[Enzymes with EC numbers; n = 72] LL₃ Diel₃ DD₃ LL₆ Diel₆ DD₆ DD₃ LL₃ Diel₃ DD₆ LL₆ Diel₆ K15509 hpsN; sulfopropanediol 3-dehydrogenase [EC:1.1.1.308] SAR116_2138 histidinol dehydrogenase K15509 hpsN; sulfopropanediol 3-dehydrogenase [EC:1.1.1.308] SAR116_0046 histidinol dehydrogenase SAR116_2446 hypothetical protein K19265 gpr; L-glyceraldehyde 3-phosphate reductase [EC:1.1.1.-] SAR116_1224 hypothetical protein K21430 ylil; aldose sugar dehydrogenase [EC:1.1.5.-] K23463 tgnC; (Z)-2-((N-methylformamido)methylene)-5-hydroxybutyrolactone dehydrogenase [EC:1.2.1.-] SAR116_2117 aldehyde dehydrogenase family protein K03518 coxS; aerobic carbon-monoxide dehydrogenase small subunit [EC:1.2.5.3] SAR116_1387 putative carbon monoxide dehydrogenase small chain K03518 coxS; aerobic carbon-monoxide dehydrogenase small subunit [EC:1.2.5.3] SAR116_2163 (2Fe-2S)-binding protein K03519 coxM; aerobic carbon-monoxide dehydrogenase medium subunit [EC:1.2.5.3] SAR116_1386 molybdopterin dehydrogenase K03519 coxM; aerobic carbon-monoxide dehydrogenase medium subunit [EC:1.2.5.3] SAR116_2165 Carbon-monoxide dehydrogenase (acceptor) K03520 coxL; aerobic carbon-monoxide dehydrogenase large subunit [EC:1.2.5.3] SAR116_2164 Carbon-monoxide dehydrogenase K03520 coxL; aerobic carbon-monoxide dehydrogenase large subunit [EC:1.2.5.3] SAR116_0095 Carbon-monoxide dehydrogenase (acceptor) K00311 ETFDH; electron-transferring-flavoprotein dehydrogenase [EC:1.5.5.1] SAR116_1662 Dehydrogenase K18208 RNLS; renalase [EC:1.6.3.5] SAR116_2453 FAD dependent oxidoreductase K07304 msrA; peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11] SAR116_0728 peptide methionine sulfoxide reductase K07305 msrB; peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12] SAR116 0096 methionine-R-sulfoxide reductase K11209 yghU; GSH-dependent disulfide-bond oxidoreductase [EC:1.8.4.-] SAR116_0657 glutathione S-transferase-like protein K07393 ECM4; glutathionyl-hydroquinone reductase [EC:1.8.5.7] SAR116_2019 putative glutathione S-transferase protein K07147 msrP; methionine sulfoxide reductase catalytic subunit [EC:1.8.-.-] SAR116_2216 twin-arginine translocation pathway signal precursor K17893 AOX1; ubiquinol oxidase [EC:1.10.3.11] SAR116_0177 Alternative oxidase K00428 E1.11.1.5; cytochrome c peroxidase [EC:1.11.1.5] SAR116_0251 Di-heme cytochrome c peroxidase K03564 BCP; thioredoxin-dependent peroxiredoxin [EC:1.11.1.24] SAR116_1028 alkyl hydroperoxide reductase/Thiol specific antioxidant/Mal allergen K24158 prx; thioredoxin-dependent peroxiredoxin [EC:1.11.1.24] SAR116_0079 Peroxidase K06911 PIR; quercetin 2,3-dioxygenase [EC:1.13.11.24] SAR116_1544 pirin family protein K21817 blh; beta-carotene 15,15'-dioxygenase [EC:1.13.11.63] SAR116_2131 possible transmembrane protein K00464 diox1; all-trans-8'-apo-beta-carotenal 15,15'-oxygenase [EC:1.13.11.75] SAR116_2357 probable dioxygenase signal peptide protein SAR116_0954 2OG-Fe(II) oxygenase K07336 K07336; PKHD-type hydroxylase [EC:1.14.11.-] K22342 dmmA; dimethylamine monooxygenase subunit A [EC:1.14.13.238] SAR116_0238 hypothetical protein K22343 dmmB; dimethylamine monooxygenase subunit B [EC:1.14.13.238] SAR116_0237 oxidoreductase NAD-binding domain/2Fe-2S iron-sulfur cluster binding domain protein K22344 dmmC; dimethylamine monooxygenase subunit C [EC:1.14.13.238] SAR116_0236 hypothetical protein SAR116_2118 bacterial luciferase family protein K23464 tgnB; flavin-dependent trigonelline monooxygenase, oxygenase component [EC:1.14.14.-] SAR116_0898 oxidoreductase FAD/NAD(P)-binding protein K00528 fpr; ferredoxin/flavodoxin---NADP+ reductase [EC:1.18.1.2 1.19.1.1] K00537 arsC; arsenate reductase (glutaredoxin) [EC:1.20.4.1] SAR116_1456 arsenate reductase K03741 arsC; arsenate reductase (thioredoxin) [EC:1.20.4.4] SAR116_1998 arsenate reductase K00573 E2.1.1.77; protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77] SAR116_0410 protein-L-isoaspartate O-methyltransferase K00573 E2.1.1.77; protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77] SAR116_0429 protein-L-isoaspartate(D-aspartate) O-methyltransferase K00574 cfa; cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79] SAR116_0580 Cyclopropane-fatty-acyl-phospholipid synthase K00574 cfa; cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79] SAR116_0655 Cyclopropane-fatty-acyl-phospholipid synthase K00612 nodU; carbamoyltransferase [EC:2.1.3.-] SAR116_0987 predicted carbamoyl transferase K03820 Int; apolipoprotein N-acyltransferase [EC:2.3.1.269] SAR116_1009 apolipoprotein N-acyltransferase K03820 Int; apolipoprotein N-acyltransferase [EC:2.3.1.269] SAR116_1586 Apolipoprotein N-acyltransferase K03824 yhbS; putative acetyltransferase [EC:2.3.1.-] SAR116_1273 hypothetical protein K03824 yhbS; putative acetyltransferase [EC:2.3.1.-] SAR116_0701 hypothetical protein K03824 yhbS; putative acetyltransferase [EC:2.3.1.-] SAR116_1519 hypothetical protein K00684 aat; leucyl/phenylalanyl-tRNA---protein transferase [EC:2.3.2.6] SAR116_1041 leucyl/phenylalanyl-tRNA--protein transferase K21420 bpt; leucyl-tRNA---protein transferase [EC:2.3.2.29] SAR116_0527 Putative arginyl-tRNA:protein arginylyltransferase K17251 pglB; undecaprenyl-diphosphooligosaccharide---protein glycotransferase [EC:2.4.99.19] SAR116_1659 oligosaccharide transferase K13292 lgt; phosphatidylglycerol---prolipoprotein diacylglyceryl transferase [EC:2.5.1.145] SAR116_2197 prolipoprotein diacylglyceryl transferase K09773 ppsR; [pyruvate, water dikinase]-phosphate phosphotransferase / [pyruvate, water dikinase] kinase [EC:2.7.4.28 2.7.11.33] SAR116_1639 hypothetical protein K00982 glnE; [glutamine synthetase] adenylyltransferase / [glutamine synthetase]-adenylyl-L-tyrosine phosphorylase [EC:2.7.7.42 2.7.7.89] SAR116_2480 (Glutamate--ammonia-ligase) adenylyltransferase K08997 SELENOO; serine/tyrosine/threonine adenylyltransferase [EC:2.7.7.-] SAR116_2540 protein of unknown function UPF0061 K07107 ybgC; acyl-CoA thioester hydrolase [EC:3.1.2.-] SAR116_2295 4-hydroxybenzoyl-CoA thioesterase K08296 sixA; phosphohistidine phosphatase [EC:3.1.3.-] SAR116_0445 putative phosphohistidine phosphatase K01133 betC; choline-sulfatase [EC:3.1.6.6] SAR116_2122 Sulfatase K03424 tatD; TatD DNase family protein [EC:3.1.21.-] K01185 E3.2.1.17; lysozyme [EC:3.2.1.17] SAR116_2269 chain A K01286 E3.4.16.4; D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4] SAR116_1050 D-alanyl-D-alanine carboxypeptidase K01447 xlyAB; N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28] SAR116_2145 Negative regulator of beta-lactamase expression SAR116_2073 N-acyl-D-amino acid deacylase family protein K06015 E3.5.1.81; N-acyl-D-amino-acid deacylase [EC:3.5.1.81] K01462 PDF; peptide deformylase [EC:3.5.1.88] SAR116_1493 peptide deformylase protein K11206 NIT1; deaminated glutathione amidase [EC:3.5.1.128] SAR116_1917 Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase K01463 bshB1; N-acetylglucosamine malate deacetylase 1 [EC:3.5.1.-] SAR116_2151 hypothetical protein K23465 tgnD; (E)-2-((N-methylformamido)methylene)succinate hydrolase [EC:3.5.1.-] SAR116_2119 3-oxoadipate enol-lactonase family protein K18456 E3.5.4.32; 8-oxoguanine deaminase [EC:3.5.4.32] SAR116_1373 hydroxydechloroatrazine ethylaminohydrolase K20762 scnC; thiocyanate hydrolase subunit gamma [EC:3.5.5.8] SAR116_1730 nitrile hydratase K09022 ridA; 2-iminobutanoate/2-iminopropanoate deaminase [EC:3.5.99.10] SAR116_0033 hypothetical protein K07766 E3.6.1.52; diphosphoinositol-polyphosphate diphosphatase [EC:3.6.1.52] SAR116_0476 NUDIX hydrolase K23997 nnr; ADP-dependent NAD(P)H-hydrate dehydratase / NAD(P)H-hydrate epimerase [EC:4.2.1.136 5.1.99.6] SAR116_0130 hypothetical protein K01726 GAMMACA; gamma-carbonic anhydrase [EC:4.2.1.-] SAR116_1423 hexapeptide transferase family protein K01751 E4.3.1.15; diaminopropionate ammonia-lyase [EC:4.3.1.15] SAR116_0768 diaminopropionate ammonia-lyase K01802 E5.2.1.8; peptidylprolyl isomerase [EC:5.2.1.8] SAR116_2176 peptidyl prolyl cis-trans isomerase (rotamase B) SAR116_0899 hypothetical protein K22131 otnl; 2-dehydrotetronate isomerase [EC:5.3.1.35] K01949 gmaS; glutamate---methylamine ligase [EC:6.3.4.12] SAR116_1707 glutamine synthetase III

Log₂ fold change

-6 -4 -2 0 2 4 6