

| Accession | Name | Description |
|-----------|-----------------|---|
| TIGR00001 | rpml_bact | ribosomal protein bL35 |
| TIGR00002 | S16 | ribosomal protein bS16 |
| TIGR00006 | TIGR00006 | 16S rRNA (cytosine(1402)-N(4))-methyltransferase |
| TIGR00007 | TIGR00007 | 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase |
| TIGR00008 | infA | translation initiation factor IF-1 |
| TIGR00009 | L28 | ribosomal protein bL28 |
| TIGR00012 | L29 | ribosomal protein uL29 |
| TIGR00014 | arsC | arsenate reductase (glutaredoxin) |
| TIGR00016 | ackA | acetate kinase |
| TIGR00017 | cmk | cytidylate kinase |
| TIGR00018 | panC | pantoate--beta-alanine ligase |
| TIGR00019 | prfA | peptide chain release factor 1 |
| TIGR00020 | prfB | peptide chain release factor 2 |
| TIGR00021 | rpiA | ribose 5-phosphate isomerase A |
| TIGR00023 | TIGR00023 | acyl-phosphate glycerol 3-phosphate acyltransferase |
| TIGR00029 | S20 | ribosomal protein bS20 |
| TIGR00030 | S21p | ribosomal protein bS21 |
| TIGR00031 | UDP-GALP_mutase | UDP-galactopyranose mutase |
| TIGR00032 | argG | argininosuccinate synthase |
| TIGR00033 | aroC | chorismate synthase |
| TIGR00034 | aroFGH | 3-deoxy-7-phosphoheptulonate synthase |
| TIGR00036 | dapB | 4-hydroxy-tetrahydrodipicolinate reductase |
| TIGR00038 | efp | translation elongation factor P |
| TIGR00041 | DTMP_kinase | dTMP kinase |
| TIGR00042 | TIGR00042 | non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family |
| TIGR00043 | TIGR00043 | rRNA maturation RNase YbeY |
| TIGR00048 | rRNA_mod_RlmN | 23S rRNA (adenine(2503)-C(2))-methyltransferase |
| TIGR00054 | TIGR00054 | RIP metalloprotease RseP |
| TIGR00055 | uppS | di-trans,poly-cis-decaprenylcistransferase |
| TIGR00057 | TIGR00057 | tRNA threonylcarbamoyl adenosine modification protein, Sua5/YciO/YrdC/YwlC family |
| TIGR00059 | L17 | ribosomal protein bL17 |
| TIGR00060 | L18_bact | ribosomal protein uL18 |
| TIGR00061 | L21 | ribosomal protein bL21 |
| TIGR00062 | L27 | ribosomal protein bL27 |

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| TIGR00063 | folE | GTP cyclohydrolase I |
| TIGR00064 | ftsY | signal recognition particle-docking protein FtsY |
| TIGR00065 | ftsZ | cell division protein FtsZ |
| TIGR00066 | g_glut_trans | gamma-glutamyltransferase |
| TIGR00067 | glut_race | glutamate racemase |
| TIGR00068 | glyox_l | lactoylglutathione lyase |
| TIGR00070 | hisG | ATP phosphoribosyltransferase |
| TIGR00071 | hisT_truA | tRNA pseudouridine(38-40) synthase |
| TIGR00073 | hypB | hydrogenase accessory protein HypB |
| TIGR00074 | hypC_hupF | hydrogenase assembly chaperone HypC/HupF |
| TIGR00075 | hypD | hydrogenase expression/formation protein HypD |
| TIGR00077 | lspA | signal peptidase II |
| TIGR00078 | nadC | nicotinate-nucleotide diphosphorylase (carboxylating) |
| TIGR00079 | pept_deformyl | peptide deformylase |
| TIGR00080 | pimt | protein-L-isoaspartate O-methyltransferase |
| TIGR00081 | purC | phosphoribosylaminoimidazolesuccinocarboxamide synthase |
| TIGR00082 | rbfA | ribosome-binding factor A |
| TIGR00083 | ribF | riboflavin biosynthesis protein RibF |
| TIGR00084 | ruvA | Holliday junction DNA helicase RuvA |
| TIGR00086 | smpB | SsrA-binding protein |
| TIGR00087 | surE | 5'/3'-nucleotidase SurE |
| TIGR00088 | trmD | tRNA (guanine(37)-N(1))-methyltransferase |
| TIGR00090 | rsfS_ijap_ybeB | ribosome silencing factor |
| TIGR00091 | TIGR00091 | tRNA (guanine-N(7))-methyltransferase |
| TIGR00095 | TIGR00095 | 16S rRNA (guanine(966)-N(2))-methyltransferase RsmD |
| TIGR00096 | TIGR00096 | 16S rRNA (cytidine(1402)-2'-O)-methyltransferase |
| TIGR00100 | hypA | hydrogenase nickel insertion protein HypA |
| TIGR00101 | ureG | urease accessory protein UreG |
| TIGR00103 | DNA_YbaB_EbfC | DNA-binding protein, YbaB/EbfC family |
| TIGR00104 | tRNA_TsaA | tRNA-Thr(GGU) m(6)t(6)A37 methyltransferase TsaA |
| TIGR00105 | L31 | ribosomal protein bL31 |
| TIGR00107 | deoD | purine nucleoside phosphorylase |
| TIGR00109 | hemH | ferrochelatase |
| TIGR00110 | ilvD | dihydroxy-acid dehydratase |
| TIGR00112 | proC | pyrroline-5-carboxylate reductase |
| TIGR00113 | queA | S-adenosylmethionine:tRNA ribosyltransferase-isomerase |

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| TIGR00114 | lumazine-synth | 6,7-dimethyl-8-ribityllumazine synthase |
| TIGR00115 | tig | trigger factor |
| TIGR00116 | tsf | translation elongation factor Ts |
| TIGR00117 | acnB | aconitate hydratase 2 |
| TIGR00118 | acolac_lg | acetolactate synthase, large subunit, biosynthetic type |
| TIGR00119 | acolac_sm | acetolactate synthase, small subunit |
| TIGR00120 | ArgJ | glutamate N-acetyltransferase/amino-acid acetyltransferase |
| TIGR00123 | cbiM | cobalamin biosynthesis protein CbiM |
| TIGR00124 | cit_ly_ligase | [citrate (pro-3S)-lyase] ligase |
| TIGR00126 | deoC | deoxyribose-phosphate aldolase |
| TIGR00127 | nadp_idh_euk | isocitrate dehydrogenase, NADP-dependent |
| TIGR00128 | fabD | malonyl CoA-acyl carrier protein transacylase |
| TIGR00129 | fdhD_narQ | formate dehydrogenase family accessory protein FdhD |
| TIGR00131 | gal_kin | galactokinase |
| TIGR00132 | gatA | aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, A subunit |
| TIGR00133 | gatB | aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, B subunit |
| TIGR00135 | gatC | aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, C subunit |
| TIGR00136 | gidA | tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA |
| TIGR00137 | gid_trmFO | tRNA:m(5)U-54 methyltransferase |
| TIGR00138 | rsmG_gidB | 16S rRNA (guanine(527)-N(7))-methyltransferase RsmG |
| TIGR00140 | hupD | hydrogenase expression/formation protein |
| TIGR00142 | hycl | hydrogenase maturation peptidase Hycl |
| TIGR00143 | hypF | carbamoyltransferase HypF |
| TIGR00150 | T6A_YjeE | tRNA threonylcarbamoyl adenosine modification protein YjeE |
| TIGR00152 | TIGR00152 | dephospho-CoA kinase |
| TIGR00154 | ispE | 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase |
| TIGR00157 | TIGR00157 | ribosome small subunit-dependent GTPase A |
| TIGR00158 | L9 | ribosomal protein bL9 |
| TIGR00160 | MGSA | methylglyoxal synthase |
| TIGR00163 | PS_decarb | phosphatidylserine decarboxylase |
| TIGR00165 | S18 | ribosomal protein bS18 |

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| TIGR00166 | S6 | ribosomal protein bS6 |
| TIGR00168 | infC | translation initiation factor IF-3 |
| TIGR00169 | leuB | 3-isopropylmalate dehydrogenase |
| TIGR00172 | maf | septum formation protein Maf |
| TIGR00173 | menD | 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase |
| TIGR00174 | miaA | tRNA dimethylallyltransferase |
| TIGR00176 | mobB | molybdopterin-guanine dinucleotide biosynthesis protein B |
| TIGR00178 | monomer_idh | isocitrate dehydrogenase, NADP-dependent |
| TIGR00179 | murB | UDP-N-acetylenolpyruvoylglicosamine reductase |
| TIGR00181 | pepF | oligoendopeptidase F |
| TIGR00182 | plsX | fatty acid/phospholipid synthesis protein PlsX |
| TIGR00183 | prok_nadp_idh | isocitrate dehydrogenase, NADP-dependent |
| TIGR00184 | purA | adenylosuccinate synthase |
| TIGR00185 | tRNA_yibK_trmL | tRNA (cytidine(34)-2'-O)-methyltransferase |
| TIGR00187 | ribE | riboflavin synthase, alpha subunit |
| TIGR00188 | rnpA | ribonuclease P protein component |
| TIGR00189 | tesB | acyl-CoA thioesterase II |
| TIGR00190 | thiC | phosphomethylpyrimidine synthase |
| TIGR00191 | thrB | homoserine kinase |
| TIGR00195 | exoDNase_III | exodeoxyribonuclease III |
| TIGR00198 | cat_per_HPI | catalase/peroxidase HPI |
| TIGR00202 | csrA | carbon storage regulator |
| TIGR00203 | cydB | cytochrome d ubiquinol oxidase, subunit II |
| TIGR00204 | dxs | 1-deoxy-D-xylulose-5-phosphate synthase |
| TIGR00205 | fliE | flagellar hook-basal body complex protein FliE |
| TIGR00206 | fliF | flagellar M-ring protein FliF |
| TIGR00207 | fliG | flagellar motor switch protein FliG |
| TIGR00208 | fliS | flagellar protein FliS |
| TIGR00209 | galT_1 | galactose-1-phosphate uridylyltransferase |
| TIGR00210 | gltS | sodium/glutamate symporter |
| TIGR00212 | hemC | hydroxymethylbilane synthase |
| TIGR00214 | lipB | lipoyl(octanoyl) transferase |
| TIGR00215 | lpxB | lipid-A-disaccharide synthase |
| TIGR00216 | ispH_lytB | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase |
| TIGR00217 | malQ | 4-alpha-glucanotransferase |
| TIGR00218 | manA | mannose-6-phosphate isomerase, class I |
| TIGR00219 | mreC | rod shape-determining protein MreC |

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| TIGR00220 | mscL | large conductance mechanosensitive channel protein |
| TIGR00221 | nagA | N-acetylglucosamine-6-phosphate deacetylase |
| TIGR00222 | panB | 3-methyl-2-oxobutanoate hydroxymethyltransferase |
| TIGR00223 | panD | aspartate 1-decarboxylase |
| TIGR00224 | pckA | phosphoenolpyruvate carboxykinase (ATP) |
| TIGR00228 | ruvC | crossover junction endodeoxyribonuclease RuvC |
| TIGR00230 | sfsA | sugar fermentation stimulation protein |
| TIGR00232 | tktlase_bact | transketolase |
| TIGR00233 | trpS | tryptophan-tRNA ligase |
| TIGR00234 | tyrS | tyrosine-tRNA ligase |
| TIGR00235 | udk | uridine kinase |
| TIGR00236 | wecB | UDP-N-acetylglucosamine 2-epimerase |
| TIGR00237 | xseA | exodeoxyribonuclease VII, large subunit |
| TIGR00239 | 2oxo_dh_E1 | oxoglutarate dehydrogenase (succinyl-transferring), E1 component |
| TIGR00240 | ATCase_reg | aspartate carbamoyltransferase, regulatory subunit |
| TIGR00242 | TIGR00242 | division/cell wall cluster transcriptional repressor MraZ |
| TIGR00243 | Dxr | 1-deoxy-D-xylulose 5-phosphate reductoisomerase |
| TIGR00244 | TIGR00244 | transcriptional regulator NrdR |
| TIGR00246 | tRNA_RlmH_YbeA | rRNA large subunit m3Psi methyltransferase RlmH |
| TIGR00249 | sixA | phosphohistidine phosphatase SixA |
| TIGR00256 | TIGR00256 | D-tyrosyl-tRNA(Tyr) deacylase |
| TIGR00260 | thrC | threonine synthase |
| TIGR00262 | trpA | tryptophan synthase, alpha subunit |
| TIGR00263 | trpB | tryptophan synthase, beta subunit |
| TIGR00273 | TIGR00273 | iron-sulfur cluster-binding protein |
| TIGR00274 | TIGR00274 | N-acetylmuramic acid 6-phosphate etherase |
| TIGR00276 | TIGR00276 | epoxyqueuosine reductase |
| TIGR00278 | TIGR00278 | putative membrane protein insertion efficiency factor |
| TIGR00281 | TIGR00281 | segregation and condensation protein B |
| TIGR00287 | cas1 | CRISPR-associated endonuclease Cas1 |
| TIGR00302 | TIGR00302 | phosphoribosylformylglycinamide synthase, purS protein |
| TIGR00312 | cbiD | cobalamin biosynthesis protein CbiD |
| TIGR00313 | cobQ | cobyric acid synthase CobQ |
| TIGR00317 | cobS | cobalamin 5'-phosphate synthase |
| TIGR00325 | lpxC | UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine |

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| | | deacetylase |
| TIGR00326 | eubact_ribD | riboflavin biosynthesis protein RibD |
| TIGR00328 | flhB | flagellar biosynthetic protein FlhB |
| TIGR00330 | glpX | fructose-1,6-bisphosphatase, class II |
| TIGR00331 | hrcA | heat-inducible transcription repressor HrcA |
| TIGR00333 | nrdI | nrdI protein |
| TIGR00334 | 5S_RNA_mat_M5 | ribonuclease M5 |
| TIGR00337 | PyrG | CTP synthase |
| TIGR00338 | serB | phosphoserine phosphatase SerB |
| TIGR00343 | TIGR00343 | pyridoxal 5'-phosphate synthase, synthase subunit Pdx1 |
| TIGR00344 | alaS | alanine--tRNA ligase |
| TIGR00347 | bioD | dethiobiotin synthase |
| TIGR00351 | narI | respiratory nitrate reductase, gamma subunit |
| TIGR00353 | nrfE | cytochrome c-type biogenesis protein CcmF |
| TIGR00355 | purH | phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase |
| TIGR00359 | cello_pts_IIC | PTS system, cellobiose-specific IIC component |
| TIGR00361 | ComEC_Rec2 | DNA internalization-related competence protein ComEC/Rec2 |
| TIGR00362 | DnaA | chromosomal replication initiator protein DnaA |
| TIGR00364 | TIGR00364 | queuosine biosynthesis protein QueC |
| TIGR00365 | TIGR00365 | monothiol glutaredoxin, Grx4 family |
| TIGR00372 | cas4 | CRISPR-associated protein Cas4 |
| TIGR00378 | cax | calcium/proton exchanger |
| TIGR00379 | cobB | cobyric acid a,c-diamide synthase |
| TIGR00380 | cobD | cobalamin biosynthesis protein CobD |
| TIGR00382 | clpX | ATP-dependent Clp protease, ATP-binding subunit ClpX |
| TIGR00383 | corA | magnesium and cobalt transport protein CorA |
| TIGR00387 | glcD | glycolate oxidase, subunit GlcD |
| TIGR00389 | glyS_dimeric | glycine--tRNA ligase |
| TIGR00390 | hslU | ATP-dependent protease HslVU, ATPase subunit |
| TIGR00392 | ileS | isoleucine--tRNA ligase |
| TIGR00396 | leuS_bact | leucine--tRNA ligase |
| TIGR00402 | napF | ferredoxin-type protein NapF |
| TIGR00406 | prmA | ribosomal protein L11 methyltransferase |
| TIGR00408 | proS_fam_I | proline--tRNA ligase |
| TIGR00409 | proS_fam_II | proline--tRNA ligase |
| TIGR00414 | serS | serine--tRNA ligase |

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| TIGR00416 | sms | DNA repair protein RadA |
| TIGR00417 | speE | spermidine synthase |
| TIGR00418 | thrS | threonine--tRNA ligase |
| TIGR00419 | tim | triose-phosphate isomerase |
| TIGR00420 | trmU | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase |
| TIGR00422 | valS | valine--tRNA ligase |
| TIGR00430 | Q_tRNA_tgt | tRNA-guanine transglycosylase |
| TIGR00431 | TruB | tRNA pseudouridine(55) synthase |
| TIGR00433 | bioB | biotin synthase |
| TIGR00435 | cysS | cysteine--tRNA ligase |
| TIGR00436 | era | GTP-binding protein Era |
| TIGR00438 | rrmJ | ribosomal RNA large subunit methyltransferase J |
| TIGR00439 | ftsX | putative protein insertion permease FtsX |
| TIGR00440 | glnS | glutamine--tRNA ligase |
| TIGR00441 | gmhA | phosphoheptose isomerase |
| TIGR00442 | hisS | histidine--tRNA ligase |
| TIGR00443 | hisZ_biosyn_reg | ATP phosphoribosyltransferase, regulatory subunit |
| TIGR00445 | mraY | phospho-N-acetylmuramoyl-pentapeptide-transferase |
| TIGR00447 | pth | aminoacyl-tRNA hydrolase |
| TIGR00450 | mnmE_trmE_thdF | tRNA modification GTPase TrmE |
| TIGR00452 | TIGR00452 | tRNA (mo5U34)-methyltransferase |
| TIGR00456 | argS | arginine--tRNA ligase |
| TIGR00457 | asnS | asparagine--tRNA ligase |
| TIGR00459 | aspS_bact | aspartate--tRNA ligase |
| TIGR00460 | fmt | methionyl-tRNA formyltransferase |
| TIGR00461 | gcvP | glycine dehydrogenase |
| TIGR00462 | genX | EF-P lysine aminoacylase GenX |
| TIGR00464 | gltX_bact | glutamate--tRNA ligase |
| TIGR00465 | ilvC | ketol-acid reductoisomerase |
| TIGR00466 | kdsB | 3-deoxy-D-manno-octulosonate cytidylyltransferase |
| TIGR00468 | pheS | phenylalanine--tRNA ligase, alpha subunit |
| TIGR00472 | pheT_bact | phenylalanine--tRNA ligase, beta subunit |
| TIGR00473 | pssA | CDP-diacylglycerol-serine O-phosphatidyltransferase |
| TIGR00474 | selA | L-seryl-tRNA(Sec) selenium transferase |
| TIGR00475 | selB | selenocysteine-specific translation elongation factor |
| TIGR00476 | selD | selenide, water dikinase |
| TIGR00477 | tehB | tellurite resistance protein TehB |

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| TIGR00479 | rumA | 23S rRNA (uracil-5-)-methyltransferase RumA |
| TIGR00482 | TIGR00482 | nicotinate (nicotinamide) nucleotide adenyllyltransferase |
| TIGR00484 | EF-G | translation elongation factor G |
| TIGR00485 | EF-Tu | translation elongation factor Tu |
| TIGR00487 | IF-2 | translation initiation factor IF-2 |
| TIGR00492 | alr | alanine racemase |
| TIGR00493 | clpP | ATP-dependent Clp endopeptidase, proteolytic subunit ClpP |
| TIGR00496 | frr | ribosome recycling factor |
| TIGR00497 | hsdM | type I restriction-modification system, M subunit |
| TIGR00498 | lexA | repressor LexA |
| TIGR00499 | lysS_bact | lysine--tRNA ligase |
| TIGR00500 | met_pdase_I | methionine aminopeptidase, type I |
| TIGR00502 | nagB | glucosamine-6-phosphate deaminase |
| TIGR00503 | prfC | peptide chain release factor 3 |
| TIGR00504 | pyro_pdase | pyroglutamyl-peptidase I |
| TIGR00508 | bioA | adenosylmethionine-8-amino-7-oxononanoate transaminase |
| TIGR00510 | lipA | lipoyl synthase |
| TIGR00512 | salvage_mtnA | S-methyl-5-thioribose-1-phosphate isomerase |
| TIGR00513 | accA | acetyl-CoA carboxylase, carboxyl transferase, alpha subunit |
| TIGR00514 | accC | acetyl-CoA carboxylase, biotin carboxylase subunit |
| TIGR00515 | accD | acetyl-CoA carboxylase, carboxyl transferase, beta subunit |
| TIGR00517 | acyl_carrier | acyl carrier protein |
| TIGR00518 | alaDH | alanine dehydrogenase |
| TIGR00521 | coaBC_dfp | phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase |
| TIGR00525 | folB | dihydronopterin aldolase |
| TIGR00527 | gcvH | glycine cleavage system H protein |
| TIGR00528 | gcvT | glycine cleavage system T protein |
| TIGR00531 | BCCP | acetyl-CoA carboxylase, biotin carboxyl carrier protein |
| TIGR00532 | HMG_CoA_R_NAD | hydroxymethylglutaryl-CoA reductase, degradative |
| TIGR00534 | OpcA | glucose-6-phosphate dehydrogenase assembly protein OpcA |
| TIGR00538 | hemN | oxygen-independent coproporphyrinogen III oxidase |
| TIGR00544 | Igt | prolipoprotein diacylglycerol transferase |

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| TIGR00546 | Int | apolipoprotein N-acyltransferase |
| TIGR00547 | lolA | outer membrane lipoprotein carrier protein LolA |
| TIGR00548 | lolB | outer membrane lipoprotein LolB |
| TIGR00549 | mevalon_kin | mevalonate kinase |
| TIGR00550 | nadA | quinolinate synthetase complex, A subunit |
| TIGR00551 | nadB | L-aspartate oxidase |
| TIGR00553 | pabB | aminodeoxychorismate synthase, component I |
| TIGR00554 | panK_bact | pantothenate kinase |
| TIGR00555 | panK_eukar | pantothenate kinase |
| TIGR00557 | pdxA | 4-hydroxythreonine-4-phosphate dehydrogenase PdxA |
| TIGR00558 | pdxH | pyridoxamine 5'-phosphate oxidase |
| TIGR00559 | pdxJ | pyridoxine 5'-phosphate synthase |
| TIGR00560 | pgsA | CDP-diacylglycerol--glycerol-3-phosphate 3- phosphatidyltransferase |
| TIGR00561 | pntA | NAD(P)(+)-transhydrogenase (AB-specific), alpha subunit |
| TIGR00562 | proto_IX_ox | protoporphyrinogen oxidase |
| TIGR00563 | rsmB | 16S rRNA (cytosine(967)-C(5))-methyltransferase |
| TIGR00564 | trpE_most | anthranilate synthase component I |
| TIGR00565 | trpE_proteo | anthranilate synthase component I |
| TIGR00568 | alkb | alkylated DNA repair protein AlkB |
| TIGR00575 | dnlj | DNA ligase, NAD-dependent |
| TIGR00577 | fpg | DNA-formamidopyrimidine glycosylase |
| TIGR00580 | mfd | transcription-repair coupling factor |
| TIGR00581 | moaC | molybdenum cofactor biosynthesis protein C |
| TIGR00593 | pola | DNA polymerase I |
| TIGR00595 | priA | primosomal protein N' |
| TIGR00609 | recB | exodeoxyribonuclease V, beta subunit |
| TIGR00612 | ispG_gcpE | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase |
| TIGR00613 | reco | DNA repair protein RecO |
| TIGR00615 | recR | recombination protein RecR |
| TIGR00628 | ung | uracil-DNA glycosylase |
| TIGR00634 | recN | DNA repair protein RecN |
| TIGR00635 | rvuB | Holliday junction DNA helicase RuvB |
| TIGR00639 | PurN | phosphoribosylglycinamide formyltransferase |
| TIGR00642 | mmCoA_mut_beta | methylmalonyl-CoA mutase, small subunit |
| TIGR00643 | recG | ATP-dependent DNA helicase RecG |
| TIGR00644 | recJ | single-stranded-DNA-specific exonuclease RecJ |

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| TIGR00647 | DNA_bind_WhiA | DNA-binding protein WhiA |
| TIGR00648 | recU | recombination protein U |
| TIGR00651 | pta | phosphate acetyltransferase |
| TIGR00652 | DapF | diaminopimelate epimerase |
| TIGR00653 | GlnA | glutamine synthetase, type I |
| TIGR00655 | PurU | formyltetrahydrofolate deformylase |
| TIGR00656 | asp_kin_monofn | aspartate kinase, monofunctional class |
| TIGR00658 | orni_carb_tr | ornithine carbamoyltransferase |
| TIGR00663 | dnan | DNA polymerase III, beta subunit |
| TIGR00664 | DNA_III_psi | DNA polymerase III, psi subunit |
| TIGR00665 | DnaB | replicative DNA helicase |
| TIGR00666 | PBP4 | D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase |
| TIGR00667 | aat | leucyl/phenylalanyl-tRNA--protein transferase |
| TIGR00668 | apaH | bis(5'-nucleosyl)-tetraphosphatase (symmetrical) |
| TIGR00669 | asnA | aspartate--ammonia ligase |
| TIGR00670 | asp_carb_tr | aspartate carbamoyltransferase |
| TIGR00672 | cdh | CDP-diacylglycerol diphosphatase |
| TIGR00673 | cynS | cyanase |
| TIGR00674 | dapA | 4-hydroxy-tetrahydrodipicolinate synthase |
| TIGR00676 | fadh2 | methylenetetrahydrofolate reductase [NAD(P)H] |
| TIGR00679 | hpr-ser | HPr(Ser) kinase/phosphatase |
| TIGR00680 | kdpA | K+-transporting ATPase, A subunit |
| TIGR00681 | kdpC | K+-transporting ATPase, C subunit |
| TIGR00682 | lpxK | tetraacyldisaccharide 4'-kinase |
| TIGR00683 | nanA | N-acetylneuraminate lyase |
| TIGR00684 | narJ | nitrate reductase molybdenum cofactor assembly chaperone |
| TIGR00685 | T6PP | trehalose-phosphatase |
| TIGR00687 | pyridox_kin | pyridoxal kinase |
| TIGR00690 | rpoZ | DNA-directed RNA polymerase, omega subunit |
| TIGR00692 | tdh | L-threonine 3-dehydrogenase |
| TIGR00695 | uxuA | mannonate dehydratase |
| TIGR00700 | GABAtrnsam | 4-aminobutyrate transaminase |
| TIGR00705 | SppA_67K | signal peptide peptidase SppA, 67K type |
| TIGR00708 | cobA | cob(I)yrinic acid a,c-diamide adenosyltransferase |
| TIGR00713 | hemL | glutamate-1-semialdehyde-2,1-aminomutase |
| TIGR00714 | hscB | Fe-S protein assembly co-chaperone HscB |
| TIGR00715 | precorr6x_red | precorrin-6x reductase |
| TIGR00716 | rnhC | ribonuclease HIII |

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| TIGR00717 | rpsA | ribosomal protein bS1 |
| TIGR00718 | sda_alpha | L-serine dehydratase, iron-sulfur-dependent, alpha subunit |
| TIGR00719 | sda_beta | L-serine dehydratase, iron-sulfur-dependent, beta subunit |
| TIGR00720 | sda_mono | L-serine ammonia-lyase |
| TIGR00731 | bL25_bact_ctc | ribosomal protein bL25, Ctc-form |
| TIGR00732 | dprA | DNA protecting protein DprA |
| TIGR00739 | yajC | preprotein translocase, YajC subunit |
| TIGR00740 | TIGR00740 | tRNA (cmo5U34)-methyltransferase |
| TIGR00746 | arcC | carbamate kinase |
| TIGR00749 | glk | glucokinase |
| TIGR00750 | lao | LAO/AO transport system ATPase |
| TIGR00751 | menA | 1,4-dihydroxy-2-naphthoate octaprenyltransferase |
| TIGR00753 | undec_PP_bacA | undecaprenyl-diphosphatase UppP |
| TIGR00754 | bfr | bacterioferritin |
| TIGR00755 | ksgA | ribosomal RNA small subunit methyltransferase A |
| TIGR00759 | aceE | pyruvate dehydrogenase (acetyl-transferring), homodimeric type |
| TIGR00760 | araD | L-ribulose-5-phosphate 4-epimerase |
| TIGR00763 | lon | endopeptidase La |
| TIGR00764 | lon_rel | putative ATP-dependent protease |
| TIGR00766 | TIGR00766 | inner membrane protein YhjD |
| TIGR00767 | rho | transcription termination factor Rho |
| TIGR00780 | ccоЁ | cytochrome c oxidase, cbb3-type, subunit I |
| TIGR00781 | ccоЁ | cytochrome c oxidase, cbb3-type, subunit II |
| TIGR00782 | ccоЁ | cytochrome c oxidase, cbb3-type, subunit III |
| TIGR00794 | kup | potassium uptake protein |
| TIGR00796 | livcs | branched-chain amino acid transport system II carrier protein |
| TIGR00809 | secB | protein-export chaperone SecB |
| TIGR00810 | secG | preprotein translocase, SecG subunit |
| TIGR00832 | acr3 | arsenical-resistance protein |
| TIGR00838 | argH | argininosuccinate lyase |
| TIGR00839 | aspA | aspartate ammonia-lyase |
| TIGR00847 | ccoS | cytochrome oxidase maturation protein, cbb3-type |
| TIGR00855 | L12 | ribosomal protein bL12 |
| TIGR00856 | pyrC_dimer | dihydroorotase, homodimeric type |
| TIGR00858 | bioF | 8-amino-7-oxononanoate synthase |
| TIGR00871 | zwf | glucose-6-phosphate dehydrogenase |

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| TIGR00872 | gnd_rel | 6-phosphogluconate dehydrogenase (decarboxylating) |
| TIGR00873 | gnd | 6-phosphogluconate dehydrogenase (decarboxylating) |
| TIGR00874 | talAB | transaldolase |
| TIGR00875 | fsa_talC_mipB | fructose-6-phosphate aldolase |
| TIGR00876 | tal_mycobact | transaldolase |
| TIGR00908 | 2A0305 | ethanolamine permease |
| TIGR00922 | nusG | transcription termination/antitermination factor NusG |
| TIGR00928 | purB | adenylosuccinate lyase |
| TIGR00936 | ahcY | adenosylhomocysteinase |
| TIGR00938 | thrB_alt | homoserine kinase |
| TIGR00945 | tatC | twin arginine-targeting protein translocase TatC |
| TIGR00952 | S15_bact | ribosomal protein uS15 |
| TIGR00959 | ffh | signal recognition particle protein |
| TIGR00962 | atpA | ATP synthase F1, alpha subunit |
| TIGR00963 | secA | preprotein translocase, SecA subunit |
| TIGR00964 | secE_bact | preprotein translocase, SecE subunit |
| TIGR00965 | dapD | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase |
| TIGR00967 | 3a0501s007 | preprotein translocase, SecY subunit |
| TIGR00970 | leuA_yeast | 2-isopropylmalate synthase |
| TIGR00973 | leuA_bact | 2-isopropylmalate synthase |
| TIGR00977 | citramal_synth | citramalate synthase |
| TIGR00979 | fumC_II | fumarate hydratase, class II |
| TIGR00981 | rpsL_bact | ribosomal protein uS12 |
| TIGR00987 | himA | integration host factor, alpha subunit |
| TIGR00988 | hip | integration host factor, beta subunit |
| TIGR00997 | ispZ | intracellular septation protein A |
| TIGR01001 | metA | homoserine O-succinyltransferase |
| TIGR01009 | rpsC_bact | ribosomal protein uS3 |
| TIGR01011 | rpsB_bact | ribosomal protein uS2 |
| TIGR01015 | hmgA | homogentisate 1,2-dioxygenase |
| TIGR01017 | rpsD_bact | ribosomal protein uS4 |
| TIGR01021 | rpsE_bact | ribosomal protein uS5 |
| TIGR01022 | rpmJ_bact | ribosomal protein bL36 |
| TIGR01023 | rpmG_bact | ribosomal protein bL33 |
| TIGR01024 | rplS_bact | ribosomal protein bL19 |
| TIGR01029 | rpsG_bact | ribosomal protein uS7 |

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| TIGR01030 | rpmH_bact | ribosomal protein bL34 |
| TIGR01031 | rpmF_bact | ribosomal protein bL32 |
| TIGR01032 | rplT_bact | ribosomal protein bL20 |
| TIGR01034 | metK | methionine adenosyltransferase |
| TIGR01035 | hemA | glutamyl-tRNA reductase |
| TIGR01036 | pyrD_sub2 | dihydroorotate dehydrogenase (fumarate) |
| TIGR01039 | atpD | ATP synthase F1, beta subunit |
| TIGR01044 | rplV_bact | ribosomal protein uL22 |
| TIGR01047 | nspC | carboxynorspermidine decarboxylase |
| TIGR01048 | lysA | diaminopimelate decarboxylase |
| TIGR01049 | rpsJ_bact | ribosomal protein uS10 |
| TIGR01050 | rpsS_bact | ribosomal protein uS19 |
| TIGR01051 | topA_bact | DNA topoisomerase I |
| TIGR01055 | parE_Gneg | DNA topoisomerase IV, B subunit |
| TIGR01058 | parE_Gpos | DNA topoisomerase IV, B subunit |
| TIGR01059 | gyrB | DNA gyrase, B subunit |
| TIGR01060 | eno | phosphopyruvate hydratase |
| TIGR01061 | parC_Gpos | DNA topoisomerase IV, A subunit |
| TIGR01062 | parC_Gneg | DNA topoisomerase IV, A subunit |
| TIGR01063 | gyrA | DNA gyrase, A subunit |
| TIGR01064 | pyruv_kin | pyruvate kinase |
| TIGR01066 | rplM_bact | ribosomal protein uL13 |
| TIGR01067 | rplN_bact | ribosomal protein uL14 |
| TIGR01068 | thioredoxin | thioredoxin |
| TIGR01070 | mutS1 | DNA mismatch repair protein MutS |
| TIGR01071 | rplO_bact | ribosomal protein uL15 |
| TIGR01072 | murA | UDP-N-acetylglucosamine 1-carboxyvinyltransferase |
| TIGR01073 | pcrA | ATP-dependent DNA helicase PcrA |
| TIGR01074 | rep | ATP-dependent DNA helicase Rep |
| TIGR01075 | uvrD | DNA helicase II |
| TIGR01078 | arcA | arginine deiminase |
| TIGR01079 | rplX_bact | ribosomal protein uL24 |
| TIGR01081 | mpl | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase |
| TIGR01082 | murC | UDP-N-acetylmuramate--L-alanine ligase |
| TIGR01083 | nth | endonuclease III |
| TIGR01084 | mutY | A/G-specific adenine glycosylase |
| TIGR01086 | fucA | L-fuculose phosphate aldolase |
| TIGR01087 | murD | UDP-N-acetylmuramoylalanine--D-glutamate ligase |
| TIGR01088 | aroQ | 3-dehydroquinate dehydratase, type II |

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| TIGR01089 | fucI | L-fucose isomerase |
| TIGR01090 | apt | adenine phosphoribosyltransferase |
| TIGR01091 | upp | uracil phosphoribosyltransferase |
| TIGR01099 | galU | UTP--glucose-1-phosphate uridylyltransferase |
| TIGR01102 | yscR | type III secretion apparatus protein, YscR/HrcR family |
| TIGR01103 | fliP | flagellar biosynthetic protein FlIP |
| TIGR01104 | V_PPase | V-type H(+)-translocating pyrophosphatase |
| TIGR01105 | galF | regulatory protein GalF |
| TIGR01108 | oadA | oxaloacetate decarboxylase alpha subunit |
| TIGR01110 | mdcA | malonate decarboxylase, alpha subunit |
| TIGR01118 | lacA | galactose-6-phosphate isomerase, LacA subunit |
| TIGR01119 | lacB | galactose-6-phosphate isomerase, LacB subunit |
| TIGR01120 | rpiB | ribose 5-phosphate isomerase B |
| TIGR01121 | D_amino_aminoT | D-amino-acid transaminase |
| TIGR01122 | ilvE_I | branched-chain amino acid aminotransferase |
| TIGR01123 | ilvE_II | branched-chain amino acid aminotransferase |
| TIGR01124 | ilvA_2Cterm | threonine ammonia-lyase, biosynthetic |
| TIGR01125 | TIGR01125 | ribosomal protein S12 methylthiotransferase RimO |
| TIGR01127 | ilvA_1Cterm | threonine ammonia-lyase |
| TIGR01128 | holA | DNA polymerase III, delta subunit |
| TIGR01131 | ATP_synt_6_or_A | ATP synthase F0, A subunit |
| TIGR01132 | pgm | phosphoglucomutase, alpha-D-glucose phosphate-specific |
| TIGR01133 | murG | undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase |
| TIGR01134 | purF | amidophosphoribosyltransferase |
| TIGR01135 | glmS | glutamine-fructose-6-phosphate transaminase (isomerizing) |
| TIGR01137 | cysta_beta | cystathionine beta-synthase |
| TIGR01138 | cysM | cysteine synthase B |
| TIGR01139 | cysK | cysteine synthase A |
| TIGR01140 | L_thr_O3P_dcar | threonine-phosphate decarboxylase |
| TIGR01141 | hisC | histidinol-phosphate transaminase |
| TIGR01142 | purT | phosphoribosylglycinamide formyltransferase 2 |
| TIGR01144 | ATP_synt_b | ATP synthase F0, B subunit |
| TIGR01145 | ATP_synt_delta | ATP synthase F1, delta subunit |
| TIGR01146 | ATPsyn_F1gamma | ATP synthase F1, gamma subunit |
| TIGR01163 | rpe | ribulose-phosphate 3-epimerase |
| TIGR01164 | rplP_bact | ribosomal protein uL16 |

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| TIGR01169 | rplA_bact | ribosomal protein uL1 |
| TIGR01171 | rplB_bact | ribosomal protein uL2 |
| TIGR01172 | cysE | serine O-acetyltransferase |
| TIGR01173 | glmU | UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase |
| TIGR01174 | ftsA | cell division protein FtsA |
| TIGR01176 | fum_red_Fp | fumarate reductase (quinol), flavoprotein subunit |
| TIGR01178 | ade | adenine deaminase |
| TIGR01179 | galE | UDP-glucose 4-epimerase GalE |
| TIGR01181 | dTDP_gluc_dehyt | dTDP-glucose 4,6-dehydratase |
| TIGR01196 | edd | phosphogluconate dehydratase |
| TIGR01202 | bchC | chlorophyll synthesis pathway protein BchC |
| TIGR01203 | HGPRTase | hypoxanthine phosphoribosyltransferase |
| TIGR01207 | rmlA | glucose-1-phosphate thymidylyltransferase |
| TIGR01208 | rmlA_long | glucose-1-phosphate thymidylyltransferase |
| TIGR01214 | rmlD | dTDP-4-dehydrorhamnose reductase |
| TIGR01215 | minE | cell division topological specificity factor MinE |
| TIGR01216 | ATP_synt_epsilon | ATP synthase F1, epsilon subunit |
| TIGR01217 | ac_ac_CoA_syn | acetoacetate-CoA ligase |
| TIGR01220 | Pmev_kin_Gr_pos | phosphomevalonate kinase |
| TIGR01221 | rmlC | dTDP-4-dehydrorhamnose 3,5-epimerase |
| TIGR01222 | minC | septum site-determining protein MinC |
| TIGR01224 | hutI | imidazolonepropionase |
| TIGR01225 | hutH | histidine ammonia-lyase |
| TIGR01227 | hutG | formimidoylglutamase |
| TIGR01228 | hutU | urocanate hydratase |
| TIGR01229 | rocF_arginase | arginase |
| TIGR01230 | agmatinase | agmatinase |
| TIGR01231 | lacC | tagatose-6-phosphate kinase |
| TIGR01232 | lacD | tagatose 1,6-diphosphate aldolase |
| TIGR01233 | lacG | 6-phospho-beta-galactosidase |
| TIGR01234 | L-ribulokinase | ribulokinase |
| TIGR01235 | pyruv_carbox | pyruvate carboxylase |
| TIGR01236 | D1pyr5carbox1 | 1-pyrroline-5-carboxylate dehydrogenase |
| TIGR01237 | D1pyr5carbox2 | putative delta-1-pyrroline-5-carboxylate dehydrogenase |
| TIGR01239 | galT_2 | galactose-1-phosphate uridylyltransferase |
| TIGR01240 | mevDPdecarb | diphosphomevalonate decarboxylase |
| TIGR01246 | dapE_proteo | succinyl-diaminopimelate desuccinylase |

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| TIGR01249 | pro_imino_pep_1 | prolyl aminopeptidase |
| TIGR01252 | acetolac_decarb | alpha-acetolactate decarboxylase |
| TIGR01255 | pyr_form_ly_1 | formate acetyltransferase |
| TIGR01260 | ATP_synt_c | ATP synthase F0, C subunit |
| TIGR01262 | maiA | maleylacetoacetate isomerase |
| TIGR01263 | 4HPPD | 4-hydroxyphenylpyruvate dioxygenase |
| TIGR01266 | fum_ac_acetase | fumarylacetoacetate |
| TIGR01267 | Phe4hydrox_mono | phenylalanine-4-hydroxylase |
| TIGR01273 | speA | arginine decarboxylase |
| TIGR01280 | xseB | exodeoxyribonuclease VII, small subunit |
| TIGR01292 | TRX_reduct | thioredoxin-disulfide reductase |
| TIGR01296 | asd_B | aspartate-semialdehyde dehydrogenase |
| TIGR01298 | RNaseT | ribonuclease T |
| TIGR01302 | IMP_dehydrog | inosine-5'-monophosphate dehydrogenase |
| TIGR01305 | GMP_reduct_1 | guanosine monophosphate reductase |
| TIGR01306 | GMP_reduct_2 | guanosine monophosphate reductase |
| TIGR01307 | pgm_bpd_ind | phosphoglycerate mutase (2,3-diphosphoglycerate-independent) |
| TIGR01308 | rpmD_bact | ribosomal protein uL30 |
| TIGR01311 | glycerol_kin | glycerol kinase |
| TIGR01312 | XylB | xylulokinase |
| TIGR01314 | gntK_FGGY | gluconate kinase |
| TIGR01320 | mal_quin_oxido | malate dehydrogenase (acceptor) |
| TIGR01321 | TrpR | trp operon repressor |
| TIGR01324 | cysta_beta_ly_B | cystathionine beta-lyase |
| TIGR01325 | O_suc_HS_sulf | O-succinylhomoserine sulfhydrylase |
| TIGR01327 | PGDH | phosphoglycerate dehydrogenase |
| TIGR01331 | bisphos_cysQ | 3'(2'),5'-bisphosphate nucleotidase |
| TIGR01341 | aconitase_1 | aconitate hydratase 1 |
| TIGR01344 | malate_syn_A | malate synthase A |
| TIGR01345 | malate_syn_G | malate synthase G |
| TIGR01346 | isocit_lyase | isocitrate lyase |
| TIGR01347 | sucB | dihydrolipoyllysine-residue succinyltransferase, E2 component of oxoglutarate dehydrogenase (succinyl-transferring) complex |
| TIGR01348 | PDHac_trf_long | dihydrolipoyllysine-residue acetyltransferase |
| TIGR01349 | PDHac_trf_mito | pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase |
| TIGR01350 | lipoamide_DH | dihydrolipoyl dehydrogenase |
| TIGR01354 | cyt_deam_tetra | cytidine deaminase |

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| TIGR01355 | cyt_deam_dimer | cytidine deaminase |
| TIGR01356 | aroA | 3-phosphoshikimate 1-carboxyvinyltransferase |
| TIGR01357 | aroB | 3-dehydroquinate synthase |
| TIGR01358 | DAHP_synth_II | 3-deoxy-7-phosphoheptulonate synthase |
| TIGR01362 | KDO8P_synth | 3-deoxy-8-phosphooctulonate synthase |
| TIGR01364 | serC_1 | phosphoserine transaminase |
| TIGR01366 | serC_3 | putative phosphoserine aminotransferase |
| TIGR01371 | met_syn_B12ind | 5-methyltetrahydropteroylglutamate--homocysteine S-methyltransferase |
| TIGR01378 | thi_PPkinase | thiamine pyrophosphokinase |
| TIGR01379 | thiL | thiamine-phosphate kinase |
| TIGR01380 | glut_syn | glutathione synthase |
| TIGR01388 | rnd | ribonuclease D |
| TIGR01389 | recQ | ATP-dependent DNA helicase RecQ |
| TIGR01390 | CycNucDiestase | 2',3'-cyclic-nucleotide 2'-phosphodiesterase |
| TIGR01392 | homoserO_Ac_trn | homoserine O-acetyltransferase |
| TIGR01393 | lepA | elongation factor 4 |
| TIGR01394 | TypA_BipA | GTP-binding protein TypA/BipA |
| TIGR01395 | FlgC | flagellar basal-body rod protein FlgC |
| TIGR01396 | FlgB | flagellar basal-body rod protein FlgB |
| TIGR01397 | fliM_switch | flagellar motor switch protein FliM |
| TIGR01398 | FlhA | flagellar biosynthesis protein FlhA |
| TIGR01400 | fliR | flagellar biosynthetic protein FliR |
| TIGR01401 | fliR_like_III | type III secretion apparatus protein SpaR/YscT/HrcT |
| TIGR01402 | fliQ | flagellar biosynthetic protein FliQ |
| TIGR01405 | polC_Gram_pos | DNA polymerase III, alpha subunit, Gram-positive type |
| TIGR01406 | dnaQ_proteo | DNA polymerase III, epsilon subunit |
| TIGR01410 | tatB | twin arginine-targeting protein translocase TatB |
| TIGR01416 | Rieske_proteo | ubiquinol-cytochrome c reductase, iron-sulfur subunit |
| TIGR01418 | PEP_synth | phosphoenolpyruvate synthase |
| TIGR01419 | nitro_reg_IIA | PTS IIA-like nitrogen-regulatory protein PtsN |
| TIGR01421 | gluta_reduc_1 | glutathione-disulfide reductase |
| TIGR01422 | phosphonatase | phosphonoacetaldehyde hydrolase |
| TIGR01424 | gluta_reduc_2 | glutathione-disulfide reductase |
| TIGR01428 | HAD_type_II | haloacid dehalogenase, type II |
| TIGR01430 | aden_deam | adenosine deaminase |
| TIGR01432 | QOXA | cytochrome aa3 quinol oxidase, subunit II |
| TIGR01433 | CyoA | ubiquinol oxidase, subunit II |

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| TIGR01434 | glu_cys_ligase | glutamate--cysteine ligase |
| TIGR01436 | glu_cys_lig_pln | glutamate--cysteine ligase |
| TIGR01447 | recD | exodeoxyribonuclease V, alpha subunit |
| TIGR01449 | PGP_bact | phosphoglycolate phosphatase, bacterial |
| TIGR01450 | recC | exodeoxyribonuclease V, gamma subunit |
| TIGR01455 | glmM | phosphoglucosamine mutase |
| TIGR01461 | greB | transcription elongation factor GreB |
| TIGR01464 | hemE | uroporphyrinogen decarboxylase |
| TIGR01465 | cobM_cbiF | precorrin-4 C11-methyltransferase |
| TIGR01467 | cobi_cbiL | precorrin-2 C(20)-methyltransferase |
| TIGR01472 | gmd | GDP-mannose 4,6-dehydratase |
| TIGR01473 | cyoE_ctaB | protoheme IX farnesyltransferase |
| TIGR01474 | ubiA_proteo | 4-hydroxybenzoate polyprenyl transferase |
| TIGR01479 | GMP_PMI | mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase |
| TIGR01481 | ccpA | catabolite control protein A |
| TIGR01496 | DHPS | dihydropteroate synthase |
| TIGR01497 | kdpB | K+-transporting ATPase, B subunit |
| TIGR01498 | folK | 2-amino-4-hydroxy-6- hydroxymethylidihydropteridine diphosphokinase |
| TIGR01504 | glyox_carbo_lig | glyoxylate carboligase |
| TIGR01505 | tartro_sem_red | 2-hydroxy-3-oxopropionate reductase |
| TIGR01510 | coaD_prev_kdtB | pantetheine-phosphate adenylyltransferase |
| TIGR01511 | ATPase-IB1_Cu | copper-translocating P-type ATPase |
| TIGR01512 | ATPase-IB2_Cd | cadmium-translocating P-type ATPase |
| TIGR01514 | NAPRTase | nicotinate phosphoribosyltransferase |
| TIGR01515 | branching_enzym | 1,4-alpha-glucan branching enzyme |
| TIGR01517 | ATPase-IIB_Ca | calcium-translocating P-type ATPase, PMCA-type |
| TIGR01518 | g3p_cytidyltrns | glycerol-3-phosphate cytidylyltransferase |
| TIGR01520 | FruBisAldo_II_A | fructose-bisphosphate aldolase, class II |
| TIGR01521 | FruBisAldo_II_B | fructose-bisphosphate aldolase, class II, Calvin cycle subtype |
| TIGR01523 | ATPase-IID_K-Na | potassium/sodium efflux P-type ATPase, fungal-type |
| TIGR01524 | ATPase-IIIB_Mg | magnesium-translocating P-type ATPase |
| TIGR01529 | argR_whole | arginine repressor |
| TIGR01532 | E4PD_g-proteo | erythrose-4-phosphate dehydrogenase |
| TIGR01533 | lipo_e_P4 | 5'-nucleotidase, lipoprotein e(P4) family |
| TIGR01534 | GAPDH-I | glyceraldehyde-3-phosphate dehydrogenase, type I |
| TIGR01536 | asn_synth_AEB | asparagine synthetase (glutamine-hydrolyzing) |

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| TIGR01553 | formate-DH-alpha | formate dehydrogenase-N alpha subunit |
| TIGR01562 | FdhE | formate dehydrogenase accessory protein FdhE |
| TIGR01573 | cas2 | CRISPR-associated endonuclease Cas2 |
| TIGR01574 | miaB-methiolase | tRNA-i(6)A37 thiotransferase enzyme MiaB |
| TIGR01575 | rimI | ribosomal-protein-alanine acetyltransferase |
| TIGR01580 | narG | nitrate reductase, alpha subunit |
| TIGR01582 | FDH-beta | formate dehydrogenase, beta subunit |
| TIGR01583 | formate-DH-gamm | formate dehydrogenase, gamma subunit |
| TIGR01584 | citF | citrate lyase, alpha subunit |
| TIGR01588 | citE | citrate (pro-3S)-lyase, beta subunit |
| TIGR01591 | Fdh-alpha | formate dehydrogenase, alpha subunit |
| TIGR01608 | citD | citrate lyase acyl carrier protein |
| TIGR01632 | L11_bact | ribosomal protein uL11 |
| TIGR01660 | narH | nitrate reductase, beta subunit |
| TIGR01682 | moaD | molybdopterin converting factor, subunit 1 |
| TIGR01683 | thiS | thiamine biosynthesis protein ThiS |
| TIGR01688 | dltC | D-alanine--poly(phosphoribitol) ligase, subunit 2 |
| TIGR01691 | enolase-ppase | 2,3-diketo-5-methylthio-1-phosphopentane phosphatase |
| TIGR01692 | HIBADH | 3-hydroxyisobutyrate dehydrogenase |
| TIGR01693 | UTase_glnD | protein-P-II uridylyltransferase |
| TIGR01694 | MTAP | methylthioadenosine phosphorylase |
| TIGR01695 | murJ_mviN | murein biosynthesis integral membrane protein MurJ |
| TIGR01696 | deoB | phosphopentomutase |
| TIGR01700 | PNPH | purine nucleoside phosphorylase I, inosine and guanosine-specific |
| TIGR01703 | hybrid_clust | hydroxylamine reductase |
| TIGR01704 | MTA/SAH-Nsdase | MTA/SAH nucleosidase |
| TIGR01706 | NAPA | periplasmic nitrate reductase, large subunit |
| TIGR01707 | gspl | type II secretion system protein I |
| TIGR01708 | typell_sec_gspH | type II secretion system protein H |
| TIGR01709 | typell_sec_gspL | type II secretion system protein L |
| TIGR01710 | typell_sec_gspG | type II secretion system protein G |
| TIGR01711 | gspJ | type II secretion system protein J |
| TIGR01713 | typell_sec_gspC | type II secretion system protein C |
| TIGR01717 | AMP-nucleosdse | AMP nucleosidase |
| TIGR01718 | Uridine-psphlse | uridine phosphorylase |
| TIGR01722 | MMSDH | methylmalonate-semialdehyde dehydrogenase (acylating) |

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| TIGR01734 | D-ala-DACP-lig | D-alanine--poly(phosphoribitol) ligase, subunit 1 |
| TIGR01735 | FGAM_synt | phosphoribosylformylglycinamide synthase |
| TIGR01736 | FGAM_synth_II | phosphoribosylformylglycinamide synthase II |
| TIGR01737 | FGAM_synth_I | phosphoribosylformylglycinamide synthase I |
| TIGR01738 | bioH | pimelyl-[acyl-carrier protein] methyl ester esterase |
| TIGR01743 | purR_Bsub | pur operon repressor PurR |
| TIGR01744 | XPRTase | xanthine phosphoribosyltransferase |
| TIGR01745 | asd_gamma | aspartate-semialdehyde dehydrogenase |
| TIGR01748 | rhaA | L-rhamnose isomerase |
| TIGR01749 | fabA | beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabA |
| TIGR01750 | fabZ | beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ |
| TIGR01752 | flav_long | flavodoxin |
| TIGR01753 | flav_short | flavodoxin |
| TIGR01755 | flav_wrbA | NAD(P)H:quinone oxidoreductase, type IV |
| TIGR01763 | MalateDH_bact | malate dehydrogenase, NAD-dependent |
| TIGR01771 | L-LDH-NAD | L-lactate dehydrogenase |
| TIGR01772 | MDH_euk_gproteo | malate dehydrogenase, NAD-dependent |
| TIGR01773 | GABAperm | GABA permease |
| TIGR01779 | TonB-B12 | TonB-dependent vitamin B12 receptor |
| TIGR01788 | Glu-decarb-GAD | glutamate decarboxylase |
| TIGR01792 | urease_alpha | urease, alpha subunit |
| TIGR01798 | cit_synth_I | citrate (Si)-synthase |
| TIGR01804 | BADH | betaine-aldehyde dehydrogenase |
| TIGR01806 | CM_mono2 | putative chorismate mutase |
| TIGR01810 | betA | choline dehydrogenase |
| TIGR01814 | kynureninase | kynureninase |
| TIGR01816 | sdhA_forward | succinate dehydrogenase, flavoprotein subunit |
| TIGR01818 | ntrC | nitrogen regulation protein NR(I) |
| TIGR01819 | F420_cofD | 2-phospho-L-lactate transferase |
| TIGR01822 | 2am3keto_CoA | glycine C-acetyltransferase |
| TIGR01828 | pyru_phos_dikin | pyruvate, phosphate dikinase |
| TIGR01830 | 3oxo_ACP_reduc | 3-oxoacyl-[acyl-carrier-protein] reductase |
| TIGR01832 | kduD | 2-deoxy-D-gluconate 3-dehydrogenase |
| TIGR01835 | HMG-CoA-S_prok | hydroxymethylglutaryl-CoA synthase |
| TIGR01848 | PHA_reg_PhaR | polyhydroxyalkanoate synthesis repressor PhaR |
| TIGR01850 | argC | N-acetyl-gamma-glutamyl-phosphate reductase |
| TIGR01852 | lipid_A_lpxA | acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase |

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| TIGR01853 | lipid_A_lpxD | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase LpxD |
| TIGR01854 | lipid_A_lpxH | UDP-2,3-diacylglicosamine diphosphatase |
| TIGR01855 | IMP_synth_hisH | imidazole glycerol phosphate synthase, glutamine amidotransferase subunit |
| TIGR01858 | tag_bisphos_ald | class II aldolase, tagatose bisphosphate family |
| TIGR01859 | fruc Bis ald_ | fructose-1,6-bisphosphate aldolase, class II |
| TIGR01868 | casD_Cas5e | CRISPR-associated protein Cas5/CasD, subtype I-E/ECOLI |
| TIGR01873 | cas_CT1978 | CRISPR-associated endoribonuclease Cas2, subtype I-E/ECOLI |
| TIGR01882 | peptidase-T | peptidase T |
| TIGR01885 | Orn_aminotrans | ornithine--oxo-acid transaminase |
| TIGR01890 | N-Ac-Glu-synth | amino-acid N-acetyltransferase |
| TIGR01892 | AcOrn-deacetyl | acetylornithine deacetylase (ArgE) |
| TIGR01907 | casE_Cse3 | CRISPR-associated protein Cas6/Cse3/CasE, subtype I-E/ECOLI |
| TIGR01916 | F420_cofE | coenzyme F420-0:L-glutamate ligase |
| TIGR01923 | menE | O-succinylbenzoate-CoA ligase |
| TIGR01924 | rsbW_low_gc | anti-sigma B factor |
| TIGR01927 | menC_gamma/gm+ | o-succinylbenzoate synthase |
| TIGR01928 | menC_lowGC/arch | o-succinylbenzoate synthase |
| TIGR01929 | menB | naphthoate synthase |
| TIGR01931 | cysJ | sulfite reductase [NADPH] flavoprotein, alpha-component |
| TIGR01932 | hfIC | HfIC protein |
| TIGR01933 | hfIK | HfIK protein |
| TIGR01936 | nqrA | NADH:ubiquinone oxidoreductase, Na(+) -translocating, A subunit |
| TIGR01937 | nqrB | NADH:ubiquinone oxidoreductase, Na(+) -translocating, B subunit |
| TIGR01938 | nqrC | NADH:ubiquinone oxidoreductase, Na(+) -translocating, C subunit |
| TIGR01939 | nqrD | NADH:ubiquinone oxidoreductase, Na(+) -translocating, D subunit |
| TIGR01940 | nqrE | NADH:ubiquinone oxidoreductase, Na(+) -translocating, E subunit |
| TIGR01941 | nqrF | NADH:ubiquinone oxidoreductase, Na(+) -translocating, F subunit |
| TIGR01950 | SoxR | redox-sensitive transcriptional activator SoxR |
| TIGR01951 | nusB | transcription antitermination factor NusB |

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| TIGR01955 | RfaH | transcription elongation factor/antiterminator RfaH |
| TIGR01959 | nuoF_fam | NADH oxidoreductase (quinone), F subunit |
| TIGR01966 | RNasePH | ribonuclease PH |
| TIGR01967 | DEAH_box_HrpA | RNA helicase HrpA |
| TIGR01968 | minD_bact | septum site-determining protein MinD |
| TIGR01970 | DEAH_box_HrpB | ATP-dependent helicase HrpB |
| TIGR01973 | NuoG | NADH dehydrogenase (quinone), G subunit |
| TIGR01975 | isoAsp_dipep | beta-aspartyl peptidase |
| TIGR01978 | sufC | FeS assembly ATPase SufC |
| TIGR01980 | sufB | FeS assembly protein SufB |
| TIGR01981 | sufD | FeS assembly protein SufD |
| TIGR01982 | UbiB | 2-polypropenylphenol 6-hydroxylase |
| TIGR01983 | UbiG | 3-demethylubiquinone-9 3-O-methyltransferase |
| TIGR01984 | UbiH | 2-polypropenyl-6-methoxyphenol 4-hydroxylase |
| TIGR01990 | bPGM | beta-phosphoglucomutase |
| TIGR01991 | HscA | Fe-S protein assembly chaperone HscA |
| TIGR01994 | SUF_scaf_2 | SUF system FeS assembly protein, NifU family |
| TIGR01997 | sufA_proteo | FeS assembly scaffold SufA |
| TIGR02006 | IscS | cysteine desulfurase IscS |
| TIGR02007 | fdx_isc | ferredoxin, 2Fe-2S type, ISC system |
| TIGR02010 | IscR | iron-sulfur cluster assembly transcription factor IscR |
| TIGR02011 | IscA | iron-sulfur cluster assembly protein IscA |
| TIGR02012 | tigrfam_recA | protein RecA |
| TIGR02013 | rpoB | DNA-directed RNA polymerase, beta subunit |
| TIGR02017 | hutG_amidohyd | N-formylglutamate deformylase |
| TIGR02018 | his_ut_repres | histidine utilization repressor |
| TIGR02022 | hutF | formiminoglutamate deiminase |
| TIGR02027 | rpoA | DNA-directed RNA polymerase, alpha subunit |
| TIGR02033 | D-hydantoinase | dihydropyrimidinase |
| TIGR02035 | D_Ser_am_lyase | D-serine ammonia-lyase |
| TIGR02036 | dsdC | D-serine deaminase transcriptional activator |
| TIGR02038 | protease_degS | periplasmic serine peptidase DegS |
| TIGR02041 | CysI | sulfite reductase (NADPH) hemoprotein, beta-component |
| TIGR02043 | ZntR | Zn(II)-responsive transcriptional regulator |
| TIGR02044 | CueR | Cu(I)-responsive transcriptional regulator |
| TIGR02057 | PAPS_reductase | phosphoadenosine phosphosulfate reductase |
| TIGR02062 | RNase_B | exoribonuclease II |
| TIGR02063 | RNase_R | ribonuclease R |
| TIGR02067 | his_9_HisN | histidinol-phosphatase |

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| TIGR02070 | mono_pep_trsgly | monofunctional biosynthetic peptidoglycan transglycosylase |
| TIGR02071 | PBP_1b | penicillin-binding protein 1B |
| TIGR02072 | BioC | malonyl-acyl carrier protein O-methyltransferase BioC |
| TIGR02073 | PBP_1c | penicillin-binding protein 1C |
| TIGR02075 | pyrH_bact | UMP kinase |
| TIGR02079 | THD1 | threonine dehydratase |
| TIGR02080 | O_succ_thio_ly | O-succinylhomoserine (thiol)-lyase |
| TIGR02081 | metW | methionine biosynthesis protein MetW |
| TIGR02082 | metH | methionine synthase |
| TIGR02085 | meth_trns_rumB | 23S rRNA (uracil-5-)methyltransferase RumB |
| TIGR02089 | TTC | tartrate dehydrogenase |
| TIGR02091 | glgC | glucose-1-phosphate adenylyltransferase |
| TIGR02100 | glgX_debranch | glycogen debranching enzyme GlgX |
| TIGR02105 | III_needle | type III secretion apparatus needle protein |
| TIGR02106 | cyd_oper_ybgT | cyd operon protein YbgT |
| TIGR02108 | PQQ_syn_pqqB | coenzyme PQQ biosynthesis protein B |
| TIGR02109 | PQQ_syn_pqqE | coenzyme PQQ biosynthesis enzyme PqqE |
| TIGR02111 | PQQ_syn_pqqC | coenzyme PQQ biosynthesis protein C |
| TIGR02112 | cyd_oper_ybgE | cyd operon protein YbgE |
| TIGR02115 | potass_kdpF | K+-transporting ATPase, F subunit |
| TIGR02116 | toxin_Txe_YoeB | addiction module toxin, Txe/YoeB family |
| TIGR02120 | GspF | type II secretion system protein F |
| TIGR02124 | hypE | hydrogenase expression/formation protein HypE |
| TIGR02125 | CytB-hydrogenase | Ni/Fe-hydrogenase, b-type cytochrome subunit |
| TIGR02127 | pyrF_sub2 | orotidine 5'-phosphate decarboxylase |
| TIGR02134 | transald_staph | transaldolase |
| TIGR02135 | phoU_full | phosphate transport system regulatory protein PhoU |
| TIGR02143 | trmA_only | tRNA (uracil(54)-C(5))-methyltransferase |
| TIGR02150 | IPP_isom_1 | isopentenyl-diphosphate delta-isomerase |
| TIGR02151 | IPP_isom_2 | isopentenyl-diphosphate delta-isomerase, type 2 |
| TIGR02152 | D_ribokin_bact | ribokinase |
| TIGR02154 | PhoB | phosphate regulon transcriptional regulatory protein PhoB |
| TIGR02155 | PA_CoA_ligase | phenylacetate-CoA ligase |
| TIGR02159 | PA_CoA_Oxy4 | phenylacetate-CoA oxygenase, PaaJ subunit |
| TIGR02162 | torC | trimethylamine-N-oxide reductase c-type cytochrome TorC |

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| TIGR02164 | torA | trimethylamine-N-oxide reductase TorA |
| TIGR02168 | SMC_prok_B | chromosome segregation protein SMC |
| TIGR02170 | thyX | thymidylate synthase, flavin-dependent |
| TIGR02176 | pyruv_ox_red | pyruvate:ferredoxin (flavodoxin) oxidoreductase |
| TIGR02181 | GRX_bact | glutaredoxin 3 |
| TIGR02182 | GRXB | glutaredoxin, GrxB family |
| TIGR02183 | GRXA | glutaredoxin, GrxA family |
| TIGR02188 | Ac_CoA_lig_AcsA | acetate--CoA ligase |
| TIGR02191 | RNaseIII | ribonuclease III |
| TIGR02193 | heptsyl_trn_I | lipopolysaccharide heptosyltransferase I |
| TIGR02195 | heptsyl_trn_II | lipopolysaccharide heptosyltransferase II |
| TIGR02197 | heptose_epim | ADP-glyceromanno-heptose 6-epimerase |
| TIGR02201 | heptsyl_trn_III | putative lipopolysaccharide heptosyltransferase III |
| TIGR02203 | MsbA_lipidA | lipid A export permease/ATP-binding protein MsbA |
| TIGR02205 | septum_zipA | cell division protein ZipA |
| TIGR02208 | lipid_A_msbB | lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase |
| TIGR02209 | ftsL_broad | cell division protein FtsL |
| TIGR02210 | rodA_shape | rod shape-determining protein RodA |
| TIGR02211 | LolD_lipo_ex | lipoprotein releasing system, ATP-binding protein |
| TIGR02213 | loliE_release | lipoprotein releasing system, transmembrane protein LoliE |
| TIGR02223 | ftsN | cell division protein FtsN |
| TIGR02224 | recomb_XerC | tyrosine recombinase XerC |
| TIGR02225 | recomb_XerD | tyrosine recombinase XerD |
| TIGR02227 | sigpep_I_bact | signal peptidase I |
| TIGR02248 | mutH_TIGR | DNA mismatch repair endonuclease MutH |
| TIGR02254 | YjjG/YfnB | noncanonical pyrimidine nucleotidase, YjjG family |
| TIGR02257 | cobalto_cobN | cobaltochelatase, CobN subunit |
| TIGR02258 | 2_5_ligase | 2'-5' RNA ligase |
| TIGR02272 | gentisate_1_2 | gentisate 1,2-dioxygenase |
| TIGR02273 | 16S_RimM | 16S rRNA processing protein RimM |
| TIGR02274 | dCTP_deam | deoxycytidine triphosphate deaminase |
| TIGR02275 | DHB_AMP_lig | (2,3-dihydroxybenzoyl)adenylate synthase |
| TIGR02278 | PaaN-DH | phenylacetic acid degradation protein paaN |
| TIGR02280 | PaaB1 | phenylacetate degradation probable enoyl-CoA hydratase PaaB |
| TIGR02282 | MltB | lytic murein transglycosylase B |
| TIGR02286 | PaaD | phenylacetic acid degradation protein PaaD |
| TIGR02296 | HpaC | 4-hydroxyphenylacetate 3-monoxygenase, |

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| | | reductase component |
| TIGR02297 | HpaA | 4-hydroxyphenylacetate catabolism regulatory protein HpaA |
| TIGR02298 | HpaD_Fe | 3,4-dihydroxyphenylacetate 2,3-dioxygenase |
| TIGR02299 | HpaE | 5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase |
| TIGR02310 | HpaB-2 | 4-hydroxyphenylacetate 3-monoxygenase, oxygenase component |
| TIGR02311 | Hpal | 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase |
| TIGR02312 | HpaH | 2-oxo-hepta-3-ene-1,7-dioic acid hydratase |
| TIGR02316 | propion_prpE | propionate--CoA ligase |
| TIGR02317 | prpB | methylisocitrate lyase |
| TIGR02318 | phosphono_phnM | phosphonate metabolism protein PhnM |
| TIGR02322 | phosphon_PhN | phosphonate metabolism protein/1,5-bisphosphokinase (PRPP-forming) PhnN |
| TIGR02323 | CP_lyasePhnK | phosphonate C-P lyase system protein PhnK |
| TIGR02324 | CP_lyasePhnL | phosphonate C-P lyase system protein PhnL |
| TIGR02325 | C_P_lyase_phnF | phosphonate metabolism transcriptional regulator PhnF |
| TIGR02326 | transamin_PhW | 2-aminoethylphosphonate--pyruvate transaminase |
| TIGR02329 | propionate_PrpR | propionate catabolism operon regulatory protein PrpR |
| TIGR02330 | prpD | 2-methylcitrate dehydratase |
| TIGR02332 | HpaX | 4-hydroxyphenylacetate permease |
| TIGR02333 | 2met_isocit_dHY | 2-methylisocitrate dehydratase, Fe/S-dependent |
| TIGR02334 | prpF | probable AcnD-accessory protein PrpF |
| TIGR02337 | HpaR | homoprotocatechuate degradation operon regulator, HpaR |
| TIGR02348 | GroEL | chaperonin GroL |
| TIGR02349 | DnaJ_bact | chaperone protein DnaJ |
| TIGR02350 | prok_dnaK | chaperone protein DnaK |
| TIGR02351 | thiH | thiazole biosynthesis protein ThiH |
| TIGR02352 | thiamin_ThiO | glycine oxidase ThiO |
| TIGR02355 | moeB | molybdopterin synthase sulfurylase MoeB |
| TIGR02356 | adenyl_thiF | thiazole biosynthesis adenylyltransferase ThiF |
| TIGR02360 | pbenz_hydroxyl | 4-hydroxybenzoate 3-monoxygenase |
| TIGR02363 | dhaK1 | dihydroxyacetone kinase, DhaK subunit |
| TIGR02365 | dha_L_ycgS | dihydroxyacetone kinase, L subunit |
| TIGR02380 | ECA_wecA | undecaprenyl-phosphate alpha-N-acetylglucosaminy 1-phosphatetransferase |
| TIGR02381 | cspD | cold shock domain protein CspD |

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| TIGR02382 | wecD_rffC | TDP-D-fucosamine acetyltransferase |
| TIGR02383 | Hfq | RNA chaperone Hfq |
| TIGR02386 | rpoC_TIGR | DNA-directed RNA polymerase, beta' subunit |
| TIGR02392 | rpoH_proteo | alternative sigma factor RpoH |
| TIGR02394 | rpoS_proteo | RNA polymerase sigma factor RpoS |
| TIGR02395 | rpoN_sigma | RNA polymerase sigma-54 factor |
| TIGR02397 | dnaX_nterm | DNA polymerase III, subunit gamma and tau |
| TIGR02400 | trehalose_OtsA | alpha,alpha-trehalose-phosphate synthase (UDP-forming) |
| TIGR02401 | trehalose_TreY | malto-oligosyltrehalose synthase |
| TIGR02402 | trehalose_TreZ | malto-oligosyltrehalose trehalohydrolase |
| TIGR02403 | trehalose_treC | alpha,alpha-phosphotrehalase |
| TIGR02404 | trehalos_R_Bsub | trehalose operon repressor |
| TIGR02405 | trehalos_R_Ecol | trehalose operon repressor |
| TIGR02412 | pepN_strep_liv | aminopeptidase N |
| TIGR02414 | pepN_proteo | aminopeptidase N |
| TIGR02418 | acolac_catab | acetolactate synthase, catabolic |
| TIGR02420 | dksA | RNA polymerase-binding protein DksA |
| TIGR02422 | protocat_beta | protocatechuate 3,4-dioxygenase, beta subunit |
| TIGR02423 | protocat_alpha | protocatechuate 3,4-dioxygenase, alpha subunit |
| TIGR02425 | decarb_PcaC | 4-carboxymuconolactone decarboxylase |
| TIGR02426 | protocat_pcaB | 3-carboxy-cis,cis-muconate cycloisomerase |
| TIGR02427 | protocat_pcaD | 3-oxoadipate enol-lactonase |
| TIGR02430 | pcaF | 3-oxoadipyl-CoA thiolase |
| TIGR02435 | CobG | precorrin-3B synthase |
| TIGR02437 | FadB | fatty oxidation complex, alpha subunit FadB |
| TIGR02440 | FadJ | fatty oxidation complex, alpha subunit FadJ |
| TIGR02445 | fadA | acetyl-CoA C-acyltransferase FadA |
| TIGR02446 | FadI | acetyl-CoA C-acyltransferase FadI |
| TIGR02473 | flagell_FliJ | flagellar export protein FliJ |
| TIGR02475 | CobW | cobalamin biosynthesis protein CobW |
| TIGR02476 | BluB | 5,6-dimethylbenzimidazole synthase |
| TIGR02482 | PFKA_ATP | 6-phosphofructokinase |
| TIGR02487 | NrdD | anaerobic ribonucleoside-triphosphate reductase |
| TIGR02488 | flgG_G_neg | flagellar basal-body rod protein FlgG |
| TIGR02490 | flgF | flagellar basal-body rod protein FlgF |
| TIGR02491 | NrdG | anaerobic ribonucleoside-triphosphate reductase activating protein |
| TIGR02492 | flgK_ends | flagellar hook-associated protein FlgK |
| TIGR02493 | PFLA | pyruvate formate-lyase 1-activating enzyme |

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| TIGR02499 | HrpE_YscL_not | type III secretion apparatus protein, HrpE/YscL family |
| TIGR02500 | type_III_yscD | type III secretion apparatus protein, YscD/HrpQ family |
| TIGR02504 | NrdJ_Z | ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent |
| TIGR02506 | NrdE_NrdA | ribonucleoside-diphosphate reductase, alpha subunit |
| TIGR02516 | type_III_yscC | type III secretion outer membrane pore, YscC/HrcC family |
| TIGR02517 | type_II_gspD | type II secretion system protein D |
| TIGR02521 | type_IV_pilW | type IV pilus biogenesis/stability protein PilW |
| TIGR02523 | type_IV_pilV | type IV pilus modification protein PilV |
| TIGR02528 | EutP | ethanolamine utilization protein, EutP |
| TIGR02533 | type_II_gspE | type II secretion system protein E |
| TIGR02538 | type_IV_pilB | type IV-A pilus assembly ATPase PilB |
| TIGR02541 | flagell_FlgJ | flagellar rod assembly protein/muramidase FlgJ |
| TIGR02544 | III_secr_YscJ | type III secretion apparatus lipoprotein, YscJ/HrcJ family |
| TIGR02546 | III_secr_ATP | type III secretion apparatus H+-transporting two-sector ATPase |
| TIGR02547 | casA_cse1 | CRISPR type I-E/ECOLI-associated protein CasA/Cse1 |
| TIGR02548 | casB_cse2 | CRISPR type I-E/ECOLI-associated protein CasB/Cse2 |
| TIGR02550 | flagell_flgL | flagellar hook-associated protein 3 |
| TIGR02551 | SpaO_YscQ | type III secretion apparatus protein, YscQ/HrcQ family |
| TIGR02552 | LcrH_SycD | type III secretion low calcium response chaperone LcrH/SycD |
| TIGR02568 | LcrE | type III secretion regulator YopN/LcrE/InvE/MxiC |
| TIGR02571 | ComEB | ComE operon protein 2 |
| TIGR02607 | antidote_HigA | addiction module antidote protein, HigA family |
| TIGR02614 | ftsW | cell division protein FtsW |
| TIGR02622 | CDP_4_6_dhtase | CDP-glucose 4,6-dehydratase |
| TIGR02623 | G1P_cyt_trans | glucose-1-phosphate cytidylyltransferase |
| TIGR02624 | rhamnu_1P_ald | rhamnulose-1-phosphate aldolase |
| TIGR02625 | YiiL_rotase | L-rhamnose mutarotase |
| TIGR02627 | rhamnulo_kin | rhamnulokinase |
| TIGR02628 | fuculo_kin_coli | L-fuculokinase |
| TIGR02630 | xylose_isom_A | xylose isomerase |
| TIGR02636 | galM_Leloir | galactose mutarotase |
| TIGR02638 | lactal_redase | lactaldehyde reductase |

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| TIGR02639 | ClpA | ATP-dependent Clp protease ATP-binding subunit ClpA |
| TIGR02643 | T_phosphoryl | thymidine phosphorylase |
| TIGR02648 | rep_term_tus | DNA replication terminus site-binding protein |
| TIGR02651 | RNase_Z | ribonuclease Z |
| TIGR02665 | molyb_mobA | molybdenum cofactor guanylyltransferase |
| TIGR02666 | moaA | molybdenum cofactor biosynthesis protein A |
| TIGR02667 | moaB_proteo | molybdenum cofactor biosynthesis protein B |
| TIGR02673 | FtsE | cell division ATP-binding protein FtsE |
| TIGR02690 | resist_ArsH | arsenical resistance protein ArsH |
| TIGR02691 | arsC_pl258_fam | arsenate reductase (thioredoxin) |
| TIGR02692 | tRNA_CCA_actino | CCA tRNA nucleotidyltransferase |
| TIGR02705 | nudix_YtkD | nucleoside triphosphatase YtkD |
| TIGR02713 | allophanate_hyd | allophanate hydrolase |
| TIGR02720 | pyruv_oxi_spxB | pyruvate oxidase |
| TIGR02721 | ycfN_thiK | thiamine kinase |
| TIGR02727 | MTHFS_bact | 5-formyltetrahydrofolate cyclo-ligase |
| TIGR02729 | Obg_CgtA | Obg family GTPase CgtA |
| TIGR02745 | ccoG_rdxA_fixG | cytochrome c oxidase accessory protein CcoG |
| TIGR02748 | GerC3_HepT | heptaprenyl diphosphate synthase component II |
| TIGR02772 | Ku_bact | Ku protein |
| TIGR02773 | addB_Gpos | helicase-exonuclease AddAB, AddB subunit |
| TIGR02776 | NHEJ_ligase_prk | DNA ligase D |
| TIGR02785 | addA_Gpos | helicase-exonuclease AddAB, AddA subunit |
| TIGR02787 | codY_Gpos | GTP-sensing transcriptional pleiotropic repressor CodY |
| TIGR02793 | nikR | nickel-responsive transcriptional regulator NikR |
| TIGR02794 | tolA_full | protein TolA |
| TIGR02795 | tol_pal_ybgF | tol-pal system protein YbgF |
| TIGR02796 | tolQ | protein TolQ |
| TIGR02797 | exbB | tonB-system energizer ExbB |
| TIGR02799 | thio_ybgC | tol-pal system-associated acyl-CoA thioesterase |
| TIGR02800 | propeller_TolB | Tol-Pal system beta propeller repeat protein TolB |
| TIGR02801 | tolR | protein TolR |
| TIGR02802 | Pal_lipo | peptidoglycan-associated lipoprotein |
| TIGR02803 | ExbD_1 | TonB system transport protein ExbD |
| TIGR02810 | agaZ_gatZ | D-tagatose-bisphosphate aldolase, class II, non-catalytic subunit |
| TIGR02812 | fadR_gamma | fatty acid metabolism transcriptional regulator FadR |
| TIGR02818 | adh_III_F_hyde | S-(hydroxymethyl)glutathione dehydrogenase/class |

| | | |
|-----------|-----------------|---|
| | | III alcohol dehydrogenase |
| TIGR02821 | fghA_este_D | S-formylglutathione hydrolase |
| TIGR02842 | CyoC | cytochrome o ubiquinol oxidase, subunit III |
| TIGR02843 | CyoB | cytochrome o ubiquinol oxidase, subunit I |
| TIGR02847 | CyoD | cytochrome o ubiquinol oxidase subunit IV |
| TIGR02866 | CoxB | cytochrome c oxidase, subunit II |
| TIGR02882 | QoxB | cytochrome aa3 quinol oxidase, subunit I |
| TIGR02891 | CtaD_CoxA | cytochrome c oxidase, subunit I |
| TIGR02897 | QoxC | cytochrome aa3 quinol oxidase, subunit III |
| TIGR02901 | QoxD | cytochrome aa3 quinol oxidase, subunit IV |
| TIGR02918 | TIGR02918 | accessory Sec system glycosylation protein GtfA |
| TIGR02919 | TIGR02919 | accessory Sec system glycosyltransferase GtfB |
| TIGR02939 | RpoE_Sigma70 | RNA polymerase sigma factor RpoE |
| TIGR02941 | Sigma_B | RNA polymerase sigma-B factor |
| TIGR02951 | DMSO_dmsB | dimethylsulfoxide reductase, chain B |
| TIGR02955 | TMAO_TorT | TMAO reductase system periplasmic protein TorT |
| TIGR02956 | TMAO_torS | TMAO reductase system sensor TorS |
| TIGR02961 | allantoicase | allantoicase |
| TIGR02962 | hdxy_isourate | hydroxyisourate hydrolase |
| TIGR02963 | xanthine_xdhA | xanthine dehydrogenase, small subunit |
| TIGR02964 | xanthine_xdhC | xanthine dehydrogenase accessory protein XdhC |
| TIGR02965 | xanthine_xdhB | xanthine dehydrogenase, molybdopterin binding subunit |
| TIGR02966 | phoR_proteo | phosphate regulon sensor kinase PhoR |
| TIGR02967 | guan_deamin | guanine deaminase |
| TIGR02968 | succ_dehyd_anc | |
| TIGR02970 | succ_dehyd_cytB | succinate dehydrogenase, cytochrome b556 subunit |
| TIGR02974 | phageshock_pspF | psp operon transcriptional activator |
| TIGR02998 | RraA_entero | regulator of ribonuclease activity A |
| TIGR03002 | outer_YhbN_LptA | lipopolysaccharide transport periplasmic protein LptA |
| TIGR03010 | sulf_tusC_dsrF | sulfur relay protein TusC/DsrF |
| TIGR03023 | WcaJ_sugtrans | undecaprenyl-phosphate glucose phosphotransferase |
| TIGR03036 | trp_2_3_diox | tryptophan 2,3-dioxygenase |
| TIGR03064 | sortase_srtB | sortase, SrtB family |
| TIGR03072 | release_prfH | putative peptide chain release factor H |
| TIGR03081 | metmalonyl_epim | methylmalonyl-CoA epimerase |
| TIGR03130 | malonate_delta | malonate decarboxylase acyl carrier protein |

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| TIGR03131 | malonate_mdcH | malonate decarboxylase, epsilon subunit |
| TIGR03132 | malonate_mdcB | triphosphoribosyl-dephospho-CoA synthase MdcB |
| TIGR03133 | malonate_beta | biotin-independent malonate decarboxylase, beta subunit |
| TIGR03134 | malonate_gamma | biotin-independent malonate decarboxylase, gamma subunit |
| TIGR03135 | malonate_mdcG | malonate decarboxylase holo-[acyl-carrier-protein] synthase |
| TIGR03137 | AhpC | peroxiredoxin |
| TIGR03138 | QueF | queuine synthase |
| TIGR03139 | QueF-II | 7-cyano-7-deazaguanine reductase |
| TIGR03140 | AhpF | alkyl hydroperoxide reductase subunit F |
| TIGR03144 | cytochr_II_ccsB | cytochrome c-type biogenesis protein CcsB |
| TIGR03146 | cyt_nit_nrfB | cytochrome c nitrite reductase, pentaheme subunit |
| TIGR03148 | cyt_nit_nrfD | cytochrome c nitrite reductase, NrfD subunit |
| TIGR03149 | cyt_nit_nrfC | cytochrome c nitrite reductase, Fe-S protein |
| TIGR03150 | fabF | beta-ketoacyl-acyl-carrier-protein synthase II |
| TIGR03156 | GTP_HflX | GTP-binding protein HflX |
| TIGR03160 | cobT_DBIPRT | nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase |
| TIGR03162 | ribazole_cobC | alpha-ribazole phosphatase |
| TIGR03167 | tRNA_sel_U_synt | tRNA 2-selenouridine synthase |
| TIGR03175 | AlID | ureidoglycolate dehydrogenase |
| TIGR03176 | AlIC | allantoate amidohydrolase |
| TIGR03177 | pilus_cpaB | Flp pilus assembly protein CpaB |
| TIGR03178 | allantoinase | allantoinase |
| TIGR03181 | PDH_E1_alpha_x | pyruvate dehydrogenase (acetyl-transferring) E1 component, alpha subunit |
| TIGR03182 | PDH_E1_alpha_y | pyruvate dehydrogenase (acetyl-transferring) E1 component, alpha subunit |
| TIGR03215 | ac_ald_DH_ac | acetaldehyde dehydrogenase (acetylating) |
| TIGR03217 | 4OH_2_O_val_ald | 4-hydroxy-2-oxovalerate aldolase |
| TIGR03220 | catechol_dmpE | 2-oxopent-4-enoate hydratase |
| TIGR03221 | muco_delta | muconolactone delta-isomerase |
| TIGR03234 | OH-pyruv-isom | hydroxypyruvate isomerase |
| TIGR03239 | GarL | 2-dehydro-3-deoxyglucarate aldolase |
| TIGR03240 | arg_catab_astD | succinylglutamate-semialdehyde dehydrogenase |
| TIGR03241 | arg_catab_astB | succinylarginine dihydrolase |
| TIGR03242 | arg_catab_astE | succinylglutamate desuccinylase |
| TIGR03244 | arg_catab_AstA | arginine N-succinyltransferase |
| TIGR03247 | glucar-dehydr | glucarate dehydratase |

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| TIGR03248 | galactar-dH20 | galactarate dehydratase |
| TIGR03254 | oxalate_oxc | oxalyl-CoA decarboxylase |
| TIGR03263 | guanyl_kin | guanylate kinase |
| TIGR03284 | thym_sym | thymidylate synthase |
| TIGR03292 | PhnH_redo | phosphonate C-P lyase system protein PhnH |
| TIGR03293 | PhnG_redo | phosphonate C-P lyase system protein PhnG |
| TIGR03300 | assembly_YfgL | outer membrane assembly lipoprotein YfgL |
| TIGR03303 | OM_YaeT | outer membrane protein assembly complex, YaeT protein |
| TIGR03307 | PhnP | phosphonate metabolism protein PhnP |
| TIGR03319 | RNase_Y | ribonuclease Y |
| TIGR03328 | salvage_mtnB | methylthioribulose-1-phosphate dehydratase |
| TIGR03330 | SAM_DCase_Bsu | S-adenosylmethionine decarboxylase proenzyme |
| TIGR03331 | SAM_DCase_Eco | S-adenosylmethionine decarboxylase proenzyme |
| TIGR03345 | VI_ClpV1 | type VI secretion ATPase, ClpV1 family |
| TIGR03346 | chaperone_ClpB | ATP-dependent chaperone protein ClpB |
| TIGR03356 | BGL | beta-galactosidase |
| TIGR03365 | Bsubt_queE | 7-cyano-7-deazaguanosine (preQ0) biosynthesis protein QueE |
| TIGR03367 | queuosine_QueD | queuosine biosynthesis protein QueD |
| TIGR03369 | cellulose_bcsE | cellulose biosynthesis protein BcsE |
| TIGR03371 | cellulose_yhjQ | cellulose synthase operon protein YhjQ |
| TIGR03372 | putres_am_tran | putrescine aminotransferase |
| TIGR03374 | ABALDH | 1-pyrroline dehydrogenase |
| TIGR03377 | glycerol3P_GlpA | glycerol-3-phosphate dehydrogenase, anaerobic, A subunit |
| TIGR03378 | glycerol3P_GlpB | glycerol-3-phosphate dehydrogenase, anaerobic, B subunit |
| TIGR03379 | glycerol3P_GlpC | glycerol-3-phosphate dehydrogenase, anaerobic, C subunit |
| TIGR03380 | agmatine_aguA | agmatine deiminase |
| TIGR03381 | agmatine_aguB | N-carbamoylputrescine amidase |
| TIGR03384 | betaine_BetI | transcriptional repressor BetI |
| TIGR03385 | CoA_CoA_reduc | CoA-disulfide reductase |
| TIGR03391 | FeS_syn_CsdE | cysteine desulfurase, sulfur acceptor subunit CsdE |
| TIGR03392 | FeS_syn_CsdA | cysteine desulfurase, catalytic subunit CsdA |
| TIGR03395 | sphingomy | sphingomyelin phosphodiesterase |
| TIGR03399 | RNA_3prim_cycl | RNA 3'-phosphate cyclase |
| TIGR03402 | FeS_nifS | cysteine desulfurase NifS |
| TIGR03412 | iscX_yfhJ | FeS assembly protein IscX |

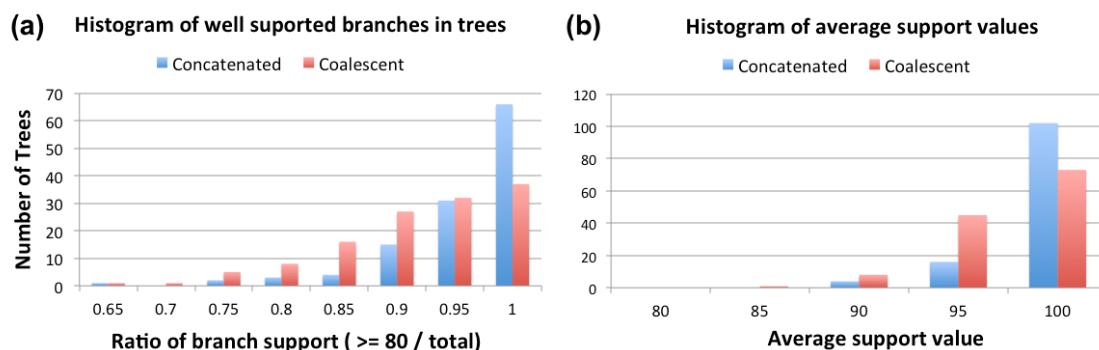
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| TIGR03413 | GSH_gloB | hydroxyacylglutathione hydrolase |
| TIGR03420 | DnaA_homol_Hda | DnaA regulatory inactivator Hda |
| TIGR03421 | FeS_CyaY | iron donor protein CyaY |
| TIGR03423 | pbp2_mrdA | penicillin-binding protein 2 |
| TIGR03426 | shape_MreD | rod shape-determining protein MreD |
| TIGR03438 | egtD_ergothio | dimethylhistidine N-methyltransferase |
| TIGR03461 | pabC_Proteo | aminodeoxychorismate lyase |
| TIGR03465 | HpnD | squalene synthase HpND |
| TIGR03493 | cellulose_BcsF | cellulose biosynthesis operon protein BcsF/YhjT |
| TIGR03496 | FliI_clade1 | flagellar protein export ATPase FliI |
| TIGR03499 | FlhF | flagellar biosynthesis protein FlhF |
| TIGR03500 | FliO_TIGR | flagellar biosynthetic protein FliO |
| TIGR03528 | 2_3_DAP_am_ly | diaminopropionate ammonia-lyase |
| TIGR03532 | DapD_Ac | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase |
| TIGR03533 | L3_gln_methyl | protein-(glutamine-N5) methyltransferase, ribosomal protein L3-specific |
| TIGR03534 | RF_mod_PrmC | protein-(glutamine-N5) methyltransferase, release factor-specific |
| TIGR03538 | DapC_gpp | succinyldiaminopimelate transaminase |
| TIGR03565 | alk_sulf_monoox | alkanesulfonate monooxygenase, FMNH(2)-dependent |
| TIGR03566 | FMN_reduc_MsuE | FMN reductase |
| TIGR03567 | FMN_reduc_SsuE | FMN reductase |
| TIGR03568 | NeuC_NnaA | UDP-N-acetyl-D-glucosamine 2-epimerase, UDP-hydrolysing |
| TIGR03591 | polynuc_phos | polyribonucleotide nucleotidyltransferase |
| TIGR03594 | GTPase_EngA | ribosome-associated GTPase EngA |
| TIGR03596 | GTPase_YlqF | ribosome biogenesis GTP-binding protein YlqF |
| TIGR03597 | GTPase_YqeH | ribosome biogenesis GTPase YqeH |
| TIGR03598 | GTPase_YsxC | ribosome biogenesis GTP-binding protein YsxC |
| TIGR03610 | RutC | pyrimidine utilization protein C |
| TIGR03611 | RutD | pyrimidine utilization protein D |
| TIGR03614 | RutB | pyrimidine utilization protein B |
| TIGR03625 | L3_bact | 50S ribosomal protein uL3 |
| TIGR03631 | uS13_bact | ribosomal protein uS13 |
| TIGR03632 | uS11_bact | ribosomal protein uS11 |
| TIGR03635 | uS17_bact | ribosomal protein uS17 |
| TIGR03652 | FeS_repair_RIC | iron-sulfur cluster repair di-iron protein |
| TIGR03654 | L6_bact | ribosomal protein uL6 |

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| TIGR03692 | ATP_dep_HslV | ATP-dependent protease HslVU, peptidase subunit |
| TIGR03695 | menH_SHCHC | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase |
| TIGR03702 | lip_kinase_YegS | lipid kinase YegS |
| TIGR03703 | plsB | glycerol-3-phosphate O-acyltransferase |
| TIGR03705 | poly_P_kin | polyphosphate kinase 1 |
| TIGR03707 | PPK2_P_aer | polyphosphate kinase 2 |
| TIGR03711 | acc_sec_asp3 | accessory Sec system protein Asp3 |
| TIGR03712 | acc_sec_asp2 | accessory Sec system protein Asp2 |
| TIGR03713 | acc_sec_asp1 | accessory Sec system protein Asp1 |
| TIGR03723 | T6A_TsaD_YgjD | tRNA threonylcarbamoyl adenosine modification protein TsaD |
| TIGR03725 | T6A_YeaZ | tRNA threonylcarbamoyl adenosine modification protein YeaZ |
| TIGR03800 | PLP_synth_Pdx2 | pyridoxal 5'-phosphate synthase, glutaminase subunit Pdx2 |
| TIGR03814 | Gln_ase | glutaminase A |
| TIGR03818 | MotA1 | flagellar motor stator protein MotA |
| TIGR03821 | EFP_modif_epmB | EF-P beta-lysylation protein EpmB |
| TIGR03823 | FliZ | flagellar regulatory protein FliZ |
| TIGR03824 | FlgM_jcvi | flagellar biosynthesis anti-sigma factor FlgM |
| TIGR03828 | pfkB | 1-phosphofructokinase |
| TIGR03838 | queuosine_YadB | glutamyl-queuosine tRNA(Asp) synthetase |
| TIGR03859 | PQQ_PqqD | coenzyme PQQ biosynthesis protein PqqD |
| TIGR03926 | T7_EssB | type VII secretion protein EssB |
| TIGR03927 | T7SS_EssA_Firm | type VII secretion protein EssA |
| TIGR03928 | T7_EssCb_Firm | type VII secretion protein EssC |
| TIGR03937 | PgaC_IcaA | poly-beta-1,6 N-acetyl-D-glucosamine synthase |
| TIGR03938 | deacetyl_PgaB | poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB |
| TIGR03939 | PGA_TPR_OMP | poly-beta-1,6 N-acetyl-D-glucosamine export porin PgaA |
| TIGR03940 | PGA_PgaD | poly-beta-1,6-N-acetyl-D-glucosamine biosynthesis protein PgaD |
| TIGR03942 | sulfatase_rSAM | anaerobic sulfatase maturase |
| TIGR03944 | dehyd_SbnB_fam | 2,3-diaminopropionate biosynthesis protein SbnB |
| TIGR03945 | PLP_SbnA_fam | 2,3-diaminopropionate biosynthesis protein SbnA |
| TIGR03951 | Fe_III_red_FhuF | siderophore-iron reductase FhuF |
| TIGR03953 | rplD_bact | 50S ribosomal protein uL4 |
| TIGR03998 | thiol_BshC | bacillithiol biosynthesis cysteine-adding enzyme BshC |

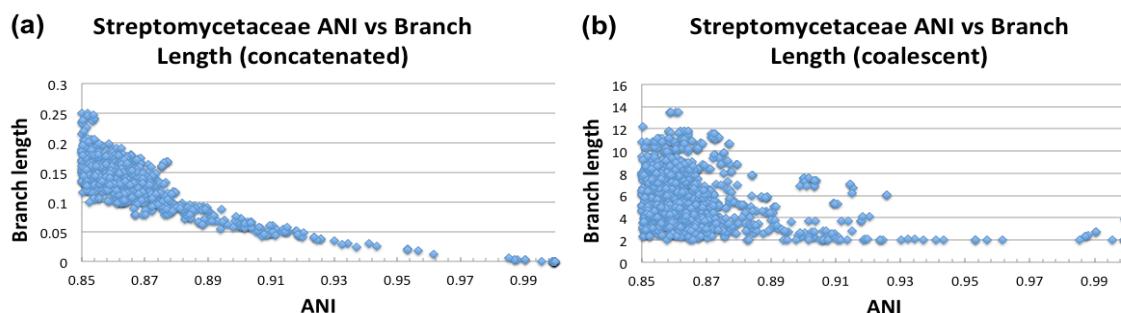
| | | |
|-------------------|-----------------|---|
| TIGR03999 | thiol_BshA | N-acetyl-alpha-D-glucosaminyL-malate synthase BshA |
| TIGR04000 | thiol_BshB2 | bacillithiol biosynthesis deacetylase BshB2 |
| TIGR04004 | WcaM | colanic acid biosynthesis protein WcaM |
| TIGR04005 | wcaL | colanic acid biosynthesis glycosyltransferase WcaL |
| TIGR04007 | wcal | colanic acid biosynthesis glycosyltransferase Wcal |
| TIGR04008 | WcaF | colanic acid biosynthesis acetyltransferase WcaF |
| TIGR04009 | wcaE | colanic acid biosynthesis glycosyltransferase WcaE |
| TIGR04010 | WcaD | putative colanic acid polymerase WcaD |
| TIGR04015 | WcaC | colanic acid biosynthesis glycosyltransferase WcaC |
| TIGR04016 | WcaB | colanic acid biosynthesis acetyltransferase WcaB |
| TIGR04017 | WcaA | colanic acid biosynthesis glycosyltransferase WcaA |
| TIGR04091 | LTA_dltB | D-alanyl-lipoteichoic acid biosynthesis protein DltB |
| TIGR04092 | LTA_DltD | D-alanyl-lipoteichoic acid biosynthesis protein DltD |
| TIGR04239 | rhombo_GlpG | rhomboid family protease GlpG |
| TIGR04265 | bac_cardiolipin | cardiolipin synthase |
| TIGR04274 | hypoxanDNAglyco | DNA-deoxyinosine glycosylase |
| TIGR04306 | salvage_TenA | thiaminase II |
| TIGR04316 | dhbA_paeA | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase |
| TIGR04322 | rSAM_QueE_Ecoli | putative 7-cyano-7-deazaguanosine (preQ0) biosynthesis protein QueE |
| TIGR04365 | spare_glycyl | autonomous glycyl radical cofactor GrcA |
| TIGR04377 | myo_inos_iolD | 3,5/4-trihydroxycyclohexa-1,2-dione hydrolase |
| TIGR04378 | myo_inos_iolB | 5-deoxy-glucuronate isomerase |
| TIGR04379 | myo_inos_iolE | myo-inosose-2 dehydratase |
| TIGR04380 | myo_inos_iolG | inositol 2-dehydrogenase |
| TIGR04416 | group_II_RT_mat | group II intron reverse transcriptase/maturase |
| TIGR04430 | OM_asym_MlaD | outer membrane lipid asymmetry maintenance protein MlaD |
| TIGR04478 | rSAM_YfkAB | radical SAM/CxCxxxxC motif protein YfkAB |
| TIGR04502 | microcomp_EutL | microcompartment protein EutL |
| TIGR04567 | RNAP_delt_lowGC | DNA-directed RNA polymerase delta subunit |
| PF00166.17 | PF00166.17 | Chaperonin 10 Kd subunit |
| PF00118.20 | PF00118.20 | TCP-1/cpn60 chaperonin family |
| PF01025.15 | PF01025.15 | GrpE |
| PF01795.15 | PF01795.15 | MraW methylase family |
| PF00162.15 | PF00162.15 | Phosphoglycerate kinase |
| PF00466.16 | PF00466.16 | Ribosomal protein L10 |
| PF00276.16 | PF00276.16 | Ribosomal protein L23 |
| PF00297.18 | PF00297.18 | Ribosomal protein L3 |

| | | |
|-------------------|------------|---------------------------------|
| PF00573.18 | PF00573.18 | Ribosomal protein L4 |
| PF00281.15 | PF00281.15 | Ribosomal protein L5 |
| PF00347.19 | PF00347.19 | Ribosomal protein L6 |
| PF00411.15 | PF00411.15 | Ribosomal protein S11 |
| PF00416.18 | PF00416.18 | Ribosomal protein S13/S18 |
| PF00253.17 | PF00253.17 | Ribosomal protein S14p/S29e |
| PF00366.16 | PF00366.16 | Ribosomal protein S17 |
| PF00410.15 | PF00410.15 | Ribosomal protein S8 |
| PF00380.15 | PF00380.15 | Ribosomal protein S9/S16 |
| PF00464.15 | PF00464.15 | Serine hydroxymethyltransferase |
| PF00750.15 | PF00750.15 | tRNA synthetases class I (R) |

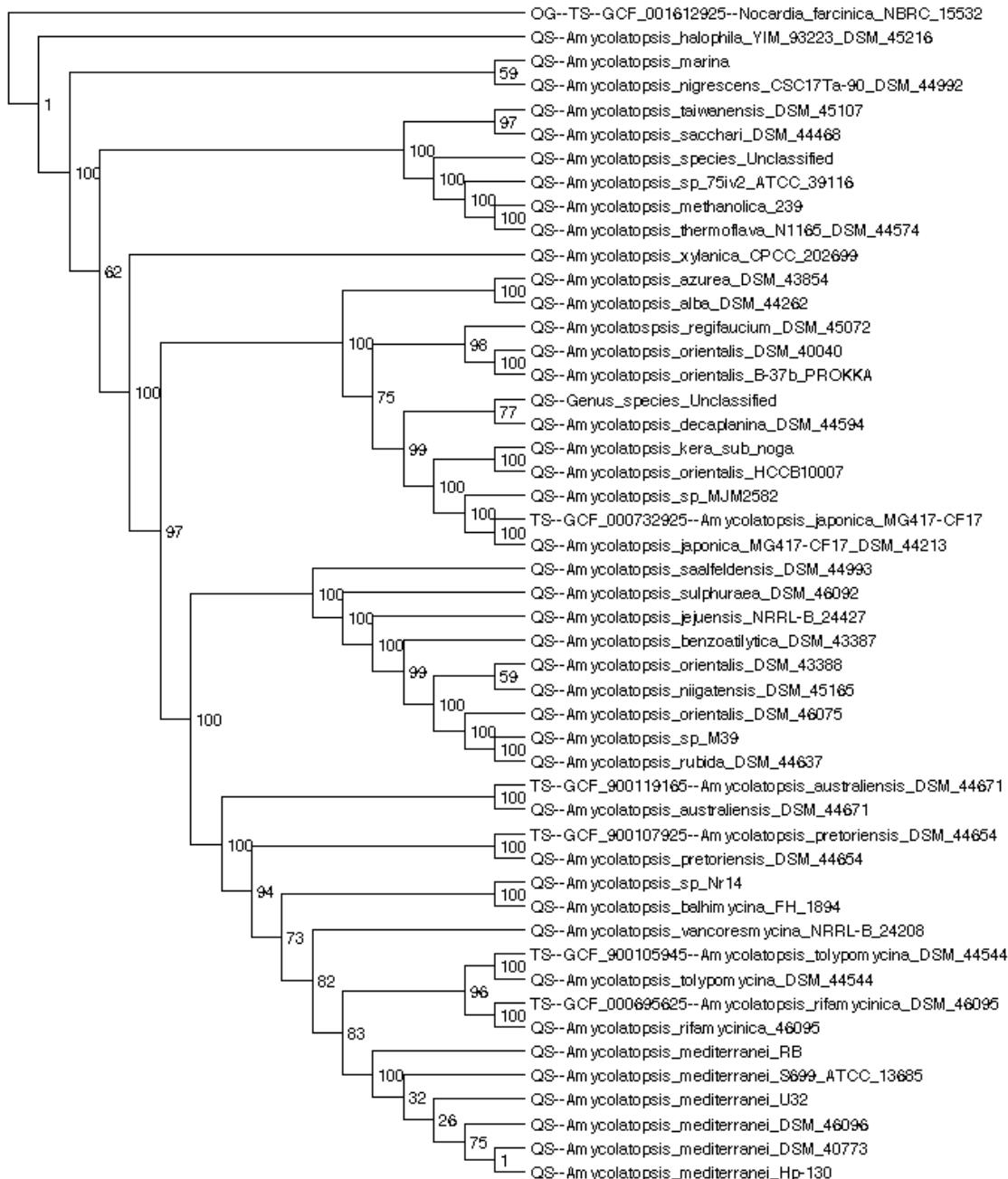
Supplemental S1. Table of housekeeping genes used for single copy gene screening



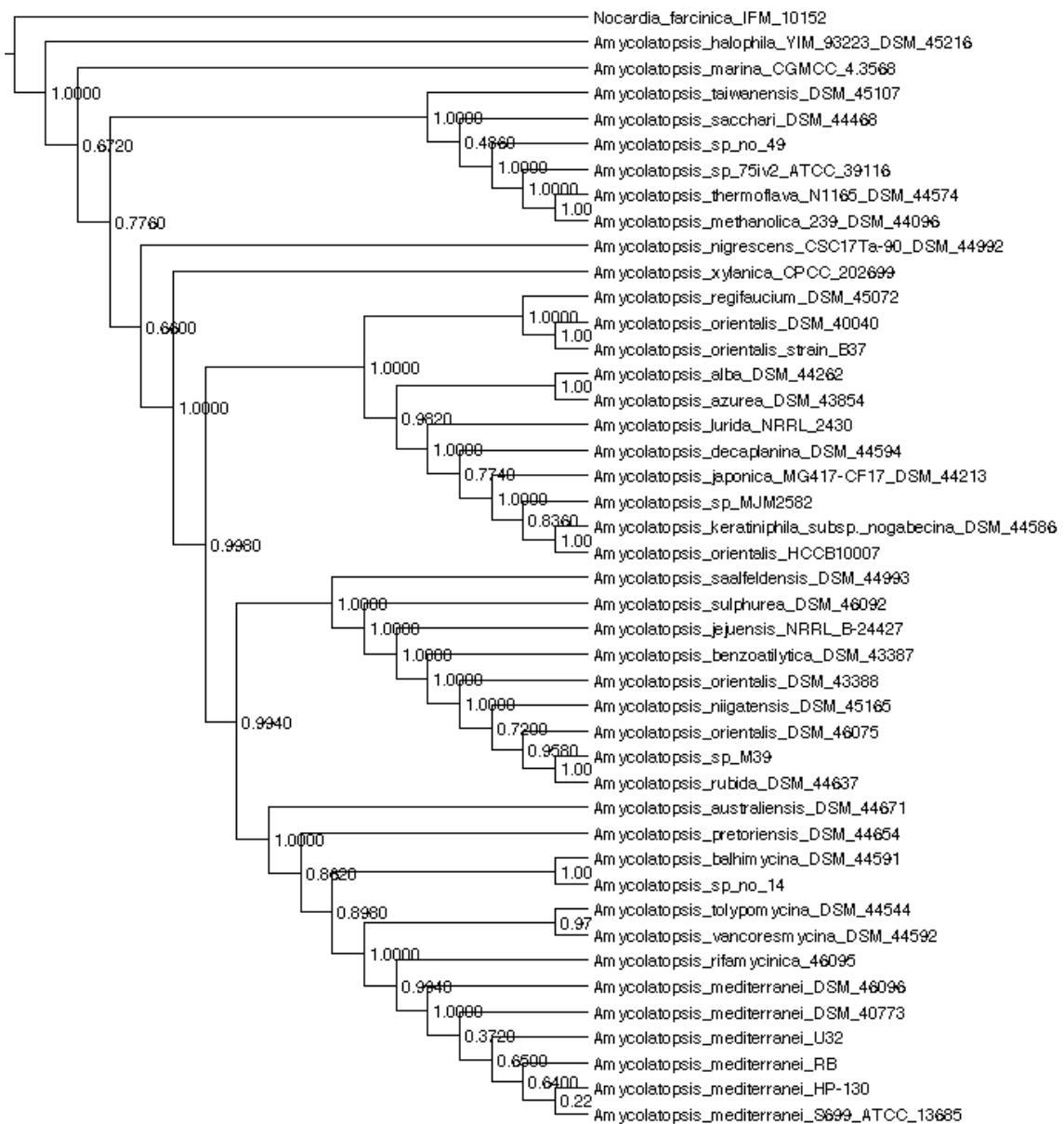
Supplemental S2. Bootstrap support values of auto-generated family trees for concatenated and coalescent workflow (blue and red respectively). (a) Ratio of well supported branches (80 or greater) versus all branches in a tree. (b) Average support values of all branches.



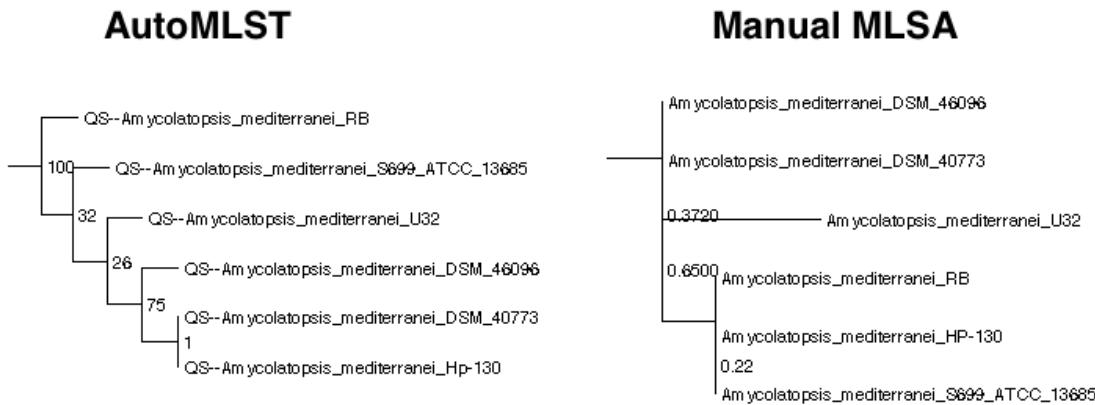
Supplemental S3. ANI values versus pairwise branch distances for the Streptomycetaceae family generated in autoMLST. (a) Concatenated workflow (b) Coalescent workflow.



Supplemental S4. *Amycolatopsis* species tree generated with autoMLST in denovo mode. Default settings were used with 1000 bootstrap replicates, values shown from 0-100.



Supplemental S5. Manually generated *Amycolatopsis* species tree using 7 housekeeping genes as described in Ademek et al (1). 500 Bootstrap replicates were used with values shown between 0–1.0



Supplemental S6. Comparison of multi-furcation differences in *A. Mediteranei* clade; AutoMLST versus Manual workflow shows resolved bi-furcation albeit with weak bootstrap support.

Supplemental Methods

Two additional validations were performed to supplement ANI clade designations. First, a survey of all bootstrap support values, a measure of branch confidence, was recorded from all family trees generated for both the concatenated and coalescent approach. These values were taken from each branch in a tree, including internal branches, and were summarized. One measure is the ratio of well-supported branches (over 80) versus all branches. Next, tree branch lengths were used to confirm correlation of pairwise ANI values with pairwise distances within the output tree for all pairs that showed an ANI over 85%. Branch distances were extracted using the ETE toolkit (2) for python and compared to corresponding pairs of ANI values as determined via MASH (3). All values were then summarized via the Pearson correlation coefficient as detailed in Alanjary et al. (4)

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