | 7.22% | 1 | 3 | 3 | 4 | 693 |
| 227 | P25567 | RNA-binding protein SRO9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRO9 PE=1 SV=2 - [SRO9_YEAST] | 16.08 | 14.06% | 1 | 3 | 3 | 4 | 434 |

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| 228 | P00931 | Tryptophan synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP5 PE=1 SV=1 - [TRP_YEAST] | 16.04 | 8.06% | 1 | 3 | 3 | 4 | 707 |
| 229 | P05749 | 60S ribosomal protein L22-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL22A PE=1 SV=3 - [RL22A_YEAST] | 15.34 | 32.23% | 1 | 2 | 2 | 4 | 121 |

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| 230 | P25045 | Serine palmitoyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LCB1 PE=1 SV=2 - [LCB1_YEAST] | 15.23 | 13.08% | 1 | 4 | 4 | 4 | 558 |
| 231 | P42943 | T-complex protein 1 subunit eta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT7 PE=1 SV=1 - [TCPH_YEAST] | 14.98 | 8.55% | 1 | 3 | 3 | 4 | 550 |

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| 232 | P21524 | Ribonucleoside-diphosphate reductase large chain 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR1 PE=1 SV=2 - [RIR1_YEAST] | 14.65 | 6.64% | 1 | 4 | 4 | 4 | 888 |
| 233 | Q03940 | RuvB-like protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RVB1 PE=1 SV=1 - [RUVB1_YEAST] | 14.46 | 16.85% | 1 | 4 | 4 | 4 | 463 |

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| 234 | P20606 | Small COPII coat GTPase SAR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAR1 PE=1 SV=1 - [SAR1_YEAST] | 14.08 | 24.74% | 5 | 3 | 3 | 4 | 190 |
| 235 | P38805 | Ribosome production factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPF1 PE=1 SV=1 - [RPF1_YEAST] | 13.78 | 19.32% | 1 | 4 | 4 | 4 | 295 |

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| 236 | P33892 | eIF-2-alpha kinase activator GCN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN1 PE=1 SV=1 - [GCN1_YEAST] | 13.43 | 2.25% | 1 | 3 | 4 | 4 | 2672 |
| 237 | P00942 | Triosephosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPI1 PE=1 SV=2 - [TPIS_YEAST] | 13.17 | 26.21% | 1 | 4 | 4 | 4 | 248 |

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| 238 | P36008 | Elongation factor 1-gamma 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TEF4 PE=1 SV=1 - [EF1G2_YEAST] | 12.9 | 9.71% | 1 | 3 | 3 | 4 | 412 |
| 239 | P39692 | Sulfite reductase [NADPH] flavoprotein component OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET10 PE=1 SV=2 - [MET10_YEAST] | 12.64 | 5.51% | 1 | 4 | 4 | 4 | 1035 |

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| 240 | P38910 | 10 kDa heat shock protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP10 PE=1 SV=1 - [CH10_YEAST] | 12.62 | 63.21% | 1 | 4 | 4 | 4 | 106 |
| 241 | P33201 | Ribosome assembly factor MRT4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRT4 PE=1 SV=1 - [MRT4_YEAST] | 12.38 | 16.53% | 1 | 3 | 3 | 4 | 236 |

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| 242 | P54839 | Hydroxymethylglutaryl-CoA synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG13 PE=1 SV=1 - [HMCS_YEAST] | 12.35 | 10.59% | 1 | 4 | 4 | 4 | 491 |
| 243 | P12945 | N-terminal acetyltransferase A complex subunit NAT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAT1 PE=1 SV=2 - [NAT1_YEAST] | 12.1 | 8.08% | 1 | 4 | 4 | 4 | 854 |

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| 244 | Q12680 | Glutamate synthase [NADH] OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLT1 PE=1 SV=2 - [GLT1_YEAST] | 11.57 | 2.75% | 1 | 3 | 4 | 4 | 2145 |
| 245 | P23641 | Mitochondrial phosphate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MIR1 PE=1 SV=1 - [MPCP_YEAST] | 11.44 | 19.29% | 1 | 4 | 4 | 4 | 311 |

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| 246 | P00958 | Methionine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MES1 PE=1 SV=4 - [SYMC_YEAST] | 11.26 | 3.46% | 1 | 2 | 2 | 4 | 751 |
| 247 | P38689 | Ribose-phosphate pyrophosphokinase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS3 PE=1 SV=1 - [KPR3_YEAST] | 11.15 | 11.88% | 1 | 3 | 3 | 4 | 320 |

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| 248 | P40525 | 60S ribosomal protein L34-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL34B PE=1 SV=1 - [RL34B_YEAST] | 11.03 | 23.14% | 2 | 3 | 3 | 4 | 121 |
| 249 | P39109 | Metal resistance protein YCF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCF1 PE=1 SV=2 - [YCFI_YEAST] | 10.96 | 1.91% | 1 | 2 | 2 | 4 | 1515 |

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| 250 | P05747 | 60S ribosomal protein L29 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL29 PE=1 SV=3 - [RL29_YEAST] | 10.47 | 13.56% | 1 | 1 | 1 | 4 | 59 |
| 251 | A6ZV85 | Pescadillo homolog OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NOP7 PE=3 SV=1 - [PESC_YEAS7] | 10.46 | 7.93% | 2 | 4 | 4 | 4 | 605 |

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| 252 | P32582 | Cystathionine beta-synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYS4 PE=1 SV=1 - [CBS_YEAST] | 14.31 | 10.85% | 1 | 3 | 3 | 3 | 507 |
| 253 | P38353 | Sec sixty-one protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSH1 PE=1 SV=1 - [SSH1_YEAST] | 13.28 | 7.14% | 1 | 2 | 2 | 3 | 490 |

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| 254 | P04173 | 3-isopropylmalate dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU2 PE=1 SV=4 - [LEU3_YEAST] | 12.24 | 11.81% | 1 | 2 | 2 | 3 | 364 |
| 255 | P39990 | 13 kDa ribonucleoprotein-associated protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SNU13 PE=1 SV=1 - [SNU13_YEAST] | 11.63 | 23.81% | 2 | 2 | 2 | 3 | 126 |

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| 256 | P40531 | Protein GVP36 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GVP36 PE=1 SV=1 - [GVP36_YEAST] | 11.58 | 15.34% | 1 | 3 | 3 | 3 | 326 |
| 257 | P32368 | Phosphoinositide phosphatase SAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAC1 PE=1 SV=1 - [SAC1_YEAST] | 11.56 | 5.14% | 1 | 2 | 2 | 3 | 623 |

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| 258 | P31412 | V-type proton ATPase subunit C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA5 PE=1 SV=4 - [VATC_YEAST] | 11.4 | 14.29% | 1 | 3 | 3 | 3 | 392 |
| 259 | P33322 | H/ACA ribonucleoprotein complex subunit CBF5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CBF5 PE=1 SV=1 - [CBF5_YEAST] | 11.25 | 7.25% | 1 | 2 | 2 | 3 | 483 |

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| 260 | P32449 | Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO4 PE=1 SV=2 - [AROG_YEAST] | 11.01 | 11.35% | 1 | 3 | 3 | 3 | 370 |
| 261 | P16603 | NADPH--cytochrome P450 reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NCP1 PE=1 SV=3 - [NCPR_YEAST] | 10.77 | 6.95% | 1 | 2 | 2 | 3 | 691 |

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| 262 | P40215 | External NADH-ubiquinone oxidoreductase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NDE1 PE=1 SV=1 - [NDH1_YEAST] | 10.76 | 5.89% | 1 | 2 | 2 | 3 | 560 |
| 263 | P25694 | Cell division control protein 48 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC48 PE=1 SV=3 - [CDC48_Y | 10.53 | 3.83% | 1 | 2 | 2 | 3 | 835 |

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| 264 | P35691 | Translationally-controlled tumor protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA19 PE=1 SV=1 - [TCTP_YEAST] | 10.48 | 17.37% | 1 | 3 | 3 | 3 | 167 |
| 265 | P43555 | Protein EMP47 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMP47 PE=1 SV=1 - [EMP47_YEAST] | 10.36 | 9.44% | 1 | 3 | 3 | 3 | 445 |

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| 266 | P32589 | Heat shock protein homolog SSE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSE1 PE=1 SV=4 - [HSP7F_YEAST] | 10.25 | 5.63% | 3 | 3 | 3 | 3 | 693 |
| 267 | Q12754 | Ribosomal RNA-processing protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP12 PE=1 SV=1 - [RRP12_YEAST] | 10.15 | 4.89% | 1 | 3 | 3 | 3 | 1228 |

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| 268 | A6ZUA1 | ATP-dependent RNA helicase DBP3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP3 PE=3 SV=1 - [DBP3_YEAS7] | 10.14 | 10.71% | 3 | 3 | 3 | 3 | 523 |
| 269 | P25349 | Flavoprotein-like protein YCP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YCP4 PE=1 SV=1 - [YCP4_YEAST] | 10.04 | 13.36% | 1 | 2 | 2 | 3 | 247 |

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| 270 | P32476 | Squalene monooxygenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG1 PE=1 SV=2 - [ERG1_YEAST] | 9.99 | 5.24% | 1 | 2 | 2 | 3 | 496 |
| 271 | P22137 | Clathrin heavy chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CHC1 PE=1 SV=1 - [CLH_YEAST] | 9.94 | 3.51% | 1 | 3 | 3 | 3 | 1653 |

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| 272 | P40506 | Phosphopantothenate--cysteine ligase CAB2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CAB2 PE=1 SV=2 - [PPCS_YEAST] | 9.75 | 10.68% | 1 | 2 | 2 | 3 | 365 |
| 273 | P35180 | Mitochondrial import receptor subunit TOM20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TOM20 PE=1 SV=1 - [TOM20_YEAST] | 9.69 | 27.32% | 1 | 3 | 3 | 3 | 183 |

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| 274 | Q04067 | Eukaryotic translation initiation factor 3 subunit G OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF35 PE=1 SV=1 - [EIF3G_YEAST] | 9.65 | 21.90% | 2 | 3 | 3 | 3 | 274 |
| 275 | P40462 | Protein TMA108 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA108 PE=1 SV=1 - [TM108_YEAST] | 9.63 | 6.55% | 1 | 3 | 3 | 3 | 946 |

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| 276 | P04802 | Aspartate--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DPS1 PE=1 SV=3 - [SYDC_YEAST] | 9.61 | 5.21% | 1 | 2 | 2 | 3 | 557 |
| 277 | A6ZVM6 | NADH-cytochrome b5 reductase 1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=CBR1 PE=3 SV=2 - [NCB5R_YEAS7] | 9.24 | 14.08% | 2 | 3 | 3 | 3 | 284 |

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| 278 | P32911 | Eukaryotic translation initiation factor eIF-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUI1 PE=1 SV=1 - [SUI1_YEAST] | 9.15 | 35.19% | 1 | 3 | 3 | 3 | 108 |
| 279 | P32565 | 26S proteasome regulatory subunit RPN2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN2 PE=1 SV=4 - [RPN2_YEAST] | 9.05 | 5.19% | 1 | 3 | 3 | 3 | 945 |

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| 280 | P32386 | ATP-dependent bile acid permease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBT1 PE=1 SV=2 - [YBT1_YEAST] | 8.99 | 1.99% | 2 | 3 | 3 | 3 | 1661 |
| 281 | P04911 | Histone H2A.1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HTA1 PE=1 SV=2 - [H2A1_YEAST] | 8.98 | 29.55% | 9 | 3 | 3 | 3 | 132 |

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| 282 | P41819 | Dimethyladenosine transferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DIM1 PE=3 SV=1 - [DIM1_YEAST] | 8.97 | 14.78% | 2 | 3 | 3 | 3 | 318 |
| 283 | Q06205 | FK506-binding protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPR4 PE=1 SV=1 - [FKBP4_YEAST] | 8.95 | 9.69% | 2 | 1 | 2 | 3 | 392 |

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| 284 | P32495 | H/ACA ribonucleoprotein complex subunit NHP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NHP2 PE=1 SV=2 - [NHP2_YEAST] | 8.95 | 18.59% | 1 | 2 | 2 | 3 | 156 |
| 285 | P54837 | Endoplasmic reticulum vesicle protein 25 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERV25 PE=1 SV=1 - [TMEDA_ | 8.85 | 17.54% | 1 | 3 | 3 | 3 | 211 |

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| 286 | P25605 | Acetolactate synthase small subunit, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILV6 PE=1 SV=2 - [ILV6_YEAST] | 8.81 | 16.18% | 1 | 3 | 3 | 3 | 309 |
| 287 | P30624 | Long-chain-fatty-acid--CoA ligase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAA1 PE=1 SV=1 - [LCF1_YEAST] | 8.79 | 6.43% | 1 | 3 | 3 | 3 | 700 |

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| 288 | Q07938 | S-methyl-5'-thioadenosine phosphorylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MEU1 PE=1 SV=1 - [MTAP_YEAST] | 8.77 | 12.76% | 1 | 3 | 3 | 3 | 337 |
| 289 | P14906 | Protein translocation protein SEC63 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC63 PE=1 SV=2 - [SEC63_YEAST] | 8.75 | 6.64% | 1 | 3 | 3 | 3 | 663 |

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| 290 | P05694 | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET6 PE=1 SV=4 - [METE_YEAST] | 8.69 | 5.87% | 1 | 3 | 3 | 3 | 767 |
| 291 | P41277 | Glycerol-1-phosphate phosphohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPP1 PE=1 SV=3 - [GPP1_YEAST] | 8.6 | 19.60% | 2 | 3 | 3 | 3 | 250 |

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| 292 | P39940 | E3 ubiquitin-protein ligase RSP5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RSP5 PE=1 SV=1 - [RSP5_YEAST] | 8.49 | 6.92% | 1 | 3 | 3 | 3 | 809 |
| 293 | P00899 | Anthranilate synthase component 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP2 PE=1 SV=4 - [TRPE_YEAST] | 8.44 | 7.50% | 1 | 3 | 3 | 3 | 507 |

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| 294 | P47154 | CAAX prenyl protease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STE24 PE=1 SV=1 - [STE24_YEAST] | 8.38 | 6.84% | 1 | 2 | 2 | 3 | 453 |
| 295 | A6ZPA9 | Ribosome biogenesis protein YTM1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=YTM1 PE=3 SV=1 - [YTM1_YEAS7] | 8.31 | 9.13% | 1 | 3 | 3 | 3 | 460 |

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| 296 | Q12746 | Plasma membrane-associated coenzyme Q6 reductase PGA3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGA3 PE=1 SV=1 - [PGA3_YEAST] | 8.27 | 14.74% | 1 | 3 | 3 | 3 | 312 |
| 297 | P00937 | Multifunctional tryptophan biosynthesis protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TRP3 PE=1 SV=2 - [TRPG_YEAST] | 8.07 | 11.36% | 1 | 3 | 3 | 3 | 484 |

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| 298 | P41338 | Acetyl-CoA acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG10 PE=1 SV=3 - [THIL_YEAST] | 8.06 | 9.55% | 2 | 3 | 3 | 3 | 398 |
| 299 | P25582 | 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SPB1 PE=1 SV=2 - [SPB1_YEAST] | 7.9 | 3.92% | 1 | 2 | 2 | 3 | 841 |

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| 300 | P04801 | Threonine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=THS1 PE=1 SV=2 - [SYTC_YEAST] | 7.83 | 4.77% | 1 | 3 | 3 | 3 | 734 |
| 301 | P32466 | Low-affinity glucose transporter HXT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXT3 PE=1 SV=1 - [HXT3_YEAST] | 10.01 | 7.76% | 1 | 2 | 2 | 2 | 567 |

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| 302 | Q02256 | Tyrosine-protein phosphatase YVH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YVH1 PE=1 SV=1 - [PVH1_YEAST] | 9.42 | 10.16% | 1 | 2 | 2 | 2 | 364 |
| 303 | P31116 | Homoserine dehydrogenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOM6 PE=1 SV=1 - [DHOM_YEAST] | 9.11 | 7.52% | 1 | 1 | 1 | 2 | 359 |

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| 304 | P02557 | Tubulin beta chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB2 PE=1 SV=2 - [TBB_YEA | 8.85 | 10.28% | 1 | 2 | 2 | 2 | 457 |
| 305 | P32352 | C-8 sterol isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG2 PE=1 SV=1 - [ERG2_YEAST] | 8.75 | 13.06% | 1 | 2 | 2 | 2 | 222 |

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| 306 | P56628 | 60S ribosomal protein L22-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL22B PE=1 SV=2 - [RL22B_YEAST] | 8.75 | 32.79% | 1 | 2 | 2 | 2 | 122 |
| 307 | Q04697 | Glucose-signaling factor 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GSF2 PE=1 SV=1 - [GSF2_YEAST] | 8.45 | 9.43% | 1 | 2 | 2 | 2 | 403 |

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| 308 | P07284 | Serine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SES1 PE=1 SV=2 - [SYSC_YEAST] | 8.43 | 8.44% | 1 | 2 | 2 | 2 | 462 |
| 309 | P09734 | Tubulin alpha-3 chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB3 PE=1 SV=1 - [TBA3_YEAST] | 8.21 | 8.09% | 1 | 1 | 2 | 2 | 445 |

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| 310 | P16387 | Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDA1 PE=1 SV=2 - [ODPA_YEAST] | 8.15 | 7.14% | 1 | 2 | 2 | 2 | 420 |
| 311 | P38779 | Proteasome-interacting protein CIC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CIC1 PE=1 SV=1 - [CIC1_YEAST] | 8.12 | 8.51% | 1 | 2 | 2 | 2 | 376 |

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| 312 | P09064 | Eukaryotic translation initiation factor 2 subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUI3 PE=1 SV=2 - [IF2B_YEAST] | 8.11 | 13.68% | 1 | 2 | 2 | 2 | 285 |
| 313 | Q12117 | Protein MRH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRH1 PE=1 SV=1 - [MRH1_YEAST] | 7.63 | 10.31% | 1 | 2 | 2 | 2 | 320 |

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| 314 | Q12449 | Hsp90 co-chaperone AHA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AHA1 PE=1 SV=1 - [AHA1_YEAST] | 7.56 | 8.00% | 1 | 2 | 2 | 2 | 350 |
| 315 | P36049 | rRNA-processing protein EBP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EBP2 PE=1 SV=1 - [EBP2_YEAST] | 7.5 | 7.03% | 1 | 2 | 2 | 2 | 427 |

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| 316 | P38013 | Peroxiredoxin AHP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AHP1 PE=1 SV=4 - [AHP1_YEAST] | 7.48 | 11.36% | 1 | 1 | 1 | 2 | 176 |
| 317 | P53235 | Eukaryotic translation initiation factor 2A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGR054W PE=1 SV=1 - [EIF2A_YEAST] | 7.43 | 4.67% | 1 | 2 | 2 | 2 | 642 |

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| 318 | P12709 | Glucose-6-phosphate isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PGI1 PE=1 SV=3 - [G6PI_YEAST] | 7.42 | 5.23% | 1 | 2 | 2 | 2 | 554 |
| 319 | P38789 | Ribosome biogenesis protein SSF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSF1 PE=1 SV=1 - [SSF1_YEAST] | 7.41 | 6.84% | 2 | 2 | 2 | 2 | 453 |

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| 320 | P40693 | Ribosome biogenesis protein RLP7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLP7 PE=1 SV=1 - [RLP7_YEAST] | 7.35 | 8.70% | 1 | 2 | 2 | 2 | 322 |
| 321 | P09733 | Tubulin alpha-1 chain OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TUB1 PE=1 SV=2 - [TBA1_YEAST] | 7.33 | 8.05% | 1 | 1 | 2 | 2 | 447 |

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| 322 | P37838 | Nucleolar protein 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP4 PE=1 SV=1 - [NOP4_YEAST] | 7.29 | 4.96% | 1 | 2 | 2 | 2 | 685 |
| 323 | Q8J1F8 | Histone H2B.2 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=HTB2 PE=3 SV=3 - [H2B2_ASHGO] | 7.22 | 19.69% | 6 | 2 | 2 | 2 | 127 |

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| 324 | Q12335 | Protoplast secreted protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PST2 PE=1 SV=1 - [PST2_YEAST] | 7.21 | 19.70% | 1 | 2 | 2 | 2 | 198 |
| 325 | Q12522 | Eukaryotic translation initiation factor 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF6 PE=1 SV=1 - [IF6_YEAST] | 7.19 | 12.65% | 1 | 2 | 2 | 2 | 245 |

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| 326 | Q12450 | Protein ERP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERP4 PE=1 SV=1 - [ERP4_YEAST] | 7.17 | 4.83% | 2 | 1 | 1 | 2 | 207 |
| 327 | A6ZNQ1 | ATP-dependent RNA helicase DBP5 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP5 PE=3 SV=1 - [DBP5_YEAS7] | 7.14 | 5.39% | 1 | 2 | 2 | 2 | 482 |

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| 328 | P12688 | Serine/threonine-protein kinase YPK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPK1 PE=1 SV=2 - [YPK1_YEAST] | 7.14 | 5.88% | 1 | 2 | 2 | 2 | 680 |
| 329 | P22768 | Argininosuccinate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARG1 PE=1 SV=3 - [ASSY_YEAST] | 6.95 | 4.52% | 1 | 1 | 1 | 2 | 420 |

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| 330 | P05453 | Eukaryotic peptide chain release factor GTP-binding subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SUP35 PE=1 SV=1 - [ERF3_YEAST] | 6.94 | 5.40% | 1 | 2 | 2 | 2 | 685 |
| 331 | P25293 | Nucleosome assembly protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAP1 PE=1 SV=2 - [NAP1_YEAST] | 6.94 | 11.27% | 1 | 2 | 2 | 2 | 417 |

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| 332 | P35844 | Oxysterol-binding protein homolog 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KES1 PE=1 SV=1 - [KES1_YEAST] | 6.94 | 6.68% | 1 | 2 | 2 | 2 | 434 |
| 333 | P38911 | FK506-binding nuclear protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FPR3 PE=1 SV=2 - [FKBP3_YEAST] | 6.89 | 9.25% | 2 | 1 | 2 | 2 | 411 |

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| 334 | P00128 | Cytochrome b-c1 complex subunit 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QCR7 PE=1 SV=2 - [QCR7_YEAST] | 6.89 | 15.75% | 1 | 1 | 1 | 2 | 127 |
| 335 | P18562 | Uracil phosphoribosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUR1 PE=1 SV=2 - [UPP_YEAST] | 6.8 | 12.50% | 1 | 2 | 2 | 2 | 216 |

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| 336 | P32598 | Serine/threonine-protein phosphatase PP1-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLC7 PE=1 SV=1 - [PP12_YEAST] | 6.79 | 10.90% | 1 | 2 | 2 | 2 | 312 |
| 337 | P21264 | Phosphoribosylaminoimidazole carboxylase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE2 PE=1 SV=1 - [PUR6_YEAST] | 6.78 | 6.65% | 1 | 2 | 2 | 2 | 571 |

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| 338 | Q03862 | Probable metalloprotease ARX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARX1 PE=1 SV=1 - [ARX1_YEAST] | 6.69 | 8.09% | 1 | 2 | 2 | 2 | 593 |
| 339 | Q01939 | 26S proteasome regulatory subunit 8 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT6 PE=1 SV=4 - [PRS8_YEAST] | 6.66 | 9.38% | 1 | 2 | 2 | 2 | 405 |

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| 340 | P39935 | Eukaryotic initiation factor 4F subunit p150 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIF4631 PE=1 SV=2 - [IF4F1_YEAST] | 6.6 | 2.42% | 1 | 1 | 1 | 2 | 952 |
| 341 | A6ZSX1 | ATP-dependent rRNA helicase RRP3 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=RRP3 PE=3 SV=1 - [RRP3_YEAS7] | 6.47 | 4.19% | 2 | 2 | 2 | 2 | 501 |

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| 342 | P06780 | GTP-binding protein RHO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RHO1 PE=1 SV=3 - [RHO1_YEAST] | 6.45 | 16.27% | 1 | 2 | 2 | 2 | 209 |
| 343 | P21576 | Vacuolar protein sorting-associated protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VPS1 PE=1 SV=2 - [VPS1_YEAST] | 6.36 | 5.40% | 1 | 2 | 2 | 2 | 704 |

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| 344 | P14832 | Peptidyl-prolyl cis-trans isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CPR1 PE=1 SV=3 - [CYPH_YEAST] | 6.33 | 14.20% | 1 | 2 | 2 | 2 | 162 |
| 345 | P47124 | Putative glycosyltransferase HOC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HOC1 PE=1 SV=3 - [HOC1_YEAST] | 6.31 | 10.35% | 1 | 2 | 2 | 2 | 396 |

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| 346 | P41911 | Glycerol-3-phosphate dehydrogenase [NAD(+)] 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GPD2 PE=1 SV=2 - [GPD2_YEAST] | 6.21 | 7.95% | 1 | 2 | 2 | 2 | 440 |
| 347 | P41810 | Coatomer subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC26 PE=1 SV=2 - [COPB_YEAST] | 6.21 | 3.60% | 1 | 2 | 2 | 2 | 973 |

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| 348 | Q04013 | Citrate/oxoglutarate carrier protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHM2 PE=1 SV=1 - [YHM2_YEAST] | 6.19 | 3.82% | 1 | 1 | 1 | 2 | 314 |
| 349 | P32074 | Coatomer subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC21 PE=1 SV=2 - [COPG_YEAST] | 6.16 | 2.99% | 1 | 2 | 2 | 2 | 935 |

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| 350 | Q06287 | Ribosomal RNA small subunit methyltransferase NEP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMG1 PE=1 SV=1 - [NEP1_YEAST] | 6.1 | 11.51% | 1 | 2 | 2 | 2 | 252 |
| 351 | P07244 | Bifunctional purine biosynthetic protein ADE5,7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE5,7 PE=1 SV=1 - [PUR2_YEAST] | 6.05 | 3.87% | 1 | 2 | 2 | 2 | 802 |

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| 352 | P39744 | Nucleolar complex protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOC2 PE=1 SV=2 - [NOC2_YEAST] | 5.92 | 2.96% | 1 | 2 | 2 | 2 | 710 |
| 353 | P0CX33 | 40S ribosomal protein S30-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS30A PE=1 SV=1 - [RS30A_YEAST] | 5.92 | 17.46% | 1 | 2 | 2 | 2 | 63 |

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| 354 | P17064 | Purine-cytosine permease FCY2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FCY2 PE=1 SV=2 - [FCY2_YEAST] | 5.87 | 2.63% | 1 | 2 | 2 | 2 | 533 |
| 355 | P35178 | Ribosomal RNA-processing protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP1 PE=1 SV=2 - [RRP1_YEAST] | 5.83 | 9.35% | 1 | 2 | 2 | 2 | 278 |

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| 356 | O74302 | Transposon Ty1-DR4 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TY1A-DR4 PE=2 SV=1 - [YD13A_YEAST] | 5.79 | 10.45% | 50 | 2 | 2 | 2 | 440 |
| 357 | P53914 | RNA cytidine acetyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KRE33 PE=1 SV=1 - [NAT10_YEAST] | 5.68 | 1.23% | 1 | 1 | 1 | 2 | 1056 |

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| 358 | P11076 | ADP-ribosylation factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARF1 PE=1 SV=3 - [ARF1_YEAST] | 5.65 | 17.68% | 3 | 2 | 2 | 2 | 181 |
| 359 | P08417 | Fumarate hydratase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FUM1 PE=1 SV=2 - [FUMH_YEAST] | 5.57 | 1.84% | 1 | 1 | 1 | 2 | 488 |

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| 360 | P53622 | Coatomer subunit alpha OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COP1 PE=1 SV=2 - [COPA_YEAST] | 5.46 | 2.41% | 1 | 1 | 2 | 2 | 1201 |
| 361 | P14843 | Phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARO3 PE=1 SV=1 - [AROF_YEAST] | 5.46 | 7.84% | 1 | 2 | 2 | 2 | 370 |

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| 362 | Q06506 | Ribosomal RNA-processing protein 9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRP9 PE=1 SV=1 - [RRP9_YEAST] | 5.39 | 6.11% | 1 | 2 | 2 | 2 | 573 |
| 363 | A6ZVE9 | Regulator of rDNA transcription 14 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=RRT14 PE=3 SV=1 - [RRT14_YEAS7] | 5.37 | 9.71% | 4 | 1 | 1 | 2 | 206 |

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| 364 | P53313 | Protein SDA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SDA1 PE=1 SV=1 - [SDA1_YEAST] | 5.35 | 3.26% | 1 | 2 | 2 | 2 | 767 |
| 365 | P41058 | 40S ribosomal protein S29-B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS29B PE=1 SV=3 - [RS29B_YEAST] | 5.3 | 14.29% | 1 | 1 | 1 | 2 | 56 |

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| 366 | P14020 | Dolichol-phosphate mannosyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DPM1 PE=1 SV=3 - [DPM1_YEAST] | 5.25 | 7.87% | 1 | 2 | 2 | 2 | 267 |
| 367 | P07703 | DNA-directed RNA polymerases I and III subunit RPAC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPC40 PE=1 SV=1 - [RPAC1_YEAST] | 5.23 | 9.25% | 1 | 2 | 2 | 2 | 335 |

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| 368 | P02309 | Histone H4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HHF1 PE=1 SV=2 - [H4_YEAST] | 5.22 | 14.56% | 2 | 2 | 2 | 2 | 103 |
| 369 | P53131 | Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP43 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRP43 PE=1 SV=1 - [PRP43_YEAST] | 5.21 | 3.39% | 1 | 2 | 2 | 2 | 767 |

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| 370 | P06106 | Homocysteine/cysteine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET17 PE=1 SV=3 - [CYSD_YEAST] | 5.18 | 8.11% | 1 | 2 | 2 | 2 | 444 |
| 371 | P01123 | GTP-binding protein YPT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPT1 PE=1 SV=2 - [YPT1_YEAST] | 5.16 | 23.79% | 1 | 2 | 2 | 2 | 206 |

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| 372 | P32939 | GTP-binding protein YPT7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPT7 PE=1 SV=1 - [YPT7_YEAST] | 5.14 | 12.02% | 1 | 2 | 2 | 2 | 208 |
| 373 | P00410 | Cytochrome c oxidase subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX2 PE=1 SV=1 - [COX2_YEAST] | 5.11 | 14.74% | 2 | 2 | 2 | 2 | 251 |

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| 374 | Q12136 | Something about silencing protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAS10 PE=1 SV=1 - [SAS10_Y | 4.96 | 1.80% | 1 | 1 | 1 | 2 | 610 |
| 375 | P09624 | Dihydrolipoyl dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LPD1 PE=1 SV=1 - [DLDH_YEAST] | 4.95 | 3.81% | 1 | 2 | 2 | 2 | 499 |

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| 376 | P35997 | 40S ribosomal protein S27-A OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPS27A PE=1 SV=1 - [RS27A_YEAST] | 4.87 | 23.17% | 2 | 2 | 2 | 2 | 82 |
| 377 | P53742 | Nucleolar GTP-binding protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOG2 PE=1 SV=1 - [NOG2_YEAST] | 4.85 | 4.94% | 1 | 2 | 2 | 2 | 486 |

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| 378 | Q9LIK9 | ATP sulfurylase 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=APS1 PE=1 SV=1 - [APS1_ARATH] | 4.82 | 4.10% | 1 | 1 | 1 | 2 | 463 |
| 379 | P0CS90 | Heat shock protein SSC1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSC1 PE=1 SV=1 - [HSP77_YEAST] | 4.73 | 4.28% | 2 | 1 | 2 | 2 | 654 |

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| 380 | P42945 | U3 small nucleolar RNA-associated protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP10 PE=1 SV=1 - [UTP10_YEAST] | 4.7 | 1.53% | 1 | 2 | 2 | 2 | 1769 |
| 381 | P47068 | Myosin tail region-interacting protein MTI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BBC1 PE=1 SV=2 - [BBC1_YEAST] | 4.7 | 1.04% | 1 | 1 | 1 | 2 | 1157 |

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| 382 | P00546 | Cyclin-dependent kinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC28 PE=1 SV=1 - [CDK1_YEAST] | 4.6 | 6.38% | 4 | 2 | 2 | 2 | 298 |
| 383 | Q12000 | Translation machinery-associated protein 46 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA46 PE=1 SV=2 - [TMA46_YEAST] | 4.49 | 6.09% | 1 | 2 | 2 | 2 | 345 |

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| 384 | Q12166 | 2-isopropylmalate synthase 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU9 PE=1 SV=1 - [LEU9_YEAST] | 4.47 | 4.64% | 1 | 1 | 2 | 2 | 604 |
| 385 | P06208 | 2-isopropylmalate synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU4 PE=1 SV=1 - [LEU1_YEAST] | 4.41 | 2.75% | 1 | 1 | 2 | 2 | 619 |

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| 386 | P40422 | DNA-directed RNA polymerases I, II, and III subunit RPABC4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPC10 PE=1 SV=1 - [RPAB4_YEAST] | 5.37 | 28.57% | 1 | 1 | 1 | 1 | 70 |
| 387 | P38861 | 60S ribosomal export protein NMD3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NMD3 PE=1 SV=3 - [NMD3_YEAST] | 5.04 | 3.28% | 1 | 1 | 1 | 1 | 518 |

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| 388 | P53295 | Ribosome-interacting GTPase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RBG2 PE=1 SV=1 - [RBG2_YEAST] | 5.03 | 5.98% | 1 | 1 | 1 | 1 | 368 |
| 389 | P53889 | Uncharacterized mitochondrial hydrolase FMP41 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FMP41 PE=1 SV=1 - [FMP41_YEAST] | 5.03 | 10.04% | 1 | 1 | 1 | 1 | 259 |

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| 390 | P47019 | Ribosome biogenesis protein ALB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALB1 PE=1 SV=1 - [ALB1_YEAST] | 5.01 | 14.29% | 1 | 1 | 1 | 1 | 175 |
| 391 | P40362 | U3 small nucleolar RNA-associated protein 18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP18 PE=1 SV=1 - [UTP18_YEAST] | 4.96 | 3.54% | 1 | 1 | 1 | 1 | 594 |

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| 392 | P47089 | Translation machinery-associated protein 22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TMA22 PE=1 SV=1 - [DENR_YEAST] | 4.9 | 8.59% | 1 | 1 | 1 | 1 | 198 |
| 393 | P25655 | General negative regulator of transcription subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC39 PE=1 SV=3 - [NOT1_YEAST] | 4.88 | 0.71% | 1 | 1 | 1 | 1 | 2108 |

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| 394 | P22214 | Protein transport protein SEC22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC22 PE=1 SV=1 - [SEC22_YEAST] | 4.86 | 7.48% | 1 | 1 | 1 | 1 | 214 |
| 395 | Q06344 | Pre-rRNA-processing protein ESF1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ESF1 PE=1 SV=1 - [ESF1_YEAST] | 4.84 | 2.87% | 1 | 1 | 1 | 1 | 628 |

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| 396 | P49723 | Ribonucleoside-diphosphate reductase small chain 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RNR4 PE=1 SV=1 - [RIR4_YEAST] | 4.83 | 5.51% | 1 | 1 | 1 | 1 | 345 |
| 397 | P53276 | U3 small nucleolar RNA-associated protein 8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UTP8 PE=1 SV=1 - [UTP8_YEAST] | 4.81 | 2.52% | 1 | 1 | 1 | 1 | 713 |

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| 398 | P40075 | Vesicle-associated membrane protein-associated protein SCS2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SCS2 PE=1 SV=3 - [SCS2_YEAST] | 4.74 | 9.84% | 1 | 1 | 1 | 1 | 244 |
| 399 | P07256 | Cytochrome b-c1 complex subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COR1 PE=1 SV=1 - [QCR1_YEAST] | 4.71 | 5.69% | 1 | 1 | 1 | 1 | 457 |

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| 400 | P32288 | Glutamine synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLN1 PE=1 SV=4 - [GLNA_YE | 4.6 | 4.32% | 1 | 1 | 1 | 1 | 370 |
| 401 | P41543 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=OST1 PE=1 SV=1 - [OST1_YEAST] | 4.49 | 4.41% | 1 | 1 | 1 | 1 | 476 |

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| 402 | Q08548 | Lysophospholipid acyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALE1 PE=1 SV=1 - [ALE1_YEAST] | 4.49 | 2.42% | 1 | 1 | 1 | 1 | 619 |
| 403 | A6ZML0 | Protein YIM1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=YIM1 PE=3 SV=1 - [YIM1_YEAS7] | 4.48 | 5.75% | 3 | 1 | 1 | 1 | 365 |

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| 404 | P40970 | Serine palmitoyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LCB2 PE=1 SV=1 - [LCB2_YEAST] | 4.48 | 5.70% | 1 | 1 | 1 | 1 | 561 |
| 405 | P20107 | Zinc/cadmium resistance protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ZRC1 PE=1 SV=2 - [ZRC1_YEAST] | 4.41 | 3.85% | 1 | 1 | 1 | 1 | 442 |

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| 406 | P35723 | Endoplasmic reticulum transmembrane protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YET1 PE=1 SV=2 - [YET1_YEAST] | 4.38 | 12.62% | 1 | 1 | 1 | 1 | 206 |
| 407 | P53723 | UPF0674 endoplasmic reticulum membrane protein YNR021W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YNR021W PE=1 SV=3 - [YN8B_YEAST] | 4.33 | 4.21% | 1 | 1 | 1 | 1 | 404 |

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| 408 | P10622 | 60S acidic ribosomal protein P1-beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPP1B PE=1 SV=3 - [RLA3_YEAST] | 4.19 | 15.09% | 1 | 1 | 1 | 1 | 106 |
| 409 | P09436 | Isoleucine--tRNA ligase, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ILS1 PE=1 SV=1 - [SYIC_YEAST] | 4.04 | 2.99% | 1 | 1 | 1 | 1 | 1072 |

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| 410 | P08067 | Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RIP1 PE=1 SV=1 - [UCRI_YEAST] | 4.01 | 10.70% | 1 | 1 | 1 | 1 | 215 |
| 411 | P07260 | Eukaryotic translation initiation factor 4E OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC33 PE=1 SV=1 - [IF4E_YEAST] | 4 | 7.51% | 1 | 1 | 1 | 1 | 213 |

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| 412 | P04050 | DNA-directed RNA polymerase II subunit RPB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPO21 PE=1 SV=2 - [RPB1_YEAST] | 3.99 | 1.04% | 1 | 1 | 1 | 1 | 1733 |
| 413 | P32419 | Malate dehydrogenase, peroxisomal OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MDH3 PE=1 SV=3 - [MDHP_YEAST] | 3.98 | 4.08% | 1 | 1 | 1 | 1 | 343 |

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| 414 | P39727 | ER-derived vesicles protein ERV46 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERV46 PE=1 SV=2 - [ERV46_YEAST] | 3.98 | 3.37% | 1 | 1 | 1 | 1 | 415 |
| 415 | A6ZT02 | Low-affinity glucose transporter HXT4 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=HXT4 PE=3 SV=1 - [HXT4_YEAS7] | 3.94 | 2.26% | 4 | 1 | 1 | 1 | 576 |

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| 416 | P51601 | GTP cyclohydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FOL2 PE=1 SV=1 - [GCH1_YEAST] | 3.91 | 8.64% | 1 | 1 | 1 | 1 | 243 |
| 417 | A6ZL22 | Cell wall protein ECM33 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ECM33 PE=3 SV=2 - [ECM33_YEAS7] | 3.85 | 3.50% | 4 | 1 | 1 | 1 | 429 |

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| 418 | P16550 | Protein APA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=APA1 PE=1 SV=4 - [APA1_YEAST] | 3.75 | 5.61% | 1 | 1 | 1 | 1 | 321 |
| 419 | P07264 | 3-isopropylmalate dehydratase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LEU1 PE=1 SV=3 - [LEUC_YEAST] | 3.63 | 2.18% | 1 | 1 | 1 | 1 | 779 |

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| 420 | P32621 | Guanosine-diphosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GDA1 PE=1 SV=1 - [GDA1_YEAST] | 3.62 | 6.56% | 1 | 1 | 1 | 1 | 518 |
| 421 | P32803 | Endosomal protein P24B OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EMP24 PE=1 SV=1 - [EMP24_YEAST] | 3.6 | 6.90% | 1 | 1 | 1 | 1 | 203 |

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| 422 | P38764 | 26S proteasome regulatory subunit RPN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN1 PE=1 SV=3 - [RPN1_YEAST] | 3.59 | 1.71% | 1 | 1 | 1 | 1 | 993 |
| 423 | P32366 | V-type proton ATPase subunit d OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VMA6 PE=1 SV=2 - [VA0D_YEAST] | 3.59 | 8.12% | 1 | 1 | 1 | 1 | 345 |

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| 424 | P32528 | Urea amidolyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DUR1,2 PE=1 SV=2 - [DUR1_YEAST] | 3.57 | 1.80% | 1 | 1 | 1 | 1 | 1835 |
| 425 | P38295 | Medium-chain fatty acid ethyl ester synthase/esterase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=EHT1 PE=1 SV=1 - [MCFS2_YEAST] | 3.57 | 4.66% | 1 | 1 | 1 | 1 | 451 |

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| 426 | P10962 | Protein MAK16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAK16 PE=1 SV=2 - [MAK16_YEAST] | 3.54 | 4.58% | 1 | 1 | 1 | 1 | 306 |
| 427 | Q99207 | Nucleolar complex protein 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP14 PE=1 SV=1 - [NOP14_Y | 3.53 | 1.98% | 1 | 1 | 1 | 1 | 810 |

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| 428 | P38137 | Peroxisomal-coenzyme A synthetase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PCS60 PE=1 SV=1 - [FAT2_YEAST] | 3.52 | 3.31% | 1 | 1 | 1 | 1 | 543 |
| 429 | P49095 | Glycine dehydrogenase (decarboxylating), mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCV2 PE=1 SV=1 - [GCSP_YEAST] | 3.5 | 1.74% | 1 | 1 | 1 | 1 | 1034 |

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| 430 | Q07381 | Ribosome biogenesis protein TSR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TSR1 PE=1 SV=1 - [TSR1_YEAST] | 3.5 | 2.16% | 1 | 1 | 1 | 1 | 788 |
| 431 | P46971 | Dolichyl-phosphate-mannose--protein mannosyltransferase 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT4 PE=1 SV=1 - [PMT4_YEAST] | 3.47 | 1.84% | 1 | 1 | 1 | 1 | 762 |

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| 432 | P46672 | tRNA-aminoacylation cofactor ARC1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARC1 PE=1 SV=2 - [ARC1_YEAST] | 3.47 | 4.26% | 1 | 1 | 1 | 1 | 376 |
| 433 | Q02196 | Adenylyl-sulfate kinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET14 PE=1 SV=1 - [KAPS_YEAST] | 3.42 | 6.93% | 2 | 1 | 1 | 1 | 202 |

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| 434 | Q02776 | Mitochondrial import inner membrane translocase subunit TIM50 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM50 PE=1 SV=1 - [TIM50_YEAST] | 3.4 | 2.94% | 1 | 1 | 1 | 1 | 476 |
| 435 | P40303 | Proteasome subunit alpha type-4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE6 PE=1 SV=1 - [PSA4_YEAST] | 3.38 | 5.51% | 1 | 1 | 1 | 1 | 254 |

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| 436 | Q00764 | Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPS1 PE=1 SV=2 - [TPS1_YEAST] | 3.37 | 3.23% | 1 | 1 | 1 | 1 | 495 |
| 437 | Q01560 | Nucleolar protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NPL3 PE=1 SV=1 - [NOP3_YEAST] | 3.37 | 3.38% | 1 | 1 | 1 | 1 | 414 |

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| 438 | P33775 | Dolichyl-phosphate-mannose--protein mannosyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT1 PE=1 SV=1 - [PMT1_YEAST] | 3.32 | 2.08% | 1 | 1 | 1 | 1 | 817 |
| 439 | P28834 | Isocitrate dehydrogenase [NAD] subunit 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IDH1 PE=1 SV=2 - [IDH1_YEAST] | 3.32 | 5.00% | 1 | 1 | 1 | 1 | 360 |

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| 440 | Q01080 | DNA-directed RNA polymerase I subunit RPA49 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA49 PE=1 SV=2 - [RPA49_YEAST] | 3.31 | 3.61% | 1 | 1 | 1 | 1 | 415 |
| 441 | P15705 | Heat shock protein STI1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=STI1 PE=1 SV=1 - [STI1_YEAST] | 3.3 | 2.72% | 1 | 1 | 1 | 1 | 589 |

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| 442 | Q12447 | Polyamine N-acetyltransferase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PAA1 PE=1 SV=1 - [PAA1_YEAST] | 3.3 | 6.81% | 1 | 1 | 1 | 1 | 191 |
| 443 | P40825 | Alanine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALA1 PE=1 SV=3 - [SYA_YEAST] | 3.29 | 1.42% | 1 | 1 | 1 | 1 | 983 |

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| 444 | P09457 | ATP synthase subunit 5, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP5 PE=1 SV=1 - [ATPO_YEAST] | 3.27 | 8.02% | 1 | 1 | 1 | 1 | 212 |
| 445 | P22146 | 1,3-beta-glucanosyltransferase GAS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GAS1 PE=1 SV=2 - [GAS1_YEAST] | 3.26 | 3.04% | 1 | 1 | 1 | 1 | 559 |

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| 446 | P32583 | Suppressor protein SRP40 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP40 PE=1 SV=2 - [SRP40_YEAST] | 3.24 | 2.96% | 1 | 1 | 1 | 1 | 406 |
| 447 | P11154 | Pyruvate carboxylase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PYC1 PE=1 SV=2 - [PYC1_YEAST] | 3.24 | 1.02% | 2 | 1 | 1 | 1 | 1178 |

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| 448 | P46956 | Inorganic phosphate transporter PHO86 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PHO86 PE=1 SV=1 - [PHO86_YEAST] | 3.22 | 5.47% | 1 | 1 | 1 | 1 | 311 |
| 449 | Q74ZA9 | GTP-binding nuclear protein GSP1/Ran OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=GSP1 PE=3 SV=1 - [GSP1_ASHGO] | 3.21 | 7.94% | 4 | 1 | 1 | 1 | 214 |

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| 450 | P18759 | Vesicular-fusion protein SEC18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC18 PE=1 SV=2 - [SEC18_YEAST] | 3.21 | 3.03% | 1 | 1 | 1 | 1 | 758 |
| 451 | Q07915 | Ribosome biogenesis protein RLP24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RLP24 PE=1 SV=1 - [RLP24_YEAST] | 3.18 | 5.03% | 1 | 1 | 1 | 1 | 199 |

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| 452 | P38968 | Protein transport protein SEC31 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC31 PE=1 SV=3 - [SEC31_YEAST] | 3.17 | 1.18% | 1 | 1 | 1 | 1 | 1273 |
| 453 | P38077 | ATP synthase subunit gamma, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ATP3 PE=1 SV=1 - [ATPG_YEAST] | 3.16 | 8.04% | 1 | 1 | 1 | 1 | 311 |

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| 454 | Q12159 | RNA annealing protein YRA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YRA1 PE=1 SV=2 - [YRA1_YEAST] | 3.16 | 5.31% | 1 | 1 | 1 | 1 | 226 |
| 455 | Q04491 | Protein transport protein SEC13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC13 PE=1 SV=1 - [SEC13_YEAST] | 3.15 | 4.04% | 1 | 1 | 1 | 1 | 297 |

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| 456 | A6ZU71 | Ribosome biogenesis protein NSA1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=NSA1 PE=3 SV=1 - [NSA1_YEAS7] | 3.14 | 2.81% | 2 | 1 | 1 | 1 | 463 |
| 457 | B3LRE5 | Fe-S cluster assembly protein DRE2 OS=Saccharomyces cerevisiae (strain RM11-1a) OX=285006 GN=DRE2 PE=3 SV=1 - [DRE2_YEAS1] | 3.11 | 6.03% | 2 | 1 | 1 | 1 | 348 |

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| 458 | P33204 | Actin-related protein 2/3 complex subunit 4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARC19 PE=1 SV=2 - [ARPC4_YEAST] | 3.1 | 9.36% | 1 | 1 | 1 | 1 | 171 |
| 459 | P32602 | Alpha-soluble NSF attachment protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC17 PE=1 SV=4 - [SEC17_YEAST] | 3.1 | 5.14% | 1 | 1 | 1 | 1 | 292 |

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| 460 | P40312 | Cytochrome b5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYB5 PE=1 SV=2 - [CYB5_YEAST] | 3.09 | 10.83% | 1 | 1 | 1 | 1 | 120 |
| 461 | P38972 | Phosphoribosylformylglycinamidine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ADE6 PE=1 SV=2 - [PUR4_YEAST] | 3.07 | 1.91% | 1 | 1 | 1 | 1 | 1358 |

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| 462 | P32342 | Signal recognition particle subunit SRP21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SRP21 PE=1 SV=3 - [SRP21_YEAST] | 3.02 | 6.59% | 1 | 1 | 1 | 1 | 167 |
| 463 | P40032 | Prolyl 3,4-dihydroxylase TPA1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TPA1 PE=1 SV=1 - [TPA1_YEAST] | 3.02 | 3.26% | 1 | 1 | 1 | 1 | 644 |

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| 464 | O74700 | Mitochondrial import inner membrane translocase subunit TIM9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM9 PE=1 SV=1 - [TIM9_YEAST] | 3.01 | 16.09% | 1 | 1 | 1 | 1 | 87 |
| 465 | P25342 | Cell division control protein 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC10 PE=1 SV=1 - [CDC10_Y | 3 | 8.70% | 1 | 1 | 1 | 1 | 322 |

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| 466 | P29311 | Protein BMH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BMH1 PE=1 SV=4 - [BMH1_YEAST] | 2.98 | 8.61% | 2 | 1 | 1 | 1 | 267 |
| 467 | P48813 | High-affinity glutamine permease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GNP1 PE=1 SV=2 - [GNP1_YEAST] | 2.98 | 2.71% | 1 | 1 | 1 | 1 | 663 |

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| 468 | P40580 | Benzil reductase ((S)-benzoin forming) IRC24 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IRC24 PE=1 SV=1 - [BZRD_YEAST] | 2.98 | 4.56% | 1 | 1 | 1 | 1 | 263 |
| 469 | P31382 | Dolichyl-phosphate-mannose--protein mannosyltransferase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PMT2 PE=1 SV=2 - [PMT2_YEAST] | 2.96 | 1.71% | 1 | 1 | 1 | 1 | 759 |

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| 470 | P40078 | Ribosome biogenesis protein NSA2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NSA2 PE=1 SV=1 - [NSA2_YEAST] | 2.94 | 10.34% | 1 | 1 | 1 | 1 | 261 |
| 471 | Q12265 | Ribose-phosphate pyrophosphokinase 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS5 PE=1 SV=1 - [KPR5_YEAST] | 2.93 | 2.22% | 1 | 1 | 1 | 1 | 496 |

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| 472 | P38088 | Glycine--tRNA ligase 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GRS1 PE=1 SV=3 - [SYG_YEAST] | 2.93 | 2.17% | 1 | 1 | 1 | 1 | 690 |
| 473 | P07139 | 3-isopropylmalate dehydrogenase OS=Candida maltosa OX=5479 GN=LEU2 PE=3 SV=1 - [LEU3_CANMA] | 2.93 | 3.75% | 1 | 1 | 1 | 1 | 373 |

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| 474 | P39107 | Mannan polymerase complexes subunit MNN9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN9 PE=1 SV=3 - [MNN9_YEAST] | 2.93 | 2.78% | 1 | 1 | 1 | 1 | 395 |
| 475 | P25635 | Periodic tryptophan protein 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PWP2 PE=1 SV=2 - [PWP2_YEAST] | 2.92 | 1.08% | 1 | 1 | 1 | 1 | 923 |

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| 476 | P07806 | Valine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VAS1 PE=1 SV=2 - [SYV_YEAST] | 2.91 | 1.18% | 1 | 1 | 1 | 1 | 1104 |
| 477 | P07257 | Cytochrome b-c1 complex subunit 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=QCR2 PE=1 SV=1 - [QCR2_YEAST] | 2.91 | 4.08% | 1 | 1 | 1 | 1 | 368 |

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| 478 | P32502 | Translation initiation factor eIF-2B subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCD7 PE=1 SV=1 - [EI2BB_YEAST] | 2.89 | 2.89% | 1 | 1 | 1 | 1 | 381 |
| 479 | P46985 | Probable alpha-1,6-mannosyltransferase MNN11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN11 PE=1 SV=2 - [MNN11_YEAST] | 2.88 | 5.92% | 1 | 1 | 1 | 1 | 422 |

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| 480 | P22147 | 5'-3' exoribonuclease 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=XRN1 PE=1 SV=1 - [XRN1_YEAST] | 2.86 | 0.92% | 1 | 1 | 1 | 1 | 1528 |
| 481 | A6ZYI0 | Adenylate kinase OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ADK1 PE=3 SV=1 - [KAD2_YEAS7] | 2.85 | 5.86% | 2 | 1 | 1 | 1 | 222 |

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| 482 | P39954 | Adenosylhomocysteinase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SAH1 PE=1 SV=1 - [SAHH_YEAST] | 2.84 | 2.23% | 1 | 1 | 1 | 1 | 449 |
| 483 | P27810 | Alpha-1,2 mannosyltransferase KTR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=KTR1 PE=1 SV=1 - [KTR1_YEAST] | 2.83 | 3.05% | 1 | 1 | 1 | 1 | 393 |

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| 484 | A6ZPU3 | ATP-dependent RNA helicase DBP4 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=DBP4 PE=3 SV=1 - [DBP4_YEAS7] | 2.83 | 1.43% | 2 | 1 | 1 | 1 | 770 |
| 485 | P32457 | Cell division control protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC3 PE=1 SV=3 - [CDC3_YEAST] | 2.8 | 4.81% | 1 | 1 | 1 | 1 | 520 |

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| 486 | P40509 | Coatomer subunit epsilon OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SEC28 PE=1 SV=2 - [COPE_YEAST] | 2.75 | 3.04% | 1 | 1 | 1 | 1 | 296 |
| 487 | P52871 | Protein transport protein SBH2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SBH2 PE=1 SV=1 - [SC6B2_YEAST] | 2.74 | 14.77% | 1 | 1 | 1 | 1 | 88 |

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| 488 | A5DWE2 | Histone H3.1/H3.2 OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) OX=379508 GN=HHT1 PE=3 SV=1 - [H31_LODEL] | 2.73 | 6.62% | 3 | 1 | 1 | 1 | 136 |
| 489 | P00817 | Inorganic pyrophosphatase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=IPP1 PE=1 SV=4 - [IPYR_YEAST] | 2.72 | 5.57% | 1 | 1 | 1 | 1 | 287 |

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| 490 | P38694 | Putative aldehyde dehydrogenase-like protein YHR039C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MSC7 PE=1 SV=1 - [MSC7_YEAST] | 2.69 | 2.17% | 1 | 1 | 1 | 1 | 644 |
| 491 | P48239 | Glutathione S-transferase omega-like 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GTO1 PE=1 SV=1 - [GTO1_YEAST] | 2.68 | 4.21% | 1 | 1 | 1 | 1 | 356 |

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| 492 | P53860 | Phosphatidylinositol transfer protein PDR16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDR16 PE=1 SV=1 - [PDR16_YEAST] | 2.68 | 4.56% | 1 | 1 | 1 | 1 | 351 |
| 493 | P54783 | D-arabinono-1,4-lactone oxidase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ALO1 PE=1 SV=1 - [ALO_YEAST] | 2.67 | 2.09% | 1 | 1 | 1 | 1 | 526 |

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| 494 | P32263 | Pyrroline-5-carboxylate reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRO3 PE=1 SV=1 - [P5CR_YEAST] | 2.66 | 4.55% | 1 | 1 | 1 | 1 | 286 |
| 495 | P25555 | Single-strand telomeric DNA-binding protein GBP2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GBP2 PE=1 SV=1 - [GBP2_YEAST] | 2.66 | 2.81% | 1 | 1 | 1 | 1 | 427 |

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| 496 | Q12434 | Rho GDP-dissociation inhibitor OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RDI1 PE=1 SV=1 - [GDIR_YEAST] | 2.66 | 10.40% | 1 | 1 | 1 | 1 | 202 |
| 497 | P53326 | Uncharacterized protein YGR266W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YGR266W PE=1 SV=1 - [YG5L_YEAST] | 2.66 | 2.14% | 1 | 1 | 1 | 1 | 701 |

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| 498 | P32468 | Cell division control protein 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CDC12 PE=1 SV=1 - [CDC12_Y | 2.64 | 4.18% | 1 | 1 | 1 | 1 | 407 |
| 499 | Q01852 | Mitochondrial import inner membrane translocase subunit TIM44 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TIM44 PE=1 SV=1 - [TIM44_YEAST] | 2.63 | 3.02% | 1 | 1 | 1 | 1 | 431 |

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| 500 | P07263 | Histidine--tRNA ligase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HTS1 PE=1 SV=2 - [SYH_YEAST] | 2.62 | 4.58% | 1 | 1 | 1 | 1 | 546 |
| 501 | Q04225 | Ribosome assembly protein RRB1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RRB1 PE=1 SV=1 - [RRB1_YEAST] | 2.62 | 2.94% | 1 | 1 | 1 | 1 | 511 |

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| 502 | P00427 | Cytochrome c oxidase subunit 6, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=COX6 PE=1 SV=1 - [COX6_YEAST] | 2.59 | 12.84% | 1 | 1 | 1 | 1 | 148 |
| 503 | P47169 | Sulfite reductase [NADPH] subunit beta OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET5 PE=1 SV=1 - [MET5_YEAST] | 2.57 | 0.76% | 1 | 1 | 1 | 1 | 1442 |

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| 504 | P38800 | Membrane-anchored lipid-binding protein LAM4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LAM4 PE=1 SV=1 - [LAM4_YEAST] | 2.57 | 1.71% | 1 | 1 | 1 | 1 | 1345 |
| 505 | P39077 | T-complex protein 1 subunit gamma OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT3 PE=1 SV=2 - [TCPG_YEAST] | 2.56 | 2.25% | 1 | 1 | 1 | 1 | 534 |

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| 506 | P40495 | Homoisocitrate dehydrogenase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LYS12 PE=1 SV=1 - [LYS12_YEAST] | 2.54 | 3.23% | 1 | 1 | 1 | 1 | 371 |
| 507 | Q07451 | Endoplasmic reticulum transmembrane protein 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YET3 PE=1 SV=1 - [YET3_YEAST] | 2.53 | 5.42% | 1 | 1 | 1 | 1 | 203 |

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| 508 | P38202 | UPF0642 protein YBL028C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBL028C PE=1 SV=1 - [YBC8_YEAST] | 2.53 | 10.38% | 1 | 1 | 1 | 1 | 106 |
| 509 | P04806 | Hexokinase-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HXK1 PE=1 SV=2 - [HXKA_YEAST] | 2.53 | 1.65% | 2 | 1 | 1 | 1 | 485 |

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| 510 | P47006 | DNA-directed RNA polymerase I subunit RPA34 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPA34 PE=1 SV=1 - [RPA34_YEAST] | 2.51 | 7.73% | 1 | 1 | 1 | 1 | 233 |
| 511 | Q75EU0 | V-type proton ATPase subunit e OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=VMA9 PE=3 SV=1 - [VA0E_ASHGO] | 2.51 | 13.89% | 2 | 1 | 1 | 1 | 72 |

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| 512 | P33767 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=WBP1 PE=1 SV=1 - [OSTB_YEAST] | 2.5 | 3.26% | 1 | 1 | 1 | 1 | 430 |
| 513 | P39676 | Flavohemoprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YHB1 PE=1 SV=2 - [FHP_YEAST] | 2.5 | 3.76% | 1 | 1 | 1 | 1 | 399 |

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| 514 | Q04373 | Pumilio homology domain family member 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PUF6 PE=1 SV=1 - [PUF6_YEAST] | 2.5 | 1.83% | 1 | 1 | 1 | 1 | 656 |
| 515 | P42900 | Sigma-like sequence protein 1, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SLS1 PE=1 SV=1 - [SLS1_YEAST] | 2.49 | 2.33% | 1 | 1 | 1 | 1 | 643 |

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| 516 | Q12176 | Ribosome biogenesis protein MAK21 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAK21 PE=1 SV=1 - [MAK21_YEAST] | 2.49 | 0.98% | 1 | 1 | 1 | 1 | 1025 |
| 517 | P36047 | Protein phosphatase 1 regulatory subunit SDS22 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SDS22 PE=1 SV=1 - [SDS22_YEAST] | 2.47 | 4.73% | 1 | 1 | 1 | 1 | 338 |

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| 518 | Q08235 | Ribosome biogenesis protein BRX1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=BRX1 PE=1 SV=2 - [BRX1_YEAST] | 2.47 | 6.19% | 1 | 1 | 1 | 1 | 291 |
| 519 | Q07362 | Protein PBP4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PBP4 PE=1 SV=1 - [PBP4_YEAST] | 2.46 | 12.43% | 1 | 1 | 1 | 1 | 185 |

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| 520 | P38069 | Alpha-1,2-mannosyltransferase MNN2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN2 PE=1 SV=1 - [MNN2_YEAST] | 2.46 | 2.85% | 1 | 1 | 1 | 1 | 597 |
| 521 | P40413 | T-complex protein 1 subunit epsilon OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCT5 PE=1 SV=3 - [TCPE_YEAST] | 2.46 | 1.78% | 1 | 1 | 1 | 1 | 562 |

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| 522 | P31373 | Cystathionine gamma-lyase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYS3 PE=1 SV=2 - [CYS3_YEAST] | 2.46 | 2.79% | 1 | 1 | 1 | 1 | 394 |
| 523 | Q01217 | Protein ARG5,6, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARG5,6 PE=1 SV=1 - [ARG56_YEAST] | 2.46 | 2.67% | 1 | 1 | 1 | 1 | 863 |

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| 524 | Q02895 | Putative aryl-alcohol dehydrogenase AAD16 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=AAD16 PE=1 SV=1 - [AAD16_YEAST] | 2.45 | 5.26% | 1 | 1 | 1 | 1 | 342 |
| 525 | P38355 | Uncharacterized transporter YBR287W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YBR287W PE=1 SV=1 - [YB8B_YEAST] | 2.42 | 6.09% | 1 | 1 | 1 | 1 | 427 |

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| 526 | P08536 | Sulfate adenylyltransferase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MET3 PE=1 SV=2 - [MET3_YEAST] | 2.42 | 4.70% | 1 | 1 | 1 | 1 | 511 |
| 527 | P36160 | Ribosome biogenesis protein RPF2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPF2 PE=1 SV=1 - [RPF2_YEAST] | 2.42 | 2.62% | 1 | 1 | 1 | 1 | 344 |

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| 528 | Q12466 | Tricalbin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TCB1 PE=1 SV=1 - [TCB1_YEAST] | 2.41 | 0.93% | 1 | 1 | 1 | 1 | 1186 |
| 529 | P36044 | Protein MNN4 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MNN4 PE=4 SV=2 - [MNN4_YEAST] | 2.4 | 3.06% | 1 | 1 | 1 | 1 | 1178 |

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| 530 | P0C2J2 | Transposon Ty2-GR1 Gag polyprotein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=TY2A-GR1 PE=5 SV=1 - [YG21A_YEAST] | 2.4 | 3.65% | 22 | 1 | 1 | 1 | 438 |
| 531 | Q05359 | Protein ERP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERP1 PE=1 SV=1 - [ERP1_YEAST] | 2.4 | 5.48% | 1 | 1 | 1 | 1 | 219 |

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| 532 | P21965 | Protein kinase MCK1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MCK1 PE=1 SV=1 - [MCK1_YEAST] | 2.4 | 4.53% | 1 | 1 | 1 | 1 | 375 |
| 533 | P23639 | Proteasome subunit alpha type-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRE8 PE=1 SV=1 - [PSA2_YEAST] | 2.4 | 4.80% | 1 | 1 | 1 | 1 | 250 |

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| 534 | P40087 | DNA damage-inducible protein 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DDI1 PE=1 SV=1 - [DDI1_YEAST] | 2.39 | 3.50% | 1 | 1 | 1 | 1 | 428 |
| 535 | P20791 | Ras-related protein Rab-8B OS=Dictyostelium discoideum OX=44689 GN=rab8B PE=2 SV=1 - [RAB8B_DICDI] | 2.39 | 5.42% | 3 | 1 | 1 | 1 | 203 |

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| 536 | P24276 | Protein SSD1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=SSD1 PE=1 SV=1 - [SSD1_YEAST] | 2.38 | 1.60% | 1 | 1 | 1 | 1 | 1250 |
| 537 | P07143 | Cytochrome c1, heme protein, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CYT1 PE=1 SV=1 - [CY1_YEAST] | 2.38 | 4.21% | 1 | 1 | 1 | 1 | 309 |

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| 538 | P36015 | Synaptobrevin homolog YKT6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YKT6 PE=1 SV=1 - [YKT6_YEAST] | 2.37 | 5.00% | 2 | 1 | 1 | 1 | 200 |
| 539 | P32337 | Importin subunit beta-3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PSE1 PE=1 SV=2 - [IMB3_YEAST] | 2.37 | 1.38% | 1 | 1 | 1 | 1 | 1089 |

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| 540 | Q06107 | Uncharacterized TLC domain-containing protein YPR114W OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YPR114W PE=1 SV=1 - [YP114_YEAST] | 2.37 | 3.17% | 1 | 1 | 1 | 1 | 315 |
| 541 | P28000 | DNA-directed RNA polymerases I and III subunit RPAC2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPC19 PE=1 SV=1 - [RPAC2_YEAST] | 2.36 | 10.56% | 1 | 1 | 1 | 1 | 142 |

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| 542 | Q9HF51 | GTP-binding protein RHO3 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=RHO3 PE=3 SV=1 - [RHO3_ASHGO] | 2.35 | 4.02% | 2 | 1 | 1 | 1 | 224 |
| 543 | Q08689 | N-alpha-acetyltransferase NAT5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NAT5 PE=1 SV=1 - [NAT5_YEAST] | 2.35 | 7.95% | 1 | 1 | 1 | 1 | 176 |

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| 544 | Q03559 | Uncharacterized protein YMR295C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=YMR295C PE=1 SV=1 - [YM8V_YEAST] | 2.33 | 5.58% | 1 | 1 | 1 | 1 | 197 |
| 545 | Q05775 | Eukaryotic translation initiation factor 3 subunit J OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HCR1 PE=1 SV=1 - [EIF3J_YEAST] | 2.33 | 4.15% | 1 | 1 | 1 | 1 | 265 |

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| 546 | P04650 | 60S ribosomal protein L39 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPL39 PE=1 SV=3 - [RL39_YEAST] | 2.33 | 21.57% | 1 | 1 | 1 | 1 | 51 |
| 547 | Q8X1F5 | Autophagy-related protein 18 OS=Komagataella pastoris OX=4922 GN=ATG18 PE=3 SV=1 - [ATG18_P | 2.32 | 3.31% | 1 | 1 | 1 | 1 | 543 |

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| 548 | Q12377 | 26S proteasome regulatory subunit RPN6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPN6 PE=1 SV=3 - [RPN6_YEAST] | 2.31 | 2.30% | 1 | 1 | 1 | 1 | 434 |
| 549 | Q757U3 | Enoyl-[acyl-carrier-protein] reductase, mitochondrial OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=ETR1 PE=3 SV=2 - [ETR1_ASHGO] | 2.31 | 5.05% | 1 | 1 | 1 | 1 | 376 |

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| 550 | Q04779 | Transcriptional regulatory protein RCO1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RCO1 PE=1 SV=1 - [RCO1_YEAST] | 2.3 | 2.05% | 1 | 1 | 1 | 1 | 684 |
| 551 | P32895 | Ribose-phosphate pyrophosphokinase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PRS1 PE=1 SV=1 - [KPR1_YEAST] | 2.29 | 2.58% | 1 | 1 | 1 | 1 | 427 |

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| 552 | P21269 | CCA tRNA nucleotidyltransferase, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CCA1 PE=1 SV=1 - [CCA1_YEAST] | 2.29 | 2.93% | 1 | 1 | 1 | 1 | 546 |
| 553 | P17967 | Protein disulfide-isomerase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDI1 PE=1 SV=2 - [PDI_YEAST] | 2.28 | 2.30% | 1 | 1 | 1 | 1 | 522 |

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| 554 | P19454 | Casein kinase II subunit alpha' OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=CKA2 PE=1 SV=2 - [CSK22_YEAST] | 2.28 | 2.95% | 1 | 1 | 1 | 1 | 339 |
| 555 | P53731 | Actin-related protein 2/3 complex subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ARC35 PE=1 SV=1 - [ARPC2_YEAST] | 2.25 | 2.92% | 1 | 1 | 1 | 1 | 342 |

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| 556 | P40327 | 26S proteasome regulatory subunit 4 homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RPT2 PE=1 SV=3 - [PRS4_YEAST] | 2.25 | 2.75% | 1 | 1 | 1 | 1 | 437 |
| 557 | P29704 | Squalene synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ERG9 PE=1 SV=2 - [FDFT_YEAST] | 2.24 | 2.25% | 1 | 1 | 1 | 1 | 444 |

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| 558 | A6ZU15 | ATP-dependent RNA helicase ROK1 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ROK1 PE=3 SV=1 - [ROK1_YEAS7] | 2.23 | 2.48% | 2 | 1 | 1 | 1 | 564 |
| 559 | Q04217 | Probable ATP-dependent RNA helicase DHR1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ECM16 PE=1 SV=1 - [DHR1_YEAST] | 2.23 | 1.18% | 1 | 1 | 1 | 1 | 1267 |

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| 560 | P53721 | Respiratory supercomplex factor 2, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RCF2 PE=1 SV=1 - [RCF2_YEAST] | 2.23 | 4.91% | 1 | 1 | 1 | 1 | 224 |
| 561 | A6ZR36 | Altered inheritance of mitochondria protein 9, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=AIM9 PE=3 SV=1 - [AIM9_YEAS7] | 2.22 | 2.23% | 5 | 1 | 1 | 1 | 627 |

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| 562 | P53927 | Ribosome biogenesis protein 15 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NOP15 PE=1 SV=1 - [NOP15_Y | 2.21 | 4.09% | 1 | 1 | 1 | 1 | 220 |
| 563 | P08466 | Mitochondrial nuclease OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=NUC1 PE=1 SV=1 - [NUC1_YEAST] | 2.21 | 3.95% | 1 | 1 | 1 | 1 | 329 |

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| 564 | Q01662 | Methionine aminopeptidase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MAP1 PE=1 SV=2 - [MAP1_YEAST] | 2.21 | 2.58% | 1 | 1 | 1 | 1 | 387 |
| 565 | P50085 | Prohibitin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PHB2 PE=1 SV=2 - [PHB2_YEAST] | 2.2 | 3.55% | 1 | 1 | 1 | 1 | 310 |

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| 566 | A7A1P0 | Serine/threonine-protein kinase STE11 OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=STE11 PE=3 SV=1 - [STE11_YEAS7] | 2.2 | 1.12% | 2 | 1 | 1 | 1 | 717 |
| 567 | P40046 | Vacuolar transporter chaperone 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=VTC1 PE=1 SV=3 - [VTC1_YEAST] | 2.2 | 7.75% | 1 | 1 | 1 | 1 | 129 |

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| 568 | P36022 | Dynein heavy chain, cytoplasmic OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=DYN1 PE=1 SV=1 - [DYHC_YEAST] | 2.19 | 0.51% | 1 | 1 | 1 | 1 | 4092 |
| 569 | P33302 | Pleiotropic ABC efflux transporter of multiple drugs OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PDR5 PE=1 SV=1 - [PDR5_YEAST] | 2.18 | 0.86% | 1 | 1 | 1 | 1 | 1511 |

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| 570 | P25037 | Ubiquitin carboxyl-terminal hydrolase 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=UBP1 PE=1 SV=2 - [UBP1_YEAST] | 2.18 | 1.11% | 1 | 1 | 1 | 1 | 809 |
| 571 | P40961 | Prohibitin-1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PHB1 PE=1 SV=2 - [PHB1_YEAST] | 2.17 | 4.53% | 1 | 1 | 1 | 1 | 287 |

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| 572 | P33399 | La protein homolog OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=LHP1 PE=1 SV=2 - [LHP1_YEAST] | 2.16 | 3.64% | 1 | 1 | 1 | 1 | 275 |
| 573 | P38251 | Replication factor C subunit 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=RFC5 PE=1 SV=1 - [RFC5_YEAST] | 2.15 | 2.26% | 1 | 1 | 1 | 1 | 354 |

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| 574 | P43535 | Protein GCN20 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GCN20 PE=1 SV=1 - [GCN20_YEAST] | 2.14 | 1.06% | 1 | 1 | 1 | 1 | 752 |
| 575 | P20084 | 54S ribosomal protein L33, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=MRPL33 PE=1 SV=4 - [RM33_YEAST] | 2.14 | 12.79% | 1 | 1 | 1 | 1 | 86 |

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| 576 | A6ZRM0 | Adenylosuccinate synthetase OS=Saccharomyces cerevisiae (strain YJM789) OX=307796 GN=ADE12 PE=3 SV=1 - [PURA_YEAS7] | 2.13 | 1.85% | 5 | 1 | 1 | 1 | 433 |
| 577 | P13188 | Glutamine--tRNA ligase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=GLN4 PE=1 SV=2 - [SYQ_YEAST] | 2.13 | 0.99% | 1 | 1 | 1 | 1 | 809 |

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| 578 | P39002 | Long-chain-fatty-acid--CoA ligase 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=FAA3 PE=1 SV=1 - [LCF3_YEAST] | 2.12 | 1.30% | 1 | 1 | 1 | 1 | 694 |
| 579 | P53918 | Uncharacterized transporter ESBP6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=ESBP6 PE=1 SV=1 - [ESBP6_YEAST] | 2.12 | 1.93% | 1 | 1 | 1 | 1 | 673 |

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| 580 | Q750X3 | Pre-mRNA-splicing factor CLF1 OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) OX=284811 GN=CLF1 PE=3 SV=1 - [CLF1_ASHGO] | 2.1 | 2.05% | 1 | 1 | 1 | 1 | 683 |
| 581 | P31539 | Heat shock protein 104 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=HSP104 PE=1 SV=2 - [HS104_YEAST] | 2.1 | 1.54% | 1 | 1 | 1 | 1 | 908 |