**Table S5.** Selected genes related to C cycling and their abundances at different revegetation types. JM: *Juglans mandshurica*; QM: *Quercus mongolica*; CB: Conifer-broadleaf forest; LG: *Larix gmelinii*; PK: *Pinus koraiensis*.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| taxonomy | QM | CB | PK | LG | JM | Definition |
|  | Carbon fixation | | | | | |
| K00024 | 0.000511 | 0.000483 | 0.000499 | 0.000502 | 0.000524 | mdh; malate dehydrogenase [EC:1.1.1.37] |
| K00029 | 0.000806 | 0.000779 | 0.000753 | 0.000711 | 0.000763 | E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40] |
| K00031 | 0.000931 | 0.000849 | 0.000808 | 0.000787 | 0.000982 | IDH1, IDH2, icd; isocitrate dehydrogenase [EC:1.1.1.42] |
| K00134 | 0.000681 | 0.000572 | 0.000564 | 0.000549 | 0.000636 | GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] |
| K00150 | 2.29E-05 | 1.18E-05 | 3E-05 | 2.06E-05 | 3.53E-05 | gap2; glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) [EC:1.2.1.59] |
| K00169 | 6.12E-05 | 3.94E-05 | 6.07E-05 | 4.98E-05 | 6.91E-05 | porA; pyruvate ferredoxin oxidoreductase alpha subunit [EC:1.2.7.1] |
| K00170 | 5.42E-05 | 2.36E-05 | 4.88E-05 | 4.54E-05 | 5.07E-05 | porB; pyruvate ferredoxin oxidoreductase beta subunit [EC:1.2.7.1] |
| K00171 | 3.43E-05 | 1.97E-05 | 3.09E-05 | 3.06E-05 | 4.71E-05 | porD; pyruvate ferredoxin oxidoreductase delta subunit [EC:1.2.7.1] |
| K00172 | 1.05E-05 | 4.94E-06 | 1.88E-05 | 9.17E-06 | 1.26E-05 | porG; pyruvate ferredoxin oxidoreductase gamma subunit [EC:1.2.7.1] |
| K00174 | 0.001077 | 0.001034 | 0.001022 | 0.001021 | 0.001043 | korA, oorA, oforA; 2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3 1.2. |
| K00175 | 0.000583 | 0.000545 | 0.000579 | 0.00059 | 0.000614 | korB, oorB, oforB; 2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase subunit beta [EC:1.2.7.3 1.2.7 |
| K00176 | 3.37E-06 | 4.07E-06 | 6.85E-06 | 8.08E-06 | 1.55E-06 | korD, oorD; 2-oxoglutarate ferredoxin oxidoreductase subunit delta [EC:1.2.7.3] |
| K00177 | 5.33E-06 | 7.66E-06 | 1.17E-05 | 1.67E-05 | 7.34E-06 | korC, oorC; 2-oxoglutarate ferredoxin oxidoreductase subunit gamma [EC:1.2.7.3] |
| K00198 | 0 | 0 | 5.07E-07 | 5.11E-07 | 0 | cooS, acsA; anaerobic carbon-monoxide dehydrogenase catalytic subunit [EC:1.2.7.4] |
| K00239 | 0.001512 | 0.00143 | 0.001427 | 0.001375 | 0.001535 | sdhA, frdA; succinate dehydrogenase / fumarate reductase, flavoprotein subunit [EC:1.3.5.1 1.3.5.4] |
| K00240 | 0.000619 | 0.000647 | 0.000614 | 0.000618 | 0.000634 | sdhB, frdB; succinate dehydrogenase / fumarate reductase, iron-sulfur subunit [EC:1.3.5.1 1.3.5.4] |
| K00241 | 0.000272 | 0.000261 | 0.000267 | 0.00026 | 0.000251 | sdhC, frdC; succinate dehydrogenase / fumarate reductase, cytochrome b subunit |
| K00242 | 8.84E-05 | 0.000104 | 9.17E-05 | 8.26E-05 | 7.69E-05 | sdhD, frdD; succinate dehydrogenase / fumarate reductase, membrane anchor subunit |
| K00244 | 0.000287 | 0.000215 | 0.000301 | 0.000301 | 0.000355 | frdA; fumarate reductase flavoprotein subunit [EC:1.3.5.4] |
| K00245 | 7.98E-05 | 5.46E-05 | 7.63E-05 | 7.34E-05 | 8.76E-05 | frdB; fumarate reductase iron-sulfur subunit [EC:1.3.5.4] |
| K00246 | 4.59E-05 | 1.61E-05 | 2.39E-05 | 3.84E-05 | 4.33E-05 | frdC; fumarate reductase subunit C |
| K00247 | 2.15E-05 | 1.31E-05 | 1.93E-05 | 2E-05 | 1.66E-05 | frdD; fumarate reductase subunit D |
| K00297 | 0.000569 | 0.000587 | 0.000626 | 0.000591 | 0.000581 | metF, MTHFR; methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20] |
| K00615 | 0.001726 | 0.001788 | 0.001691 | 0.00168 | 0.001743 | E2.2.1.1, tktA, tktB; transketolase [EC:2.2.1.1] |
| K00625 | 0.000248 | 0.00021 | 0.000241 | 0.000215 | 0.000229 | E2.3.1.8, pta; phosphate acetyltransferase [EC:2.3.1.8] |
| K00626 | 0.002238 | 0.002032 | 0.002002 | 0.001905 | 0.002125 | E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9] |
| K00814 | 0 | 5.58E-07 | 1.87E-06 | 0 | 1.17E-06 | GPT, ALT; alanine transaminase [EC:2.6.1.2] |
| K00855 | 5.43E-05 | 5.47E-05 | 4.15E-05 | 4.62E-05 | 3.83E-05 | PRK, prkB; phosphoribulokinase [EC:2.7.1.19] |
| K00925 | 0.000577 | 0.000676 | 0.000574 | 0.000644 | 0.000511 | ackA; acetate kinase [EC:2.7.2.1] |
| K00927 | 0.000517 | 0.000514 | 0.000529 | 0.000501 | 0.000529 | PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3] |
| K01006 | 0.001204 | 0.001206 | 0.001245 | 0.00116 | 0.00126 | ppdK; pyruvate, orthophosphate dikinase [EC:2.7.9.1] |
| K01007 | 0.000594 | 0.000566 | 0.000532 | 0.000516 | 0.000657 | pps, ppsA; pyruvate, water dikinase [EC:2.7.9.2] |
| K01086 | 7.98E-06 | 8.9E-06 | 5.5E-06 | 3.46E-06 | 4.77E-06 | fbp-SEBP; fructose-1,6-bisphosphatase I / sedoheptulose-1,7-bisphosphatase [EC:3.1.3.11 3.1.3.37] |
| K01491 | 0.000363 | 0.000382 | 0.000394 | 0.000402 | 0.000349 | folD; methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase [EC: |
| K01595 | 0.00057 | 0.000552 | 0.000505 | 0.000532 | 0.000566 | ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31] |
| K01601 | 9.41E-05 | 8.6E-05 | 8.15E-05 | 7.36E-05 | 8.44E-05 | rbcL; ribulose-bisphosphate carboxylase large chain [EC:4.1.1.39] |
| K01610 | 0.000458 | 0.000473 | 0.000466 | 0.000412 | 0.00045 | E4.1.1.49, pckA; phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49] |
| K01623 | 0.000359 | 0.000359 | 0.000295 | 0.000355 | 0.000349 | ALDO; fructose-bisphosphate aldolase, class I [EC:4.1.2.13] |
| K01624 | 0.00023 | 0.000216 | 0.000169 | 0.00016 | 0.000195 | FBA, fbaA; fructose-bisphosphate aldolase, class II [EC:4.1.2.13] |
| K01676 | 0.000472 | 0.000409 | 0.00042 | 0.000391 | 0.000461 | E4.2.1.2A, fumA, fumB; fumarate hydratase, class I [EC:4.2.1.2] |
| K01677 | 3E-05 | 2.13E-05 | 3.27E-05 | 2.31E-05 | 4.05E-05 | E4.2.1.2AA, fumA; fumarate hydratase subunit alpha [EC:4.2.1.2] |
| K01678 | 6.94E-06 | 3.3E-06 | 7.83E-06 | 5.51E-06 | 1.6E-05 | E4.2.1.2AB, fumB; fumarate hydratase subunit beta [EC:4.2.1.2] |
| K01679 | 0.000738 | 0.000751 | 0.000661 | 0.000651 | 0.000693 | E4.2.1.2B, fumC, FH; fumarate hydratase, class II [EC:4.2.1.2] |
| K01681 | 0.001563 | 0.001451 | 0.001467 | 0.001396 | 0.001605 | ACO, acnA; aconitate hydratase [EC:4.2.1.3] |
| K01682 | 2.6E-05 | 2.03E-05 | 1.97E-05 | 9.5E-06 | 3.58E-05 | acnB; aconitate hydratase 2 / 2-methylisocitrate dehydratase [EC:4.2.1.3 4.2.1.99] |
| K01807 | 0.000181 | 0.000172 | 0.000187 | 0.000181 | 0.000148 | rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6] |
| K01808 | 0.000197 | 0.000219 | 0.000206 | 0.000217 | 0.000209 | rpiB; ribose 5-phosphate isomerase B [EC:5.3.1.6] |
| K01847 | 0.000471 | 0.000462 | 0.000404 | 0.000371 | 0.000345 | MUT; methylmalonyl-CoA mutase [EC:5.4.99.2] |
| K01848 | 0.000809 | 0.000733 | 0.000919 | 0.000872 | 0.000826 | E5.4.99.2A, mcmA1; methylmalonyl-CoA mutase, N-terminal domain [EC:5.4.99.2] |
| K01902 | 0.000499 | 0.000491 | 0.00043 | 0.000425 | 0.000495 | sucD; succinyl-CoA synthetase alpha subunit [EC:6.2.1.5] |
| K01903 | 0.000729 | 0.000682 | 0.000672 | 0.000681 | 0.000707 | sucC; succinyl-CoA synthetase beta subunit [EC:6.2.1.5] |
| K01938 | 0.000398 | 0.000371 | 0.000374 | 0.000331 | 0.000418 | fhs; formate--tetrahydrofolate ligase [EC:6.3.4.3] |
| K01958 | 0.000298 | 0.000335 | 0.000304 | 0.000322 | 0.000303 | PC, pyc; pyruvate carboxylase [EC:6.4.1.1] |
| K01959 | 1.41E-05 | 1.01E-05 | 1.81E-05 | 1.61E-05 | 1.87E-05 | pycA; pyruvate carboxylase subunit A [EC:6.4.1.1] |
| K01960 | 2.37E-05 | 1.68E-05 | 4.22E-05 | 3.28E-05 | 3.76E-05 | pycB; pyruvate carboxylase subunit B [EC:6.4.1.1] |
| K01961 | 0.000866 | 0.000834 | 0.000873 | 0.000831 | 0.000851 | accC; acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14] |
| K01962 | 0.000413 | 0.000444 | 0.000452 | 0.000478 | 0.000432 | accA; acetyl-CoA carboxylase carboxyl transferase subunit alpha [EC:6.4.1.2 2.1.3.15] |
| K01963 | 0.000399 | 0.000367 | 0.00041 | 0.000429 | 0.000396 | accD; acetyl-CoA carboxylase carboxyl transferase subunit beta [EC:6.4.1.2 2.1.3.15] |
| K02160 | 0.000216 | 0.000227 | 0.000236 | 0.000246 | 0.000186 | accB, bccP; acetyl-CoA carboxylase biotin carboxyl carrier protein |
| K02446 | 0.00019 | 0.000193 | 0.000178 | 0.000213 | 0.000188 | glpX; fructose-1,6-bisphosphatase II [EC:3.1.3.11] |
| K03737 | 0.000471 | 0.000405 | 0.000506 | 0.000448 | 0.000479 | por, nifJ; pyruvate-ferredoxin/flavodoxin oxidoreductase [EC:1.2.7.1 1.2.7.-] |
| K03841 | 9.52E-05 | 8.81E-05 | 0.000101 | 8.92E-05 | 0.000109 | FBP, fbp; fructose-1,6-bisphosphatase I [EC:3.1.3.11] |
| K05298 | 0 | 5.58E-07 | 1.49E-06 | 9.81E-07 | 2.36E-06 | GAPA; glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [EC:1.2.1.13] |
| K05299 | 1.61E-05 | 3.73E-06 | 1.78E-05 | 1.44E-05 | 2.08E-05 | fdhA; formate dehydrogenase (NADP+) alpha subunit [EC:1.17.1.10] |
| K05606 | 0.000122 | 0.000147 | 0.000151 | 0.000163 | 0.000158 | MCEE, epi; methylmalonyl-CoA/ethylmalonyl-CoA epimerase [EC:5.1.99.1] |
| K08691 | 9.36E-05 | 9.87E-05 | 0.000105 | 9.27E-05 | 9.95E-05 | mcl; malyl-CoA/(S)-citramalyl-CoA lyase [EC:4.1.3.24 4.1.3.25] |
| K09709 | 0.0001 | 8.74E-05 | 8.57E-05 | 7.42E-05 | 7.54E-05 | meh; 3-methylfumaryl-CoA hydratase [EC:4.2.1.153] |
| K11532 | 0.000145 | 0.000137 | 0.000128 | 0.000108 | 0.000114 | glpX-SEBP; fructose-1,6-bisphosphatase II / sedoheptulose-1,7-bisphosphatase [EC:3.1.3.11 3.1.3.37] |
| K13788 | 2.22E-05 | 2.34E-05 | 1.35E-05 | 1.15E-05 | 7.95E-06 | pta; phosphate acetyltransferase [EC:2.3.1.8] |
| K14138 | 1.16E-06 | 0 | 0 | 0 | 0 | acsB; acetyl-CoA synthase [EC:2.3.1.169] |
| K14449 | 9.67E-05 | 0.000109 | 0.000103 | 9.32E-05 | 8.98E-05 | mch, mcd; 2-methylfumaryl-CoA hydratase [EC:4.2.1.148] |
| K14454 | 0 | 0 | 0 | 5.2E-07 | 0 | GOT1; aspartate aminotransferase, cytoplasmic [EC:2.6.1.1] |
| K14465 | 2.62E-06 | 0 | 2.23E-06 | 2.74E-06 | 1.92E-06 | K14465; succinate semialdehyde reductase (NADPH) [EC:1.1.1.-] |
| K14467 | 1.23E-06 | 0 | 0 | 0 | 1.32E-06 | 4hbl; 4-hydroxybutyrate---CoA ligase (AMP-forming) [EC:6.2.1.40] |
| K14469 | 3.69E-06 | 3.35E-06 | 5.93E-06 | 5.77E-06 | 1.48E-06 | K14469; acrylyl-CoA reductase (NADPH) / 3-hydroxypropionyl-CoA dehydratase / 3-hydroxypropionyl-CoA |
| K14470 | 1.64E-05 | 3.08E-05 | 1.21E-05 | 1.44E-05 | 2.3E-05 | mct; 2-methylfumaryl-CoA isomerase [EC:5.4.1.3] |
| K14471 | 1.42E-06 | 6.62E-06 | 2.98E-06 | 1.4E-06 | 2.57E-06 | smtA1; succinyl-CoA:(S)-malate CoA-transferase subunit A [EC:2.8.3.22] |
| K14472 | 7.34E-06 | 4.55E-06 | 4.83E-06 | 6.31E-06 | 6.78E-06 | smtB; succinyl-CoA:(S)-malate CoA-transferase subunit B [EC:2.8.3.22] |
| K14534 | 4.1E-05 | 4.14E-05 | 3.85E-05 | 2.77E-05 | 5.86E-05 | abfD; 4-hydroxybutyryl-CoA dehydratase / vinylacetyl-CoA-Delta-isomerase [EC:4.2.1.120 5.3.3.3] |
| K15016 | 1.77E-05 | 1.03E-05 | 2.24E-05 | 1.77E-05 | 2.58E-05 | K15016; enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.35] |
| K15019 | 2.47E-05 | 7.24E-06 | 1.47E-05 | 8.15E-06 | 2.57E-05 | K15019; 3-hydroxypropionyl-coenzyme A dehydratase [EC:4.2.1.116] |
| K15020 | 6.13E-07 | 8.37E-07 | 1.52E-06 | 9.17E-07 | 1.33E-06 | K15020; acryloyl-coenzyme A reductase [EC:1.3.1.84] |
| K15022 | 1.17E-05 | 5E-06 | 5.14E-06 | 8.6E-06 | 1.61E-05 | fdhB; formate dehydrogenase (NADP+) beta subunit [EC:1.17.1.10] |
| K15024 | 3.59E-06 | 3.45E-06 | 5.19E-06 | 4.87E-06 | 3.18E-06 | K15024; putative phosphotransacetylase [EC:2.3.1.8] |
| K15038 | 0 | 0 | 0 | 0 | 7.98E-07 | K15038; succinyl-CoA reductase [EC:1.2.1.76] |
| K15052 | 1.27E-05 | 6.94E-06 | 8.11E-06 | 8.92E-06 | 1.43E-05 | K15052; propionyl-CoA carboxylase [EC:6.4.1.3 2.1.3.15] |
| K15230 | 7.85E-06 | 2.58E-06 | 6.27E-06 | 3.95E-06 | 9.9E-06 | aclA; ATP-citrate lyase alpha-subunit [EC:2.3.3.8] |
| K15231 | 5.19E-06 | 1.75E-06 | 6.41E-06 | 5.61E-06 | 1.11E-05 | aclB; ATP-citrate lyase beta-subunit [EC:2.3.3.8] |
| K15232 | 2.2E-05 | 1.42E-05 | 1.94E-05 | 1.6E-05 | 2.68E-05 | ccsA; citryl-CoA synthetase large subunit [EC:6.2.1.18] |
| K15234 | 9.68E-06 | 3.72E-06 | 1.11E-05 | 4.67E-06 | 9.03E-06 | ccl; citryl-CoA lyase [EC:4.1.3.34] |
| K18209 | 5.96E-06 | 7.93E-06 | 1.1E-05 | 7.1E-06 | 1.04E-05 | tfrA; fumarate reductase (CoM/CoB) subunit A [EC:1.3.4.1] |
|  | methane metabolism | | | | | |
| K00018 | 6.62E-05 | 6.23E-05 | 4.88E-05 | 5.67E-05 | 5.57E-05 | hprA; glycerate dehydrogenase [EC:1.1.1.29] |
| K00024 | 0.000511 | 0.000483 | 0.000499 | 0.000502 | 0.000524 | mdh; malate dehydrogenase [EC:1.1.1.37] |
| K00200 | 0.000104 | 8.79E-05 | 9.61E-05 | 7.06E-05 | 0.000112 | fwdA, fmdA; formylmethanofuran dehydrogenase subunit A [EC:1.2.7.12] |
| K00201 | 5.18E-05 | 3.37E-05 | 4.25E-05 | 3.1E-05 | 6.08E-05 | fwdB, fmdB; formylmethanofuran dehydrogenase subunit B [EC:1.2.7.12] |
| K00202 | 2.21E-05 | 1.61E-05 | 2.77E-05 | 1.87E-05 | 3.92E-05 | fwdC, fmdC; formylmethanofuran dehydrogenase subunit C [EC:1.2.7.12] |
| K00203 | 2.08E-06 | 5.69E-07 | 3.39E-06 | 1.46E-06 | 3.74E-06 | fwdD, fmdD; formylmethanofuran dehydrogenase subunit D [EC:1.2.7.12] |
| K00205 | 2.05E-06 | 0 | 1.26E-06 | 2.98E-06 | 6.59E-07 | fwdF, fmdF; 4Fe-4S ferredoxin |
| K00320 | 0.000197 | 0.000172 | 0.000177 | 0.000203 | 0.000243 | mer; 5,10-methylenetetrahydromethanopterin reductase [EC:1.5.98.2] |
| K00577 | 1.57E-06 | 3.58E-06 | 2.88E-06 | 3.04E-06 | 6.59E-07 | mtrA; tetrahydromethanopterin S-methyltransferase subunit A [EC:2.1.1.86] |
| K00600 | 0.000708 | 0.00063 | 0.000658 | 0.000665 | 0.000718 | glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1] |
| K00625 | 0.000248 | 0.00021 | 0.000241 | 0.000215 | 0.000229 | E2.3.1.8, pta; phosphate acetyltransferase [EC:2.3.1.8] |
| K00672 | 5.31E-05 | 4.68E-05 | 3.9E-05 | 2.91E-05 | 4.91E-05 | ftr; formylmethanofuran--tetrahydromethanopterin N-formyltransferase [EC:2.3.1.101] |
| K00830 | 0.000619 | 0.000623 | 0.000607 | 0.00057 | 0.000543 | AGXT; alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminas |
| K00850 | 0.000688 | 0.000636 | 0.000676 | 0.000668 | 0.000777 | pfkA, PFK; 6-phosphofructokinase 1 [EC:2.7.1.11] |
| K00863 | 1.66E-05 | 1.97E-05 | 1.13E-05 | 9.51E-06 | 7.3E-06 | DAK, TKFC; triose/dihydroxyacetone kinase / FAD-AMP lyase (cyclizing) [EC:2.7.1.28 2.7.1.29 4.6.1.15 |
| K00925 | 0.000577 | 0.000676 | 0.000574 | 0.000644 | 0.000511 | ackA; acetate kinase [EC:2.7.2.1] |
| K01595 | 0.00057 | 0.000552 | 0.000505 | 0.000532 | 0.000566 | ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31] |
| K01624 | 0.00023 | 0.000216 | 0.000169 | 0.00016 | 0.000195 | FBA, fbaA; fructose-bisphosphate aldolase, class II [EC:4.1.2.13] |
| K01689 | 0.000694 | 0.000634 | 0.000684 | 0.000654 | 0.000701 | ENO, eno; enolase [EC:4.2.1.11] |
| K01895 | 0.00182 | 0.001662 | 0.001711 | 0.001598 | 0.001773 | ACSS, acs; acetyl-CoA synthetase [EC:6.2.1.1] |
| K03388 | 3.39E-06 | 0 | 0 | 0 | 0 | hdrA2; heterodisulfide reductase subunit A2 [EC:1.8.7.3 1.8.98.4 1.8.98.5 1.8.98.6] |
| K03841 | 9.52E-05 | 8.81E-05 | 0.000101 | 8.92E-05 | 0.000109 | FBP, fbp; fructose-1,6-bisphosphatase I [EC:3.1.3.11] |
| K04480 | 0 | 8.31E-07 | 0 | 0 | 0 | mtaB; methanol---5-hydroxybenzimidazolylcobamide Co-methyltransferase [EC:2.1.1.90] |
| K08093 | 3.26E-06 | 7.84E-06 | 1.01E-06 | 2.91E-06 | 6.59E-07 | hxlA; 3-hexulose-6-phosphate synthase [EC:4.1.2.43] |
| K08094 | 8.26E-06 | 7.99E-06 | 1.69E-06 | 1.98E-06 | 5.27E-06 | hxlB; 6-phospho-3-hexuloisomerase [EC:5.3.1.27] |
| K08264 | 3.84E-06 | 0 | 5.43E-07 | 9.9E-07 | 1.78E-06 | hdrD; heterodisulfide reductase subunit D [EC:1.8.98.1] |
| K08691 | 9.36E-05 | 9.87E-05 | 0.000105 | 9.27E-05 | 9.95E-05 | mcl; malyl-CoA/(S)-citramalyl-CoA lyase [EC:4.1.3.24 4.1.3.25] |
| K08692 | 1.28E-05 | 1.24E-05 | 1.66E-05 | 9.32E-06 | 1.04E-05 | mtkB; malate-CoA ligase subunit alpha [EC:6.2.1.9] |
| K10944 | 1.15E-05 | 4.52E-06 | 7.44E-06 | 4.98E-06 | 1.43E-05 | pmoA-amoA; methane/ammonia monooxygenase subunit A [EC:1.14.18.3 1.14.99.39] |
| K10945 | 1.74E-05 | 6.6E-06 | 9.36E-06 | 9.56E-06 | 1.33E-05 | pmoB-amoB; methane/ammonia monooxygenase subunit B |
| K10946 | 1.32E-05 | 5.6E-06 | 1.23E-05 | 1.06E-05 | 2.48E-05 | pmoC-amoC; methane/ammonia monooxygenase subunit C |
| K11261 | 1.36E-05 | 2.8E-05 | 3.02E-05 | 3.89E-05 | 1.22E-05 | fwdE, fmdE; formylmethanofuran dehydrogenase subunit E [EC:1.2.7.12] |
| K11529 | 1.02E-05 | 7.28E-06 | 8.47E-06 | 8.5E-06 | 1.19E-05 | gck, gckA, GLYCTK; glycerate 2-kinase [EC:2.7.1.165] |
| K13788 | 2.22E-05 | 2.34E-05 | 1.35E-05 | 1.15E-05 | 7.95E-06 | pta; phosphate acetyltransferase [EC:2.3.1.8] |
| K13831 | 2.12E-05 | 1.46E-05 | 2.36E-05 | 1.35E-05 | 2.5E-05 | hps-phi; 3-hexulose-6-phosphate synthase / 6-phospho-3-hexuloisomerase [EC:4.1.2.43 5.3.1.27] |
| K14028 | 2.9E-05 | 2.36E-05 | 1.95E-05 | 2.05E-05 | 4.05E-05 | mdh1, mxaF; methanol dehydrogenase (cytochrome c) subunit 1 [EC:1.1.2.7] |
| K14067 | 1.48E-05 | 1.54E-05 | 1.05E-05 | 1.18E-05 | 1.98E-05 | mtkA; malate-CoA ligase subunit beta [EC:6.2.1.9] |
| K14080 | 1.23E-06 | 0 | 2.35E-06 | 0 | 6.59E-07 | mtaA; [methyl-Co(III) methanol-specific corrinoid protein]:coenzyme M methyltransferase [EC:2.1.1.24 |
| K14083 | 0.000209 | 0.0003 | 0.000196 | 0.000219 | 0.000204 | mttB; trimethylamine---corrinoid protein Co-methyltransferase [EC:2.1.1.250] |
| K14084 | 0 | 1.37E-06 | 6.7E-07 | 2.12E-06 | 0 | mttC; trimethylamine corrinoid protein |
| K14127 | 0 | 3.07E-06 | 0 | 0 | 0 | mvhD, vhuD, vhcD; F420-non-reducing hydrogenase iron-sulfur subunit [EC:1.12.99.- 1.8.98.5 1.8.98.6] |
| K16157 | 1.13E-06 | 3.58E-06 | 2.08E-06 | 3.06E-06 | 2.5E-06 | mmoX; methane monooxygenase component A alpha chain [EC:1.14.13.25] |
| K16177 | 0 | 0 | 0 | 4.56E-07 | 1.53E-06 | mtmC; monomethylamine corrinoid protein |
| K16179 | 0 | 2.93E-06 | 1.63E-06 | 1.68E-06 | 0 | mtbC; dimethylamine corrinoid protein |
| K16370 | 1.45E-05 | 1.86E-05 | 2.77E-05 | 2.29E-05 | 1.08E-05 | pfkB; 6-phosphofructokinase 2 [EC:2.7.1.11] |
|  | carbohydrate metabolism | | | | | |
| K00001 | 0.000485 | 0.000489 | 0.0005 | 0.000524 | 0.000434 | E1.1.1.1,adh;alcoholdehydrogenase[EC:1.1.1.1] |
| K00002 | 1.91E-06 | 3.07E-06 | 5.25E-06 | 5.66E-06 | 1.91E-06 | AKR1A1,adh;alcoholdehydrogenase(NADP+)[EC:1.1.1.2] |
| K00004 | 5.14E-05 | 7.2E-05 | 5.94E-05 | 6.29E-05 | 7.48E-05 | BDH,butB;(R,R)-butanedioldehydrogenase/meso-butanedioldehydrogenase/diacetylr |
| K00005 | 1.7E-06 | 5.28E-06 | 8.23E-06 | 8.1E-06 | 7.44E-06 | gldA;glyceroldehydrogenase[EC:1.1.1.6] |
| K00007 | 1.32E-05 | 4.18E-06 | 1.32E-05 | 1.17E-05 | 1.7E-05 | dalD;D-arabinitol4-dehydrogenase[EC:1.1.1.11] |
| K00008 | 0.000369 | 0.000426 | 0.000414 | 0.000496 | 0.000357 | SORD,gutB;L-iditol2-dehydrogenase[EC:1.1.1.14] |
| K00010 | 0.000269 | 0.000273 | 0.000287 | 0.000242 | 0.000246 | iolG;myo-inositol2-dehydrogenase/D-chiro-inositol1-dehydrogenase[EC:1.1.1.181.1 |
| K00011 | 2.08E-05 | 3.07E-05 | 2.3E-05 | 1.45E-05 | 2E-05 | AKR1B;aldehydereductase[EC:1.1.1.21] |
| K00012 | 0.000725 | 0.000729 | 0.000792 | 0.000798 | 0.000701 | UGDH,ugd;UDPglucose6-dehydrogenase[EC:1.1.1.22] |
| K00015 | 0.000352 | 0.000348 | 0.000317 | 0.000347 | 0.000316 | gyaR,GOR1;glyoxylatereductase[EC:1.1.1.26] |
| K00016 | 7.77E-05 | 0.000103 | 8.81E-05 | 8.68E-05 | 8.31E-05 | LDH,ldh;L-lactatedehydrogenase[EC:1.1.1.27] |
| K00018 | 6.62E-05 | 6.23E-05 | 4.88E-05 | 5.67E-05 | 5.57E-05 | hprA;glyceratedehydrogenase[EC:1.1.1.29] |
| K00019 | 0.0003 | 0.000261 | 0.000286 | 0.000261 | 0.00028 | E1.1.1.30,bdh;3-hydroxybutyratedehydrogenase[EC:1.1.1.30] |
| K00022 | 9.52E-06 | 5.92E-06 | 3.57E-06 | 5.28E-06 | 9.09E-06 | HADH;3-hydroxyacyl-CoAdehydrogenase[EC:1.1.1.35] |
| K00023 | 0.000248 | 0.000255 | 0.000248 | 0.000211 | 0.000237 | phbB;acetoacetyl-CoAreductase[EC:1.1.1.36] |
| K00024 | 0.000511 | 0.000483 | 0.000499 | 0.000502 | 0.000524 | mdh;malatedehydrogenase[EC:1.1.1.37] |
| K00027 | 0.000212 | 0.000216 | 0.000179 | 0.000195 | 0.000224 | ME2,sfcA,maeA;malatedehydrogenase(oxaloacetate-decarboxylating)[EC:1.1.1.38] |
| K00029 | 0.000806 | 0.000779 | 0.000753 | 0.000711 | 0.000763 | E1.1.1.40,maeB;malatedehydrogenase(oxaloacetate-decarboxylating)(NADP+)[EC:1.1.1. |
| K00030 | 0.000221 | 0.000197 | 0.000229 | 0.000232 | 0.000247 | IDH3;isocitratedehydrogenase(NAD+)[EC:1.1.1.41] |
| K00031 | 0.000931 | 0.000849 | 0.000808 | 0.000787 | 0.000982 | IDH1,IDH2,icd;isocitratedehydrogenase[EC:1.1.1.42] |
| K00032 | 6.92E-06 | 7.23E-06 | 6.05E-06 | 6.93E-06 | 3.85E-06 | E1.1.1.43;phosphogluconate2-dehydrogenase[EC:1.1.1.43] |
| K00033 | 0.00066 | 0.000753 | 0.000695 | 0.000709 | 0.000641 | PGD,gnd,gntZ;6-phosphogluconatedehydrogenase[EC:1.1.1.441.1.1.343] |
| K00034 | 9.83E-05 | 0.000133 | 0.000123 | 0.000145 | 7.8E-05 | gdh;glucose1-dehydrogenase[EC:1.1.1.47] |
| K00035 | 2.79E-05 | 2.57E-05 | 1.49E-05 | 1.74E-05 | 2.43E-05 | gal;D-galactose1-dehydrogenase[EC:1.1.1.48] |
| K00036 | 0.001325 | 0.001478 | 0.001305 | 0.001356 | 0.00121 | G6PD,zwf;glucose-6-phosphate1-dehydrogenase[EC:1.1.1.491.1.1.363] |
| K00039 | 1.74E-05 | 1.85E-05 | 8.35E-06 | 8.07E-06 | 1.24E-05 | rbtD;ribitol2-dehydrogenase[EC:1.1.1.56] |
| K00040 | 5.33E-05 | 4.33E-05 | 2.36E-05 | 3.48E-05 | 3.76E-05 | uxuB;fructuronatereductase[EC:1.1.1.57] |
| K00041 | 6.89E-06 | 9.69E-06 | 1.03E-05 | 8.83E-06 | 1.68E-05 | uxaB;tagaturonatereductase[EC:1.1.1.58] |
| K00042 | 0.000262 | 0.00024 | 0.000279 | 0.000255 | 0.000249 | garR,glxR;2-hydroxy-3-oxopropionatereductase[EC:1.1.1.60] |
| K00043 | 5.84E-06 | 5.58E-07 | 1.76E-06 | 1.77E-06 | 5.63E-06 | gbd;4-hydroxybutyratedehydrogenase[EC:1.1.1.61] |
| K00045 | 3.36E-05 | 3.84E-05 | 2.17E-05 | 2.14E-05 | 2.14E-05 | E1.1.1.67,mtlK;mannitol2-dehydrogenase[EC:1.1.1.67] |
| K00048 | 4.94E-06 | 2.15E-06 | 2.31E-06 | 3.25E-06 | 5.24E-06 | fucO;lactaldehydereductase[EC:1.1.1.77] |
| K00049 | 3.61E-06 | 3.6E-06 | 1.07E-06 | 1.55E-06 | 3.86E-06 | GRHPR;glyoxylate/hydroxypyruvatereductase[EC:1.1.1.791.1.1.81] |
| K00050 | 0.000237 | 0.000295 | 0.000285 | 0.000305 | 0.000215 | ttuD;hydroxypyruvatereductase[EC:1.1.1.81] |
| K00052 | 0.000655 | 0.00068 | 0.000723 | 0.000686 | 0.000657 | leuB,IMDH;3-isopropylmalatedehydrogenase[EC:1.1.1.85] |
| K00064 | 0.000171 | 0.000169 | 0.000137 | 0.000135 | 0.000135 | E1.1.1.122;D-threo-aldose1-dehydrogenase[EC:1.1.1.122] |
| K00065 | 0.000233 | 0.000238 | 0.000241 | 0.000234 | 0.000253 | kduD;2-dehydro-3-deoxy-D-gluconate5-dehydrogenase[EC:1.1.1.127] |
| K00066 | 0.000153 | 0.000135 | 0.00017 | 0.00016 | 0.000179 | algD;GDP-mannose6-dehydrogenase[EC:1.1.1.132] |
| K00068 | 9.32E-06 | 7.68E-06 | 6.04E-07 | 4.14E-06 | 4.36E-06 | srlD;sorbitol-6-phosphate2-dehydrogenase[EC:1.1.1.140] |
| K00074 | 0.000722 | 0.00073 | 0.000786 | 0.000761 | 0.000696 | paaH,hbd,fadB,mmgB;3-hydroxybutyryl-CoAdehydrogenase[EC:1.1.1.157] |
| K00075 | 0.000326 | 0.000325 | 0.000362 | 0.000364 | 0.000333 | murB;UDP-N-acetylmuramatedehydrogenase[EC:1.3.1.98] |
| K00078 | 0 | 3.51E-06 | 1.68E-06 | 4.56E-07 | 0 | DHDH;dihydrodioldehydrogenase/D-xylose1-dehydrogenase(NADP)[EC:1.3.1.201.1.1.1 |
| K00086 | 1.21E-06 | 2.04E-06 | 1.52E-06 | 9.81E-07 | 6.59E-07 | dhaT;1,3-propanedioldehydrogenase[EC:1.1.1.202] |
| K00090 | 1.32E-05 | 2.21E-05 | 1.78E-05 | 1.16E-05 | 2.18E-05 | ghrB;glyoxylate/hydroxypyruvate/2-ketogluconatereductase[EC:1.1.1.791.1.1.811.1.1 |
| K00100 | 0 | 6.14E-07 | 0 | 4.56E-07 | 0 | bdhAB;butanoldehydrogenase[EC:1.1.1.-] |
| K00101 | 0.000427 | 0.000462 | 0.0004 | 0.000407 | 0.000415 | lldD;L-lactatedehydrogenase(cytochrome)[EC:1.1.2.3] |
| K00102 | 0.00035 | 0.000304 | 0.000317 | 0.000292 | 0.000368 | LDHD,dld;D-lactatedehydrogenase(cytochrome)[EC:1.1.2.4] |
| K00103 | 6.52E-06 | 1.37E-05 | 6.47E-06 | 8.14E-06 | 1.03E-05 | GULO;L-gulonolactoneoxidase[EC:1.1.3.8] |
| K00104 | 0.000702 | 0.000754 | 0.000763 | 0.000755 | 0.00071 | glcD;glycolateoxidase[EC:1.1.3.15] |
| K00109 | 1.36E-05 | 7.55E-06 | 1.27E-05 | 1.33E-05 | 1.14E-05 | L2HGDH;2-hydroxyglutaratedehydrogenase[EC:1.1.99.2] |
| K00114 | 0.002869 | 0.002727 | 0.003221 | 0.003104 | 0.003064 | exaA;alcoholdehydrogenase(cytochromec)[EC:1.1.2.8] |
| K00115 | 7.91E-07 | 2.43E-06 | 5.07E-07 | 1.71E-06 | 1.72E-06 | GLD;glucose1-dehydrogenase(FAD,quinone)[EC:1.1.5.9] |
| K00116 | 5.01E-05 | 7.34E-05 | 3.34E-05 | 3.95E-05 | 4.6E-05 | mqo;malatedehydrogenase(quinone)[EC:1.1.5.4] |
| K00117 | 0.002145 | 0.001704 | 0.002221 | 0.001983 | 0.002466 | gcd;quinoproteinglucosedehydrogenase[EC:1.1.5.2] |
| K00121 | 0.000682 | 0.000746 | 0.000647 | 0.000657 | 0.000694 | frmA,ADH5,adhC;S-(hydroxymethyl)glutathionedehydrogenase/alcoholdehydrogenase[ |
| K00122 | 0.000389 | 0.000381 | 0.000383 | 0.000383 | 0.000349 | FDH;formatedehydrogenase[EC:1.17.1.9] |
| K00123 | 0.002141 | 0.002172 | 0.002088 | 0.002038 | 0.002155 | fdoG,fdhF,fdwA;formatedehydrogenasemajorsubunit[EC:1.17.1.9] |
| K00124 | 0.000399 | 0.000424 | 0.000393 | 0.000376 | 0.000386 | fdoH,fdsB;formatedehydrogenaseiron-sulfursubunit |
| K00126 | 8.85E-06 | 1.99E-05 | 1.72E-05 | 1.62E-05 | 6.71E-06 | fdsD;formatedehydrogenasesubunitdelta[EC:1.17.1.9] |
| K00127 | 0.000262 | 0.000281 | 0.000277 | 0.000273 | 0.000278 | fdoI,fdsG;formatedehydrogenasesubunitgamma |
| K00128 | 0.001742 | 0.00192 | 0.001597 | 0.00169 | 0.001621 | ALDH;aldehydedehydrogenase(NAD+)[EC:1.2.1.3] |
| K00129 | 7.11E-07 | 4.76E-06 | 1.57E-06 | 2.24E-06 | 3.01E-06 | E1.2.1.5;aldehydedehydrogenase(NAD(P)+)[EC:1.2.1.5] |
| K00131 | 2.2E-05 | 1.74E-05 | 1.58E-05 | 1.92E-05 | 3.19E-05 | gapN;glyceraldehyde-3-phosphatedehydrogenase(NADP+)[EC:1.2.1.9] |
| K00132 | 5.07E-05 | 2.74E-05 | 5.94E-05 | 4.13E-05 | 6.4E-05 | E1.2.1.10;acetaldehydedehydrogenase(acetylating)[EC:1.2.1.10] |
| K00134 | 0.000681 | 0.000572 | 0.000564 | 0.000549 | 0.000636 | GAPDH,gapA;glyceraldehyde3-phosphatedehydrogenase[EC:1.2.1.12] |
| K00135 | 0.000855 | 0.000987 | 0.000825 | 0.000898 | 0.00082 | gabD;succinate-semialdehydedehydrogenase/glutarate-semialdehydedehydrogenase[EC: |
| K00138 | 7.46E-05 | 0.000103 | 6.33E-05 | 5.19E-05 | 5.99E-05 | aldB;aldehydedehydrogenase[EC:1.2.1.-] |
| K00140 | 0.000572 | 0.000608 | 0.000581 | 0.000546 | 0.00055 | mmsA,iolA,ALDH6A1;malonate-semialdehydedehydrogenase(acetylating)/methylmalonat |
| K00150 | 2.29E-05 | 1.18E-05 | 3E-05 | 2.06E-05 | 3.53E-05 | gap2;glyceraldehyde-3-phosphatedehydrogenase(NAD(P))[EC:1.2.1.59] |
| K00156 | 0.000415 | 0.000553 | 0.000275 | 0.000342 | 0.000268 | poxB;pyruvatedehydrogenase(quinone)[EC:1.2.5.1] |
| K00158 | 1.96E-05 | 2.02E-05 | 4.06E-05 | 3.49E-05 | 1.79E-05 | E1.2.3.3,poxL;pyruvateoxidase[EC:1.2.3.3] |
| K00161 | 0.000878 | 0.000889 | 0.000823 | 0.00086 | 0.000873 | PDHA,pdhA;pyruvatedehydrogenaseE1componentalphasubunit[EC:1.2.4.1] |
| K00162 | 0.000707 | 0.000722 | 0.000689 | 0.000689 | 0.000767 | PDHB,pdhB;pyruvatedehydrogenaseE1componentbetasubunit[EC:1.2.4.1] |
| K00163 | 0.001215 | 0.001069 | 0.001207 | 0.001055 | 0.001278 | aceE;pyruvatedehydrogenaseE1component[EC:1.2.4.1] |
| K00164 | 0.001304 | 0.001314 | 0.001189 | 0.001222 | 0.00121 | OGDH,sucA;2-oxoglutaratedehydrogenaseE1component[EC:1.2.4.2] |
| K00166 | 0.000157 | 0.000173 | 0.000155 | 0.000151 | 0.00017 | BCKDHA,bkdA1;2-oxoisovaleratedehydrogenaseE1componentalphasubunit[EC:1.2.4.4] |
| K00167 | 0.000275 | 0.000241 | 0.00023 | 0.000239 | 0.000292 | BCKDHB,bkdA2;2-oxoisovaleratedehydrogenaseE1componentbetasubunit[EC:1.2.4.4] |
| K00169 | 6.12E-05 | 3.94E-05 | 6.07E-05 | 4.98E-05 | 6.91E-05 | porA;pyruvateferredoxinoxidoreductasealphasubunit[EC:1.2.7.1] |
| K00170 | 5.42E-05 | 2.36E-05 | 4.88E-05 | 4.54E-05 | 5.07E-05 | porB;pyruvateferredoxinoxidoreductasebetasubunit[EC:1.2.7.1] |
| K00171 | 3.43E-05 | 1.97E-05 | 3.09E-05 | 3.06E-05 | 4.71E-05 | porD;pyruvateferredoxinoxidoreductasedeltasubunit[EC:1.2.7.1] |
| K00172 | 1.05E-05 | 4.94E-06 | 1.88E-05 | 9.17E-06 | 1.26E-05 | porG;pyruvateferredoxinoxidoreductasegammasubunit[EC:1.2.7.1] |
| K00174 | 0.001077 | 0.001034 | 0.001022 | 0.001021 | 0.001043 | korA,oorA,oforA;2-oxoglutarate/2-oxoacidferredoxinoxidoreductasesubunitalpha[E |
| K00175 | 0.000583 | 0.000545 | 0.000579 | 0.00059 | 0.000614 | korB,oorB,oforB;2-oxoglutarate/2-oxoacidferredoxinoxidoreductasesubunitbeta[EC |
| K00176 | 3.37E-06 | 4.07E-06 | 6.85E-06 | 8.08E-06 | 1.55E-06 | korD,oorD;2-oxoglutarateferredoxinoxidoreductasesubunitdelta[EC:1.2.7.3] |
| K00177 | 5.33E-06 | 7.66E-06 | 1.17E-05 | 1.67E-05 | 7.34E-06 | korC,oorC;2-oxoglutarateferredoxinoxidoreductasesubunitgamma[EC:1.2.7.3] |
| K00209 | 4.08E-05 | 2.19E-05 | 3.13E-05 | 2.82E-05 | 2.47E-05 | fabV,ter;enoyl-[acyl-carrierprotein]reductase/trans-2-enoyl-CoAreductase(NAD+) |
| K00234 | 0 | 1.88E-06 | 1.94E-06 | 5.52E-07 | 3.07E-06 | SDHA,SDH1;succinatedehydrogenase(ubiquinone)flavoproteinsubunit[EC:1.3.5.1] |
| K00239 | 0.001512 | 0.00143 | 0.001427 | 0.001375 | 0.001535 | sdhA,frdA;succinatedehydrogenase/fumaratereductase,flavoproteinsubunit[EC:1.3 |
| K00240 | 0.000619 | 0.000647 | 0.000614 | 0.000618 | 0.000634 | sdhB,frdB;succinatedehydrogenase/fumaratereductase,iron-sulfursubunit[EC:1.3. |
| K00241 | 0.000272 | 0.000261 | 0.000267 | 0.00026 | 0.000251 | sdhC,frdC;succinatedehydrogenase/fumaratereductase,cytochromebsubunit |
| K00242 | 8.84E-05 | 0.000104 | 9.17E-05 | 8.26E-05 | 7.69E-05 | sdhD,frdD;succinatedehydrogenase/fumaratereductase,membraneanchorsubunit |
| K00244 | 0.000287 | 0.000215 | 0.000301 | 0.000301 | 0.000355 | frdA;fumaratereductaseflavoproteinsubunit[EC:1.3.5.4] |
| K00245 | 7.98E-05 | 5.46E-05 | 7.63E-05 | 7.34E-05 | 8.76E-05 | frdB;fumaratereductaseiron-sulfursubunit[EC:1.3.5.4] |
| K00246 | 4.59E-05 | 1.61E-05 | 2.39E-05 | 3.84E-05 | 4.33E-05 | frdC;fumaratereductasesubunitC |
| K00247 | 2.15E-05 | 1.31E-05 | 1.93E-05 | 2E-05 | 1.66E-05 | frdD;fumaratereductasesubunitD |
| K00248 | 0.000445 | 0.000473 | 0.000484 | 0.000505 | 0.000419 | ACADS,bcd;butyryl-CoAdehydrogenase[EC:1.3.8.1] |
| K00249 | 0.002059 | 0.001797 | 0.00182 | 0.001719 | 0.001932 | ACADM,acd;acyl-CoAdehydrogenase[EC:1.3.8.7] |
| K00281 | 0.000671 | 0.000477 | 0.00053 | 0.000484 | 0.000686 | GLDC,gcvP;glycinedehydrogenase[EC:1.4.4.2] |
| K00282 | 0.000268 | 0.000302 | 0.000302 | 0.00034 | 0.00024 | gcvPA;glycinedehydrogenasesubunit1[EC:1.4.4.2] |
| K00283 | 0.000306 | 0.000339 | 0.000348 | 0.000363 | 0.000302 | gcvPB;glycinedehydrogenasesubunit2[EC:1.4.4.2] |
| K00284 | 0.000555 | 0.000357 | 0.000511 | 0.000441 | 0.000701 | GLU,gltS;glutamatesynthase(ferredoxin)[EC:1.4.7.1] |
| K00326 | 8.94E-06 | 5.46E-06 | 9.52E-06 | 8.06E-06 | 1.43E-05 | E1.6.2.2;cytochrome-b5reductase[EC:1.6.2.2] |
| K00382 | 0.001376 | 0.001339 | 0.00131 | 0.001261 | 0.001364 | DLD,lpd,pdhD;dihydrolipoamidedehydrogenase[EC:1.8.1.4] |
| K00423 | 2.67E-06 | 4.49E-06 | 0 | 1.31E-06 | 6.59E-07 | E1.10.3.3;L-ascorbateoxidase[EC:1.10.3.3] |
| K00467 | 6.9E-06 | 1.25E-05 | 2.85E-06 | 4.63E-06 | 4.4E-06 | E1.13.12.4;lactate2-monooxygenase[EC:1.13.12.4] |
| K00469 | 2.32E-05 | 3.22E-05 | 3.15E-05 | 4.7E-05 | 2.01E-05 | MIOX;inositoloxygenase[EC:1.13.99.1] |
| K00523 | 9.62E-05 | 6.33E-05 | 0.000108 | 8.4E-05 | 0.000137 | ascD,ddhD,rfbI;CDP-4-dehydro-6-deoxyglucosereductase,E3[EC:1.17.1.1] |
| K00594 | 5.07E-05 | 7.2E-05 | 7.12E-05 | 9.06E-05 | 3.94E-05 | xyoA,aldO;alditoloxidase[EC:1.1.3.41] |
| K00600 | 0.000708 | 0.00063 | 0.000658 | 0.000665 | 0.000718 | glyA,SHMT;glycinehydroxymethyltransferase[EC:2.1.2.1] |
| K00605 | 0.000659 | 0.000742 | 0.000676 | 0.000775 | 0.000686 | gcvT,AMT;aminomethyltransferase[EC:2.1.2.10] |
| K00615 | 0.001726 | 0.001788 | 0.001691 | 0.00168 | 0.001743 | E2.2.1.1,tktA,tktB;transketolase[EC:2.2.1.1] |
| K00616 | 0.000608 | 0.00069 | 0.000631 | 0.000687 | 0.000639 | E2.2.1.2,talA,talB;transaldolase[EC:2.2.1.2] |
| K00621 | 0 | 7.75E-07 | 0 | 0 | 0 | GNPNAT1,GNA1;glucosamine-phosphateN-acetyltransferase[EC:2.3.1.4] |
| K00625 | 0.000248 | 0.00021 | 0.000241 | 0.000215 | 0.000229 | E2.3.1.8,pta;phosphateacetyltransferase[EC:2.3.1.8] |
| K00626 | 0.002238 | 0.002032 | 0.002002 | 0.001905 | 0.002125 | E2.3.1.9,atoB;acetyl-CoAC-acetyltransferase[EC:2.3.1.9] |
| K00627 | 0.000783 | 0.000806 | 0.000834 | 0.000792 | 0.000782 | DLAT,aceF,pdhC;pyruvatedehydrogenaseE2component(dihydrolipoamideacetyltransfer |
| K00634 | 9.03E-06 | 5.59E-06 | 2.42E-06 | 3.14E-06 | 7.38E-06 | ptb;phosphatebutyryltransferase[EC:2.3.1.19] |
| K00656 | 0.000288 | 0.000214 | 0.000254 | 0.000245 | 0.000335 | E2.3.1.54,pflD;formateC-acetyltransferase[EC:2.3.1.54] |
| K00658 | 0.000571 | 0.000617 | 0.000585 | 0.000599 | 0.00061 | DLST,sucB;2-oxoglutaratedehydrogenaseE2component(dihydrolipoamidesuccinyltransf |
| K00688 | 0.001828 | 0.001817 | 0.001791 | 0.0018 | 0.00181 | PYG,glgP;glycogenphosphorylase[EC:2.4.1.1] |
| K00690 | 6.84E-06 | 6.18E-06 | 4.9E-06 | 4.2E-06 | 1.75E-05 | E2.4.1.7;sucrosephosphorylase[EC:2.4.1.7] |
| K00691 | 4.47E-06 | 5.58E-07 | 3.53E-06 | 6.66E-07 | 3.29E-06 | mapA;maltosephosphorylase[EC:2.4.1.8] |
| K00692 | 0 | 0 | 1.12E-06 | 0 | 6.59E-07 | sacB;levansucrase[EC:2.4.1.10] |
| K00693 | 2.22E-06 | 0 | 0 | 1.45E-06 | 7.93E-06 | GYS;glycogensynthase[EC:2.4.1.11] |
| K00694 | 4.69E-05 | 6.35E-05 | 4.69E-05 | 4.35E-05 | 4.35E-05 | bcsA;cellulosesynthase(UDP-forming)[EC:2.4.1.12] |
| K00695 | 0 | 0 | 5.07E-07 | 1.05E-06 | 0 | E2.4.1.13;sucrosesynthase[EC:2.4.1.13] |
| K00696 | 3.71E-06 | 0 | 0 | 2.29E-06 | 1.91E-06 | E2.4.1.14;sucrose-phosphatesynthase[EC:2.4.1.14] |
| K00697 | 0.000506 | 0.000625 | 0.000587 | 0.00058 | 0.000482 | otsA;trehalose6-phosphatesynthase[EC:2.4.1.152.4.1.347] |
| K00699 | 4.46E-05 | 3.53E-05 | 3.14E-05 | 3.52E-05 | 4.58E-05 | UGT;glucuronosyltransferase[EC:2.4.1.17] |
| K00700 | 0.000936 | 0.000957 | 0.00091 | 0.000918 | 0.000994 | GBE1,glgB;1,4-alpha-glucanbranchingenzyme[EC:2.4.1.18] |
| K00701 | 2.79E-06 | 7.03E-07 | 1.01E-06 | 0 | 5.51E-06 | cgt;cyclomaltodextringlucanotransferase[EC:2.4.1.19] |
| K00702 | 4.47E-05 | 3.54E-05 | 4.35E-05 | 2.75E-05 | 5.08E-05 | E2.4.1.20;cellobiosephosphorylase[EC:2.4.1.20] |
| K00703 | 0.00042 | 0.000468 | 0.000461 | 0.000505 | 0.000427 | glgA;starchsynthase[EC:2.4.1.21] |
| K00705 | 0.000696 | 0.000722 | 0.000708 | 0.00075 | 0.000667 | malQ;4-alpha-glucanotransferase[EC:2.4.1.25] |
| K00790 | 0.000588 | 0.000537 | 0.00053 | 0.00055 | 0.000638 | murA;UDP-N-acetylglucosamine1-carboxyvinyltransferase[EC:2.5.1.7] |
| K00820 | 0.001092 | 0.001119 | 0.001116 | 0.001135 | 0.001098 | glmS,GFPT;glucosamine---fructose-6-phosphateaminotransferase(isomerizing)[EC:2.6. |
| K00822 | 0.000302 | 0.000301 | 0.000285 | 0.00027 | 0.000324 | E2.6.1.18;beta-alanine--pyruvatetransaminase[EC:2.6.1.18] |
| K00823 | 0.000332 | 0.000329 | 0.000362 | 0.000405 | 0.000301 | puuE;4-aminobutyrateaminotransferase[EC:2.6.1.19] |
| K00830 | 0.000619 | 0.000623 | 0.000607 | 0.00057 | 0.000543 | AGXT;alanine-glyoxylatetransaminase/serine-glyoxylatetransaminase/serine-pyruva |
| K00844 | 2.7E-06 | 5.58E-07 | 3.25E-06 | 5.69E-06 | 3.53E-06 | HK;hexokinase[EC:2.7.1.1] |
| K00845 | 0.000353 | 0.000487 | 0.000475 | 0.000575 | 0.000397 | glk;glucokinase[EC:2.7.1.2] |
| K00846 | 0 | 1.18E-06 | 5.07E-07 | 4.56E-07 | 7.32E-07 | KHK;ketohexokinase[EC:2.7.1.3] |
| K00847 | 0.000195 | 0.000204 | 0.000201 | 0.0002 | 0.000188 | E2.7.1.4,scrK;fructokinase[EC:2.7.1.4] |
| K00848 | 8.92E-05 | 8.83E-05 | 8.61E-05 | 0.000103 | 0.000101 | rhaB;rhamnulokinase[EC:2.7.1.5] |
| K00849 | 0.000108 | 0.000121 | 0.000125 | 0.000114 | 9.72E-05 | galK;galactokinase[EC:2.7.1.6] |
| K00850 | 0.000688 | 0.000636 | 0.000676 | 0.000668 | 0.000777 | pfkA,PFK;6-phosphofructokinase1[EC:2.7.1.11] |
| K00851 | 0.000242 | 0.000244 | 0.000189 | 0.000231 | 0.000192 | E2.7.1.12,gntK,idnK;gluconokinase[EC:2.7.1.12] |
| K00852 | 0.000145 | 0.000195 | 0.000168 | 0.00019 | 0.000152 | rbsK,RBKS;ribokinase[EC:2.7.1.15] |
| K00853 | 7.61E-05 | 0.000111 | 8.57E-05 | 0.000113 | 6.32E-05 | araB;L-ribulokinase[EC:2.7.1.16] |
| K00854 | 0.000257 | 0.000305 | 0.000268 | 0.000279 | 0.000263 | xylB,XYLB;xylulokinase[EC:2.7.1.17] |
| K00863 | 1.66E-05 | 1.97E-05 | 1.13E-05 | 9.51E-06 | 7.3E-06 | DAK,TKFC;triose/dihydroxyacetonekinase/FAD-AMPlyase(cyclizing)[EC:2.7.1.282.7 |
| K00865 | 8.13E-05 | 8.32E-05 | 6.06E-05 | 7.3E-05 | 6.21E-05 | glxK,garK;glycerate2-kinase[EC:2.7.1.165] |
| K00873 | 0.000736 | 0.000698 | 0.000673 | 0.000685 | 0.000666 | PK,pyk;pyruvatekinase[EC:2.7.1.40] |
| K00874 | 0.000245 | 0.00022 | 0.000269 | 0.000244 | 0.000255 | kdgK;2-dehydro-3-deoxygluconokinase[EC:2.7.1.45] |
| K00875 | 2.72E-05 | 3.52E-05 | 1.49E-05 | 2.51E-05 | 1.84E-05 | rbtK;D-ribulokinase[EC:2.7.1.47] |
| K00880 | 6.13E-07 | 1.08E-05 | 3.01E-06 | 9.12E-07 | 0 | lyxK;L-xylulokinase[EC:2.7.1.53] |
| K00881 | 0 | 0 | 0 | 0 | 1.15E-06 | alsK;allosekinase[EC:2.7.1.55] |
| K00882 | 2.7E-05 | 3.53E-05 | 3.85E-05 | 3.51E-05 | 2.48E-05 | fruK;1-phosphofructokinase[EC:2.7.1.56] |
| K00883 | 4.67E-05 | 3.08E-05 | 3.02E-05 | 2.07E-05 | 4.92E-05 | dgoK;2-dehydro-3-deoxygalactonokinase[EC:2.7.1.58] |
| K00884 | 6.13E-07 | 1.49E-06 | 1.01E-06 | 1.22E-06 | 2.23E-06 | NAGK,nagK;N-acetylglucosaminekinase[EC:2.7.1.59] |
| K00886 | 0.000244 | 0.000291 | 0.000221 | 0.00027 | 0.000229 | ppgK;polyphosphateglucokinase[EC:2.7.1.63] |
| K00889 | 2.44E-06 | 1.12E-06 | 3.06E-06 | 1.94E-06 | 1.58E-06 | PIP5K;1-phosphatidylinositol-4-phosphate5-kinase[EC:2.7.1.68] |
| K00895 | 4.49E-06 | 7.87E-07 | 2.13E-06 | 4.56E-07 | 7.03E-06 | pfp,PFP;diphosphate-dependentphosphofructokinase[EC:2.7.1.90] |
| K00914 | 3E-06 | 0 | 0 | 0 | 0 | PIK3C3,VPS34;phosphatidylinositol3-kinase[EC:2.7.1.137] |
| K00917 | 1.53E-05 | 1.43E-05 | 1.59E-05 | 1.53E-05 | 1.02E-05 | lacC;tagatose6-phosphatekinase[EC:2.7.1.144] |
| K00918 | 1.04E-06 | 0 | 0 | 0 | 0 | pfkC;ADP-dependentphosphofructokinase/glucokinase[EC:2.7.1.1462.7.1.147] |
| K00921 | 0 | 5.58E-07 | 0 | 0 | 0 | PIKFYVE,FAB1;1-phosphatidylinositol-3-phosphate5-kinase[EC:2.7.1.150] |
| K00925 | 0.000577 | 0.000676 | 0.000574 | 0.000644 | 0.000511 | ackA;acetatekinase[EC:2.7.2.1] |
| K00927 | 0.000517 | 0.000514 | 0.000529 | 0.000501 | 0.000529 | PGK,pgk;phosphoglyceratekinase[EC:2.7.2.3] |
| K00948 | 0.000608 | 0.000576 | 0.00059 | 0.000546 | 0.000634 | PRPS,prsA;ribose-phosphatepyrophosphokinase[EC:2.7.6.1] |
| K00963 | 0.000329 | 0.000324 | 0.000345 | 0.000365 | 0.000339 | UGP2,galU,galF;UTP--glucose-1-phosphateuridylyltransferase[EC:2.7.7.9] |
| K00965 | 0.000255 | 0.000291 | 0.00032 | 0.000337 | 0.00029 | galT,GALT;UDPglucose--hexose-1-phosphateuridylyltransferase[EC:2.7.7.12] |
| K00966 | 0.000161 | 0.000106 | 0.000125 | 0.000102 | 0.00017 | GMPP;mannose-1-phosphateguanylyltransferase[EC:2.7.7.13] |
| K00971 | 0.000217 | 0.0002 | 0.000232 | 0.000267 | 0.000204 | manC,cpsB;mannose-1-phosphateguanylyltransferase[EC:2.7.7.13] |
| K00972 | 6.14E-06 | 1.02E-05 | 1.27E-05 | 6.81E-06 | 1.41E-05 | UAP1;UDP-N-acetylglucosamine/UDP-N-acetylgalactosaminediphosphorylase[EC:2.7.7.232 |
| K00975 | 0.000585 | 0.000511 | 0.000552 | 0.000538 | 0.000588 | glgC;glucose-1-phosphateadenylyltransferase[EC:2.7.7.27] |
| K00976 | 0 | 0 | 0 | 5.61E-07 | 0 | FPGT;fucose-1-phosphateguanylyltransferase[EC:2.7.7.30] |
| K00978 | 0.000164 | 0.000175 | 0.000175 | 0.000173 | 0.000173 | rfbF;glucose-1-phosphatecytidylyltransferase[EC:2.7.7.33] |
| K00983 | 2.75E-05 | 2.49E-05 | 2.81E-05 | 3.12E-05 | 4.16E-05 | neuA;N-acylneuraminatecytidylyltransferase[EC:2.7.7.43] |
| K00992 | 0.00012 | 0.000109 | 0.000143 | 0.000127 | 0.000105 | murU;N-acetyl-alpha-D-muramate1-phosphateuridylyltransferase[EC:2.7.7.99] |
| K01003 | 7.05E-05 | 6.3E-05 | 5.46E-05 | 6.19E-05 | 7.43E-05 | bcpA;oxaloacetatedecarboxylase[EC:4.1.1.112] |
| K01006 | 0.001204 | 0.001206 | 0.001245 | 0.00116 | 0.00126 | ppdK;pyruvate,orthophosphatedikinase[EC:2.7.9.1] |
| K01007 | 0.000594 | 0.000566 | 0.000532 | 0.000516 | 0.000657 | pps,ppsA;pyruvate,waterdikinase[EC:2.7.9.2] |
| K01026 | 0.000124 | 0.00013 | 0.000112 | 0.000115 | 0.000125 | pct;propionateCoA-transferase[EC:2.8.3.1] |
| K01027 | 7.98E-05 | 5.6E-05 | 6.11E-05 | 6.1E-05 | 0.000101 | OXCT;3-oxoacidCoA-transferase[EC:2.8.3.5] |
| K01028 | 0.000201 | 0.000218 | 0.000195 | 0.000223 | 0.00019 | E2.8.3.5A,scoA;3-oxoacidCoA-transferasesubunitA[EC:2.8.3.5] |
| K01029 | 0.000201 | 0.000208 | 0.000202 | 0.000207 | 0.000182 | E2.8.3.5B,scoB;3-oxoacidCoA-transferasesubunitB[EC:2.8.3.5] |
| K01034 | 4.6E-05 | 4.43E-05 | 3.89E-05 | 4.84E-05 | 4.44E-05 | atoD;acetateCoA/acetoacetateCoA-transferasealphasubunit[EC:2.8.3.82.8.3.9] |
| K01035 | 5.77E-05 | 5.91E-05 | 4.47E-05 | 4.24E-05 | 4.88E-05 | atoA;acetateCoA/acetoacetateCoA-transferasebetasubunit[EC:2.8.3.82.8.3.9] |
| K01039 | 0.000175 | 0.000229 | 0.000214 | 0.000234 | 0.000192 | gctA;glutaconateCoA-transferase,subunitA[EC:2.8.3.12] |
| K01040 | 0.000154 | 0.000171 | 0.00018 | 0.000165 | 0.000164 | gctB;glutaconateCoA-transferase,subunitB[EC:2.8.3.12] |
| K01051 | 4.89E-05 | 4.92E-05 | 5.41E-05 | 4.76E-05 | 7.48E-05 | E3.1.1.11;pectinesterase[EC:3.1.1.11] |
| K01053 | 0.001162 | 0.001179 | 0.001224 | 0.001286 | 0.001278 | E3.1.1.17,gnl,RGN;gluconolactonase[EC:3.1.1.17] |
| K01067 | 2.29E-05 | 3.2E-05 | 3.36E-05 | 3.62E-05 | 3.27E-05 | E3.1.2.1,ACH1;acetyl-CoAhydrolase[EC:3.1.2.1] |
| K01069 | 0.000266 | 0.000263 | 0.000222 | 0.000239 | 0.000232 | gloB,gloC,HAGH;hydroxyacylglutathionehydrolase[EC:3.1.2.6] |
| K01083 | 9.36E-06 | 1.65E-06 | 3.29E-06 | 1.37E-06 | 2.06E-05 | E3.1.3.8;3-phytase[EC:3.1.3.8] |
| K01085 | 0 | 1.84E-06 | 1.33E-06 | 2.83E-06 | 0 | agp;glucose-1-phosphatase[EC:3.1.3.10] |
| K01086 | 7.98E-06 | 8.9E-06 | 5.5E-06 | 3.46E-06 | 4.77E-06 | fbp-SEBP;fructose-1,6-bisphosphataseI/sedoheptulose-1,7-bisphosphatase[EC:3.1.3.1 |
| K01087 | 0.000139 | 0.00016 | 0.000149 | 0.000139 | 0.000131 | otsB;trehalose6-phosphatephosphatase[EC:3.1.3.12] |
| K01091 | 0.000286 | 0.000311 | 0.000369 | 0.00038 | 0.000314 | gph;phosphoglycolatephosphatase[EC:3.1.3.18] |
| K01092 | 0.000499 | 0.000543 | 0.000599 | 0.000609 | 0.000537 | E3.1.3.25,IMPA,suhB;myo-inositol-1(or4)-monophosphatase[EC:3.1.3.25] |
| K01093 | 9.6E-06 | 1.48E-05 | 1.2E-05 | 1.16E-05 | 2.97E-06 | appA;4-phytase/acidphosphatase[EC:3.1.3.263.1.3.2] |
| K01103 | 3.23E-06 | 2.49E-06 | 6.23E-06 | 3.74E-06 | 4.35E-06 | PFKFB3;6-phosphofructo-2-kinase/fructose-2,6-biphosphatase3[EC:2.7.1.1053.1.3.46 |
| K01106 | 0 | 0 | 5.99E-07 | 0 | 0 | E3.1.3.56;inositol-1,4,5-trisphosphate5-phosphatase[EC:3.1.3.56] |
| K01114 | 0.000896 | 0.001461 | 0.001148 | 0.001262 | 0.000749 | plc;phospholipaseC[EC:3.1.4.3] |
| K01176 | 8.79E-05 | 0.000108 | 9.04E-05 | 9.41E-05 | 7.81E-05 | AMY,amyA,malS;alpha-amylase[EC:3.2.1.1] |
| K01177 | 0 | 5.58E-07 | 0 | 1.72E-06 | 6.59E-07 | E3.2.1.2;beta-amylase[EC:3.2.1.2] |
| K01178 | 0.000275 | 0.000388 | 0.000304 | 0.000356 | 0.000221 | SGA1;glucoamylase[EC:3.2.1.3] |
| K01179 | 0.000433 | 0.000421 | 0.00043 | 0.000423 | 0.00045 | E3.2.1.4;endoglucanase[EC:3.2.1.4] |
| K01182 | 4.92E-05 | 3.51E-05 | 2.77E-05 | 3.52E-05 | 3.15E-05 | IMA,malL;oligo-1,6-glucosidase[EC:3.2.1.10] |
| K01183 | 0.000148 | 0.00016 | 0.000189 | 0.000192 | 0.000183 | E3.2.1.14;chitinase[EC:3.2.1.14] |
| K01184 | 3.58E-05 | 3.84E-05 | 3.44E-05 | 2.73E-05 | 4.06E-05 | E3.2.1.15;polygalacturonase[EC:3.2.1.15] |
| K01187 | 0.00057 | 0.000648 | 0.000562 | 0.000682 | 0.000562 | malZ;alpha-glucosidase[EC:3.2.1.20] |
| K01188 | 0 | 0 | 5.07E-07 | 8.58E-07 | 0 | E3.2.1.21;beta-glucosidase[EC:3.2.1.21] |
| K01190 | 0.000288 | 0.000328 | 0.000306 | 0.000304 | 0.00026 | lacZ;beta-galactosidase[EC:3.2.1.23] |
| K01193 | 2.65E-05 | 5.36E-05 | 3.95E-05 | 4.85E-05 | 2.42E-05 | INV,sacA;beta-fructofuranosidase[EC:3.2.1.26] |
| K01194 | 0.000149 | 0.000238 | 0.000151 | 0.000188 | 0.000124 | TREH,treA,treF;alpha,alpha-trehalase[EC:3.2.1.28] |
| K01195 | 7.03E-05 | 9.3E-05 | 6.77E-05 | 8.3E-05 | 7.05E-05 | uidA,GUSB;beta-glucuronidase[EC:3.2.1.31] |
| K01198 | 0.000225 | 0.000223 | 0.000227 | 0.000238 | 0.000198 | xynB;xylan1,4-beta-xylosidase[EC:3.2.1.37] |
| K01200 | 6.06E-06 | 5.22E-06 | 8.77E-06 | 1.12E-05 | 8.35E-06 | pulA;pullulanase[EC:3.2.1.41] |
| K01207 | 0.00052 | 0.000514 | 0.00055 | 0.000567 | 0.000449 | nagZ;beta-N-acetylhexosaminidase[EC:3.2.1.52] |
| K01208 | 1.53E-06 | 1.95E-06 | 5.07E-07 | 3.04E-06 | 6.59E-07 | cd,ma,nplT;cyclomaltodextrinase/maltogenicalpha-amylase/neopullulanase[EC:3.2 |
| K01209 | 0.000378 | 0.000354 | 0.000399 | 0.000388 | 0.000358 | abfA;alpha-N-arabinofuranosidase[EC:3.2.1.55] |
| K01210 | 7.29E-05 | 9.86E-05 | 7.66E-05 | 5.66E-05 | 4.86E-05 | E3.2.1.58;glucan1,3-beta-glucosidase[EC:3.2.1.58] |
| K01212 | 1.1E-05 | 2.18E-05 | 1.06E-05 | 1.22E-05 | 1.16E-05 | sacC,levB;levanase[EC:3.2.1.65] |
| K01213 | 0 | 1.87E-06 | 2.84E-06 | 1.72E-06 | 4.25E-06 | E3.2.1.67;galacturan1,4-alpha-galacturonidase[EC:3.2.1.67] |
| K01214 | 0 | 0 | 0 | 6.16E-07 | 0 | ISA,treX;isoamylase[EC:3.2.1.68] |
| K01218 | 4.94E-05 | 4.72E-05 | 4.33E-05 | 5.12E-05 | 5.93E-05 | gmuG;mannanendo-1,4-beta-mannosidase[EC:3.2.1.78] |
| K01220 | 8.22E-06 | 2.02E-06 | 4.68E-06 | 4.34E-06 | 1E-05 | E3.2.1.85,lacG;6-phospho-beta-galactosidase[EC:3.2.1.85] |
| K01222 | 5.74E-05 | 6.77E-05 | 6.15E-05 | 5.03E-05 | 4.76E-05 | E3.2.1.86A,celF;6-phospho-beta-glucosidase[EC:3.2.1.86] |
| K01223 | 5.88E-06 | 4.91E-06 | 4.14E-06 | 3.95E-06 | 9.53E-06 | E3.2.1.86B,bglA;6-phospho-beta-glucosidase[EC:3.2.1.86] |
| K01226 | 0 | 2.28E-06 | 0 | 1.17E-06 | 0 | treC;trehalose-6-phosphatehydrolase[EC:3.2.1.93] |
| K01229 | 0 | 0 | 0 | 1.3E-06 | 0 | LCT;lactase-phlorizinhydrolase[EC:3.2.1.1083.2.1.62] |
| K01232 | 0 | 2.09E-06 | 9.64E-07 | 7.53E-07 | 6.59E-07 | glvA;maltose-6'-phosphateglucosidase[EC:3.2.1.122] |
| K01233 | 5.34E-06 | 7.07E-06 | 6.15E-06 | 8.06E-06 | 6.05E-06 | csn;chitosanase[EC:3.2.1.132] |
| K01236 | 0.000421 | 0.000511 | 0.000464 | 0.000482 | 0.000422 | treZ,glgZ;maltooligosyltrehalosetrehalohydrolase[EC:3.2.1.141] |
| K01432 | 0.000227 | 0.00019 | 0.000217 | 0.000186 | 0.000196 | AFMID;arylformamidase[EC:3.5.1.9] |
| K01433 | 9.52E-05 | 0.000124 | 9.66E-05 | 0.000117 | 0.000111 | purU;formyltetrahydrofolatedeformylase[EC:3.5.1.10] |
| K01443 | 0.000217 | 0.000277 | 0.000244 | 0.000322 | 0.0002 | nagA,AMDHD2;N-acetylglucosamine-6-phosphatedeacetylase[EC:3.5.1.25] |
| K01452 | 8.89E-06 | 1.95E-05 | 9.94E-06 | 1.22E-05 | 6.86E-06 | E3.5.1.41;chitindeacetylase[EC:3.5.1.41] |
| K01455 | 0.000113 | 0.000127 | 0.000123 | 0.000118 | 0.000123 | E3.5.1.49;formamidase[EC:3.5.1.49] |
| K01458 | 5.32E-05 | 5.84E-05 | 6.11E-05 | 4.98E-05 | 5.28E-05 | hutG;N-formylglutamatedeformylase[EC:3.5.1.68] |
| K01512 | 0.000106 | 0.000123 | 0.000121 | 0.000123 | 9.17E-05 | acyP;acylphosphatase[EC:3.6.1.7] |
| K01513 | 4.09E-06 | 5.51E-06 | 4.88E-06 | 6.17E-06 | 4.41E-06 | ENPP1\_3,CD203;ectonucleotidepyrophosphatase/phosphodiesterasefamilymember43103[EC |
| K01568 | 3.03E-06 | 4.36E-06 | 1.63E-06 | 1.37E-06 | 2.58E-06 | PDC,pdc;pyruvatedecarboxylase[EC:4.1.1.1] |
| K01569 | 0.000228 | 0.000328 | 0.000213 | 0.000226 | 0.000157 | oxdD;oxalatedecarboxylase[EC:4.1.1.2] |
| K01571 | 0.00012 | 0.000111 | 9.02E-05 | 0.000106 | 0.000102 | oadA;oxaloacetatedecarboxylase,alphasubunit[EC:4.1.1.112] |
| K01572 | 7.36E-06 | 4.37E-06 | 8.17E-06 | 6.96E-06 | 6.51E-06 | oadB;oxaloacetatedecarboxylase,betasubunit[EC:4.1.1.112] |
| K01574 | 0.000158 | 0.000198 | 0.00013 | 0.00013 | 0.000126 | adc;acetoacetatedecarboxylase[EC:4.1.1.4] |
| K01575 | 2.06E-05 | 1.27E-05 | 1.36E-05 | 1.1E-05 | 6.53E-06 | alsD,budA,aldC;acetolactatedecarboxylase[EC:4.1.1.5] |
| K01575 | 2.06E-05 | 1.27E-05 | 1.36E-05 | 1.1E-05 | 6.53E-06 | alsD,budA,aldC;acetolactatedecarboxylase[EC:4.1.1.5] |
| K01577 | 0.000285 | 0.000231 | 0.000233 | 0.000206 | 0.000285 | oxc;oxalyl-CoAdecarboxylase[EC:4.1.1.8] |
| K01578 | 0.000198 | 0.000229 | 0.000212 | 0.00021 | 0.000163 | MLYCD;malonyl-CoAdecarboxylase[EC:4.1.1.9] |
| K01580 | 8.94E-05 | 0.000133 | 8.11E-05 | 7.42E-05 | 8.58E-05 | E4.1.1.15,gadB,gadA,GAD;glutamatedecarboxylase[EC:4.1.1.15] |
| K01595 | 0.00057 | 0.000552 | 0.000505 | 0.000532 | 0.000566 | ppc;phosphoenolpyruvatecarboxylase[EC:4.1.1.31] |
| K01596 | 0.000451 | 0.000438 | 0.00042 | 0.00043 | 0.000487 | E4.1.1.32,pckA,PCK;phosphoenolpyruvatecarboxykinase(GTP)[EC:4.1.1.32] |
| K01601 | 9.41E-05 | 8.6E-05 | 8.15E-05 | 7.36E-05 | 8.44E-05 | rbcL;ribulose-bisphosphatecarboxylaselargechain[EC:4.1.1.39] |
| K01602 | 1.57E-05 | 2.71E-05 | 2.27E-05 | 2.01E-05 | 1.75E-05 | rbcS;ribulose-bisphosphatecarboxylasesmallchain[EC:4.1.1.39] |
| K01608 | 7.96E-05 | 7.6E-05 | 5.78E-05 | 3.92E-05 | 6.6E-05 | gcl;tartronate-semialdehydesynthase[EC:4.1.1.47] |
| K01610 | 0.000458 | 0.000473 | 0.000466 | 0.000412 | 0.00045 | E4.1.1.49,pckA;phosphoenolpyruvatecarboxykinase(ATP)[EC:4.1.1.49] |
| K01615 | 4.06E-06 | 2.32E-06 | 2.25E-06 | 2.43E-06 | 7.17E-06 | gcdA;glutaconyl-CoAdecarboxylase[EC:4.1.1.70] |
| K01619 | 0.000168 | 0.000168 | 0.000191 | 0.000206 | 0.000173 | deoC,DERA;deoxyribose-phosphatealdolase[EC:4.1.2.4] |
| K01621 | 0.000929 | 0.001211 | 0.000978 | 0.001022 | 0.000889 | xfp,xpk;xylulose-5-phosphate/fructose-6-phosphatephosphoketolase[EC:4.1.2.94.1.2. |
| K01622 | 1.49E-05 | 6.38E-06 | 7.55E-06 | 1.24E-05 | 2.6E-05 | K01622;fructose1,6-bisphosphatealdolase/phosphatase[EC:4.1.2.133.1.3.11] |
| K01623 | 0.000359 | 0.000359 | 0.000295 | 0.000355 | 0.000349 | ALDO;fructose-bisphosphatealdolase,classI[EC:4.1.2.13] |
| K01624 | 0.00023 | 0.000216 | 0.000169 | 0.00016 | 0.000195 | FBA,fbaA;fructose-bisphosphatealdolase,classII[EC:4.1.2.13] |
| K01625 | 0.000119 | 0.000133 | 0.000117 | 0.000159 | 0.000119 | eda;2-dehydro-3-deoxyphosphogluconatealdolase/(4S)-4-hydroxy-2-oxoglutaratealdola |
| K01628 | 0.000278 | 0.000243 | 0.000282 | 0.00029 | 0.000282 | fucA;L-fuculose-phosphatealdolase[EC:4.1.2.17] |
| K01629 | 0 | 0 | 0 | 0 | 9.16E-07 | rhaD;rhamnulose-1-phosphatealdolase[EC:4.1.2.19] |
| K01630 | 5.87E-05 | 5.63E-05 | 5.88E-05 | 4.93E-05 | 6.16E-05 | garL;2-dehydro-3-deoxyglucaratealdolase[EC:4.1.2.20] |
| K01631 | 4.32E-05 | 3.03E-05 | 2.11E-05 | 2.44E-05 | 2.95E-05 | dgoA;2-dehydro-3-deoxyphosphogalactonatealdolase[EC:4.1.2.21] |
| K01635 | 5.86E-05 | 9.57E-05 | 6.74E-05 | 0.000109 | 3.21E-05 | lacD;tagatose1,6-diphosphatealdolase[EC:4.1.2.40] |
| K01637 | 0.000354 | 0.000343 | 0.000311 | 0.00032 | 0.000347 | E4.1.3.1,aceA;isocitratelyase[EC:4.1.3.1] |
| K01638 | 0.000599 | 0.000498 | 0.000523 | 0.000513 | 0.00056 | aceB,glcB;malatesynthase[EC:2.3.3.9] |
| K01639 | 8.28E-06 | 5.65E-06 | 5.35E-06 | 1.02E-05 | 1.2E-05 | E4.1.3.3,nanA,NPL;N-acetylneuraminatelyase[EC:4.1.3.3] |
| K01640 | 0.000389 | 0.000365 | 0.000344 | 0.000337 | 0.000359 | E4.1.3.4,HMGCL,hmgL;hydroxymethylglutaryl-CoAlyase[EC:4.1.3.4] |
| K01641 | 2.43E-05 | 1.67E-05 | 1.89E-05 | 1.55E-05 | 2.49E-05 | E2.3.3.10;hydroxymethylglutaryl-CoAsynthase[EC:2.3.3.10] |
| K01647 | 0.001229 | 0.001135 | 0.001123 | 0.001074 | 0.001307 | CS,gltA;citratesynthase[EC:2.3.3.1] |
| K01648 | 0 | 0 | 2.97E-06 | 6.02E-07 | 0 | ACLY;ATPcitrate(pro-S)-lyase[EC:2.3.3.8] |
| K01649 | 0.00124 | 0.001176 | 0.001208 | 0.001175 | 0.001291 | leuA,IMS;2-isopropylmalatesynthase[EC:2.3.3.13] |
| K01652 | 0.003902 | 0.003524 | 0.003879 | 0.003589 | 0.00395 | E2.2.1.6L,ilvB,ilvG,ilvI;acetolactatesynthaseI/II/IIIlargesubunit[EC:2.2.1.6] |
| K01653 | 0.000198 | 0.000205 | 0.000215 | 0.000226 | 0.000213 | E2.2.1.6S,ilvH,ilvN;acetolactatesynthaseI/IIIsmallsubunit[EC:2.2.1.6] |
| K01654 | 8.47E-05 | 9.27E-05 | 9.94E-05 | 9.25E-05 | 0.000105 | E2.5.1.56,neuB;N-acetylneuraminatesynthase[EC:2.5.1.56] |
| K01655 | 0 | 1.41E-06 | 9.24E-07 | 3.56E-06 | 0 | LYS21,LYS20;homocitratesynthase[EC:2.3.3.14] |
| K01659 | 0.000122 | 0.000102 | 0.000126 | 0.000103 | 0.000122 | prpC;2-methylcitratesynthase[EC:2.3.3.5] |
| K01676 | 0.000472 | 0.000409 | 0.00042 | 0.000391 | 0.000461 | E4.2.1.2A,fumA,fumB;fumaratehydratase,classI[EC:4.2.1.2] |
| K01677 | 3E-05 | 2.13E-05 | 3.27E-05 | 2.31E-05 | 4.05E-05 | E4.2.1.2AA,fumA;fumaratehydratasesubunitalpha[EC:4.2.1.2] |
| K01678 | 6.94E-06 | 3.3E-06 | 7.83E-06 | 5.51E-06 | 1.6E-05 | E4.2.1.2AB,fumB;fumaratehydratasesubunitbeta[EC:4.2.1.2] |
| K01679 | 0.000738 | 0.000751 | 0.000661 | 0.000651 | 0.000693 | E4.2.1.2B,fumC,FH;fumaratehydratase,classII[EC:4.2.1.2] |
| K01681 | 0.001563 | 0.001451 | 0.001467 | 0.001396 | 0.001605 | ACO,acnA;aconitatehydratase[EC:4.2.1.3] |
| K01682 | 2.6E-05 | 2.03E-05 | 1.97E-05 | 9.5E-06 | 3.58E-05 | acnB;aconitatehydratase2/2-methylisocitratedehydratase[EC:4.2.1.34.2.1.99] |
| K01684 | 0.000249 | 0.000241 | 0.000241 | 0.000261 | 0.000269 | dgoD;galactonatedehydratase[EC:4.2.1.6] |
| K01685 | 0.000289 | 0.000265 | 0.000267 | 0.000265 | 0.000276 | uxaA;altronatehydrolase[EC:4.2.1.7] |
| K01686 | 0.000169 | 0.000177 | 0.000183 | 0.000187 | 0.000176 | uxuA;mannonatedehydratase[EC:4.2.1.8] |
| K01689 | 0.000694 | 0.000634 | 0.000684 | 0.000654 | 0.000701 | ENO,eno;enolase[EC:4.2.1.11] |
| K01690 | 5.19E-05 | 5.27E-05 | 3.45E-05 | 3.05E-05 | 5.06E-05 | edd;phosphogluconatedehydratase[EC:4.2.1.12] |
| K01692 | 0.00082 | 0.000857 | 0.000837 | 0.000782 | 0.000815 | paaF,echA;enoyl-CoAhydratase[EC:4.2.1.17] |
| K01699 | 2.43E-05 | 3.88E-05 | 2.41E-05 | 2.29E-05 | 3.27E-05 | pduC;propanedioldehydrataselargesubunit[EC:4.2.1.28] |
| K01703 | 0.000983 | 0.000894 | 0.000965 | 0.000954 | 0.001083 | leuC,IPMI-L;3-isopropylmalate/(R)-2-methylmalatedehydrataselargesubunit[EC:4.2.1 |
| K01704 | 0.000354 | 0.00037 | 0.00038 | 0.000368 | 0.000363 | leuD,IPMI-S;3-isopropylmalate/(R)-2-methylmalatedehydratasesmallsubunit[EC:4.2.1 |
| K01706 | 0.000102 | 7.5E-05 | 9.07E-05 | 6.59E-05 | 9.4E-05 | gudD;glucaratedehydratase[EC:4.2.1.40] |
| K01707 | 2.04E-05 | 1.71E-05 | 1.61E-05 | 1E-05 | 2.27E-05 | kdgD;5-dehydro-4-deoxyglucaratedehydratase[EC:4.2.1.41] |
| K01708 | 7.57E-05 | 4.83E-05 | 3.1E-05 | 3.93E-05 | 5.55E-05 | garD;galactaratedehydratase[EC:4.2.1.42] |
| K01709 | 8.03E-05 | 5.82E-05 | 9.13E-05 | 9.69E-05 | 7.5E-05 | rfbG;CDP-glucose4,6-dehydratase[EC:4.2.1.45] |
| K01711 | 0.000413 | 0.000426 | 0.000435 | 0.000421 | 0.000408 | gmd,GMDS;GDPmannose4,6-dehydratase[EC:4.2.1.47] |
| K01715 | 0.000395 | 0.000451 | 0.000364 | 0.000396 | 0.000424 | crt;enoyl-CoAhydratase[EC:4.2.1.17] |
| K01720 | 0.000489 | 0.000579 | 0.000442 | 0.000502 | 0.000454 | prpD;2-methylcitratedehydratase[EC:4.2.1.79] |
| K01728 | 0.0001 | 4.86E-05 | 6.44E-05 | 5.31E-05 | 0.00013 | pel;pectatelyase[EC:4.2.2.2] |
| K01729 | 4.6E-06 | 3.74E-06 | 3.87E-06 | 2.44E-06 | 2.63E-06 | algL;poly(beta-D-mannuronate)lyase[EC:4.2.2.3] |
| K01730 | 3.95E-05 | 3.12E-05 | 3.67E-05 | 3.5E-05 | 5.09E-05 | ogl;oligogalacturonidelyase[EC:4.2.2.6] |
| K01734 | 1.26E-05 | 9.06E-06 | 1.91E-05 | 9.75E-06 | 2.42E-05 | mgsA;methylglyoxalsynthase[EC:4.2.3.3] |
| K01759 | 0.000232 | 0.000247 | 0.000268 | 0.000229 | 0.000254 | GLO1,gloA;lactoylglutathionelyase[EC:4.4.1.5] |
| K01771 | 0 | 7.42E-07 | 6.85E-07 | 8.3E-07 | 1.91E-06 | plc;1-phosphatidylinositolphosphodiesterase[EC:4.6.1.13] |
| K01782 | 0.000576 | 0.000558 | 0.000518 | 0.000526 | 0.00049 | fadJ;3-hydroxyacyl-CoAdehydrogenase/enoyl-CoAhydratase/3-hydroxybutyryl-CoAepi |
| K01783 | 0.000364 | 0.000362 | 0.000363 | 0.000386 | 0.000366 | rpe,RPE;ribulose-phosphate3-epimerase[EC:5.1.3.1] |
| K01784 | 0.001248 | 0.001212 | 0.001343 | 0.001413 | 0.001263 | galE,GALE;UDP-glucose4-epimerase[EC:5.1.3.2] |
| K01785 | 0.000274 | 0.000276 | 0.000275 | 0.000276 | 0.000272 | galM,GALM;aldose1-epimerase[EC:5.1.3.3] |
| K01787 | 2.83E-06 | 1.79E-06 | 2.21E-06 | 1.37E-06 | 2.64E-06 | RENBP;N-acylglucosamine2-epimerase[EC:5.1.3.8] |
| K01788 | 4.04E-06 | 1.58E-06 | 1.7E-06 | 4.56E-07 | 2.82E-06 | nanE;N-acylglucosamine-6-phosphate2-epimerase[EC:5.1.3.9] |
| K01791 | 0.000196 | 0.000194 | 0.000243 | 0.000227 | 0.000214 | wecB;UDP-N-acetylglucosamine2-epimerase(non-hydrolysing)[EC:5.1.3.14] |
| K01792 | 2.74E-05 | 5.72E-05 | 3.07E-05 | 4.4E-05 | 2.05E-05 | E5.1.3.15;glucose-6-phosphate1-epimerase[EC:5.1.3.15] |
| K01795 | 9.76E-06 | 5.58E-07 | 5.07E-07 | 0 | 1.59E-05 | algG;mannuronan5-epimerase[EC:5.1.3.37] |
| K01799 | 0.000273 | 0.000217 | 0.000252 | 0.000236 | 0.000293 | nicE,maiA;maleateisomerase[EC:5.2.1.1] |
| K01803 | 0.000321 | 0.000328 | 0.000333 | 0.000342 | 0.000316 | TPI,tpiA;triosephosphateisomerase(TIM)[EC:5.3.1.1] |
| K01804 | 7.18E-05 | 0.000101 | 8.12E-05 | 8.16E-05 | 6.97E-05 | araA;L-arabinoseisomerase[EC:5.3.1.4] |
| K01805 | 0.000255 | 0.000225 | 0.000202 | 0.000186 | 0.000258 | xylA;xyloseisomerase[EC:5.3.1.5] |
| K01805 | 0.000255 | 0.000225 | 0.000202 | 0.000186 | 0.000258 | xylA;xyloseisomerase[EC:5.3.1.5] |
| K01807 | 0.000181 | 0.000172 | 0.000187 | 0.000181 | 0.000148 | rpiA;ribose5-phosphateisomeraseA[EC:5.3.1.6] |
| K01808 | 0.000197 | 0.000219 | 0.000206 | 0.000217 | 0.000209 | rpiB;ribose5-phosphateisomeraseB[EC:5.3.1.6] |
| K01809 | 0.000158 | 0.000201 | 0.000181 | 0.000213 | 0.000134 | manA,MPI;mannose-6-phosphateisomerase[EC:5.3.1.8] |
| K01810 | 0.00073 | 0.000689 | 0.000734 | 0.000732 | 0.000734 | GPI,pgi;glucose-6-phosphateisomerase[EC:5.3.1.9] |
| K01812 | 0.000128 | 0.000126 | 0.000144 | 0.000153 | 0.000117 | uxaC;glucuronateisomerase[EC:5.3.1.12] |
| K01813 | 2.47E-05 | 1.32E-05 | 1.35E-05 | 2.37E-05 | 4.62E-05 | rhaA;L-rhamnoseisomerase[EC:5.3.1.14] |
| K01815 | 1.8E-05 | 1.81E-05 | 8.56E-06 | 1.32E-05 | 2.26E-05 | kduI;4-deoxy-L-threo-5-hexosulose-uronateketol-isomerase[EC:5.3.1.17] |
| K01816 | 0.000284 | 0.000286 | 0.000299 | 0.000278 | 0.000262 | hyi,gip;hydroxypyruvateisomerase[EC:5.3.1.22] |
| K01818 | 6.33E-06 | 5.82E-06 | 7.37E-06 | 2.26E-06 | 3.3E-06 | fucI;L-fucose/D-arabinoseisomerase[EC:5.3.1.255.3.1.3] |
| K01820 | 9.93E-05 | 0.00011 | 9.68E-05 | 0.000107 | 0.000109 | rhaA;L-rhamnoseisomerase/sugarisomerase[EC:5.3.1.145.3.1.-] |
| K01825 | 1.43E-05 | 1.93E-05 | 1.15E-05 | 1.12E-05 | 2.29E-05 | fadB;3-hydroxyacyl-CoAdehydrogenase/enoyl-CoAhydratase/3-hydroxybutyryl-CoAepi |
| K01834 | 0.000148 | 0.000129 | 0.000143 | 0.000126 | 0.000168 | PGAM,gpmA;2,3-bisphosphoglycerate-dependentphosphoglyceratemutase[EC:5.4.2.11] |
| K01835 | 0.000663 | 0.000704 | 0.000655 | 0.000667 | 0.000681 | pgm;phosphoglucomutase[EC:5.4.2.2] |
| K01838 | 2.05E-05 | 2.32E-05 | 2.27E-05 | 2.66E-05 | 1.79E-05 | pgmB;beta-phosphoglucomutase[EC:5.4.2.6] |
| K01839 | 0.000133 | 0.000119 | 0.000158 | 0.000157 | 0.00014 | deoB;phosphopentomutase[EC:5.4.2.7] |
| K01840 | 0.000289 | 0.000237 | 0.000261 | 0.000221 | 0.000345 | manB;phosphomannomutase[EC:5.4.2.8] |
| K01846 | 1.27E-06 | 0 | 7.71E-07 | 2.91E-06 | 0 | glmS,mutS,mamA;methylaspartatemutasesigmasubunit[EC:5.4.99.1] |
| K01847 | 0.000471 | 0.000462 | 0.000404 | 0.000371 | 0.000345 | MUT;methylmalonyl-CoAmutase[EC:5.4.99.2] |
| K01848 | 0.000809 | 0.000733 | 0.000919 | 0.000872 | 0.000826 | E5.4.99.2A,mcmA1;methylmalonyl-CoAmutase,N-terminaldomain[EC:5.4.99.2] |
| K01849 | 0.000102 | 0.000107 | 0.000105 | 0.000114 | 0.000111 | E5.4.99.2B,mcmA2;methylmalonyl-CoAmutase,C-terminaldomain[EC:5.4.99.2] |
| K01854 | 5.33E-05 | 5.83E-05 | 5.88E-05 | 4.66E-05 | 4.8E-05 | glf;UDP-galactopyranosemutase[EC:5.4.99.9] |
| K01858 | 0.000391 | 0.000393 | 0.000398 | 0.000403 | 0.000442 | INO1,ISYNA1;myo-inositol-1-phosphatesynthase[EC:5.5.1.4] |
| K01895 | 0.00182 | 0.001662 | 0.001711 | 0.001598 | 0.001773 | ACSS,acs;acetyl-CoAsynthetase[EC:6.2.1.1] |
| K01896 | 3.92E-06 | 4.95E-06 | 4.53E-06 | 5.32E-06 | 6.59E-07 | ACSM;medium-chainacyl-CoAsynthetase[EC:6.2.1.2] |
| K01899 | 0 | 8.53E-07 | 1.01E-06 | 1.35E-06 | 0 | LSC1;succinyl-CoAsynthetasealphasubunit[EC:6.2.1.46.2.1.5] |
| K01900 | 2.52E-06 | 9.8E-06 | 4.64E-06 | 8.57E-06 | 4.72E-06 | LSC2;succinyl-CoAsynthetasebetasubunit[EC:6.2.1.46.2.1.5] |
| K01902 | 0.000499 | 0.000491 | 0.00043 | 0.000425 | 0.000495 | sucD;succinyl-CoAsynthetasealphasubunit[EC:6.2.1.5] |
| K01903 | 0.000729 | 0.000682 | 0.000672 | 0.000681 | 0.000707 | sucC;succinyl-CoAsynthetasebetasubunit[EC:6.2.1.5] |
| K01905 | 3.44E-05 | 3E-05 | 3E-05 | 3.61E-05 | 4.38E-05 | acdA;acetate---CoAligase(ADP-forming)subunitalpha[EC:6.2.1.13] |
| K01907 | 0.000285 | 0.000266 | 0.000237 | 0.000216 | 0.000288 | AACS,acsA;acetoacetyl-CoAsynthetase[EC:6.2.1.16] |
| K01908 | 0.000396 | 0.000362 | 0.000419 | 0.00034 | 0.000393 | prpE;propionyl-CoAsynthetase[EC:6.2.1.17] |
| K01915 | 0.002064 | 0.00181 | 0.001806 | 0.001705 | 0.002096 | glnA,GLUL;glutaminesynthetase[EC:6.3.1.2] |
| K01958 | 0.000298 | 0.000335 | 0.000304 | 0.000322 | 0.000303 | PC,pyc;pyruvatecarboxylase[EC:6.4.1.1] |
| K01959 | 1.41E-05 | 1.01E-05 | 1.81E-05 | 1.61E-05 | 1.87E-05 | pycA;pyruvatecarboxylasesubunitA[EC:6.4.1.1] |
| K01960 | 2.37E-05 | 1.68E-05 | 4.22E-05 | 3.28E-05 | 3.76E-05 | pycB;pyruvatecarboxylasesubunitB[EC:6.4.1.1] |
| K01961 | 0.000866 | 0.000834 | 0.000873 | 0.000831 | 0.000851 | accC;acetyl-CoAcarboxylase,biotincarboxylasesubunit[EC:6.4.1.26.3.4.14] |
| K01962 | 0.000413 | 0.000444 | 0.000452 | 0.000478 | 0.000432 | accA;acetyl-CoAcarboxylasecarboxyltransferasesubunitalpha[EC:6.4.1.22.1.3.15] |
| K01963 | 0.000399 | 0.000367 | 0.00041 | 0.000429 | 0.000396 | accD;acetyl-CoAcarboxylasecarboxyltransferasesubunitbeta[EC:6.4.1.22.1.3.15] |
| K01965 | 0.000254 | 0.000295 | 0.00025 | 0.000201 | 0.000243 | PCCA,pccA;propionyl-CoAcarboxylasealphachain[EC:6.4.1.3] |
| K01965 | 0.000254 | 0.000295 | 0.00025 | 0.000201 | 0.000243 | PCCA,pccA;propionyl-CoAcarboxylasealphachain[EC:6.4.1.3] |
| K01966 | 0.00065 | 0.000565 | 0.000551 | 0.000541 | 0.000631 | PCCB,pccB;propionyl-CoAcarboxylasebetachain[EC:6.4.1.32.1.3.15] |
| K02080 | 6.13E-07 | 1.65E-06 | 2.92E-06 | 2.37E-06 | 2.55E-06 | agaI;galactosamine-6-phosphateisomerase[EC:5.3.1.-] |
| K02160 | 0.000216 | 0.000227 | 0.000236 | 0.000246 | 0.000186 | accB,bccP;acetyl-CoAcarboxylasebiotincarboxylcarrierprotein |
| K02377 | 0.000262 | 0.00023 | 0.000274 | 0.000253 | 0.000247 | TSTA3,fcl;GDP-L-fucosesynthase[EC:1.1.1.271] |
| K02437 | 0.00017 | 0.000182 | 0.000181 | 0.000219 | 0.000189 | gcvH,GCSH;glycinecleavagesystemHprotein |
| K02438 | 0.001411 | 0.001444 | 0.001279 | 0.001279 | 0.001337 | glgX;glycogendebranchingenzyme[EC:3.2.1.196] |
| K02446 | 0.00019 | 0.000193 | 0.000178 | 0.000213 | 0.000188 | glpX;fructose-1,6-bisphosphataseII[EC:3.1.3.11] |
| K02472 | 7.58E-05 | 8.26E-05 | 9.04E-05 | 9.67E-05 | 7.89E-05 | wecC;UDP-N-acetyl-D-mannosaminuronicaciddehydrogenase[EC:1.1.1.336] |
| K02473 | 6.75E-05 | 4.18E-05 | 7.12E-05 | 3.83E-05 | 7.43E-05 | wbpP;UDP-N-acetylglucosamine4-epimerase[EC:5.1.3.7] |
| K02474 | 0.000159 | 0.000125 | 0.000188 | 0.000145 | 0.000191 | wbpO;UDP-N-acetyl-D-galactosaminedehydrogenase[EC:1.1.1.-] |
| K02564 | 0.000124 | 0.000164 | 0.000189 | 0.000212 | 0.000162 | nagB,GNPDA;glucosamine-6-phosphatedeaminase[EC:3.5.99.6] |
| K02594 | 1.96E-05 | 1.77E-05 | 1.42E-05 | 1.48E-05 | 1.07E-05 | nifV;homocitratesynthaseNifV[EC:2.3.3.14] |
| K02744 | 1.23E-06 | 5.58E-07 | 1.8E-06 | 2.45E-06 | 2E-06 | PTS-Aga-EIIA,agaF;PTSsystem,N-acetylgalactosamine-specificIIAcomponent[EC:2.7.1 |
| K02746 | 0 | 7.42E-07 | 0 | 0 | 1.32E-06 | PTS-Aga-EIIC,agaW;PTSsystem,N-acetylgalactosamine-specificIICcomponent |
| K02750 | 0 | 0 | 0 | 1.16E-06 | 6.59E-07 | PTS-Glv-EIIC,glvC,malP,aglA;PTSsystem,alpha-glucoside-specificIICcomponent |
| K02752 | 0 | 8.37E-07 | 0 | 0 | 0 | PTS-Asc-EIIB,ascF;PTSsystem,beta-glucoside(arbutin/salicin/cellobiose)-specificI |
| K02759 | 7.66E-07 | 0 | 0 | 0 | 0 | PTS-Cel-EIIA,celC,chbA;PTSsystem,cellobiose-specificIIAcomponent[EC:2.7.1.196 |
| K02761 | 6.6E-06 | 4.03E-06 | 2.9E-06 | 3.53E-06 | 9.46E-06 | PTS-Cel-EIIC,celB,chbC;PTSsystem,cellobiose-specificIICcomponent |
| K02768 | 1.54E-05 | 1.05E-05 | 1.53E-05 | 1.42E-05 | 2.34E-05 | PTS-Fru-EIIA,fruB;PTSsystem,fructose-specificIIAcomponent[EC:2.7.1.202] |
| K02769 | 3.66E-06 | 5.36E-06 | 5.07E-07 | 9.03E-07 | 4.92E-06 | PTS-Fru-EIIB,fruA;PTSsystem,fructose-specificIIBcomponent[EC:2.7.1.202] |
| K02770 | 1.2E-05 | 5.72E-06 | 3.18E-06 | 5.13E-06 | 8.85E-06 | PTS-Fru-EIIC,fruA;PTSsystem,fructose-specificIICcomponent |
| K02774 | 0 | 0 | 5.07E-07 | 5.52E-07 | 0 | PTS-Gat-EIIB,gatB,sgcB;PTSsystem,galactitol-specificIIBcomponent[EC:2.7.1.200] |
| K02778 | 3.22E-05 | 1.76E-05 | 1.58E-05 | 2.04E-05 | 2.87E-05 | PTS-Glc-EIIB,ptsG;PTSsystem,glucose-specificIIBcomponent[EC:2.7.1.199] |
| K02779 | 2.58E-05 | 7.52E-06 | 1.82E-05 | 1.43E-05 | 2.27E-05 | PTS-Glc-EIIC,ptsG;PTSsystem,glucose-specificIICcomponent |
| K02781 | 0 | 1.94E-06 | 0 | 0 | 0 | PTS-Gut-EIIA,srlB;PTSsystem,glucitol/sorbitol-specificIIAcomponent[EC:2.7.1.198 |
| K02791 | 0 | 1E-06 | 7.36E-07 | 0 | 0 | PTS-MalGlc-EIIC,malX;PTSsystem,maltose/glucose-specificIICcomponent |
| K02793 | 9.33E-05 | 7.18E-05 | 8.62E-05 | 8.17E-05 | 9.59E-05 | PTS-Man-EIIA,manX;PTSsystem,mannose-specificIIAcomponent[EC:2.7.1.191] |
| K02794 | 3.34E-06 | 5.84E-06 | 1.04E-06 | 3.01E-06 | 0 | PTS-Man-EIIB,manX;PTSsystem,mannose-specificIIBcomponent[EC:2.7.1.191] |
| K02795 | 7.79E-06 | 2.98E-06 | 5.07E-07 | 3.75E-06 | 6E-06 | PTS-Man-EIIC,manY;PTSsystem,mannose-specificIICcomponent |
| K02796 | 3.26E-06 | 8.95E-06 | 1.21E-05 | 1.06E-05 | 1.98E-06 | PTS-Man-EIID,manZ;PTSsystem,mannose-specificIIDcomponent |
| K02798 | 0 | 0 | 0 | 0 | 1.09E-06 | PTS-Mtl-EIIA,mtlA,cmtB;PTSsystem,mannitol-specificIIAcomponent[EC:2.7.1.197] |
| K02799 | 1.58E-06 | 1.38E-06 | 3.14E-06 | 1.66E-06 | 1.6E-06 | PTS-Mtl-EIIB,mtlA,cmtA;PTSsystem,mannitol-specificIIBcomponent[EC:2.7.1.197] |
| K02800 | 4.45E-06 | 8.26E-07 | 3.26E-06 | 4.62E-06 | 1.22E-06 | PTS-Mtl-EIIC,mtlA,cmtA;PTSsystem,mannitol-specificIICcomponent |
| K02803 | 1.82E-05 | 2.09E-05 | 1.74E-05 | 1.06E-05 | 1.38E-05 | PTS-Nag-EIIB,nagE;PTSsystem,N-acetylglucosamine-specificIIBcomponent[EC:2.7.1.1 |
| K02804 | 1.05E-05 | 1.26E-05 | 7.37E-06 | 1.51E-05 | 1.14E-05 | PTS-Nag-EIIC,nagE;PTSsystem,N-acetylglucosamine-specificIICcomponent |
| K02821 | 1.32E-05 | 6.52E-06 | 2.17E-05 | 1.3E-05 | 2.7E-05 | PTS-Ula-EIIA,ulaC,sgaA;PTSsystem,ascorbate-specificIIAcomponent[EC:2.7.1.194] |
| K03077 | 5.74E-06 | 1.07E-05 | 5.13E-06 | 6.4E-06 | 2.23E-06 | araD,ulaF,sgaE,sgbE;L-ribulose-5-phosphate4-epimerase[EC:5.1.3.4] |
| K03079 | 4.91E-06 | 1.32E-06 | 2.12E-06 | 2.12E-06 | 2.47E-06 | ulaE,sgaU,sgbU;L-ribulose-5-phosphate3-epimerase[EC:5.1.3.22] |
| K03331 | 4.55E-06 | 3.13E-06 | 1.73E-06 | 2.3E-06 | 3.18E-06 | DCXR;L-xylulosereductase[EC:1.1.1.10] |
| K03332 | 1.58E-05 | 9.52E-06 | 2.68E-05 | 2.97E-05 | 2.38E-05 | fruA;fructanbeta-fructosidase[EC:3.2.1.80] |
| K03335 | 0.000157 | 0.000182 | 0.000129 | 0.000141 | 0.000127 | iolE;inososedehydratase[EC:4.2.1.44] |
| K03336 | 0.000194 | 0.000277 | 0.000185 | 0.000216 | 0.000183 | iolD;3D-(3,5/4)-trihydroxycyclohexane-1,2-dioneacylhydrolase(decyclizing)[EC:3.7.1 |
| K03337 | 8.66E-05 | 0.000101 | 5.98E-05 | 8.68E-05 | 7.81E-05 | iolB;5-deoxy-glucuronateisomerase[EC:5.3.1.30] |
| K03338 | 0.000136 | 0.000135 | 9.75E-05 | 9.59E-05 | 0.000102 | iolC;5-dehydro-2-deoxygluconokinase[EC:2.7.1.92] |
| K03366 | 7.46E-05 | 5.11E-05 | 7.33E-05 | 6.52E-05 | 8.06E-05 | butA,budC;meso-butanedioldehydrogenase/(S,S)-butanedioldehydrogenase/diacetyl |
| K03416 | 7.36E-06 | 2.23E-05 | 8.4E-06 | 6.96E-06 | 7E-06 | E2.1.3.1-5S;methylmalonyl-CoAcarboxyltransferase5Ssubunit[EC:2.1.3.1] |
| K03417 | 0.000213 | 0.00019 | 0.000188 | 0.000195 | 0.000199 | prpB;methylisocitratelyase[EC:4.1.3.30] |
| K03418 | 0.000107 | 0.000112 | 0.000104 | 9.53E-05 | 0.000109 | E3.5.1.56;N,N-dimethylformamidase[EC:3.5.1.56] |
| K03431 | 0.000514 | 0.000487 | 0.000482 | 0.00048 | 0.000488 | glmM;phosphoglucosaminemutase[EC:5.4.2.10] |
| K03476 | 1.6E-06 | 2.05E-06 | 2.34E-06 | 2.15E-06 | 0 | ulaG;L-ascorbate6-phosphatelactonase[EC:3.1.1.-] |
| K03737 | 0.000471 | 0.000405 | 0.000506 | 0.000448 | 0.000479 | por,nifJ;pyruvate-ferredoxin/flavodoxinoxidoreductase[EC:1.2.7.11.2.7.-] |
| K03738 | 0.000212 | 0.000123 | 0.000195 | 0.000178 | 0.000279 | aor;aldehyde:ferredoxinoxidoreductase[EC:1.2.7.5] |
| K03777 | 1.56E-05 | 1.64E-05 | 1.44E-05 | 1E-05 | 9.12E-06 | dld;D-lactatedehydrogenase(quinone)[EC:1.1.5.12] |
| K03778 | 5.12E-05 | 4.09E-05 | 4.94E-05 | 5.35E-05 | 4.94E-05 | ldhA;D-lactatedehydrogenase[EC:1.1.1.28] |
| K03779 | 3.56E-05 | 4.57E-05 | 4.58E-05 | 4.28E-05 | 4.43E-05 | ttdA;L(+)-tartratedehydratasealphasubunit[EC:4.2.1.32] |
| K03780 | 3.84E-05 | 3.63E-05 | 5.67E-05 | 5.19E-05 | 4.66E-05 | ttdB;L(+)-tartratedehydratasebetasubunit[EC:4.2.1.32] |
| K03781 | 0.000823 | 0.000835 | 0.000654 | 0.000635 | 0.000817 | katE,CAT,catB,srpA;catalase[EC:1.11.1.6] |
| K03821 | 0.000916 | 0.000903 | 0.000739 | 0.000723 | 0.00081 | phbC,phaC;polyhydroxyalkanoatesynthasesubunitPhaC[EC:2.3.1.-] |
| K03841 | 9.52E-05 | 8.81E-05 | 0.000101 | 8.92E-05 | 0.000109 | FBP,fbp;fructose-1,6-bisphosphataseI[EC:3.1.3.11] |
| K04020 | 0 | 0 | 3.42E-06 | 7.98E-07 | 0 | eutD;phosphotransacetylase |
| K04021 | 3.3E-05 | 3.45E-05 | 3.01E-05 | 3.4E-05 | 3.83E-05 | eutE;aldehydedehydrogenase |
| K04022 | 0 | 0 | 7.97E-07 | 1.78E-06 | 6.59E-07 | eutG;alcoholdehydrogenase |
| K04041 | 2.02E-05 | 2.04E-05 | 2.34E-05 | 1.65E-05 | 3.59E-05 | fbp3;fructose-1,6-bisphosphataseIII[EC:3.1.3.11] |
| K04042 | 0.000474 | 0.000486 | 0.000488 | 0.000503 | 0.000469 | glmU;bifunctionalUDP-N-acetylglucosaminepyrophosphorylase/Glucosamine-1-phosphate |
| K04072 | 2.23E-05 | 1.67E-05 | 1.62E-05 | 1.76E-05 | 3.55E-05 | adhE;acetaldehydedehydrogenase/alcoholdehydrogenase[EC:1.2.1.101.1.1.1] |
| K04073 | 1.51E-05 | 2.41E-05 | 1.89E-05 | 1.36E-05 | 1.25E-05 | mhpF;acetaldehydedehydrogenase[EC:1.2.1.10] |
| K04618 | 7.39E-06 | 1.56E-05 | 1.08E-05 | 1.35E-05 | 1.15E-05 | GAOA;galactoseoxidase[EC:1.1.3.9] |
| K04835 | 1.75E-05 | 1.48E-05 | 1.06E-05 | 9.01E-06 | 1.27E-05 | mal;methylaspartateammonia-lyase[EC:4.3.1.2] |
| K05304 | 6.77E-06 | 4.8E-06 | 7.89E-06 | 6.45E-06 | 1.84E-05 | NANS,SAS;sialicacidsynthase[EC:2.5.1.562.5.1.572.5.1.132] |
| K05305 | 0 | 8.48E-07 | 4.07E-06 | 9.12E-07 | 0 | FUK;fucokinase[EC:2.7.1.52] |
| K05308 | 6.8E-06 | 4.11E-06 | 2.88E-06 | 4.57E-06 | 2.82E-06 | gnaD;gluconate/galactonatedehydratase[EC:4.2.1.140] |
| K05341 | 6.53E-06 | 5.95E-06 | 7.13E-06 | 4.62E-06 | 1.05E-05 | E2.4.1.4;amylosucrase[EC:2.4.1.4] |
| K05342 | 0.000134 | 0.000181 | 0.00012 | 0.000112 | 0.000128 | E2.4.1.64;alpha,alpha-trehalosephosphorylase[EC:2.4.1.64] |
| K05343 | 0.001001 | 0.001103 | 0.000941 | 0.000969 | 0.00094 | treS;maltosealpha-D-glucosyltransferase/alpha-amylase[EC:5.4.99.163.2.1.1] |
| K05349 | 0.00091 | 0.001126 | 0.000935 | 0.000989 | 0.000836 | bglX;beta-glucosidase[EC:3.2.1.21] |
| K05350 | 0.000328 | 0.000361 | 0.000327 | 0.000305 | 0.000295 | bglB;beta-glucosidase[EC:3.2.1.21] |
| K05351 | 1.15E-06 | 3.1E-06 | 7.95E-06 | 1.76E-06 | 4.8E-06 | E1.1.1.9;D-xylulosereductase[EC:1.1.1.9] |
| K05605 | 3.67E-06 | 2.86E-06 | 2.54E-06 | 1.89E-06 | 4.67E-06 | HIBCH;3-hydroxyisobutyryl-CoAhydrolase[EC:3.1.2.4] |
| K05606 | 0.000122 | 0.000147 | 0.000151 | 0.000163 | 0.000158 | MCEE,epi;methylmalonyl-CoA/ethylmalonyl-CoAepimerase[EC:5.1.99.1] |
| K05774 | 2.77E-05 | 2.15E-05 | 1.73E-05 | 2.41E-05 | 1.76E-05 | phnN;ribose1,5-bisphosphokinase[EC:2.7.4.23] |
| K05947 | 2.68E-06 | 1.47E-06 | 1.55E-06 | 4.47E-06 | 1.19E-05 | E2.4.1.217;mannosyl-3-phosphoglyceratesynthase[EC:2.4.1.217] |
| K05973 | 0.000214 | 0.000195 | 0.000211 | 0.00018 | 0.000232 | phaZ;poly(3-hydroxybutyrate)depolymerase[EC:3.1.1.75] |
| K05988 | 0 | 8.03E-07 | 1.85E-06 | 4.56E-07 | 0 | dexA;dextranase[EC:3.2.1.11] |
| K06044 | 0.000587 | 0.000674 | 0.000615 | 0.000665 | 0.000607 | treY,glgY;(1->4)-alpha-D-glucan1-alpha-D-glucosylmutase[EC:5.4.99.15] |
| K06118 | 5.94E-05 | 9.84E-05 | 4.88E-05 | 7.09E-05 | 3.74E-05 | SQD1,sqdB;UDP-sulfoquinovosesynthase[EC:3.13.1.1] |
| K06151 | 0.000567 | 0.000678 | 0.000664 | 0.000682 | 0.000486 | E1.1.99.3A;gluconate2-dehydrogenasealphachain[EC:1.1.99.3] |
| K06152 | 0.000174 | 0.00024 | 0.000223 | 0.000226 | 0.000165 | E1.1.99.3G;gluconate2-dehydrogenasegammachain[EC:1.1.99.3] |
| K06606 | 6.83E-06 | 1.14E-05 | 9.26E-06 | 5.54E-06 | 1.45E-05 | iolI;2-keto-myo-inositolisomerase[EC:5.3.99.11] |
| K06617 | 0 | 0 | 0 | 0 | 7.25E-07 | E2.4.1.82;raffinosesynthase[EC:2.4.1.82] |
| K06859 | 5.26E-06 | 8.91E-06 | 3.49E-06 | 9.37E-06 | 6.8E-06 | pgi1;glucose-6-phosphateisomerase,archaeal[EC:5.3.1.9] |
| K07024 | 0.000255 | 0.000308 | 0.00027 | 0.000313 | 0.000247 | SPP;sucrose-6-phosphatase[EC:3.1.3.24] |
| K07026 | 9.6E-06 | 1.86E-05 | 2.27E-05 | 2.41E-05 | 2E-05 | E3.1.3.70;mannosyl-3-phosphoglyceratephosphatase[EC:3.1.3.70] |
| K07046 | 0.000419 | 0.00044 | 0.000429 | 0.000446 | 0.000439 | K07046;L-fuconolactonase[EC:3.1.1.-] |
| K07102 | 0.000283 | 0.000276 | 0.000279 | 0.000269 | 0.000285 | amgK;N-acetylmuramate1-kinase[EC:2.7.1.221] |
| K07106 | 0.000179 | 0.000195 | 0.000233 | 0.000257 | 0.000187 | murQ;N-acetylmuramicacid6-phosphateetherase[EC:4.2.1.126] |
| K07130 | 7.46E-05 | 6.54E-05 | 6.21E-05 | 7.63E-05 | 6.92E-05 | kynB;arylformamidase[EC:3.5.1.9] |
| K07246 | 0.000328 | 0.000302 | 0.000313 | 0.000307 | 0.000347 | ttuC,dmlA;tartratedehydrogenase/decarboxylase/D-malatedehydrogenase[EC:1.1.1.93 |
| K07248 | 1.21E-05 | 1.22E-05 | 6.95E-06 | 7.87E-06 | 7.39E-06 | aldA;lactaldehydedehydrogenase/glycolaldehydedehydrogenase[EC:1.2.1.221.2.1.21] |
| K07250 | 0.000171 | 0.000196 | 0.000201 | 0.000228 | 0.000199 | gabT;4-aminobutyrateaminotransferase/(S)-3-amino-2-methylpropionatetransaminase[ |
| K07281 | 7.74E-05 | 0.000118 | 9.19E-05 | 9.92E-05 | 5.44E-05 | ipct;1L-myo-inositol1-phosphatecytidylyltransferase[EC:2.7.7.74] |
| K07291 | 3.78E-05 | 4.02E-05 | 2.62E-05 | 3.7E-05 | 3.2E-05 | dipps;CDP-L-myo-inositolmyo-inositolphosphotransferase[EC:2.7.8.34] |
| K07404 | 0.000375 | 0.000391 | 0.000428 | 0.000441 | 0.000417 | pgl;6-phosphogluconolactonase[EC:3.1.1.31] |
| K07405 | 4.25E-05 | 4.27E-05 | 4.89E-05 | 7.11E-05 | 3.56E-05 | E3.2.1.1A;alpha-amylase[EC:3.2.1.1] |
| K07406 | 4.85E-05 | 5.81E-05 | 3.41E-05 | 3.62E-05 | 5.44E-05 | melA;alpha-galactosidase[EC:3.2.1.22] |
| K07407 | 0.000243 | 0.000339 | 0.00037 | 0.000402 | 0.000251 | E3.2.1.22B,galA,rafA;alpha-galactosidase[EC:3.2.1.22] |
| K07511 | 2.05E-06 | 7.74E-06 | 8.52E-06 | 6.91E-06 | 4.22E-06 | ECHS1;enoyl-CoAhydratase[EC:4.2.1.17] |
| K07514 | 3.04E-06 | 5.29E-06 | 4.94E-06 | 3.11E-06 | 4.89E-06 | EHHADH;enoyl-CoAhydratase/3-hydroxyacyl-CoAdehydrogenase/3,2-trans-enoyl-CoAis |
| K07515 | 1.23E-06 | 3.06E-06 | 1.87E-06 | 4.84E-06 | 6.59E-07 | HADHA;enoyl-CoAhydratase/long-chain3-hydroxyacyl-CoAdehydrogenase[EC:4.2.1.171 |
| K07516 | 0.000838 | 0.000834 | 0.000863 | 0.000907 | 0.000844 | fadN;3-hydroxyacyl-CoAdehydrogenase[EC:1.1.1.35] |
| K07518 | 2.28E-05 | 1.95E-05 | 2.23E-05 | 3.38E-05 | 3.55E-05 | E3.1.1.22;hydroxybutyrate-dimerhydrolase[EC:3.1.1.22] |
| K07806 | 1.57E-05 | 5.88E-06 | 1.67E-05 | 1.41E-05 | 2.42E-05 | arnB,pmrH;UDP-4-amino-4-deoxy-L-arabinose-oxoglutarateaminotransferase[EC:2.6.1.87 |
| K07967 | 6.13E-07 | 5.58E-07 | 0 | 0 | 1.57E-06 | B4GALT2;beta-1,4-galactosyltransferase2[EC:2.4.1.222.4.1.902.4.1.382.4.1.-] |
| K08068 | 3.86E-06 | 6.19E-06 | 2.2E-06 | 3.77E-06 | 6.59E-06 | siaA,neuC1;UDP-N-acetylglucosamine2-epimerase(hydrolysing)[EC:3.2.1.183] |
| K08080 | 0 | 2.7E-06 | 0 | 4.56E-07 | 0 | CMAH;CMP-N-acetylneuraminatemonooxygenase[EC:1.14.18.2] |
| K08092 | 1.31E-05 | 9.36E-06 | 1.17E-05 | 1.04E-05 | 1.87E-05 | dlgD;3-dehydro-L-gulonate2-dehydrogenase[EC:1.1.1.130] |
| K08093 | 3.26E-06 | 7.84E-06 | 1.01E-06 | 2.91E-06 | 6.59E-07 | hxlA;3-hexulose-6-phosphatesynthase[EC:4.1.2.43] |
| K08094 | 8.26E-06 | 7.99E-06 | 1.69E-06 | 1.98E-06 | 5.27E-06 | hxlB;6-phospho-3-hexuloisomerase[EC:5.3.1.27] |
| K08232 | 4.28E-06 | 8.65E-06 | 9.46E-06 | 8.35E-06 | 4.23E-06 | E1.6.5.4;monodehydroascorbatereductase(NADH)[EC:1.6.5.4] |
| K08261 | 1.32E-05 | 1.48E-05 | 1.21E-05 | 1.01E-05 | 1.22E-05 | E1.1.99.21;D-sorbitoldehydrogenase(acceptor)[EC:1.1.99.21] |
| K08302 | 3.51E-06 | 1.67E-06 | 1.15E-06 | 4.21E-06 | 3.75E-06 | gatY-kbaY;tagatose1,6-diphosphatealdolaseGatY/KbaY[EC:4.1.2.40] |
| K08318 | 1.68E-05 | 1.5E-05 | 1.61E-05 | 2.56E-05 | 2.21E-05 | yihU;4-hydroxybutyratedehydrogenase/sulfolactaldehyde3-reductase[EC:1.1.1.611.1 |
| K08322 | 7.02E-06 | 7.18E-06 | 5.26E-06 | 9.5E-06 | 1E-05 | rspB;L-gulonate5-dehydrogenase[EC:1.1.1.380] |
| K08323 | 0.000149 | 0.000148 | 0.000143 | 0.000156 | 0.000148 | rspA,manD;mannonatedehydratase[EC:4.2.1.8] |
| K08324 | 1.34E-05 | 2.18E-05 | 7.95E-06 | 1.61E-05 | 9.82E-06 | sad;succinate-semialdehydedehydrogenase[EC:1.2.1.161.2.1.24] |
| K08678 | 0.000173 | 0.000171 | 0.000198 | 0.000163 | 0.000155 | UXS1,uxs;UDP-glucuronatedecarboxylase[EC:4.1.1.35] |
| K08679 | 0.00023 | 0.000261 | 0.000275 | 0.000266 | 0.000249 | E5.1.3.6;UDP-glucuronate4-epimerase[EC:5.1.3.6] |
| K08691 | 9.36E-05 | 9.87E-05 | 0.000105 | 9.27E-05 | 9.95E-05 | mcl;malyl-CoA/(S)-citramalyl-CoAlyase[EC:4.1.3.244.1.3.25] |
| K08692 | 1.28E-05 | 1.24E-05 | 1.66E-05 | 9.32E-06 | 1.04E-05 | mtkB;malate-CoAligasesubunitalpha[EC:6.2.1.9] |
| K09011 | 9.32E-06 | 7.54E-06 | 8.37E-06 | 1.21E-05 | 2.12E-05 | cimA;(R)-citramalatesynthase[EC:2.3.1.182] |
| K09699 | 6.78E-05 | 7.37E-05 | 5.3E-05 | 7.35E-05 | 6.47E-05 | DBT,bkdB;2-oxoisovaleratedehydrogenaseE2component(dihydrolipoyltransacylase)[E |
| K09788 | 1.27E-05 | 1.14E-05 | 7.43E-06 | 4.15E-06 | 1.33E-05 | prpF;2-methylaconitateisomerase[EC:5.3.3.-] |
| K09988 | 5.09E-06 | 3.53E-06 | 2.52E-06 | 6.07E-07 | 4.02E-06 | lyxA;D-lyxoseketol-isomerase[EC:5.3.1.15] |
| K10011 | 2.83E-05 | 8.22E-06 | 1.74E-05 | 1.71E-05 | 2.76E-05 | arnA,pmrI;UDP-4-amino-4-deoxy-L-arabinoseformyltransferase/UDP-glucuronicacidde |
| K10012 | 0.000126 | 0.000124 | 0.000124 | 0.000138 | 0.000108 | arnC,pmrF;undecaprenyl-phosphate4-deoxy-4-formamido-L-arabinosetransferase[EC:2.4 |
| K10046 | 4.7E-06 | 1.64E-06 | 1.77E-06 | 1.37E-06 | 0 | GME;GDP-D-mannose3',5'-epimerase[EC:5.1.3.185.1.3.-] |
| K10046 | 4.7E-06 | 1.64E-06 | 1.77E-06 | 1.37E-06 | 0 | GME;GDP-D-mannose3',5'-epimerase[EC:5.1.3.185.1.3.-] |
| K10047 | 1.15E-06 | 2.31E-06 | 2.05E-06 | 1.35E-06 | 6.57E-06 | VTC4;inositol-phosphatephosphatase/L-galactose1-phosphatephosphatase[EC:3.1.3.2 |
| K10047 | 1.15E-06 | 2.31E-06 | 2.05E-06 | 1.35E-06 | 6.57E-06 | VTC4;inositol-phosphatephosphatase/L-galactose1-phosphatephosphatase[EC:3.1.3.2 |
| K10218 | 9.3E-05 | 9.16E-05 | 8.13E-05 | 7.78E-05 | 7.09E-05 | ligK,galC;4-hydroxy-4-methyl-2-oxoglutaratealdolase[EC:4.1.3.17] |
| K10705 | 0 | 0 | 8.07E-07 | 0 | 0 | GAPDHS;glyceraldehyde-3-phosphatedehydrogenase,spermatogenic[EC:1.2.1.12] |
| K10977 | 1.74E-05 | 2.7E-05 | 2.76E-05 | 3.31E-05 | 3.2E-05 | aksA;methanogenhomocitratesynthase[EC:2.3.3.142.3.3.-] |
| K11263 | 9.41E-05 | 9.26E-05 | 7.24E-05 | 6.73E-05 | 0.000104 | bccA,pccA;acetyl-CoA/propionyl-CoAcarboxylase,biotincarboxylase,biotincarboxyl |
| K11264 | 5.94E-06 | 1.26E-05 | 1.05E-05 | 1.04E-05 | 1.1E-05 | scpB,mmcD;methylmalonyl-CoAdecarboxylase[EC:7.2.4.3] |
| K11381 | 0.000543 | 0.000555 | 0.000529 | 0.000595 | 0.000538 | bkdA;2-oxoisovaleratedehydrogenaseE1component[EC:1.2.4.4] |
| K11472 | 0.000245 | 0.000266 | 0.000263 | 0.00026 | 0.000233 | glcE;glycolateoxidaseFADbindingsubunit |
| K11473 | 0.00034 | 0.000403 | 0.000421 | 0.000444 | 0.000388 | glcF;glycolateoxidaseiron-sulfursubunit |
| K11517 | 5.04E-05 | 5.49E-05 | 6.43E-05 | 6.11E-05 | 7.36E-05 | HAO;(S)-2-hydroxy-acidoxidase[EC:1.1.3.15] |
| K11528 | 1.15E-05 | 1.85E-05 | 1.46E-05 | 1.02E-05 | 5.93E-06 | glmU;UDP-N-acetylglucosaminepyrophosphorylase[EC:2.7.7.23] |
| K11529 | 1.02E-05 | 7.28E-06 | 8.47E-06 | 8.5E-06 | 1.19E-05 | gck,gckA,GLYCTK;glycerate2-kinase[EC:2.7.1.165] |
| K11532 | 0.000145 | 0.000137 | 0.000128 | 0.000108 | 0.000114 | glpX-SEBP;fructose-1,6-bisphosphataseII/sedoheptulose-1,7-bisphosphatase[EC:3.1.3 |
| K11645 | 0.000176 | 0.000139 | 0.000178 | 0.000149 | 0.000187 | fbaB;fructose-bisphosphatealdolase,classI[EC:4.1.2.13] |
| K12111 | 0 | 1.48E-06 | 1.05E-06 | 1.8E-06 | 0 | ebgA;evolvedbeta-galactosidasesubunitalpha[EC:3.2.1.23] |
| K12308 | 9.8E-05 | 0.000176 | 0.00013 | 0.000162 | 8.01E-05 | bgaB,lacA;beta-galactosidase[EC:3.2.1.23] |
| K12373 | 0.000208 | 0.000296 | 0.000275 | 0.00033 | 0.000205 | HEXA\_B;hexosaminidase[EC:3.2.1.52] |
| K12409 | 1.61E-06 | 5.58E-07 | 7.41E-07 | 1.48E-06 | 9.43E-07 | GNE;bifunctionalUDP-N-acetylglucosamine2-epimerase/N-acetylmannosaminekinase[EC |
| K12446 | 2.75E-05 | 1.35E-05 | 2.54E-05 | 1.58E-05 | 3.41E-05 | E2.7.1.46;L-arabinokinase[EC:2.7.1.46] |
| K12448 | 6.39E-05 | 7.43E-05 | 7.57E-05 | 7.6E-05 | 4.21E-05 | UXE,uxe;UDP-arabinose4-epimerase[EC:5.1.3.5] |
| K12449 | 4.71E-06 | 2.96E-06 | 1.98E-06 | 2.58E-06 | 6.8E-06 | AXS;UDP-apiose/xylosesynthase |
| K12450 | 0 | 0 | 1.15E-06 | 0 | 0 | RHM;UDP-glucose4,6-dehydratase[EC:4.2.1.76] |
| K12451 | 0 | 8.37E-07 | 0 | 2.57E-06 | 1.85E-06 | UER1;3,5-epimerase/4-reductase[EC:5.1.3.-1.1.1.-] |
| K12452 | 7.38E-05 | 4.19E-05 | 6.35E-05 | 7.33E-05 | 5.01E-05 | ascC,ddhC,rfbH;CDP-4-dehydro-6-deoxyglucosereductase,E1[EC:1.17.1.1] |
| K12454 | 0.000155 | 0.000193 | 0.000196 | 0.000213 | 0.00014 | rfbE;CDP-paratose2-epimerase[EC:5.1.3.10] |
| K12660 | 2.9E-06 | 1.12E-06 | 1.98E-06 | 0 | 2.16E-06 | rhmA;2-dehydro-3-deoxy-L-rhamnonatealdolase[EC:4.1.2.53] |
| K12661 | 1.46E-05 | 1.85E-05 | 1.31E-05 | 9.56E-06 | 1.8E-05 | LRA3,yfaW;L-rhamnonatedehydratase[EC:4.2.1.90] |
| K12972 | 0.000127 | 0.000128 | 0.000136 | 0.00012 | 0.000112 | ghrA;glyoxylate/hydroxypyruvatereductase[EC:1.1.1.791.1.1.81] |
| K13010 | 0.000115 | 0.000136 | 0.000152 | 0.000169 | 0.000159 | per,rfbE;perosaminesynthetase[EC:2.6.1.102] |
| K13014 | 7.12E-06 | 4.95E-06 | 4E-06 | 5.24E-06 | 6.59E-07 | arnD;undecaprenylphosphate-alpha-L-ara4FNdeformylase[EC:3.5.1.-] |
| K13015 | 0.000338 | 0.000368 | 0.00041 | 0.000406 | 0.000365 | wbpA;UDP-N-acetyl-D-glucosaminedehydrogenase[EC:1.1.1.136] |
| K13016 | 1.31E-05 | 6.26E-06 | 2.24E-05 | 1.56E-05 | 1.52E-05 | wbpB;UDP-N-acetyl-2-amino-2-deoxyglucuronatedehydrogenase[EC:1.1.1.335] |
| K13017 | 2.51E-05 | 2.38E-05 | 2.42E-05 | 1.43E-05 | 2.3E-05 | wbpE,wlbC;UDP-2-acetamido-2-deoxy-ribo-hexuluronateaminotransferase[EC:2.6.1.98] |
| K13018 | 4.66E-05 | 4.4E-05 | 8.55E-05 | 9.19E-05 | 6.49E-05 | wbpD,wlbB;UDP-2-acetamido-3-amino-2,3-dideoxy-glucuronateN-acetyltransferase[EC:2. |
| K13019 | 1.85E-05 | 2.51E-05 | 2.87E-05 | 2.98E-05 | 2.59E-05 | wbpI,wlbD;UDP-GlcNAc3NAcAepimerase[EC:5.1.3.23] |
| K13020 | 1.8E-05 | 1.64E-05 | 2.09E-05 | 2.49E-05 | 1.04E-05 | wlbA,bplA;UDP-N-acetyl-2-amino-2-deoxyglucuronatedehydrogenase[EC:1.1.1.335] |
| K13057 | 8.6E-05 | 0.00011 | 0.000111 | 0.000115 | 9.35E-05 | treT;trehalosesynthase[EC:2.4.1.245] |
| K13247 | 0 | 2.69E-06 | 2.33E-06 | 0 | 3.5E-06 | CRYL1;L-gulonate3-dehydrogenase[EC:1.1.1.45] |
| K13379 | 0 | 0 | 0 | 6.75E-07 | 0 | RGP,UTM;reversiblyglycosylatedpolypeptide/UDP-arabinopyranosemutase[EC:2.4.1.- |
| K13381 | 1.74E-06 | 0 | 2.91E-06 | 4.56E-07 | 2.8E-06 | chiA;bifunctionalchitinase/lysozyme[EC:3.2.1.143.2.1.17] |
| K13524 | 2.53E-05 | 1.82E-05 | 2.28E-05 | 1.83E-05 | 3.97E-05 | ABAT;4-aminobutyrateaminotransferase/(S)-3-amino-2-methylpropionatetransaminase[ |
| K13524 | 2.53E-05 | 1.82E-05 | 2.28E-05 | 1.83E-05 | 3.97E-05 | ABAT;4-aminobutyrateaminotransferase/(S)-3-amino-2-methylpropionatetransaminase[ |
| K13788 | 2.22E-05 | 2.34E-05 | 1.35E-05 | 1.15E-05 | 7.95E-06 | pta;phosphateacetyltransferase[EC:2.3.1.8] |
| K13810 | 0.000308 | 0.000435 | 0.000432 | 0.000496 | 0.000272 | tal-pgi;transaldolase/glucose-6-phosphateisomerase[EC:2.2.1.25.3.1.9] |
| K13831 | 2.12E-05 | 1.46E-05 | 2.36E-05 | 1.35E-05 | 2.5E-05 | hps-phi;3-hexulose-6-phosphatesynthase/6-phospho-3-hexuloisomerase[EC:4.1.2.435 |
| K13873 | 2.57E-06 | 0 | 0 | 0 | 4.65E-06 | araA;L-arabinose1-dehydrogenase[EC:1.1.1.376] |
| K13874 | 2.45E-06 | 0 | 1.16E-06 | 1.99E-06 | 3.06E-06 | K13874,araB;L-arabinonolactonase[EC:3.1.1.15] |
| K13875 | 7.34E-06 | 3.74E-06 | 2.44E-06 | 6.39E-06 | 4.82E-06 | K13875,araC;L-arabonatedehydrase[EC:4.2.1.25] |
| K13876 | 7.37E-06 | 7.27E-06 | 1.09E-05 | 6.17E-06 | 7.89E-06 | araD;2-keto-3-deoxy-L-arabinonatedehydratase[EC:4.2.1.43] |
| K13877 | 0 | 5.58E-07 | 0 | 0 | 0 | aldH;2,5-dioxopentanoatedehydrogenase[EC:1.2.1.26] |
| K13919 | 0 | 7.64E-07 | 1.44E-06 | 1.37E-06 | 0 | pduD;propanedioldehydratasemediumsubunit[EC:4.2.1.28] |
| K13920 | 3.95E-06 | 6E-06 | 3.6E-06 | 1.37E-06 | 6.14E-06 | pduE;propanedioldehydratasesmallsubunit[EC:4.2.1.28] |
| K13922 | 6.38E-06 | 7.97E-06 | 7.77E-06 | 5.01E-06 | 6.26E-06 | pduP;propionaldehydedehydrogenase[EC:1.2.1.87] |
| K13951 | 0 | 0 | 0 | 8.8E-07 | 0 | ADH1\_7;alcoholdehydrogenase43107[EC:1.1.1.1] |
| K13953 | 0.000593 | 0.000655 | 0.000598 | 0.000635 | 0.000559 | adhP;alcoholdehydrogenase,propanol-preferring[EC:1.1.1.1] |
| K13954 | 3.94E-05 | 2.58E-05 | 3.39E-05 | 3.3E-05 | 5.72E-05 | yiaY;alcoholdehydrogenase[EC:1.1.1.1] |
| K13967 | 0 | 0 | 0 | 8.26E-07 | 0 | nanEK;N-acetylmannosamine-6-phosphate2-epimerase/N-acetylmannosaminekinase[EC:5. |
| K13997 | 0 | 1.42E-06 | 1.47E-06 | 1.48E-06 | 0 | PDHX;dihydrolipoamidedehydrogenase-bindingproteinofpyruvatedehydrogenasecomplex |
| K14028 | 2.9E-05 | 2.36E-05 | 1.95E-05 | 2.05E-05 | 4.05E-05 | mdh1,mxaF;methanoldehydrogenase(cytochromec)subunit1[EC:1.1.2.7] |
| K14067 | 1.48E-05 | 1.54E-05 | 1.05E-05 | 1.18E-05 | 1.98E-05 | mtkA;malate-CoAligasesubunitbeta[EC:6.2.1.9] |
| K14085 | 7.26E-06 | 2.58E-06 | 5.07E-07 | 2.8E-06 | 9.3E-07 | ALDH7A1;aldehydedehydrogenasefamily7memberA1[EC:1.2.1.311.2.1.81.2.1.3] |
| K14259 | 3.11E-05 | 3.13E-05 | 3.95E-05 | 3.56E-05 | 4.68E-05 | kdxD;2-dehydro-3-deoxy-D-arabinonatedehydratase[EC:4.2.1.141] |
| K14268 | 1.23E-06 | 2.48E-06 | 5.07E-07 | 0 | 1.73E-06 | davT,gabT;5-aminovalerate/4-aminobutyrateaminotransferase[EC:2.6.1.482.6.1.19] |
| K14273 | 2.59E-06 | 3.15E-06 | 3.1E-06 | 2.99E-06 | 2.47E-06 | xdh;D-xylose1-dehydrogenase(NADP+)[EC:1.1.1.179] |
| K14274 | 2.41E-06 | 5.58E-07 | 2.83E-06 | 6.85E-06 | 2.49E-06 | xylC;xylonolactonase[EC:3.1.1.-] |
| K14275 | 3.98E-06 | 2.55E-06 | 5.55E-06 | 5.05E-06 | 5.06E-06 | xad;D-xylonatedehydratase[EC:4.2.1.82] |
| K14446 | 0.000169 | 0.000174 | 0.000151 | 0.000158 | 0.000132 | ccr;crotonyl-CoAcarboxylase/reductase[EC:1.3.1.85] |
| K14447 | 0.00021 | 0.000223 | 0.000207 | 0.000175 | 0.000202 | ecm;ethylmalonyl-CoAmutase[EC:5.4.99.63] |
| K14448 | 0.000131 | 0.000158 | 0.000169 | 0.000136 | 0.000168 | mcd;(2S)-methylsuccinyl-CoAdehydrogenase[EC:1.3.8.12] |
| K14449 | 9.67E-05 | 0.000109 | 0.000103 | 9.32E-05 | 8.98E-05 | mch,mcd;2-methylfumaryl-CoAhydratase[EC:4.2.1.148] |
| K14451 | 0 | 0 | 0 | 0 | 1.46E-06 | mcl2;(3S)-malyl-CoAthioesterase[EC:3.1.2.30] |
| K14471 | 1.42E-06 | 6.62E-06 | 2.98E-06 | 1.4E-06 | 2.57E-06 | smtA1;succinyl-CoA:(S)-malateCoA-transferasesubunitA[EC:2.8.3.22] |
| K14472 | 7.34E-06 | 4.55E-06 | 4.83E-06 | 6.31E-06 | 6.78E-06 | smtB;succinyl-CoA:(S)-malateCoA-transferasesubunitB[EC:2.8.3.22] |
| K14534 | 4.1E-05 | 4.14E-05 | 3.85E-05 | 2.77E-05 | 5.86E-05 | abfD;4-hydroxybutyryl-CoAdehydratase/vinylacetyl-CoA-Delta-isomerase[EC:4.2.1.120 |
| K15024 | 3.59E-06 | 3.45E-06 | 5.19E-06 | 4.87E-06 | 3.18E-06 | K15024;putativephosphotransacetylase[EC:2.3.1.8] |
| K15230 | 7.85E-06 | 2.58E-06 | 6.27E-06 | 3.95E-06 | 9.9E-06 | aclA;ATP-citratelyasealpha-subunit[EC:2.3.3.8] |
| K15231 | 5.19E-06 | 1.75E-06 | 6.41E-06 | 5.61E-06 | 1.11E-05 | aclB;ATP-citratelyasebeta-subunit[EC:2.3.3.8] |
| K15633 | 0.000281 | 0.000361 | 0.000332 | 0.000364 | 0.000248 | gpmI;2,3-bisphosphoglycerate-independentphosphoglyceratemutase[EC:5.4.2.12] |
| K15634 | 0.000343 | 0.000411 | 0.00033 | 0.000378 | 0.000354 | gpmB;probablephosphoglyceratemutase[EC:5.4.2.12] |
| K15635 | 5.33E-05 | 4.71E-05 | 5.1E-05 | 5.78E-05 | 7.71E-05 | apgM;2,3-bisphosphoglycerate-independentphosphoglyceratemutase[EC:5.4.2.12] |
| K15778 | 0.000321 | 0.000303 | 0.00032 | 0.000295 | 0.000363 | pmm-pgm;phosphomannomutase/phosphoglucomutase[EC:5.4.2.85.4.2.2] |
| K15855 | 0.000176 | 0.000294 | 0.00027 | 0.000301 | 0.000134 | csxA;exo-1,4-beta-D-glucosaminidase[EC:3.2.1.165] |
| K15856 | 5.49E-05 | 4.8E-05 | 5.97E-05 | 6.53E-05 | 6.33E-05 | rmd;GDP-4-dehydro-6-deoxy-D-mannosereductase[EC:1.1.1.281] |
| K15894 | 3.73E-05 | 3.56E-05 | 5.54E-05 | 4.94E-05 | 4.57E-05 | pseB;UDP-N-acetylglucosamine4,6-dehydratase[EC:4.2.1.115] |
| K15897 | 2.41E-06 | 0 | 0 | 0 | 1.09E-06 | pseG;UDP-2,4-diacetamido-2,4,6-trideoxy-beta-L-altropyranosehydrolase[EC:3.6.1.57] |
| K15898 | 9.83E-06 | 1.19E-06 | 1.85E-06 | 2.92E-06 | 2.81E-06 | pseI,neuB3;pseudaminicacidsynthase[EC:2.5.1.97] |
| K15899 | 0 | 0 | 7.15E-07 | 0 | 0 | pseF;pseudaminicacidcytidylyltransferase[EC:2.7.7.81] |
| K15910 | 0 | 0 | 0 | 0 | 1.6E-06 | pglE;UDP-N-acetylbacillosaminetransaminase[EC:2.6.1.34] |
| K15912 | 0 | 5.58E-07 | 1.72E-06 | 3.08E-06 | 0 | pglF;UDP-N-acetyl-D-glucosamine4,6-dehydratase[EC:4.2.1.135] |
| K15913 | 0 | 1.91E-06 | 5.07E-07 | 3.15E-06 | 6.59E-07 | pglD;UDP-N-acetylbacillosamineN-acetyltransferase[EC:2.3.1.203] |
| K15916 | 1.55E-05 | 2.46E-05 | 1.78E-05 | 1.63E-05 | 1.77E-05 | pgi-pmi;glucose/mannose-6-phosphateisomerase[EC:5.3.1.95.3.1.8] |
| K15918 | 2.05E-06 | 3.91E-06 | 2.58E-06 | 3.74E-06 | 2.35E-06 | GLYK;D-glycerate3-kinase[EC:2.7.1.31] |
| K15919 | 5.29E-06 | 5.13E-06 | 1.01E-05 | 7.02E-06 | 7.48E-06 | HPR2\_3;glyoxylate/hydroxypyruvatereductase[EC:1.1.1.791.1.1.81] |
| K15921 | 0 | 8.2E-07 | 0 | 0 | 9.76E-07 | xynD;arabinoxylanarabinofuranohydrolase[EC:3.2.1.55] |
| K16011 | 0.000219 | 0.000258 | 0.000214 | 0.000221 | 0.000194 | algA,xanB,rfbA,wbpW,pslB;mannose-1-phosphateguanylyltransferase/mannose-6-phos |
| K16011 | 0.000219 | 0.000258 | 0.000214 | 0.000221 | 0.000194 | algA,xanB,rfbA,wbpW,pslB;mannose-1-phosphateguanylyltransferase/mannose-6-phos |
| K16043 | 2.34E-05 | 2.31E-05 | 3.32E-05 | 2.95E-05 | 2.57E-05 | iolX;scyllo-inositol2-dehydrogenase(NAD+)[EC:1.1.1.370] |
| K16044 | 1.23E-06 | 6.86E-06 | 3.2E-06 | 4.68E-06 | 1.46E-06 | iolW;scyllo-inositol2-dehydrogenase(NADP+)[EC:1.1.1.371] |
| K16055 | 3.45E-05 | 4.57E-05 | 4.06E-05 | 3.99E-05 | 3.31E-05 | TPS;trehalose6-phosphatesynthase/phosphatase[EC:2.4.1.153.1.3.12] |
| K16146 | 1.08E-05 | 2.99E-05 | 9.95E-06 | 8.36E-06 | 1.24E-05 | pep2;maltokinase[EC:2.7.1.175] |
| K16147 | 0.000348 | 0.000391 | 0.000347 | 0.000382 | 0.000368 | glgE;starchsynthase(maltosyl-transferring)[EC:2.4.99.16] |
| K16148 | 5.39E-05 | 4.4E-05 | 3.17E-05 | 5.36E-05 | 3.22E-05 | glgM;alpha-maltose-1-phosphatesynthase[EC:2.4.1.342] |
| K16149 | 0.000129 | 0.000148 | 0.000116 | 0.000158 | 0.000133 | K16149;1,4-alpha-glucanbranchingenzyme[EC:2.4.1.18] |
| K16150 | 1.83E-05 | 1.34E-05 | 2.2E-05 | 1.62E-05 | 1.89E-05 | K16150;glycogensynthase[EC:2.4.1.11] |
| K16153 | 6.13E-07 | 0 | 0 | 0 | 1.71E-06 | K16153;glycogenphosphorylase/synthase[EC:2.4.1.12.4.1.11] |
| K16190 | 1.69E-05 | 8.76E-06 | 2.59E-05 | 1.73E-05 | 4.04E-05 | GLCAK;glucuronokinase[EC:2.7.1.43] |
| K16305 | 0 | 0 | 0 | 1.25E-06 | 0 | K16305;fructose-bisphosphatealdolase/6-deoxy-5-ketofructose1-phosphatesynthase[ |
| K16306 | 6.93E-06 | 6.09E-06 | 8.05E-06 | 6.34E-06 | 1.11E-05 | K16306;fructose-bisphosphatealdolase/2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate |
| K16370 | 1.45E-05 | 1.86E-05 | 2.77E-05 | 2.29E-05 | 1.08E-05 | pfkB;6-phosphofructokinase2[EC:2.7.1.11] |
| K16371 | 2.22E-05 | 5.32E-05 | 3.98E-05 | 4.04E-05 | 2.96E-05 | gatZ-kbaZ;D-tagatose-1,6-bisphosphatealdolasesubunitGatZ/KbaZ |
| K16849 | 1.3E-06 | 2.98E-06 | 1.42E-06 | 1.58E-06 | 1.28E-06 | uxaA1;altronatedehydratasesmallsubunit[EC:4.2.1.7] |
| K16850 | 2.48E-05 | 1.41E-05 | 2.3E-05 | 2.16E-05 | 3.56E-05 | uxaA2;altronatedehydrataselargesubunit[EC:4.2.1.7] |
| K16871 | 0.00016 | 0.000176 | 0.000145 | 0.000148 | 0.00014 | POP2;4-aminobutyrate---pyruvatetransaminase[EC:2.6.1.96] |
| K16881 | 8.78E-05 | 0.000103 | 0.000109 | 8.57E-05 | 9.71E-05 | K16881;mannose-1-phosphateguanylyltransferase/phosphomannomutase[EC:2.7.7.135.4. |
| K17468 | 0 | 0 | 0 | 0 | 1.02E-06 | dgaE;D-glucosaminate-6-phosphateammonia-lyase[EC:4.3.1.29] |
| K17489 | 6.33E-06 | 1.46E-05 | 1.19E-05 | 1.35E-05 | 5.23E-06 | E2.1.3.1-12S;methylmalonyl-CoAcarboxyltransferase12Ssubunit[EC:2.1.3.1] |
| K17490 | 1.82E-06 | 5.14E-06 | 9.29E-07 | 3.3E-06 | 2.23E-06 | E2.1.3.1-1.3S;methylmalonyl-CoAcarboxyltransferase1.3Ssubunit[EC:2.1.3.1] |
| K17716 | 7.19E-06 | 3.03E-06 | 1.42E-05 | 6.75E-06 | 1.17E-05 | capD;UDP-glucose4-epimerase[EC:5.1.3.2] |
| K17724 | 1.44E-05 | 9.12E-06 | 1.01E-05 | 6.3E-06 | 1.11E-05 | IRG1;aconitatedecarboxylase[EC:4.1.1.6] |
| K17742 | 1.42E-06 | 0 | 0 | 0 | 0 | SOU1;sorbosereductase[EC:1.1.1.289] |
| K17743 | 6.13E-07 | 3.5E-06 | 8.68E-07 | 9.12E-07 | 0 | XR;D-xylosereductase[EC:1.1.1.307] |
| K17744 | 1.82E-05 | 2.09E-05 | 1.61E-05 | 2.11E-05 | 2.27E-05 | GalDH;L-galactosedehydrogenase[EC:1.1.1.316] |
| K17761 | 0 | 1.24E-06 | 0 | 0 | 0 | SSADH;succinate-semialdehydedehydrogenase,mitochondrial[EC:1.2.1.24] |
| K17818 | 2.74E-06 | 4.32E-06 | 1.3E-06 | 3.66E-06 | 4.48E-06 | ARD1;D-arabinitoldehydrogenase(NADP+)[EC:1.1.1.287] |
| K17829 | 3.55E-05 | 2.71E-05 | 1.17E-05 | 1.49E-05 | 2.31E-05 | ccrA;crotonyl-CoAreductase[EC:1.3.1.86] |
| K17865 | 5.04E-05 | 4.53E-05 | 4.34E-05 | 3.94E-05 | 4.24E-05 | croR;3-hydroxybutyryl-CoAdehydratase[EC:4.2.1.55] |
| K18009 | 4.7E-05 | 3.47E-05 | 4.99E-05 | 3.91E-05 | 4.6E-05 | budC;meso-butanedioldehydrogenase/(S,S)-butanedioldehydrogenase/diacetylreduct |
| K18020 | 0 | 5.86E-07 | 1.01E-06 | 8.99E-07 | 2.88E-06 | cutA;glyceraldehydedehydrogenaselargesubunit[EC:1.2.99.8] |
| K18022 | 0 | 1.13E-06 | 1.18E-06 | 0 | 0 | cutC;glyceraldehydedehydrogenasesmallsubunit[EC:1.2.99.8] |
| K18106 | 0 | 0 | 0 | 5.61E-07 | 1.07E-06 | GAAA;D-galacturonatereductase[EC:1.1.1.-] |
| K18118 | 7.43E-06 | 1.35E-05 | 1.89E-05 | 1.77E-05 | 9.03E-06 | aarC,cat1;succinyl-CoA:acetateCoA-transferase[EC:2.8.3.18] |
| K18119 | 2.21E-05 | 2.1E-05 | 2.88E-05 | 1.94E-05 | 3.2E-05 | sucD;succinate-semialdehydedehydrogenase[EC:1.2.1.76] |
| K18121 | 5.6E-05 | 8.76E-05 | 2.93E-05 | 4.76E-05 | 4.59E-05 | GLYR;glyoxylate/succinicsemialdehydereductase[EC:1.1.1.791.1.1.-] |
| K18122 | 1.43E-05 | 1.37E-05 | 1.93E-05 | 1.77E-05 | 2.71E-05 | cat2,abfT;4-hydroxybutyrateCoA-transferase[EC:2.8.3.-] |
| K18123 | 5.61E-05 | 4.98E-05 | 6.52E-05 | 7.07E-05 | 4.99E-05 | HOGA1;4-hydroxy-2-oxoglutaratealdolase[EC:4.1.3.16] |
| K18125 | 0 | 1.26E-06 | 1.83E-06 | 5.88E-07 | 6.59E-07 | ssgdh;aldose1-dehydrogenase[NAD(P)+][EC:1.1.1.359] |
| K18223 | 4.03E-05 | 5.11E-05 | 2.76E-05 | 2.62E-05 | 3.68E-05 | prmA;propane2-monooxygenaselargesubunit[EC:1.14.13.227] |
| K18224 | 4.37E-05 | 6.45E-05 | 2.16E-05 | 2.55E-05 | 3.9E-05 | prmC;propane2-monooxygenasesmallsubunit[EC:1.14.13.227] |
| K18225 | 2.91E-05 | 4.79E-05 | 2.45E-05 | 2.63E-05 | 2.93E-05 | prmB;propanemonooxygenasereductasecomponent[EC:1.18.1.-] |
| K18226 | 1.23E-05 | 2.38E-05 | 6.31E-06 | 6.11E-06 | 5.64E-06 | prmD;propanemonooxygenasecouplingprotein |
| K18288 | 1.44E-05 | 2.56E-05 | 1.79E-05 | 8.42E-06 | 8E-06 | ict-Y;itaconateCoA-transferase[EC:2.8.3.-] |
| K18289 | 3.14E-05 | 1.39E-05 | 2.87E-05 | 2.52E-05 | 2.74E-05 | ict-P;itaconateCoA-transferase[EC:2.8.3.-2.8.3.22] |
| K18290 | 1.58E-05 | 1.67E-05 | 8.87E-06 | 8.18E-06 | 1.34E-05 | ich-Y;itaconyl-CoAhydratase[EC:4.2.1.56] |
| K18291 | 7.91E-07 | 2.89E-06 | 1.01E-06 | 2.45E-06 | 1.09E-06 | ich-P;itaconyl-CoAhydratase/mesaconyl-C4CoAhydratase[EC:4.2.1.564.2.1.-] |
| K18292 | 6.93E-06 | 5.05E-06 | 1.01E-05 | 8.05E-06 | 3.41E-06 | E4.1.3.25;(S)-citramalyl-CoAlyase[EC:4.1.3.25] |
| K18333 | 2.73E-05 | 5.42E-05 | 3.87E-05 | 6.15E-05 | 1.72E-05 | K18333;L-fucosedehydrogenase |
| K18334 | 8.3E-05 | 0.000109 | 6.82E-05 | 9.54E-05 | 0.000109 | fucD;L-fuconatedehydratase[EC:4.2.1.68] |
| K18335 | 0.000106 | 0.000136 | 0.000114 | 0.000101 | 9.68E-05 | K18335;2-keto-3-deoxy-L-fuconatedehydrogenase[EC:1.1.1.-] |
| K18336 | 2.52E-05 | 2.45E-05 | 3.27E-05 | 3.21E-05 | 2.09E-05 | K18336;2,4-diketo-3-deoxy-L-fuconatehydrolase[EC:3.7.1.-] |
| K18337 | 1.15E-05 | 1.75E-05 | 9.48E-06 | 9.3E-06 | 9.05E-06 | LRA1;L-rhamnose1-dehydrogenase[EC:1.1.1.3781.1.1.3771.1.1.173] |
| K18366 | 5.82E-06 | 9.08E-06 | 6.63E-06 | 6.63E-06 | 7.31E-06 | bphJ,xylQ,nahO,tesF;acetaldehyde/propanaldehydrogenase[EC:1.2.1.101.2.1.87] |
| K18369 | 8.97E-05 | 0.000115 | 9.97E-05 | 8.14E-05 | 8.2E-05 | adh2;alcoholdehydrogenase[EC:1.1.1.-] |
| K18371 | 2.93E-05 | 4.12E-05 | 3.02E-05 | 2.44E-05 | 2.52E-05 | acmA;acetonemonooxygenase(methylacetate-forming)[EC:1.14.13.226] |
| K18372 | 4.69E-05 | 5.12E-05 | 3.12E-05 | 2.68E-05 | 3.76E-05 | acmB;methylacetatehydrolase[EC:3.1.1.-] |
| K18382 | 3.41E-05 | 4.34E-05 | 1.6E-05 | 2.62E-05 | 2.67E-05 | adh1;NAD+-dependentsecondaryalcoholdehydrogenaseAdh1[EC:1.1.1.-] |
| K18429 | 2.53E-06 | 2.04E-06 | 6.08E-06 | 7.73E-06 | 1.76E-05 | legG,neuC2;GDP/UDP-N,N'-diacetylbacillosamine2-epimerase(hydrolysing)[EC:3.2.1.18 |
| K18430 | 1.61E-05 | 1.88E-05 | 1.6E-05 | 1.96E-05 | 2.6E-05 | legI,neuB2;N,N'-diacetyllegionaminatesynthase[EC:2.5.1.101] |
| K18431 | 3.56E-06 | 2.75E-06 | 6.61E-06 | 3.29E-06 | 5.08E-06 | legF,ptmB;CMP-N,N'-diacetyllegionaminicacidsynthase[EC:2.7.7.82] |
| K18471 | 9.56E-07 | 0 | 0 | 4.56E-07 | 0 | ydjG;methylglyoxalreductase[EC:1.1.1.-] |
| K18472 | 1.3E-05 | 1.64E-05 | 7.85E-06 | 8.32E-06 | 1.24E-05 | accD6;acetyl-CoA/propionyl-CoAcarboxylasecarboxyltransferasesubunit[EC:6.4.1.26 |
| K18649 | 1.53E-05 | 2.22E-05 | 1.65E-05 | 1.47E-05 | 1.75E-05 | IMPL2;inositol-phosphatephosphatase/L-galactose1-phosphatephosphatase/histidin |
| K18675 | 1.77E-06 | 1.82E-06 | 1.01E-06 | 0 | 0 | chbP;N,N'-diacetylchitobiosephosphorylase[EC:2.4.1.280] |
| K18676 | 4.53E-05 | 5.43E-05 | 5.2E-05 | 5.79E-05 | 5.02E-05 | gspK;glucosaminekinase[EC:2.7.1.8] |
| K18677 | 6.13E-07 | 0 | 0 | 0 | 2.77E-06 | GALAK;galacturonokinase[EC:2.7.1.44] |
| K18981 | 0.000131 | 0.000123 | 0.000122 | 0.000114 | 0.000128 | udh;uronatedehydrogenase[EC:1.1.1.203] |
| K18982 | 3.81E-05 | 2.67E-05 | 4.39E-05 | 2.93E-05 | 3.03E-05 | gli;D-galactarolactoneisomerase[EC:5.4.1.4] |
| K18983 | 0.00015 | 0.000137 | 0.000128 | 0.000115 | 0.000138 | gci;D-galactarolactonecycloisomerase[EC:5.5.1.27] |
| K19243 | 2.62E-06 | 5.58E-07 | 3.19E-06 | 2.52E-06 | 2.64E-06 | azf;NAD+dependentglucose-6-phosphatedehydrogenase[EC:1.1.1.388] |
| K19266 | 0 | 3.29E-06 | 2.43E-06 | 4.56E-07 | 0 | E1.2.1.22;lactaldehydedehydrogenase[EC:1.2.1.22] |
| K19268 | 3.17E-06 | 5.58E-07 | 3.05E-06 | 3.23E-06 | 2.8E-06 | glmE,mutE,mamB;methylaspartatemutaseepsilonsubunit[EC:5.4.99.1] |
| K19269 | 0 | 0 | 2.63E-06 | 0 | 0 | PGP,PGLP;phosphoglycolatephosphatase[EC:3.1.3.183.1.3.48] |
| K19280 | 2.35E-06 | 0 | 5.07E-07 | 4.56E-07 | 2.81E-06 | mct;succinyl-CoA:mesaconateCoAtransferase[EC:2.8.3.-] |
| K19290 | 1.21E-06 | 5.58E-07 | 2.09E-06 | 0 | 0 | alg8;mannuronansynthase[EC:2.4.1.33] |
| K19312 | 1.39E-05 | 4.68E-06 | 7.1E-06 | 6.22E-06 | 1.83E-05 | pccB;acetyl-CoA/propionyl-CoAcarboxylasecarboxyltransferasesubunit[EC:6.4.1.26 |
| K19355 | 3.3E-05 | 2.11E-05 | 1.82E-05 | 2.01E-05 | 3.78E-05 | MAN;mannanendo-1,4-beta-mannosidase[EC:3.2.1.78] |
| K19517 | 0 | 0 | 0 | 9.12E-07 | 2E-06 | MIK;1D-myo-inositol3-kinase[EC:2.7.1.64] |
| K19551 | 2.45E-06 | 0 | 0 | 0 | 4.55E-06 | pelC;pectatelyaseC[EC:4.2.2.24.2.2.10] |
| K19660 | 0 | 1.24E-06 | 0 | 0 | 0 | araDH;L-arabinose1-dehydrogenase[NAD(P)+][EC:1.1.1.376] |
| K19668 | 6.62E-05 | 6.51E-05 | 8.41E-05 | 8.03E-05 | 9.36E-05 | CBH2,cbhA;cellulose1,4-beta-cellobiosidase[EC:3.2.1.91] |
| K19709 | 0 | 0 | 0 | 5.43E-07 | 0 | ydiF;acetateCoA-transferase[EC:2.8.3.8] |
| K19745 | 0.000139 | 0.000175 | 0.000156 | 0.00013 | 0.000111 | acuI;acrylyl-CoAreductase(NADPH)[EC:1.3.1.-] |
| K19813 | 7.54E-06 | 1.81E-05 | 1.14E-05 | 1.56E-05 | 2.03E-05 | gdh;glucosedehydrogenase[EC:1.1.5.9] |
| K19956 | 0 | 0 | 0 | 1.19E-06 | 0 | sorE;L-sorbose1-phosphatereductase[EC:1.1.1.-] |
| K20023 | 9.4E-05 | 8.9E-05 | 9.79E-05 | 9.38E-05 | 9.07E-05 | talrD-galrD;L-talarate/galactaratedehydratase[EC:4.2.1.1564.2.1.42] |
| K20117 | 6.13E-07 | 8.76E-07 | 5.07E-07 | 0 | 8.44E-07 | PTS-Glc1-EIIB,ptsG,glcA,glcB;PTSsystem,glucose-specificIIBcomponent[EC:2.7.1. |
| K20370 | 2.34E-05 | 3.58E-05 | 2.99E-05 | 2.81E-05 | 1.74E-05 | PEPCK;phosphoenolpyruvatecarboxykinase(diphosphate)[EC:4.1.1.38] |
| K20455 | 6.13E-07 | 0 | 1.1E-06 | 4.56E-07 | 5.65E-06 | acnD;2-methylcitratedehydratase(2-methyl-trans-aconitateforming)[EC:4.2.1.117] |
| K20547 | 6.13E-07 | 0 | 0 | 0 | 1.44E-06 | CHIB;basicendochitinaseB[EC:3.2.1.14] |