Supplemental Table.9 Comparative ranking of pathways between *Buchnera* and other bacteria.

|  |  |  |
| --- | --- | --- |
| Pathway | Rank in others | Rank in *Buchnera* |
| aerobic respiration I (cytochrome c) | 1 | 175 |
| pyruvate fermentation to isobutanol (engineered) | 2 | 11 |
| gondoate biosynthesis (anaerobic) | 3 | 60 |
| mycolate biosynthesis | 4 | 162 |
| L-isoleucine biosynthesis II | 5 | 6 |
| fatty acid elongation -- saturated | 6 | 61 |
| L-isoleucine biosynthesis I (from threonine) | 7 | 13 |
| L-valine biosynthesis | 8 | 12 |
| oleate biosynthesis IV (anaerobic) | 9 | 54 |
| fatty acid beta-oxidation I | 10 | 1 |
| cis-vaccenate biosynthesis | 11 | 77 |
| palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate) | 12 | 71 |
| stearate biosynthesis II (bacteria and plants) | 13 | 89 |
| TCA cycle I (prokaryotic) | 14 | 3 |
| (5Z)-dodec-5-enoate biosynthesis | 15 | 39 |
| superpathway of fatty acid biosynthesis initiation (E. coli) | 16 | 59 |
| superpathway of L-serine and glycine biosynthesis I | 17 | 104 |
| CDP-diacylglycerol biosynthesis II | 18 | 42 |
| CDP-diacylglycerol biosynthesis I | 19 | 41 |
| pentose phosphate pathway (non-oxidative branch) | 20 | 5 |
| superpathway of branched amino acid biosynthesis | 21 | 14 |
| fatty acid salvage | 22 | 196 |
| superpathway of phospholipid biosynthesis I (bacteria) | 23 | 16 |
| superpathway of sulfate assimilation and cysteine biosynthesis | 24 | 38 |
| L-isoleucine biosynthesis III | 25 | 19 |
| urate biosynthesis/inosine 5'-phosphate degradation | 26 | 48 |
| 8-amino-7-oxononanoate biosynthesis I | 27 | 88 |
| sulfate reduction I (assimilatory) | 28 | 15 |
| peptidoglycan maturation (meso-diaminopimelate containing) | 29 | 9 |
| superpathway of adenosine nucleotides de novo biosynthesis I | 30 | 18 |
| superpathway of aromatic amino acid biosynthesis | 31 | 32 |
| adenosine nucleotides degradation II | 32 | 172 |
| adenosine ribonucleotides de novo biosynthesis | 33 | 33 |
| L-ornithine biosynthesis | 34 | 106 |
| superpathway of L-isoleucine biosynthesis I | 35 | 25 |
| superpathway of pyrimidine nucleobases salvage | 36 | 64 |
| superpathway of adenosine nucleotides de novo biosynthesis II | 37 | 27 |
| phosphatidylglycerol biosynthesis II (non-plastidic) | 38 | 29 |
| phosphatidylglycerol biosynthesis I (plastidic) | 39 | 28 |
| guanosine deoxyribonucleotides de novo biosynthesis II | 40 | 21 |
| adenosine deoxyribonucleotides de novo biosynthesis II | 41 | 20 |
| superpathway of L-phenylalanine biosynthesis | 42 | 31 |
| 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I | 43 | 107 |
| chorismate biosynthesis I | 44 | 56 |
| pentose phosphate pathway | 45 | 37 |
| 6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia) | 46 | 105 |
| biotin biosynthesis I | 47 | 75 |
| L-lysine biosynthesis III | 48 | 30 |
| N10-formyl-tetrahydrofolate biosynthesis | 49 | 112 |
| superpathway of L-alanine biosynthesis | 50 | 8 |
| L-lysine biosynthesis I | 51 | 52 |
| chorismate biosynthesis from 3-dehydroquinate | 52 | 79 |
| GDP-mannose biosynthesis | 53 | 187 |
| 5-aminoimidazole ribonucleotide biosynthesis I | 54 | 81 |
| TCA cycle VIII (helicobacter) | 55 | 214 |
| superpathway of pyrimidine ribonucleotides de novo biosynthesis | 56 | 44 |
| UMP biosynthesis | 57 | 45 |
| superpathway of guanosine nucleotides de novo biosynthesis I | 58 | 65 |
| superpathway of purine nucleotides de novo biosynthesis I | 59 | 62 |
| L-lysine biosynthesis VI | 60 | 36 |
| superpathway of tetrahydrofolate biosynthesis and salvage | 61 | 87 |
| L-tryptophan biosynthesis | 62 | 80 |
| superpathway of L-threonine biosynthesis | 63 | 35 |
| TCA cycle VII (acetate-producers) | 64 | 10 |
| Calvin-Benson-Bassham cycle | 65 | 40 |
| ubiquinol-9 biosynthesis (prokaryotic) | 66 | 85 |
| ubiquinol-7 biosynthesis (prokaryotic) | 67 | 84 |
| ubiquinol-10 biosynthesis (prokaryotic) | 68 | 83 |
| ubiquinol-8 biosynthesis (prokaryotic) | 69 | 82 |
| superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis | 70 | 46 |
| heme biosynthesis II (anaerobic) | 71 | 66 |
| pyrimidine deoxyribonucleotides de novo biosynthesis I | 72 | 47 |
| superpathway of guanosine nucleotides de novo biosynthesis II | 73 | 76 |
| dTDP-L-rhamnose biosynthesis I | 74 | 176 |
| superpathway of glyoxylate bypass and TCA | 75 | 173 |
| L-arginine biosynthesis III (via N-acetyl-L-citrulline) | 76 | 97 |
| superpathway of ubiquinol-8 biosynthesis (prokaryotic) | 77 | 90 |
| L-methionine biosynthesis III | 78 | 227 |
| flavin biosynthesis I (bacteria and plants) | 79 | 117 |
| superpathway of 5-aminoimidazole ribonucleotide biosynthesis | 80 | 124 |
| 5-aminoimidazole ribonucleotide biosynthesis II | 81 | 123 |
| superpathway of L-methionine biosynthesis (by sulfhydrylation) | 82 | 177 |
| gluconeogenesis I | 83 | 99 |
| guanosine ribonucleotides de novo biosynthesis | 84 | 108 |
| superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli) | 85 | 93 |
| tRNA charging | 86 | 70 |
| L-histidine biosynthesis | 87 | 111 |
| superpathway of tetrahydrofolate biosynthesis | 88 | 100 |
| phosphopantothenate biosynthesis I | 89 | 110 |
| TCA cycle VI (obligate autotrophs) | 90 | 57 |
| tetrapyrrole biosynthesis II (from glycine) | 91 | 131 |
| glucose and glucose-1-phosphate degradation | 92 | 145 |
| tetrapyrrole biosynthesis I (from glutamate) | 93 | 126 |
| preQ0 biosynthesis | 94 | 138 |
| UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) | 95 | 109 |
| polyisoprenoid biosynthesis (E. coli) | 96 | 119 |
| peptidoglycan biosynthesis I (meso-diaminopimelate containing) | 97 | 113 |
| O-antigen building blocks biosynthesis (E. coli) | 98 | 170 |
| inosine-5'-phosphate biosynthesis I | 99 | 127 |
| peptidoglycan biosynthesis III (mycobacteria) | 100 | 114 |
| pantothenate and coenzyme A biosynthesis I | 101 | 118 |
| superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis | 102 | 53 |
| L-arginine biosynthesis II (acetyl cycle) | 103 | 98 |
| superpathway of glycolysis and Entner-Doudoroff | 104 | 169 |
| inosine-5'-phosphate biosynthesis III | 105 | 135 |
| UDP-N-acetyl-D-glucosamine biosynthesis I | 106 | 125 |
| thiamin salvage II | 107 | 134 |
| mixed acid fermentation | 108 | 7 |
| superpathway of L-tyrosine biosynthesis | 109 | 43 |
| coenzyme A biosynthesis I | 110 | 128 |
| L-arginine biosynthesis I (via L-ornithine) | 111 | 101 |
| pyrimidine deoxyribonucleotide phosphorylation | 112 | 129 |
| glycolysis I (from glucose 6-phosphate) | 113 | 73 |
| guanosine nucleotides degradation III | 114 | 51 |
| L-arginine biosynthesis IV (archaebacteria) | 115 | 102 |
| superpathay of heme biosynthesis from glutamate | 116 | 136 |
| TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase) | 117 | 164 |
| methylerythritol phosphate pathway I | 118 | 133 |
| methylerythritol phosphate pathway II | 119 | 132 |
| NAD biosynthesis I (from aspartate) | 120 | 147 |
| queuosine biosynthesis | 121 | 130 |
| anhydromuropeptides recycling | 122 | 2 |
| glycolysis III (from glucose) | 123 | 96 |
| CMP-3-deoxy-D-manno-octulosonate biosynthesis I | 124 | 67 |
| superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass | 125 | 167 |
| lipid IVA biosynthesis | 126 | 116 |
| L-histidine degradation I | 127 | 157 |
| heme biosynthesis I (aerobic) | 128 | 142 |
| Kdo transfer to lipid IVA III (Chlamydia) | 129 | 140 |
| NAD salvage pathway I | 130 | 146 |
| UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing) | 131 | 115 |
| starch degradation V | 132 | 17 |
| L-leucine degradation I | 133 | 234 |
| colanic acid building blocks biosynthesis | 134 | 183 |
| TCA cycle IV (2-oxoglutarate decarboxylase) | 135 | 165 |
| glycogen degradation I (bacterial) | 136 | 4 |
| sucrose degradation III (sucrose invertase) | 137 | 121 |
| glycolysis II (from fructose 6-phosphate) | 138 | 74 |
| glyoxylate cycle | 139 | 178 |
| sucrose degradation IV (sucrose phosphorylase) | 140 | 137 |
| myo-, chiro- and scillo-inositol degradation | 141 | 160 |
| L-tyrosine degradation I | 142 | 249 |
| superpathway of L-lysine, L-threonine and L-methionine biosynthesis I | 143 | 55 |
| superpathway of purine nucleotides de novo biosynthesis II | 144 | 78 |
| superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP) | 145 | 149 |
| protocatechuate degradation II (ortho-cleavage pathway) | 146 | 254 |
| superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis | 147 | 198 |
| pyridoxal 5'-phosphate biosynthesis I | 148 | 139 |
| ppGpp biosynthesis | 149 | 86 |
| aromatic biogenic amine degradation (bacteria) | 150 | 258 |
| aspartate superpathway | 151 | 163 |
| superpathway of histidine, purine, and pyrimidine biosynthesis | 152 | 72 |
| homolactic fermentation | 153 | 92 |
| L-histidine degradation II | 154 | 159 |
| superpathway of S-adenosyl-L-methionine biosynthesis | 155 | 34 |
| glycogen biosynthesis I (from ADP-D-Glucose) | 156 | 151 |
| superpathway of pyridoxal 5'-phosphate biosynthesis and salvage | 157 | 120 |
| pyrimidine deoxyribonucleotides de novo biosynthesis II | 158 | 141 |
| 4-aminobutanoate degradation V | 159 | 225 |
| tRNA processing | 160 | 143 |
| superpathway of L-aspartate and L-asparagine biosynthesis | 161 | 122 |
| L-arginine degradation II (AST pathway) | 162 | 150 |
| octane oxidation | 163 | 241 |
| superpathway of L-methionine biosynthesis (transsulfuration) | 164 | 26 |
| D-fructuronate degradation | 165 | 188 |
| superpathway of pyrimidine deoxyribonucleoside salvage | 166 | 148 |
| superpathway of arginine and polyamine biosynthesis | 167 | 58 |
| ADP-L-glycero-beta-D-manno-heptose biosynthesis | 168 | 144 |
| superpathway of pyrimidine ribonucleosides salvage | 169 | 94 |
| purine nucleotides degradation II (aerobic) | 170 | 166 |
| 2-methylcitrate cycle II | 171 | 208 |
| L-methionine biosynthesis I | 172 | 50 |
| adenosylcobalamin salvage from cobinamide I | 173 | 211 |
| superpathway of ornithine degradation | 174 | 209 |
| L-isoleucine biosynthesis IV | 175 | 180 |
| superpathway of thiamin diphosphate biosynthesis I | 176 | 168 |
| adenosylcobalamin salvage from cobinamide II | 177 | 233 |
| adenosylcobalamin biosynthesis from cobyrinate a,c-diamide I | 178 | 239 |
| acetylene degradation | 179 | 189 |
| taxadiene biosynthesis (engineered) | 180 | 182 |
| myo-inositol degradation I | 181 | 161 |
| superpathway of (Kdo)2-lipid A biosynthesis | 182 | 103 |
| pyrimidine deoxyribonucleosides salvage | 183 | 153 |
| superpathway of polyamine biosynthesis I | 184 | 22 |
| superpathway of thiamin diphosphate biosynthesis II | 185 | 171 |
| S-adenosyl-L-methionine cycle I | 186 | 68 |
| superpathway of polyamine biosynthesis II | 187 | 207 |
| galactose degradation I (Leloir pathway) | 188 | 69 |
| 2-methylcitrate cycle I | 189 | 215 |
| cob(II)yrinate a,c-diamide biosynthesis II (late cobalt incorporation) | 190 | 259 |
| D-galacturonate degradation I | 191 | 212 |
| superpathway of beta-D-glucuronide and D-glucuronate degradation | 192 | 210 |
| methylphosphonate degradation I | 193 | 244 |
| adenine and adenosine salvage III | 194 | 152 |
| Bifidobacterium shunt | 195 | 271 |
| aromatic compounds degradation via beta-ketoadipate | 196 | 263 |
| catechol degradation III (ortho-cleavage pathway) | 197 | 262 |
| 4-deoxy-L-threo-hex-4-enopyranuronate degradation | 198 | 213 |
| dTDP-N-acetylthomosamine biosynthesis | 199 | 24 |
| palmitate biosynthesis II (bacteria and plants) | 200 | none |
| catechol degradation to beta-ketoadipate | 201 | 268 |
| arginine, ornithine and proline interconversion | 202 | 223 |
| polymyxin resistance | 203 | 158 |
| superpathway of purine deoxyribonucleosides degradation | 204 | 154 |
| superpathway of heme biosynthesis from uroporphyrinogen-III | 205 | 91 |
| urea cycle | 206 | 276 |
| superpathway of chorismate metabolism | 207 | 185 |
| 4-hydroxyphenylacetate degradation | 208 | 238 |
| superpathway of salicylate degradation | 209 | 265 |
| superpathway of pyrimidine deoxyribonucleosides degradation | 210 | 156 |
| 4-methylcatechol degradation (ortho cleavage) | 211 | 260 |
| purine ribonucleosides degradation | 212 | 155 |
| superpathway of L-tryptophan biosynthesis | 213 | 190 |
| toluene degradation III (aerobic) (via p-cresol) | 214 | 257 |
| superpathway of glucose and xylose degradation | 215 | 199 |
| enterobactin biosynthesis | 216 | 186 |
| NAD salvage pathway II | 217 | 49 |
| toluene degradation II (aerobic) (via 4-methylcatechol) | 218 | none |
| toluene degradation I (aerobic) (via o-cresol) | 219 | none |
| superpathway of N-acetylneuraminate degradation | 220 | 181 |
| thiazole biosynthesis I (E. coli) | 221 | 184 |
| superpathway of menaquinol-8 biosynthesis I | 222 | 197 |
| pyruvate fermentation to propanoate I | 223 | 280 |
| superpathway of hexuronide and hexuronate degradation | 224 | 216 |
| superpathway of menaquinol-13 biosynthesis | 225 | 202 |
| superpathway of menaquinol-11 biosynthesis | 226 | 201 |
| superpathway of menaquinol-12 biosynthesis | 227 | 200 |
| superpathway of lipopolysaccharide biosynthesis | 228 | 231 |
| phenylacetate degradation I (aerobic) | 229 | 264 |
| superpathway of menaquinol-7 biosynthesis | 230 | 204 |
| ectoine biosynthesis | 231 | 237 |
| superpathway of menaquinol-6 biosynthesis I | 232 | 206 |
| superpathway of menaquinol-10 biosynthesis | 233 | 205 |
| superpathway of menaquinol-9 biosynthesis | 234 | 203 |
| L-glutamate and L-glutamine biosynthesis | 235 | 179 |
| superpathway of hexitol degradation (bacteria) | 236 | 174 |
| incomplete reductive TCA cycle | 237 | 245 |
| superpathway of heme biosynthesis from glycine | 238 | none |
| NAD biosynthesis II (from tryptophan) | 239 | 284 |
| nitrate reduction I (denitrification) | 240 | none |
| enterobacterial common antigen biosynthesis | 241 | 95 |
| superpathway of demethylmenaquinol-8 biosynthesis | 242 | 218 |
| superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation | 243 | 192 |
| superpathway of L-arginine and L-ornithine degradation | 244 | 191 |
| formaldehyde assimilation II (RuMP Cycle) | 245 | 283 |
| thiazole biosynthesis II (Bacillus) | 246 | 193 |
| superpathway of phylloquinol biosynthesis | 247 | 226 |
| D-glucarate degradation I | 248 | 229 |
| L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde | 249 | 289 |
| hexitol fermentation to lactate, formate, ethanol and acetate | 250 | 23 |
| L-rhamnose degradation I | 251 | 220 |
| superpathway of D-glucarate and D-galactarate degradation | 252 | 230 |
| D-galactarate degradation I | 253 | 228 |
| superpathway of demethylmenaquinol-6 biosynthesis I | 254 | 222 |
| superpathway of demethylmenaquinol-9 biosynthesis | 255 | 221 |
| 1,4-dihydroxy-2-naphthoate biosynthesis I | 256 | 224 |
| 2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate | 257 | 293 |
| 2-nitrobenzoate degradation I | 258 | 292 |
| allantoin degradation to glyoxylate III | 259 | 235 |
| photorespiration | 260 | 294 |
| pyruvate fermentation to acetate and lactate II | 261 | 219 |
| formaldehyde oxidation I | 262 | 286 |
| catechol degradation I (meta-cleavage pathway) | 263 | none |
| androstenedione degradation | 264 | 297 |
| reductive TCA cycle I | 265 | 253 |
| ketogluconate metabolism | 266 | 246 |
| glucose degradation (oxidative) | 267 | 252 |
| superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation | 268 | 217 |
| superpathway of 2,3-butanediol biosynthesis | 269 | 243 |
| superpathway of phenylethylamine degradation | 270 | 267 |
| heterolactic fermentation | 271 | 281 |
| norspermidine biosynthesis | 272 | 256 |
| superpathway of fucose and rhamnose degradation | 273 | 232 |
| catechol degradation II (meta-cleavage pathway) | 274 | none |
| superpathway of (R,R)-butanediol biosynthesis | 275 | 63 |
| 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation | 276 | 278 |
| superpathway of UDP-N-acetylglucosamine-derived O-antigen building blocks biosynthesis | 277 | none |
| creatinine degradation I | 278 | none |
| superpathway of glycol metabolism and degradation | 279 | 236 |
| acetyl-CoA fermentation to butanoate II | 280 | 270 |
| methyl ketone biosynthesis | 281 | 285 |
| meta cleavage pathway of aromatic compounds | 282 | none |
| fucose degradation | 283 | 240 |
| p-cymene degradation | 284 | none |
| p-cumate degradation | 285 | none |
| toluene degradation IV (aerobic) (via catechol) | 286 | none |
| catechol degradation to 2-oxopent-4-enoate II | 287 | none |
| mono-trans, poly-cis decaprenyl phosphate biosynthesis | 288 | none |
| UDP-2,3-diacetamido-2,3-dideoxy-alpha-D-mannuronate biosynthesis | 289 | none |
| sulfoglycolysis | 290 | 242 |
| peptidoglycan biosynthesis IV (Enterococcus faecium) | 291 | none |
| L-arabinose degradation IV | 292 | none |
| cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate | 293 | 288 |
| 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate | 294 | 287 |
| glycerol degradation to butanol | 295 | 277 |
| glycogen degradation II (eukaryotic) | 296 | 302 |
| 3-phenylpropanoate degradation | 297 | 296 |
| methanol oxidation to carbon dioxide | 298 | none |
| methylgallate degradation | 299 | 248 |
| nicotinate degradation I | 300 | 295 |
| L-tryptophan degradation IX | 301 | none |
| gallate degradation I | 302 | 250 |
| gallate degradation II | 303 | 251 |
| glycine betaine degradation I | 304 | none |
| superpathway of menaquinol-8 biosynthesis II | 305 | none |
| L-tryptophan degradation XII (Geobacillus) | 306 | none |
| pyrimidine deoxyribonucleotides de novo biosynthesis III | 307 | 291 |
| superpathway of aerobic toluene degradation | 308 | none |
| syringate degradation | 309 | 255 |
| adenosylcobalamin biosynthesis II (late cobalt incorporation) | 310 | 272 |
| pyruvate fermentation to acetone | 311 | 290 |
| 2-aminophenol degradation | 312 | none |
| mycothiol biosynthesis | 313 | none |
| superpathway of L-threonine metabolism | 314 | 273 |
| teichoic acid (poly-glycerol) biosynthesis | 315 | none |
| superpathway of methylglyoxal degradation | 316 | 195 |
| 1,4-dihydroxy-6-naphthoate biosynthesis II | 317 | none |
| 1,4-dihydroxy-6-naphthoate biosynthesis I | 318 | none |
| aerobactin biosynthesis | 319 | 301 |
| CMP-legionaminate biosynthesis I | 320 | 306 |
| superpathway of sulfur oxidation (Acidianus ambivalens) | 321 | none |
| L-lysine biosynthesis II | 322 | none |
| cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion) | 323 | 261 |
| GDP-D-glycero-alpha-D-manno-heptose biosynthesis | 324 | none |
| protocatechuate degradation I (meta-cleavage pathway) | 325 | 269 |
| sucrose biosynthesis I (from photosynthesis) | 326 | 303 |
| isopropanol biosynthesis | 327 | none |
| chlorosalicylate degradation | 328 | none |
| superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate) | 329 | none |
| formaldehyde assimilation I (serine pathway) | 330 | 300 |
| vanillin and vanillate degradation II | 331 | 266 |
| 1,5-anhydrofructose degradation | 332 | none |
| superpathway of vanillin and vanillate degradation | 333 | 275 |
| vanillin and vanillate degradation I | 334 | 274 |
| mannan degradation | 335 | none |
| allantoin degradation IV (anaerobic) | 336 | 247 |
| superpathway of C1 compounds oxidation to CO2 | 337 | none |
| mevalonate pathway I | 338 | none |
| S-methyl-5-thio-alpha-D-ribose 1-phosphate degradation | 339 | none |
| ethylmalonyl-CoA pathway | 340 | none |
| adenosylcobalamin biosynthesis I (early cobalt insertion) | 341 | 282 |
| L-rhamnose degradation II | 342 | none |
| creatinine degradation II | 343 | none |
| methylaspartate cycle | 344 | 299 |
| benzoyl-CoA degradation I (aerobic) | 345 | none |
| purine nucleobases degradation I (anaerobic) | 346 | none |
| ergothioneine biosynthesis I (bacteria) | 347 | none |
| chlorophyllide a biosynthesis III (aerobic, light independent) | 348 | none |
| chlorophyllide a biosynthesis II (anaerobic) | 349 | none |
| superpathway of sulfolactate degradation | 350 | none |
| L-1,2-propanediol degradation | 351 | 194 |
| L-methionine salvage cycle III | 352 | none |
| superpathway of taurine degradation | 353 | none |
| mandelate degradation to acetyl-CoA | 354 | none |
| sucrose biosynthesis III | 355 | 305 |
| superpathway of Clostridium acetobutylicum acidogenic fermentation | 356 | none |
| nitrate reduction VI (assimilatory) | 357 | none |
| coenzyme B biosynthesis | 358 | none |
| pyrimidine deoxyribonucleotides biosynthesis from CTP | 359 | none |
| pyruvate fermentation to butanoate | 360 | none |
| starch degradation III | 361 | 298 |
| biotin biosynthesis II | 362 | none |
| naphthalene degradation to acetyl-CoA | 363 | none |
| sucrose degradation II (sucrose synthase) | 364 | none |
| isoprene biosynthesis II (engineered) | 365 | none |
| peptidoglycan biosynthesis V (beta-lactam resistance) | 366 | none |
| L-lysine fermentation to acetate and butanoate | 367 | 304 |
| peptidoglycan biosynthesis II (staphylococci) | 368 | none |
| superpathway of bacteriochlorophyll a biosynthesis | 369 | none |
| naphthalene degradation (aerobic) | 370 | none |
| nylon-6 oligomer degradation | 371 | none |
| chorismate biosynthesis II (archaea) | 372 | none |
| mandelate degradation I | 373 | none |
| chlorophyllide a biosynthesis I (aerobic, light-dependent) | 374 | none |
| L-valine degradation I | 375 | none |
| phospholipases | 376 | none |
| superpathway of mycolyl-arabinogalactan-peptidoglycan complex biosynthesis | 377 | none |
| reductive acetyl coenzyme A pathway | 378 | none |
| lactose and galactose degradation I | 379 | none |
| mycolyl-arabinogalactan-peptidoglycan complex biosynthesis | 380 | none |
| superpathway of glycerol degradation to 1,3-propanediol | 381 | 279 |
| coenzyme M biosynthesis I | 382 | none |
| succinate fermentation to butanoate | 383 | none |
| L-glutamate degradation V (via hydroxyglutarate) | 384 | none |
| sitosterol degradation to androstenedione | 385 | none |
| glycolysis V (Pyrococcus) | 386 | none |
| superpathway of the 3-hydroxypropanoate cycle | 387 | none |
| superpathway of demethylmenaquinol-6 biosynthesis II | 388 | none |
| vitamin B6 degradation | 389 | none |
| glutaryl-CoA degradation | 390 | none |
| 3-hydroxypropanoate cycle | 391 | none |
| glyoxylate assimilation | 392 | none |
| 4-coumarate degradation (anaerobic) | 393 | none |
| mannosylglycerate biosynthesis I | 394 | none |
| chitin derivatives degradation | 395 | none |
| nitrifier denitrification | 396 | none |
| starch biosynthesis | 397 | none |
| 4-hydroxyacetophenone degradation | 398 | none |
| L-glutamate degradation VIII (to propanoate) | 399 | none |
| reductive TCA cycle II | 400 | none |
| beta-alanine biosynthesis II | 401 | none |
| D-galacturonate degradation II | 402 | none |
| chondroitin sulfate degradation I (bacterial) | 403 | none |
| toluene degradation V (aerobic) (via toluene-cis-diol) | 404 | none |
| Entner-Doudoroff pathway III (semi-phosphorylative) | 405 | none |
| methanogenesis from acetate | 406 | none |
| (5R)-carbapenem carboxylate biosynthesis | 407 | none |
| neopentalenoketolactone and pentalenate biosynthesis | 408 | none |
| UTP and CTP dephosphorylation I | 409 | none |
| pyrimidine deoxyribonucleotides de novo biosynthesis IV | 410 | none |
| dTDP-N-acetylviosamine biosynthesis | 411 | none |
| biphenyl degradation | 412 | none |
| dTDP-D-desosamine biosynthesis | 413 | none |
| pentalenolactone biosynthesis | 414 | none |
| superpathway of megalomicin A biosynthesis | 415 | none |
| superpathway of erythromycin biosynthesis | 416 | none |
| erythromycin D biosynthesis | 417 | none |
| superpathway of erythromycin biosynthesis (without sugar biosynthesis) | 418 | none |
| mevalonate pathway II (archaea) | 419 | none |
| benzoyl-CoA degradation II (anaerobic) | 420 | none |
| paromamine biosynthesis I | 421 | none |