## Fsr regulon

| | | | Late log | | | | Entry Stat | | | | Early Stat | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ID | Name | PCR | Fold | *p* | Int OG1RF | Int TX5266 | Fold | *p* | Int OG1RF | Int TX5266 | Fold | *p* | Int OG1RF | Int TX5266 |
| EF0002 | DNA polymerase III, beta subunit | 488 | | | | | | | | | 3 | 0.006 | 14725 | 6699 |
| **EF0004** | **recF protein** | 497 | | | | | **3** | 0.040 | 4518 | 2259 | | | | |
| **EF0005** | **DNA gyrase, B subunit** | 498 | | | | | **3** | 0.035 | 8505 | 3569 | | | | |
| **EF0006** | **DNA gyrase, A subunit** | 497 | | | | | **3** | 0.006 | 14938 | 6162 | | | | |
| EF0012 | ribosomal protein L9 | 407 | | | | | 2 | 0.038 | 21951 | 14619 | | | | |
| EF0016 | DegV family protein | 503 | | | | | | | | | 2 | 0.036 | 4477 | 3050 |
| EF0025 | hypothetical protein | 452 | | | | | 3 | 0.008 | 6228 | 2825 | | | | |
| EF0026 | hypothetical protein | 251 | | | | | 2 | 0.013 | 3538 | 2937 | | | | |
| EF0041 | conserved hypothetical protein | 506 | | | | | 3 | 0.021 | 5770 | 3444 | | | | |
| EF0042 | 2C-methyl-D-erythritol 2,4-cyclodiphosphate syn | 463 | | | | | 2 | 0.012 | 12696 | 9071 | | | | |
| EF0076 | oxidoreductase, short chain dehydrogenase/redu | 503 | | | | | 2 | 0.011 | 41655 | 33706 | | | | |
| EF0079 | gls24 protein | 471 | | | | | | | | | 2 | 0.018 | 23057 | 16995 |
| EF0080 | gls24 protein | 506 | | | | | 2 | 0.035 | 22485 | 13985 | | | | |
| EF0081 | conserved hypothetical protein | 224 | | | | | 3 | 0.049 | 18866 | 11059 | | | | |
| EF0094 | formate/nitrite transporter family protein | 500 | -2 | 0.007 | 6960 | 9136 | | | | | | | | |
| EF0095 | conserved hypothetical protein | 494 | | | | | 2 | 0.018 | 9831 | 5749 | | | | |
| EF0097 | regulatory protein pfoR | 493 | 4 | 0.046 | 7864 | 2196 | | | | | | | | |
| EF0098 | L-serine dehydratase, iron-sulfur-dependent, bet | 514 | | | | | 2 | 0.014 | 2601 | 1426 | | | | |
| EF0099 | L-serine dehydratase, iron-sulfur-dependent, alp | 511 | 3 | 0.040 | 3460 | 1527 | | | | | | | | |
| **EF0104** | **arginine deiminase** | 502 | **-5** | 0.034 | 9974 | 17364 | **-3** | 0.000 | 30050 | 47518 | | | | |
| **EF0105** | **ornithine carbamoyltransferase, catabolic** | 499 | **-6** | 0.009 | 4229 | 13072 | **-2** | 0.007 | 41236 | 57596 | | | | |
| **EF0106** | **carbamate kinase** | 495 | **-3** | 0.010 | 4048 | 7942 | **-3** | 0.010 | 34082 | 46973 | **-4** | 0.035 | 20348 | 39863 |
| **EF0108** | **conserved hypothetical protein** | 501 | **-3** | 0.023 | 3015 | 4693 | **-3** | 0.002 | 21026 | 37091 | **-3** | 0.029 | 11364 | 28473 |
| EF0202 | phosphomethylpyrimidine kinase, putative | 498 | | | | | | | | | -3 | 0.046 | 1817 | 3792 |
| **EF0213** | **ribosomal protein L16** | 407 | | | | | **2** | 0.008 | 25764 | 17086 | | | | |
| **EF0214** | **ribosomal protein L29** | 144 | | | | | **3** | 0.021 | 4075 | 2795 | | | | |
| **EF0215** | **ribosomal protein S17** | 196 | | | | | **3** | 0.030 | 5870 | 3533 | | | | |
| **EF0216** | **ribosomal protein L14** | 297 | | | | | **2** | 0.018 | 12838 | 6663 | | | | |
| **EF0217** | **ribosomal protein L24** | 208 | | | | | **2** | 0.017 | 10366 | 5650 | | | | |
| **EF0219** | **ribosomal protein S14** | 144 | | | | | **2** | 0.001 | 10030 | 6038 | | | | |
| **EF0220** | **ribosomal protein S8** | 368 | | | | | **2** | 0.023 | 23788 | 20261 | | | | |
| **EF0221** | **ribosomal protein L6** | 488 | | | | | **3** | 0.044 | 3484 | 2075 | | | | |
| **EF0225** | **ribosomal protein L30** | 106 | | | | | **2** | 0.022 | 8840 | 5378 | | | | |
| EF0228 | adenylate kinase | 499 | | | | | 2 | 0.023 | 16041 | 9495 | | | | |
| EF0256 | peptidyl-tRNA hydrolase | 499 | | | | | 3 | 0.013 | 4387 | 2102 | 2 | 0.019 | 4367 | 2258 |
| EF0257 | transcription-repair coupling factor | 501 | 2 | 0.000 | 6823 | 3713 | 7 | 0.000 | 13528 | 3507 | 4 | 0.009 | 8559 | 3501 |
| EF0258 | low temperature requirement B protein, putative | 506 | 2 | 0.005 | 5674 | 3559 | 6 | 0.003 | 7986 | 2345 | 4 | 0.010 | 4009 | 1989 |
| EF0259 | S4 domain protein | 172 | | | | | 6 | 0.004 | 6555 | 2518 | 3 | 0.036 | 2964 | 1435 |
| EF0270 | PTS system component | 500 | | | | | | | | | -3 | 0.020 | 1212 | 2218 |
| EF0285 | dihydroorotate dehydrogenase | 505 | 2 | 0.006 | 28127 | 16305 | | | | | 2 | 0.020 | 7140 | 3977 |
| EF0291 | glycosyl hydrolase, family 1 | 503 | | | | | | | | | -4 | 0.031 | 4707 | 16249 |
| EF0292 | PTS system component | 505 | | | | | -3 | 0.015 | 3202 | 7324 | -4 | 0.021 | 2631 | 11723 |
| EF0296 | Na+/H+ exchanger family protein | 503 | | | | | 3 | 0.013 | 18889 | 10683 | | | | |
| EF0298 | cation-transporting Pase, E1-E2 family | 496 | | | | | | | | | 2 | 0.017 | 5580 | 3034 |
| EF0301 | transcriptional regulator, GntR family | 313 | -2 | 0.021 | 3354 | 3238 | | | | | | | | |
| EF0362 | chitinase, putative | 487 | | | | | 2 | 0.029 | 5000 | 2010 | | | | |
| EF0372 | DNA-binding response regulator | 500 | | | | | | | | | 2 | 0.022 | 2558 | 1520 |
| EF0377 | Ank repeat, putative | 500 | | | | | | | | | -2 | 0.006 | 3127 | 6706 |
| EF0379 | death on curing protein, putative | 297 | | | | | 2 | 0.013 | 20737 | 15285 | | | | |
| EF0396 | hypothetical protein | 495 | | | | | 3 | 0.005 | 25956 | 15315 | 2 | 0.036 | 10685 | 7941 |
| EF0397 | conserved hypothetical protein | 462 | | | | | 3 | 0.015 | 11657 | 8172 | | | | |
| EF0399 | conserved hypothetical protein | 493 | | | | | 3 | 0.016 | 4794 | 1939 | | | | |
| EF0402 | Na+/H+ antiporter | 498 | 3 | 0.002 | 12993 | 6102 | | | | | 5 | 0.033 | 11396 | 4593 |
| EF0405 | hydrolase, haloacid dehalogenase-like family | 499 | | | | | | | | | 2 | 0.012 | 22939 | 12455 |
| **EF0408** | **PTS system component** | 410 | | | | | **3** | 0.022 | 2840 | 1351 | | | | |
| **EF0411** | **PTS system component** | 498 | | | | | **12** | 0.005 | 39590 | 15549 | **13** | 0.009 | 22441 | 4250 |
| **EF0412** | **PTS system component** | 306 | | | | | **10** | 0.020 | 20563 | 7075 | **9** | 0.032 | 16795 | 3868 |
| **EF0413** | **mannitol-1-phosphate 5-dehydrogenase** | 506 | | | | | | | | | **7** | 0.005 | 41301 | 14545 |
| EF0417 | conserved hypothetical protein | 492 | -2 | 0.018 | 11185 | 15992 | | | | | | | | |
| EF0448 | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carb | 506 | | | | | 2 | 0.030 | 5420 | 2333 | | | | |
| EF0449 | hydrolase, alpha/beta hydrolase fold family | 493 | | | | | | | | | 2 | 0.049 | 10535 | 6328 |
| EF0450 | chloromuconate cycloisomerase, putative | 501 | | | | | 3 | 0.028 | 4605 | 2449 | | | | |
| EF0455 | PTS system component | 506 | | | | | | | | | 3 | 0.032 | 2102 | 1195 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| EF0458 | phosphosugar-binding transcriptional regulator, I | 491 | | | | | 2 | 0.032 | 9275 | 4757 | 3 | 0.018 | 5793 | 3035 |
| EF0459 | glucokinase regulator-related protein | 498 | | | | | | | | | 3 | 0.010 | 8356 | 4446 |
| EF0633 | tyrosyl-tRNA synthetase | 498 | | | | | | | | | 6 | 0.005 | 46986 | 19405 |
| EF0634 | decarboxylase, putative | 503 | -2 | 0.020 | 22437 | 29562 | | | | | | | | |
| EF0651 | peptidase A, putative, authentic frameshift | 494 | | | | | 4 | 0.016 | 12522 | 5294 | 3 | 0.012 | 8732 | 3959 |
| EF0670 | ribosomal small subunit pseudouridine synthase | 507 | 2 | 0.031 | 10875 | 6856 | | | | | | | | |
| EF0681 | conserved hypothetical protein | 299 | | | | | 2 | 0.050 | 27598 | 16771 | | | | |
| EF0691 | conserved hypothetical protein TIGR00091 | 495 | 2 | 0.007 | 8503 | 4512 | | | | | | | | |
| EF0703 | conserved hypothetical protein | 475 | 2 | 0.009 | 4081 | 2435 | | | | | | | | |
| EF0713 | hypothetical protein | 497 | | | | | 4 | 0.038 | 7431 | 3161 | | | | |
| EF0717 | PTS system component | 500 | | | | | 2 | 0.014 | 8285 | 5473 | | | | |
| EF0718 | carbohydrate kinase, PfkB family | 512 | | | | | 2 | 0.029 | 4070 | 2403 | | | | |
| EF0728 | RNA methyltransferase, TrmA family | 508 | | | | | 2 | 0.007 | 10549 | 5176 | | | | |
| EF0744 | sodium/dicarboxylate symporter family protein | 494 | | | | | 2 | 0.003 | 3826 | 1933 | | | | |
| EF0747 | conserved domain protein | 509 | | | | | 3 | 0.001 | 25309 | 11336 | 2 | 0.041 | 17786 | 10373 |
| EF0748 | rhodanese family protein | 499 | 2 | 0.001 | 15854 | 9837 | 3 | 0.006 | 20499 | 8975 | 3 | 0.003 | 18195 | 7799 |
| **EF0750** | **proteinase, PI-type, putative** | 210 | **3** | 0.002 | 3797 | 1731 | | | | | | | | |
| **EF0751** | **hypothetical protein** | 502 | **4** | 0.002 | 16667 | 6387 | **4** | 0.003 | 3298 | 1110 | | | | |
| **EF0752** | **hypothetical protein** | 496 | **3** | 0.002 | 13142 | 5555 | **4** | 0.003 | 2796 | 935 | | | | |
| **EF0753** | **hypothetical protein** | 497 | **4** | 0.003 | 16553 | 6484 | **4** | 0.004 | 3628 | 1214 | | | | |
| **EF0754** | **conserved hypothetical protein** | 485 | **4** | 0.004 | 20762 | 8423 | **4** | 0.002 | 4049 | 1498 | | | | |
| **EF0756** | **hypothetical protein** | 378 | **3** | 0.002 | 2143 | 1100 | | | | | | | | |
| EF0763 | excinuclease ABC, subunit A | 503 | | | | | 2 | 0.041 | 9184 | 5263 | | | | |
| EF0794 | conserved hypothetical protein | 475 | | | | | 3 | 0.004 | 6544 | 2571 | | | | |
| EF0795 | conserved hypothetical protein | 503 | | | | | 3 | 0.005 | 7371 | 3035 | | | | |
| EF0796 | acid phosphatase | 513 | | | | | 2 | 0.020 | 3486 | 2024 | | | | |
| EF0801 | leucyl-tRNA synthetase | 498 | | | | | 4 | 0.006 | 9618 | 3771 | | | | |
| EF0805 | amino acid ABC transporter, P-binding protein | 495 | -2 | 0.046 | 2592 | 3300 | | | | | | | | |
| EF0819 | hypothetical protein | 240 | | | | | | | | | 2 | 0.008 | 3825 | 2000 |
| EF0827 | oxidoreductase, Gfo/Idh/MocA family | 501 | | | | | | | | | -2 | 0.042 | 2948 | 5860 |
| EF0846 | P-dependent RNA helicase DeaD | 500 | | | | | 3 | 0.000 | 6927 | 2436 | | | | |
| EF0848 | holo-(acyl-carrier-protein) synthase | 322 | | | | | | | | | -4 | 0.023 | 1395 | 2129 |
| EF0849 | alanine racemase | 496 | | | | | | | | | -3 | 0.007 | 1106 | 2043 |
| EF0859 | cation efflux family | 499 | | | | | 2 | 0.039 | 2519 | 1794 | | | | |
| EF0861 | acetyltransferase, GN family | 378 | 2 | 0.016 | 7376 | 4502 | | | | | | | | |
| EF0862 | amino acid ABC transporter, permease protein | 503 | | | | | 2 | 0.040 | 18470 | 11907 | | | | |
| EF0879 | formamidopyrimidine-DNA glycosylase | 500 | 2 | 0.005 | 17137 | 9988 | 4 | 0.036 | 10781 | 4283 | | | | |
| EF0884 | conserved hypothetical protein | 498 | 3 | 0.032 | 2226 | 1395 | | | | | | | | |
| EF0886 | hypothetical protein | 504 | 2 | 0.000 | 5305 | 2647 | 4 | 0.005 | 7788 | 2174 | | | | |
| EF0887 | glycosyl transferase domain protein | 510 | 2 | 0.007 | 4989 | 2346 | | | | | | | | |
| EF0888 | hypothetical protein | 499 | | | | | 4 | 0.041 | 3001 | 811 | | | | |
| EF0889 | hypothetical protein | 504 | | | | | 3 | 0.022 | 2804 | 1170 | | | | |
| EF0903 | mevalonate diphosphate decarboxylase | 502 | 3 | 0.016 | 3101 | 1644 | | | | | | | | |
| EF0911 | peptide ABC transporter, P-binding protein | 500 | | | | | 4 | 0.041 | 17344 | 8066 | | | | |
| EF0912 | peptide ABC transporter, P-binding protein | 495 | | | | | 3 | 0.016 | 5494 | 2445 | 2 | 0.037 | 3282 | 1719 |
| EF0914 | translation initiation factor IF-3 | 482 | | | | | | | | | 3 | 0.019 | 19615 | 11890 |
| EF0927 | sensor histidine kinase | 494 | | | | | | | | | -2 | 0.018 | 4959 | 5030 |
| EF0939 | methylglyoxal synthase | 404 | | | | | 2 | 0.031 | 6952 | 3432 | | | | |
| EF0940 | conserved hypothetical protein | 404 | | | | | 2 | 0.022 | 12784 | 7230 | | | | |
| EF0945 | acetyltransferase, GN family | 500 | 2 | 0.022 | 8838 | 3921 | 3 | 0.024 | 3345 | 1620 | | | | |
| EF0946 | conserved hypothetical protein | 471 | | | | | 2 | 0.031 | 13801 | 7954 | 3 | 0.043 | 10917 | 4923 |
| EF0947 | hydrolase, haloacid dehalogenase-like family | 501 | | | | | | | | | 3 | 0.016 | 15211 | 7044 |
| **EF0955** | **aldose 1-epimerase, putative** | 503 | | | | | **6** | 0.003 | 7195 | 2013 | | | | |
| **EF0956** | **beta-phosphoglucomutase** | 500 | | | | | **7** | 0.006 | 11580 | 3107 | **6** | 0.008 | 7814 | 2049 |
| **EF0957** | **glycosyl transferase, family 65** | 504 | | | | | **6** | 0.009 | 13216 | 4189 | **7** | 0.007 | 12735 | 2621 |
| **EF0958** | **PTS system component** | 501 | | | | | **5** | 0.008 | 8632 | 2622 | **6** | 0.020 | 5826 | 1533 |
| EF0976 | conserved hypothetical protein | 370 | | | | | | | | | -2 | 0.034 | 2599 | 4247 |
| EF0982 | hemolysin A | 501 | | | | | 3 | 0.023 | 9188 | 4260 | 2 | 0.041 | 3754 | 2445 |
| EF1004 | glucose-6-phosphate 1-dehydrogenase | 506 | | | | | 2 | 0.006 | 15136 | 10190 | | | | |
| EF1020 | glycosyl hydrolase, family 1 | 508 | | | | | 3 | 0.026 | 12157 | 5453 | | | | |
| EF1021 | conserved hypothetical protein | 501 | | | | | | | | | 2 | 0.009 | 9689 | 5874 |
| EF1033 | 6-aminohexanoate-cyclic-dimer hydrolase, putat | 501 | | | | | | | | | 3 | 0.043 | 4458 | 1918 |
| EF1046 | pyruvate kinase | 507 | | | | | 2 | 0.012 | 27290 | 19172 | | | | |
| EF1047 | conserved hypothetical protein | 469 | | | | | | | | | 2 | 0.028 | 10663 | 4996 |
| EF1051 | sensor histidine kinase | 485 | 3 | 0.004 | 23818 | 14747 | | | | | | | | |
| EF1081 | hypothetical protein | 349 | -2 | 0.019 | 3813 | 5403 | -2 | 0.008 | 2893 | 3507 | | | | |
| **EF1090** | **hypothetical protein** | 500 | **-3** | 0.025 | 1441 | 2729 | | | | | | | | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **EF1091** | **hypothetical protein** | 500 | **-5** | 0.012 | 25172 | 34779 | | | | | | | | |
| **EF1092** | **conserved hypothetical protein** | 500 | **-4** | 0.011 | 16027 | 21743 | | | | | | | | |
| **EF1093** | **LPX-motif cell wall anchor domain protein** | 496 | **-4** | 0.005 | 24900 | 34987 | **-3** | 0.031 | 11832 | 17431 | | | | |
| **EF1094** | **LPX-site transpeptidase family protein** | 488 | **-2** | 0.019 | 9484 | 13402 | | | | | | | | |
| **EF1097** | **hypothetical protein** | 466 | **214** | 0.004 | 14581 | 316 | **10** | 0.050 | 4338 | 516 | | | | |
| EF1106 | hypothetical protein | 100 | 2 | 0.016 | 3129 | 3034 | | | | | | | | |
| EF1108 | conserved hypothetical protein | 499 | -2 | 0.015 | 9248 | 12279 | | | | | | | | |
| EF1120 | amino acid ABC transporter, P-binding protein | 507 | | | | | 4 | 0.034 | 6986 | 2259 | | | | |
| EF1152 | conserved hypothetical protein | 498 | | | | | | | | | 2 | 0.030 | 6284 | 3321 |
| EF1153 | carboxypeptidase | 500 | | | | | 2 | 0.015 | 14854 | 8725 | 2 | 0.000 | 11492 | 6884 |
| EF1154 | conserved hypothetical protein | 500 | | | | | 4 | 0.026 | 13692 | 7026 | 2 | 0.022 | 9108 | 5104 |
| EF1155 | endonuclease III | 497 | 2 | 0.007 | 17009 | 9858 | 3 | 0.005 | 13673 | 6373 | | | | |
| EF1160 | PTS system component | 500 | | | | | | | | | -2 | 0.045 | 2482 | 1871 |
| EF1167 | fructose-bisphosphate aldolase | 486 | | | | | -3 | 0.006 | 8733 | 15841 | | | | |
| EF1189 | hypothetical protein | 515 | | | | | 2 | 0.041 | 4505 | 2852 | | | | |
| EF1190 | hypothetical protein | 469 | 3 | 0.000 | 27580 | 13454 | | | | | | | | |
| EF1191 | DegV family protein | 496 | 3 | 0.010 | 30212 | 12243 | 3 | 0.048 | 6383 | 3262 | 2 | 0.026 | 3430 | 1787 |
| EF1206 | malate oxidoreductase | 500 | -2 | 0.016 | 8167 | 10520 | -5 | 0.003 | 12551 | 35780 | | | | |
| EF1207 | citrate carrier protein | 504 | | | | | -2 | 0.013 | 5629 | 7391 | | | | |
| EF1213 | acetolactate synthase | 501 | -2 | 0.010 | 14831 | 19082 | | | | | | | | |
| EF1219 | spermidine/putrescine ABC transporter, permeas | 500 | | | | | 2 | 0.004 | 2329 | 1556 | | | | |
| EF1228 | hypothetical protein | 503 | -2 | 0.004 | 8950 | 13499 | | | | | | | | |
| EF1229 | conserved hypothetical protein | 490 | -2 | 0.007 | 4375 | 6388 | | | | | | | | |
| EF1254 | ABC transporter, permease protein | 508 | 2 | 0.007 | 2269 | 1471 | | | | | | | | |
| EF1255 | ABC transporter, P-binding protein | 515 | 2 | 0.011 | 4225 | 2710 | | | | | | | | |
| EF1256 | membrane protein, putative | 410 | | | | | 2 | 0.009 | 5419 | 3027 | | | | |
| EF1271 | N utilization substance protein A | 497 | | | | | 3 | 0.005 | 4035 | 1789 | | | | |
| EF1274 | translation initiation factor IF-2 | 500 | | | | | 2 | 0.004 | 27445 | 14496 | | | | |
| EF1300 | cell division protein, FtsW/RodA/SpovE family | 501 | -2 | 0.001 | 4860 | 7110 | | | | | | | | |
| EF1306 | heat-inducible transcription repressor HrcA | 512 | | | | | 2 | 0.000 | 24776 | 15891 | | | | |
| EF1307 | heat shock protein GrpE | 481 | | | | | 2 | 0.001 | 27789 | 16407 | | | | |
| EF1308 | dnak protein | 501 | | | | | 2 | 0.000 | 24684 | 13369 | | | | |
| EF1310 | dnaJ protein | 505 | | | | | 2 | 0.012 | 10101 | 5293 | | | | |
| EF1322 | conserved hypothetical protein | 508 | | | | | 2 | 0.007 | 22665 | 14053 | 2 | 0.023 | 22751 | 13106 |
| EF1323 | conserved hypothetical protein, authentic point n | 497 | | | | | 2 | 0.007 | 30289 | 16311 | 3 | 0.032 | 25141 | 13283 |
| EF1327 | (R)-2-hydroxyglutaryl-CoA dehydratase activator | 501 | -3 | 0.006 | 16697 | 25332 | -2 | 0.021 | 4347 | 5967 | | | | |
| EF1343 | maltose ABC transporter, permease protein, put | 494 | | | | | 6 | 0.002 | 7052 | 2050 | 4 | 0.033 | 4477 | 1968 |
| EF1344 | maltose ABC transporter, permease protein | 498 | | | | | 4 | 0.025 | 4691 | 1901 | | | | |
| EF1345 | maltose ABC transporter, maltose-binding protei | 502 | | | | | 4 | 0.007 | 26745 | 13095 | 5 | 0.004 | 27207 | 8869 |
| EF1352 | cation-transporting Pase, E1-E2 family | 496 | | | | | 2 | 0.000 | 7348 | 3514 | | | | |
| EF1353 | pyruvate dehydrogenase complex, E1 componer | 493 | | | | | 2 | 0.044 | 37222 | 29195 | | | | |
| EF1376 | hypothetical protein | 496 | 3 | 0.007 | 19261 | 9070 | | | | | | | | |
| EF1404 | MutS2 family protein | 501 | | | | | | | | | 3 | 0.031 | 2837 | 1338 |
| EF1450 | conserved hypothetical protein | 474 | | | | | 2 | 0.004 | 5724 | 3258 | | | | |
| EF1451 | hypothetical protein | 219 | | | | | 2 | 0.017 | 2690 | 1788 | | | | |
| EF1494 | V-type Pase, subunit K | 391 | | | | | 2 | 0.032 | 6369 | 4093 | | | | |
| EF1496 | V-type Pase, subunit C | 488 | | | | | 2 | 0.000 | 15182 | 8176 | | | | |
| EF1497 | V-type Pase, subunit G | 285 | | | | | 2 | 0.008 | 7057 | 3608 | | | | |
| EF1498 | V-type Pase, subunit A | 500 | | | | | 2 | 0.005 | 9796 | 5697 | | | | |
| EF1499 | V-type Pase, subunit B | 499 | | | | | 2 | 0.003 | 11783 | 6427 | 2 | 0.021 | 8010 | 5113 |
| EF1500 | V-type Pase, subunit D | 489 | | | | | 3 | 0.002 | 9180 | 3941 | | | | |
| EF1501 | hypothetical protein | 261 | 2 | 0.018 | 10842 | 6088 | 4 | 0.015 | 10459 | 6171 | | | | |
| EF1515 | transcription antiterminator BglG family protein | 515 | 3 | 0.000 | 8264 | 4197 | | | | | | | | |
| EF1516 | PTS system component | 496 | 3 | 0.000 | 7494 | 3168 | | | | | | | | |
| EF1521 | DNA primase | 500 | | | | | 3 | 0.025 | 9520 | 5105 | | | | |
| EF1522 | RNA polymerase sigma-70 factor family protein | 501 | | | | | 3 | 0.014 | 8120 | 3997 | | | | |
| EF1524 | conserved hypothetical protein | 488 | | | | | 2 | 0.001 | 4211 | 2194 | | | | |
| EF1525 | ferric uptake regulator family protein | 420 | | | | | 2 | 0.021 | 8694 | 4587 | | | | |
| EF1526 | glyceraldehyde 3-phosphate dehydrogenase | 503 | | | | | 2 | 0.041 | 38442 | 27021 | | | | |
| EF1535 | conserved hypothetical protein | 497 | | | | | -2 | 0.036 | 2078 | 3419 | | | | |
| EF1541 | conserved hypothetical protein | 494 | 2 | 0.004 | 5006 | 3021 | 4 | 0.002 | 11618 | 4040 | 3 | 0.035 | 9407 | 3569 |
| EF1547 | cytidylate kinase | 500 | 3 | 0.002 | 29817 | 15920 | | | | | 4 | 0.021 | 5864 | 1815 |
| **EF1561** | **shikimate 5-dehydrogenase** | 500 | | | | | **5** | 0.016 | 12050 | 3784 | **9** | 0.036 | 10293 | 1662 |
| **EF1562** | **phospho-2-dehydro-3-deoxyheptonate aldola** | 500 | 2 | 0.032 | 38475 | 24865 | **17** | 0.016 | 42955 | 8977 | **24** | 0.010 | 38317 | 3812 |
| **EF1563** | **3-dehydroquinate synthase** | 500 | 3 | 0.008 | 16010 | 7890 | **24** | 0.015 | 28577 | 4925 | **22** | 0.004 | 26175 | 2381 |
| **EF1564** | **chorismate synthase** | 503 | 2 | 0.038 | 8740 | 4646 | **21** | 0.020 | 14845 | 2774 | **9** | 0.006 | 10042 | 1669 |
| **EF1565** | **prephenate dehydrogenase, putative** | 487 | 2 | 0.034 | 19796 | 12862 | **11** | 0.015 | 40961 | 11835 | **13** | 0.008 | 30625 | 5187 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **EF1566** | **3-phosphoshikimate 1-carboxyvinyltransfera** | 495 | | | | | **11** | 0.007 | 34102 | 8180 | **11** | 0.012 | 21811 | 4521 |
| **EF1567** | **shikimate kinase** | 444 | | | | | **4** | 0.012 | 33649 | 11644 | **8** | 0.023 | 30830 | 6805 |
| **EF1568** | **chorismate mutase/prephenate dehydratase,** | 496 | | | | | **10** | 0.010 | 18571 | 4222 | | | | |
| **EF1569** | **transcriptional regulator, PSR protein** | 499 | | | | | **5** | 0.024 | 4772 | 1871 | | | | |
| EF1573 | hypothetical protein | 212 | | | | | 2 | 0.043 | 4339 | 2474 | | | | |
| EF1574 | Na+/H+ antiporter | 500 | | | | | 2 | 0.003 | 6411 | 2977 | | | | |
| EF1586 | NADH oxidase | 501 | | | | | 2 | 0.007 | 21185 | 12763 | | | | |
| EF1590 | protease synthase and sporulation negative regu | 477 | | | | | 3 | 0.006 | 2842 | 1250 | | | | |
| EF1596 | conserved domain protein | 497 | | | | | | | | | 2 | 0.014 | 4326 | 2362 |
| EF1606 | glycosyl hydrolase, family 1 | 499 | 4 | 0.016 | 4500 | 2061 | 4 | 0.012 | 2234 | 1043 | | | | |
| EF1610 | hypothetical protein | 503 | 3 | 0.000 | 17958 | 9569 | | | | | | | | |
| **EF1616** | **conserved hypothetical protein** | 372 | | | | | | | | | **-2** | 0.013 | 2156 | 2843 |
| **EF1617** | **conserved hypothetical protein** | 416 | | | | | **-87** | 0.001 | 1862 | 23224 | **-49** | 0.002 | 1081 | 15457 |
| **EF1618** | **ethanolamine utilization protein euth** | 494 | | | | | **-63** | 0.000 | 870 | 10659 | **-32** | 0.006 | 812 | 7251 |
| **EF1619** | **carbon dioxide concentrating mechanism pro** | 241 | | | | | **-51** | 0.005 | 689 | 13721 | **-59** | 0.006 | 474 | 9739 |
| **EF1620** | **hypothetical protein** | 505 | | | | | **-95** | 0.003 | 660 | 17922 | **-63** | 0.012 | 821 | 18735 |
| **EF1621** | **conserved hypothetical protein** | 504 | | | | | **-96** | 0.004 | 997 | 24108 | **-92** | 0.008 | 691 | 13663 |
| **EF1622** | **hypothetical protein** | 501 | | | | | **-181** | 0.000 | 834 | 23003 | **-45** | 0.027 | 619 | 13530 |
| **EF1623** | **pduJ protein** | 266 | | | | | **-61** | 0.000 | 1207 | 18665 | **-45** | 0.003 | 577 | 9812 |
| **EF1624** | **aldehyde dehydrogenase, putative** | 506 | | | | | **-165** | 0.000 | 1331 | 29369 | **-77** | 0.011 | 1164 | 18215 |
| **EF1625** | **pduJ protein** | 506 | | | | | **-8** | 0.002 | 889 | 2712 | **-6** | 0.007 | 1126 | 2038 |
| **EF1627** | **ethanolamine ammonia-lyase light chain, put** | 487 | | | | | **-139** | 0.001 | 913 | 24156 | **-77** | 0.029 | 824 | 10588 |
| **EF1629** | **ethanolamine ammonia lyase large subunit** | 495 | | | | | **-288** | 0.000 | 792 | 26871 | **-86** | 0.005 | 612 | 14231 |
| **EF1630** | **chaperonin, putative, authentic frameshift** | 500 | | | | | **-107** | 0.001 | 932 | 15614 | **-43** | 0.000 | 779 | 10203 |
| **EF1632** | **histidine kinase, putative** | 503 | | | | | **-18** | 0.011 | 799 | 7581 | **-12** | 0.008 | 1793 | 7958 |
| **EF1633** | **response regulator** | 440 | | | | | **-24** | 0.010 | 1719 | 19525 | **-21** | 0.004 | 1200 | 9535 |
| **EF1634** | **propanediol utilization protein PduV** | 299 | | | | | **-85** | 0.001 | 1550 | 24497 | **-27** | 0.003 | 1325 | 8307 |
| **EF1635** | **alcohol dehydrogenase, iron-containing** | 500 | | | | | **-18** | 0.002 | 2433 | 6382 | **-7** | 0.015 | 823 | 2028 |
| **EF1637** | **conserved hypothetical protein** | 502 | | | | | **-9** | 0.011 | 817 | 4064 | | | | |
| **EF1638** | **propanediol utilization protein PduV** | 424 | | | | | **-22** | 0.003 | 631 | 4642 | | | | |
| **EF1639** | **siderophore ABC transporter, P-binding prot** | 499 | | | | | **-3** | 0.010 | 2202 | 2473 | | | | |
| **EF1640** | **hemin ABC transporter, permease protein, pu** | 500 | | | | | **-4** | 0.048 | 3023 | 4326 | | | | |
| **EF1641** | **hemin ABC transporter, hemin-binding prote** | 496 | | | | | **-4** | 0.008 | 2746 | 4801 | -2 | 0.016 | 1733 | 2386 |
| EF1655 | 2-dehydropantoate 2-reductase, putative | 502 | | | | | | | | | -6 | 0.034 | 930 | 5366 |
| **EF1658** | **branched-chain alpha-keto acid, E2 compone** | 502 | | | | | **-5** | 0.010 | 8857 | 21970 | | | | |
| **EF1659** | **branched-chain alpha-keto acid dehydrogena** | 502 | | | | | **-7** | 0.000 | 8051 | 25402 | **-8** | 0.005 | 4334 | 22514 |
| **EF1660** | **branched-chain alpha-keto acid dehydrogena** | 506 | | | | | **-8** | 0.000 | 6597 | 21725 | **-11** | 0.024 | 3205 | 20934 |
| **EF1661** | **branched-chain alpha-keto acid dehydrogena** | 495 | | | | | **-6** | 0.023 | 3825 | 14197 | | | | |
| **EF1662** | **branched-chain carboxylic acid kinase** | 498 | | | | | **-11** | 0.000 | 4200 | 19731 | | | | |
| **EF1663** | **branched-chain phosphotransacylase** | 500 | | | | | **-6** | 0.011 | 4241 | 14199 | **-6** | 0.029 | 2633 | 10899 |
| EF1679 | tail-specific protease, putative | 502 | | | | | | | | | 3 | 0.022 | 5894 | 2847 |
| EF1680 | conserved hypothetical protein | 502 | | | | | | | | | 3 | 0.018 | 3644 | 1772 |
| EF1681 | peptide methionine sulfoxide reductase | 443 | 2 | 0.000 | 15123 | 8276 | 5 | 0.018 | 12283 | 4618 | | | | |
| EF1682 | conserved hypothetical protein | 499 | 2 | 0.002 | 20168 | 11755 | 12 | 0.014 | 10880 | 2449 | 8 | 0.010 | 6683 | 1503 |
| EF1683 | Lipase/Acylhydrolase, putative | 495 | 3 | 0.002 | 11328 | 6079 | 13 | 0.019 | 8448 | 1997 | 5 | 0.043 | 4185 | 1187 |
| EF1700 | signal recognition particle protein | 500 | | | | | | | | | 2 | 0.008 | 39945 | 27054 |
| EF1701 | conserved hypothetical protein | 271 | | | | | 2 | 0.042 | 2151 | 1344 | | | | |
| EF1702 | conserved hypothetical protein | 431 | | | | | 2 | 0.027 | 10622 | 6208 | 3 | 0.003 | 9633 | 4828 |
| EF1707 | conserved hypothetical protein | 500 | | | | | -8 | 0.009 | 17735 | 45924 | -14 | 0.009 | 12097 | 51906 |
| EF1708 | conserved hypothetical protein | 497 | | | | | -9 | 0.003 | 15399 | 50360 | -11 | 0.012 | 9367 | 42145 |
| EF1712 | orotate phosphoribosyltransferase | 492 | | | | | 3 | 0.013 | 4479 | 2002 | | | | |
| EF1714 | dihydroorotate dehydrogenase | 505 | | | | | 2 | 0.014 | 4486 | 2250 | | | | |
| EF1719 | aspartate carbamoyltransferase | 512 | -2 | 0.043 | 9302 | 13045 | | | | | | | | |
| EF1720 | uracil permease | 512 | -2 | 0.022 | 6975 | 10049 | | | | | | | | |
| EF1727 | pore forming protein ebsa | 412 | 2 | 0.004 | 2561 | 1655 | | | | | | | | |
| EF1732 | ABC transporter, P-binding/permease protein | 503 | 3 | 0.008 | 9530 | 4399 | | | | | | | | |
| EF1733 | ABC transporter, P-binding/permease protein | 503 | 2 | 0.010 | 8303 | 4138 | | | | | | | | |
| EF1753 | conserved hypothetical protein | 488 | -3 | 0.007 | 9113 | 17209 | | | | | | | | |
| **EF1760** | **cell division protein FtsX, putative** | 501 | | | | | **2** | 0.001 | 9577 | 5017 | | | | |
| **EF1761** | **cell division P-binding protein FtsE** | 499 | | | | | **2** | 0.016 | 11124 | 5770 | | | | |
| **EF1762** | **peptide chain release factor 2** | 507 | | | | | **4** | 0.007 | 14261 | 4855 | **3** | 0.021 | 6852 | 4062 |
| EF1770 | hypothetical protein | 161 | | | | | | | | | 3 | 0.045 | 3641 | 1845 |
| EF1774 | conserved hypothetical protein | 490 | | | | | 2 | 0.033 | 2321 | 1250 | | | | |
| EF1803 | PTS system component | 500 | | | | | | | | | -2 | 0.002 | 1560 | 3118 |
| **EF1817** | **serine proteinase homolog** | 501 | **503** | 0.001 | 47004 | 1356 | **549** | 0.000 | 37583 | 958 | **166** | 0.015 | 35003 | 4701 |
| **EF1818** | **gelatinase** | 506 | **725** | 0.000 | 36622 | 725 | **165** | 0.002 | 17877 | 457 | **215** | 0.031 | 22598 | 1151 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **EF1820** | **AgrCfs** | 494 | **44** | 0.000 | 31041 | 3092 | **228** | 0.000 | 14704 | 474 | **33** | 0.034 | 6249 | 634 |
| **EF1821** | **agrBfs protein** | 500 | **480** | 0.001 | 42845 | 3793 | **153** | 0.007 | 20531 | 737 | **118** | 0.016 | 13257 | 495 |
| EF1826 | alcohol dehydrogenase, zinc-containing | 499 | | | | | -2 | 0.012 | 2977 | 4043 | | | | |
| EF1898 | ribosomal protein L19 | 273 | | | | | | | | | -2 | 0.040 | 5524 | 8824 |
| EF1900 | 16S rRNA processing protein RimM | 484 | | | | | | | | | 2 | 0.023 | 3281 | 2123 |
| EF1904 | conserved domain protein | 502 | | | | | 3 | 0.026 | 3118 | 1569 | | | | |
| EF1907 | maoC like domain protein | 418 | | | | | | | | | 3 | 0.029 | 17945 | 9050 |
| EF1916 | P-binding protein | 502 | 2 | 0.007 | 12288 | 6395 | | | | | | | | |
| EF1917 | P-dependent Clp protease, P-binding subunit Cl | 507 | | | | | 2 | 0.026 | 20607 | 11446 | | | | |
| EF1919 | acetyltransferase, GN family | 472 | | | | | 3 | 0.043 | 6838 | 3538 | | | | |
| EF1921 | inosine-uridine preferring nucleoside hydrolase | 502 | | | | | 3 | 0.022 | 30818 | 18386 | 5 | 0.037 | 34890 | 14010 |
| EF1927 | glycerol uptake facilitator protein, putative | 497 | | | | | -3 | 0.011 | 34100 | 53520 | -5 | 0.015 | 22875 | 48396 |
| EF1928 | aerobic glycerol-3-phosphate dehydrogenase, p | 488 | | | | | -2 | 0.006 | 41108 | 53576 | | | | |
| EF1929 | glycerol kinase | 499 | | | | | -4 | 0.002 | 27330 | 54470 | -5 | 0.027 | 15003 | 37630 |
| EF1937 | conserved hypothetical protein | 454 | 3 | 0.039 | 3286 | 1774 | | | | | | | | |
| EF1938 | calcium E1-E2-type Pase | 498 | 3 | 0.006 | 9686 | 4646 | | | | | | | | |
| EF1973 | conserved hypothetical protein TIGR00256 | 402 | | | | | 3 | 0.029 | 3695 | 1649 | | | | |
| EF1978 | DNA-3-methyladenine glycosylase | 459 | | | | | -2 | 0.033 | 2569 | 2887 | | | | |
| EF1981 | hypothetical protein | 220 | | | | | | | | | 2 | 0.013 | 3547 | 2583 |
| EF2023 | hypothetical protein | 258 | | | | | -3 | 0.006 | 2114 | 2550 | | | | |
| EF2048 | conserved hypothetical protein TIGR00048 | 501 | -2 | 0.046 | 9068 | 12418 | | | | | | | | |
| **EF2057** | **polyprenyl synthetase** | 486 | **2** | 0.007 | 14173 | 9522 | | | | | | | | |
| **EF2058** | **transport P-binding protein CydC, putative** | 496 | **3** | 0.000 | 15052 | 7297 | **7** | 0.000 | 19148 | 4714 | | | | |
| **EF2059** | **transport P-binding protein CydD, putative** | 498 | **3** | 0.003 | 28177 | 17808 | **6** | 0.000 | 18670 | 6319 | **5** | 0.003 | 12908 | 3970 |
| EF2063 | transcriptional activator, AraC family | 502 | | | | | | | | | 2 | 0.036 | 3495 | 2104 |
| EF2070 | tRNA (5-methylaminomethyl-2-thiouridylate)-met | 493 | | | | | | | | | 2 | 0.042 | 2353 | 1642 |
| **EF2075** | **iron (chelated) ABC transporter, permease pr** | 501 | | | | | **4** | 0.033 | 16799 | 7416 | **3** | 0.011 | 9671 | 4874 |
| **EF2076** | **endocarditis specific antigen** | 488 | | | | | **7** | 0.035 | 27860 | 12840 | **8** | 0.020 | 20585 | 5794 |
| **EF2077** | **ABC transporter, P-binding protein** | 494 | | | | | **3** | 0.005 | 3807 | 1566 | | | | |
| **EF2163** | **glycerophosphoryl diester phosphodiesteras** | 500 | **2** | 0.047 | 5805 | 3762 | | | | | | | | |
| **EF2165** | **NAD-dependent epimerase/dehydratase fami** | 495 | **2** | 0.014 | 9545 | 5956 | | | | | | | | |
| EF2177 | capsular polysaccharide biosynthesis glycosyltra | 492 | | | | | 5 | 0.033 | 2789 | 1205 | | | | |
| EF2178 | hypothetical protein | 497 | | | | | 6 | 0.040 | 3387 | 1574 | | | | |
| EF2179 | hypothetical protein | 497 | | | | | 3 | 0.011 | 4384 | 2182 | | | | |
| EF2180 | glycosyl transferase domain protein | 503 | | | | | 2 | 0.028 | 7941 | 4733 | | | | |
| EF2190 | glycosyl transferase domain protein | 494 | 2 | 0.001 | 8010 | 4869 | 4 | 0.007 | 3079 | 955 | | | | |
| EF2191 | dTDP-4-dehydrorhamnose reductase | 498 | | | | | 6 | 0.003 | 9093 | 2594 | | | | |
| EF2192 | dTDP-glucose 4,6-dehydratase | 503 | | | | | 3 | 0.003 | 25764 | 11666 | | | | |
| EF2193 | dTDP-4-dehydrorhamnose 3,5-epimerase | 498 | | | | | 3 | 0.016 | 15086 | 7092 | | | | |
| EF2194 | glucose-1-phosphate thymidylyltransferase | 496 | | | | | 2 | 0.023 | 5954 | 3309 | | | | |
| EF2195 | glycosyl transferase domain protein | 502 | 2 | 0.011 | 14303 | 8927 | | | | | | | | |
| EF2197 | glycosyl transferase domain protein | 509 | 2 | 0.006 | 13385 | 8190 | | | | | | | | |
| EF2204 | aminopeptidase pep, authentic frameshift | 500 | | | | | 2 | 0.022 | 9941 | 5697 | | | | |
| EF2205 | conserved hypothetical protein | 358 | | | | | 2 | 0.021 | 2169 | 1311 | | | | |
| EF2217 | alpha-1,2-mannosidase, putative | 494 | | | | | -6 | 0.015 | 9091 | 24639 | | | | |
| EF2218 | DNA-binding response regulator | 493 | | | | | 2 | 0.025 | 12952 | 6134 | | | | |
| EF2254 | hypothetical protein | 491 | | | | | | | | | -2 | 0.027 | 1918 | 4297 |
| EF2314 | bacteriocin, putative | 507 | | | | | | | | | -2 | 0.009 | 2075 | 3076 |
| EF2355 | P-dependent Clp protease, P-binding subunit Cl | 493 | | | | | | | | | 2 | 0.041 | 22400 | 15461 |
| EF2365 | xanthine phosphoribosyltransferase | 484 | 2 | 0.049 | 16283 | 9947 | | | | | | | | |
| EF2372 | aspartate aminotransferase | 498 | | | | | -2 | 0.027 | 9210 | 13356 | | | | |
| EF2377 | amino acid permease | 501 | 2 | 0.041 | 11225 | 7197 | | | | | | | | |
| **EF2378** | **DNA polymerase III, alpha subunit, Gram-pos** | 499 | | | | | **3** | 0.005 | 4650 | 2036 | | | | |
| EF2408 | hypothetical protein | 56 | -2 | 0.000 | 10256 | 13344 | | | | | | | | |
| EF2417 | ferric uptake regulator family protein | 416 | | | | | 2 | 0.049 | 4306 | 2446 | | | | |
| EF2424 | pyrroline-5-carboxylate reductase, putative | 506 | | | | | 2 | 0.047 | 3936 | 1994 | | | | |
| EF2426 | transcriptional regulator, GntR family | 497 | | | | | 2 | 0.013 | 3312 | 1722 | | | | |
| EF2433 | phosphoglycerate mutase family protein | 500 | | | | | | | | | -2 | 0.018 | 1480 | 2519 |
| EF2444 | acyl-CoA thioesterase, putative | 475 | 2 | 0.018 | 10838 | 6228 | 3 | 0.043 | 3385 | 1923 | | | | |
| EF2450 | PDZ domain protein | 507 | | | | | 2 | 0.000 | 11945 | 5756 | 3 | 0.025 | 9860 | 4763 |
| EF2451 | lipopolysaccharide core biosynthesis protein Kdt | 478 | | | | | 3 | 0.014 | 7361 | 3634 | 3 | 0.009 | 3898 | 2180 |
| EF2453 | conserved hypothetical protein | 262 | | | | | 2 | 0.038 | 5870 | 3439 | | | | |
| EF2478 | conserved hypothetical protein | 500 | | | | | 3 | 0.015 | 4869 | 2457 | | | | |
| EF2479 | conserved hypothetical protein | 484 | | | | | 3 | 0.025 | 16125 | 7891 | 3 | 0.006 | 7843 | 4135 |
| EF2496 | lipoprotein, YaeC family | 508 | | | | | | | | | 2 | 0.026 | 12228 | 7654 |
| EF2509 | azlC protein, putative | 500 | 2 | 0.028 | 8401 | 6024 | | | | | | | | |
| EF2552 | Sua5/YciO/YrdC/YwlC family protein, putative | 504 | | | | | 3 | 0.008 | 11514 | 5129 | 3 | 0.029 | 8412 | 3752 |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| EF2590 | conserved hypothetical protein | 502 | 2 | 0.000 | 10474 | 5762 | | | | | | | | | |
| EF2597 | glycosyl hydrolase, family 1 | 509 | | | | | | | | | -5 | 0.014 | 2927 | 9406 | |
| EF2603 | PTS system component | 320 | | | | | 2 | 0.022 | 14818 | 9109 | | | | | |
| EF2607 | P synthase F1, epsilon subunit | 356 | | | | | 2 | 0.003 | 27837 | 16718 | | | | | |
| EF2610 | P synthase F1, alpha subunit | 497 | | | | | 2 | 0.013 | 22034 | 14960 | | | | | |
| EF2616 | SsrA-binding protein | 444 | | | | | 2 | 0.008 | 5807 | 3252 | | | | | |
| EF2618 | carboxylesterase precursor, putative | 495 | | | | | | | | | 2 | 0.017 | 14378 | 7272 | |
| EF2620 | preprotein translocase, SecG subunit | 171 | | | | | 2 | 0.013 | 4475 | 2206 | | | | | |
| EF2621 | conserved hypothetical protein | 180 | | | | | 3 | 0.035 | 6755 | 2927 | | | | | |
| EF2643 | hypothetical protein | 490 | | | | | | | | | 3 | 0.013 | 4032 | 1737 | |
| EF2646 | conserved hypothetical protein TIGR00045 | 501 | | | | | 3 | 0.004 | 5428 | 2387 | | | | | |
| EF2654 | alcohol dehydrogenase, zinc-containing | 500 | | | | | -2 | 0.028 | 5912 | 7489 | | | | | |
| EF2659 | conserved hypothetical protein | 454 | | | | | 2 | 0.048 | 2013 | 1167 | | | | | |
| EF2665 | RNA methyltransferase, TrmH family | 441 | | | | | 2 | 0.019 | 3114 | 1623 | | | | | |
| EF2672 | conserved hypothetical protein | 497 | | | | | | | | | -3 | 0.007 | 4234 | 8053 | |
| EF2678 | arsenate reductase, putative | 366 | | | | | 3 | 0.049 | 33587 | 19729 | | | | | |
| EF2689 | exonuclease SbcC | 501 | | | | | 2 | 0.000 | 16561 | 10281 | | | | | |
| EF2698 | tellurite resistance protein | 498 | | | | | 2 | 0.032 | 29298 | 23775 | | | | | |
| EF2703 | transcriptional regulator | 498 | -2 | 0.031 | 3420 | 4347 | | | | | | | | | |
| EF2711 | transcriptional regulator, AraC family | 481 | | | | | -2 | 0.044 | 2106 | 3289 | -3 | 0.016 | 1904 | 4303 | |
| EF2719 | ribosomal protein L11 | 358 | | | | | | | | | 2 | 0.007 | 21870 | 13367 | |
| EF2720 | ABC transporter, P-binding protein | 504 | | | | | 3 | 0.030 | 32309 | 19618 | | | | | |
| EF2737 | hypothetical protein | 192 | 3 | 0.022 | 6409 | 3349 | | | | | | | | | |
| EF2743 | conserved hypothetical protein | 500 | | | | | 2 | 0.032 | 5287 | 3275 | | | | | |
| EF2744 | endoglucanase, putative | 492 | | | | | | | | | 2 | 0.016 | 5851 | 2933 | |
| EF2746 | dltD protein | 507 | | | | | 2 | 0.013 | 2946 | 1456 | | | | | |
| EF2747 | D-alanyl carrier protein | 157 | | | | | 2 | 0.010 | 1887 | 886 | | | | | |
| EF2748 | dltB protein | 492 | | | | | 3 | 0.002 | 4568 | 2130 | | | | | |
| EF2749 | D-alanine-activating enzyme, putative | 505 | | | | | 4 | 0.004 | 8118 | 2998 | | | | | |
| EF2751 | hypothetical protein | 502 | | | | | 3 | 0.007 | 9432 | 4232 | | | | | |
| EF2752 | ABC transporter, P-binding protein | 501 | | | | | 2 | 0.029 | 7700 | 4316 | | | | | |
| EF2757 | conserved hypothetical protein TIGR00245 | 500 | 2 | 0.030 | 8554 | 4798 | 3 | 0.028 | 2539 | 1251 | | | | | |
| EF2760 | conserved hypothetical protein | 336 | | | | | 2 | 0.017 | 19015 | 10752 | | | | | |
| EF2761 | conserved hypothetical protein | 507 | | | | | 2 | 0.007 | 24405 | 15639 | 2 | 0.011 | 15049 | 8994 | |
| EF2762 | DNA polymerase III, delta prime subunit, putativ | 497 | | | | | 4 | 0.013 | 22753 | 9590 | 4 | 0.020 | 15928 | 6533 | |
| EF2763 | conserved hypothetical protein | 245 | | | | | | | | | 2 | 0.029 | 10345 | 6826 | |
| EF2767 | transcriptional regulator | 505 | 2 | 0.007 | 4333 | 2500 | 3 | 0.004 | 3155 | 1526 | | | | | |
| EF2768 | conserved hypothetical protein | 514 | 2 | 0.012 | 4031 | 2778 | 3 | 0.034 | 2435 | 1192 | | | | | |
| EF2769 | ABC transporter, P-binding protein | 499 | 3 | 0.001 | 3843 | 2354 | 3 | 0.006 | 2668 | 1349 | 2 | | | | |
| EF2770 | conserved hypothetical protein | 494 | 2 | 0.010 | 3093 | 2168 | | | | | | | | | |
| EF2772 | drug transporter, putative, authentic frameshift | 502 | 2 | 0.001 | 2449 | 1473 | | | | | | | | | |
| EF2775 | phosphomethylpyrimidine kinase | 501 | 2 | 0.003 | 3317 | 2067 | | | | | | | | | |
| EF2776 | thiamine-phosphate pyrophosphorylase | 500 | 2 | 0.003 | 3262 | 2301 | | | | | | | | | |
| EF2777 | hydroxyethylthiazole kinase | 500 | 2 | 0.006 | 2436 | 1801 | | | | | | | | | |
| EF2780 | conserved hypothetical protein TIGR00103 | 293 | | | | | | | | | 2 | 0.024 | 2998 | 2053 | |
| EF2781 | DNA polymerase III, gamma and tau subunits | 500 | | | | | | | | | 2 | 0.033 | 27152 | 16519 | |
| EF2790 | rhomboid family protein | 487 | | | | | 2 | 0.049 | 5498 | 2982 | | | | | |
| EF2795 | LysM domain protein | 500 | | | | | 3 | 0.012 | 4178 | 1935 | 3 | 0.034 | 3427 | 1666 | |
| EF2860 | hypothetical protein | 497 | | | | | | | | | 4 | 0.003 | 5446 | 2218 | |
| EF2867 | conserved hypothetical protein | 499 | 2 | 0.010 | 17841 | 10017 | 2 | 0.046 | 7544 | 4448 | 2 | 0.002 | 6143 | 3680 | |
| EF2870 | conserved hypothetical protein TIGR00488 | 471 | | | | | | | | | 2 | 0.011 | 16059 | 10282 | |
| EF2871 | conserved hypothetical protein TIGR00482 | 507 | 2 | 0.005 | 28685 | 19910 | 2 | 0.016 | 7578 | 4132 | 2 | 0.014 | 6052 | 3426 | |
| EF2872 | conserved hypothetical protein TIGR00253 | 276 | | | | | 2 | 0.005 | 3979 | 1954 | 2 | 0.041 | 2982 | 1768 | |
| EF2873 | Pase of unknown function subfamily, putative | 496 | | | | | 2 | 0.030 | 4818 | 2619 | 3 | 0.039 | 4544 | 2754 | |
| EF2874 | conserved hypothetical protein | 495 | | | | | 2 | 0.028 | 2240 | 1212 | 4 | 0.035 | 2474 | 1227 | |
| EF2876 | acetyl-CoA carboxylase, carboxyl transferase be | 513 | | | | | 3 | 0.032 | 23251 | 10638 | | | | | |
| EF2877 | acetyl-CoA carboxylase, biotin carboxylase | 493 | | | | | 3 | 0.028 | 25135 | 11508 | | | | | |
| EF2878 | (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehy | 373 | | | | | 4 | 0.016 | 23577 | 9821 | 2 | 0.049 | 16360 | 9713 | |
| EF2879 | acetyl-CoA carboxylase, biotin carboxyl carrier p | 401 | | | | | 5 | 0.033 | 24340 | 9213 | 3 | 0.023 | 14537 | 7403 | |
| EF2880 | 3-oxoacyl-(acyl-carrier-protein) synthase II | 502 | | | | | 4 | 0.027 | 27778 | 10735 | 3 | 0.007 | 21491 | 11500 | |
| EF2881 | 3-oxoacyl-(acyl-carrier-protein) reductase | 496 | | | | | 3 | 0.021 | 20986 | 9427 | 2 | 0.019 | 20205 | 10268 | |
| EF2882 | malonyl CoA-acyl carrier protein transacylase | 503 | | | | | | | | | 2 | 0.016 | 11848 | 6740 | |
| EF2898 | peptidyl-prolyl cis-trans isomerase, cyclophilin-ty | 499 | | | | | | | | | 2 | 0.011 | 2923 | 1669 | |
| EF2904 | conserved hypothetical protein | 501 | | | | | | | | | -2 | 0.034 | 2410 | 3745 | |
| EF2905 | sugar ABC transporter, permease protein | 491 | | | | | -2 | 0.018 | 3854 | 4041 | | | | | |
| EF2907 | sugar ABC transporter, P-binding protein | 500 | | | | | -2 | 0.049 | 4003 | 4775 | | | | | |
| EF2911 | DNA-binding response regulator | 500 | | | | | 2 | 0.017 | 8809 | 4473 | 2 | 0.042 | 6022 | 2851 | |
| EF2915 | conserved hypothetical protein TIGR00247 | 497 | | | | | 4 | 0.005 | 10800 | 4080 | 4 | 0.036 | 7075 | 2918 | |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| EF2916 | hydrolase, haloacid dehalogenase-like family | 497 | | | | | 4 | 0.009 | 3583 | 1161 | | | | |
| EF2917 | UDP-N-acetylglucosamine 2-epimerase | 500 | | | | | 2 | 0.011 | 9890 | 4992 | 2 | 0.005 | 6236 | 3332 |
| EF2918 | ferripyochelin binding protein | 461 | | | | | 2 | 0.024 | 18361 | 9889 | 2 | 0.032 | 12121 | 5805 |
| EF2919 | ABC transporter, P-binding/permease protein | 503 | | | | | | | | | 3 | 0.010 | 4460 | 1991 |
| EF2920 | ABC transporter, P-binding/permease protein | 505 | | | | | 2 | 0.040 | 5145 | 2896 | | | | |
| EF2924 | conserved hypothetical protein | 500 | | | | | 3 | 0.003 | 8451 | 3532 | | | | |
| EF2959 | transporter, putative | 502 | | | | | 2 | 0.010 | 27895 | 16458 | | | | |
| EF2960 | ribose ABC transporter protein | 333 | | | | | | | | | 2 | 0.044 | 34872 | 19454 |
| EF2961 | ribokinase | 500 | | | | | 2 | 0.013 | 37729 | 26407 | 3 | 0.040 | 33416 | 17622 |
| EF2964 | SgaT protein, putative | 496 | | | | | -2 | 0.000 | 26736 | 37884 | | | | |
| EF2965 | conserved hypothetical protein | 228 | | | | | -3 | 0.004 | 24246 | 36387 | | | | |
| EF2966 | PTS system component | 504 | | | | | -2 | 0.001 | 22659 | 31134 | | | | |
| EF2972 | amidinotransferase family protein | 498 | | | | | 4 | 0.003 | 19571 | 7766 | 3 | 0.017 | 15778 | 7804 |
| EF2973 | alkaline phosphatase | 501 | 3 | 0.004 | 6194 | 3345 | | | | | | | | |
| EF2974 | MutS2 family protein | 495 | 3 | 0.004 | 4019 | 2203 | 2 | 0.012 | 2257 | 1145 | 3 | 0.020 | 2023 | 1045 |
| EF3003 | hypothetical protein | 475 | | | | | 2 | 0.034 | 6044 | 3231 | | | | |
| EF3005 | choloylglycine hydrolase family protein | 491 | | | | | -2 | 0.038 | 4015 | 6824 | -2 | 0.026 | 3291 | 5683 |
| EF3018 | conserved domain protein | 500 | | | | | 4 | 0.038 | 2011 | 1053 | | | | |
| EF3019 | hypothetical protein | 492 | 3 | 0.002 | 2573 | 1542 | | | | | | | | |
| EF3028 | tRNA binding domain protein | 496 | | | | | 2 | 0.013 | 13783 | 7537 | | | | |
| EF3066 | polypeptide deformylase | 494 | | | | | 2 | 0.034 | 4947 | 3012 | | | | |
| EF3091 | YitT family protein | 490 | 2 | 0.015 | 8271 | 4911 | | | | | | | | |
| EF3092 | glyoxalase family protein | 368 | 2 | 0.000 | 11167 | 6083 | | | | | | | | |
| EF3093 | conserved hypothetical protein | 445 | 3 | 0.027 | 13229 | 6688 | | | | | 3 | 0.043 | 2091 | 930 |
| **EF3094** | **cell division protein FtsY** | 499 | | | | | **2** | 0.004 | 10462 | 6198 | | | | |
| EF3109 | peptide ABC transporter, P-binding protein | 500 | 2 | 0.012 | 16865 | 10815 | | | | | | | | |
| EF3113 | P-dependent DNA helicase RecG | 499 | 4 | 0.009 | 7003 | 2835 | 2 | 0.024 | 6396 | 3156 | | | | |
| EF3121 | protein phosphatase 2C | 493 | | | | | | | | | 2 | 0.024 | 4632 | 2790 |
| EF3122 | Sun protein | 502 | | | | | 2 | 0.025 | 5358 | 3149 | | | | |
| EF3134 | 2-deydro-3-deoxyphosphogluconate aldolase/4-h | 523 | | | | | 2 | 0.019 | 26379 | 15442 | 2 | 0.015 | 25301 | 14775 |
| EF3135 | mannonate dehydratase | 499 | | | | | 2 | 0.021 | 23220 | 15034 | 2 | 0.006 | 19343 | 11109 |
| EF3136 | PTS system component | 412 | | | | | | | | | 2 | 0.035 | 26991 | 16999 |
| EF3165 | maf protein | 475 | | | | | 2 | 0.024 | 13680 | 7570 | | | | |
| EF3166 | DNA mismatch repair protein MutL | 496 | | | | | 2 | 0.008 | 15805 | 8192 | | | | |
| EF3167 | DNA mismatch repair protein MutS | 507 | | | | | 2 | 0.008 | 10428 | 5026 | 2 | 0.008 | 7409 | 4008 |
| EF3168 | conserved hypothetical protein | 350 | | | | | 2 | 0.026 | 2060 | 1094 | 2 | 0.013 | 2380 | 1534 |
| EF3173 | conserved hypothetical protein | 508 | | | | | | | | | 2 | 0.018 | 4163 | 2446 |
| EF3196 | response regulator | 517 | | | | | 2 | 0.005 | 29350 | 17896 | | | | |
| EF3197 | F domain protein | 495 | | | | | 2 | 0.006 | 28318 | 16835 | | | | |
| EF3198 | lipoprotein, YaeC family | 492 | | | | | 3 | 0.019 | 9300 | 4418 | 2 | 0.025 | 3616 | 2083 |
| EF3199 | ABC transporter, permease protein | 502 | | | | | | | | | 2 | 0.042 | 9085 | 4159 |
| EF3200 | ABC transporter, P-binding protein | 505 | | | | | 2 | 0.013 | 18539 | 9529 | | | | |
| **EF3210** | **PTS system component** | 352 | | | | | **7** | 0.001 | 8473 | 2116 | **3** | 0.027 | 3124 | 1227 |
| **EF3211** | **PTS system component** | 424 | | | | | **8** | 0.004 | 14467 | 3089 | **9** | 0.002 | 12295 | 2549 |
| **EF3212** | **PTS system component** | 496 | | | | | **6** | 0.001 | 18159 | 5022 | **5** | 0.009 | 9524 | 2378 |
| **EF3213** | **PTS system component** | 499 | | | | | **5** | 0.000 | 21235 | 6059 | **4** | 0.010 | 16792 | 5452 |
| EF3214 | sigma-54 dependent transcriptional regulator, pu | 507 | | | | | 4 | 0.003 | 7627 | 2620 | | | | |
| EF3216 | transcriptional regulator, putative | 500 | | | | | 3 | 0.016 | 2504 | 1123 | | | | |
| EF3234 | hypothetical protein | 504 | | | | | | | | | 2 | 0.006 | 2902 | 1739 |
| EF3236 | leader peptidase PilD, putative | 501 | | | | | 2 | 0.033 | 3383 | 1870 | | | | |
| EF3237 | DNA-directed RNA polymerase, beta-prime subu | 505 | | | | | 3 | 0.000 | 17726 | 7611 | | | | |
| EF3239 | conserved hypothetical protein | 145 | | | | | 2 | 0.014 | 2589 | 1563 | | | | |
| EF3245 | cell-envelope associated acid phosphatase | 501 | 2 | 0.018 | 3285 | 2306 | | | | | | | | |
| EF3256 | lipoprotein, putative | 495 | | | | | -3 | 0.008 | 11665 | 21331 | | | | |
| EF3265 | dihydropteroate synthase | 501 | | | | | 2 | 0.041 | 10854 | 5721 | 3 | 0.017 | 10025 | 4043 |
| EF3294 | conserved hypothetical protein | 499 | | | | | 3 | 0.006 | 2681 | 1160 | | | | |
| EF3296 | conserved hypothetical protein TIGR00092 | 506 | | | | | 2 | 0.012 | 16685 | 9572 | | | | |
| EF3298 | chromosome partioning protein ParB, putative | 501 | | | | | 2 | 0.037 | 8055 | 4599 | | | | |
| EF3305 | PTS system component | 293 | | | | | -3 | 0.040 | 12976 | 30323 | | | | |
| EF3306 | PTS system component | 499 | | | | | -3 | 0.032 | 12053 | 24237 | | | | |
| EF3307 | PTS system component | 428 | | | | | -3 | 0.017 | 12511 | 23676 | | | | |
| EF3308 | transcriptional activator | 420 | | | | | -2 | 0.016 | 17977 | 24944 | | | | |
| EF3309 | transcriptional antiterminator, BglG family | 497 | | | | | -3 | 0.015 | 13952 | 24273 | | | | |
| EF3311 | Glucose inhibited division protein A | 500 | 2 | 0.004 | 16153 | 10797 | 2 | 0.001 | 3964 | 2115 | 3 | 0.007 | 2329 | 1265 |
| EF3319 | citrate lyase, alpha subunit | 501 | | | | | -2 | 0.043 | 14321 | 20503 | | | | |
| EF3327 | citrate transporter | 502 | | | | | | | | | -4 | 0.048 | 1002 | 3282 |