Supplemental Table 8. Pathways ranked by activity as estimated by PICRUSt2.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Overall | | *Buchnera* alone | | All other genera | |
| fatty acid beta-oxidation I | 49990374.39 | fatty acid beta-oxidation I | 47863170.30 | aerobic respiration I (cytochrome c) | 4020259.41 |
| anhydromuropeptides recycling | 43950267.23 | anhydromuropeptides recycling | 42417511.74 | pyruvate fermentation to isobutanol (engineered) | 2772569.39 |
| TCA cycle I (prokaryotic) | 43150337.13 | TCA cycle I (prokaryotic) | 41048308.93 | gondoate biosynthesis (anaerobic) | 2763286.94 |
| glycogen degradation I (bacterial) | 41334843.09 | glycogen degradation I (bacterial) | 39880951.18 | mycolate biosynthesis | 2430000.10 |
| pentose phosphate pathway (non-oxidative branch) | 40209945.56 | pentose phosphate pathway (non-oxidative branch) | 38368121.19 | L-isoleucine biosynthesis II | 2422960.26 |
| L-isoleucine biosynthesis II | 39849625.83 | L-isoleucine biosynthesis II | 37428656.17 | fatty acid elongation -- saturated | 2396467.81 |
| mixed acid fermentation | 38199142.29 | mixed acid fermentation | 36682065.34 | L-isoleucine biosynthesis I (from threonine) | 2313292.91 |
| pyruvate fermentation to isobutanol (engineered) | 38100324.98 | superpathway of L-alanine biosynthesis | 35986568.69 | L-valine biosynthesis | 2313292.91 |
| L-valine biosynthesis | 37781648.12 | peptidoglycan maturation (meso-diaminopimelate containing) | 35935247.60 | oleate biosynthesis IV (anaerobic) | 2258649.33 |
| L-isoleucine biosynthesis I (from threonine) | 37781648.12 | TCA cycle VII (acetate-producers) | 35921454.54 | fatty acid beta-oxidation I | 2243395.81 |
| superpathway of L-alanine biosynthesis | 37772950.94 | pyruvate fermentation to isobutanol (engineered) | 35526994.20 | cis-vaccenate biosynthesis | 2222135.39 |
| TCA cycle VII (acetate-producers) | 37632344.03 | L-valine biosynthesis | 35476963.41 | palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate) | 2194399.64 |
| peptidoglycan maturation (meso-diaminopimelate containing) | 37561343.79 | L-isoleucine biosynthesis I (from threonine) | 35476963.41 | stearate biosynthesis II (bacteria and plants) | 2148106.46 |
| superpathway of branched amino acid biosynthesis | 36744146.58 | superpathway of branched amino acid biosynthesis | 34714338.68 | TCA cycle I (prokaryotic) | 2140322.97 |
| sulfate reduction I (assimilatory) | 35835117.59 | sulfate reduction I (assimilatory) | 33815384.14 | (5Z)-dodec-5-enoate biosynthesis | 2139672.10 |
| superpathway of phospholipid biosynthesis I (bacteria) | 34688494.38 | superpathway of phospholipid biosynthesis I (bacteria) | 32695985.67 | superpathway of fatty acid biosynthesis initiation (E. coli) | 2121814.72 |
| superpathway of adenosine nucleotides de novo biosynthesis I | 34337541.32 | starch degradation V | 32652900.69 | superpathway of L-serine and glycine biosynthesis I | 2114370.67 |
| L-isoleucine biosynthesis III | 34249341.67 | superpathway of adenosine nucleotides de novo biosynthesis I | 32550201.50 | CDP-diacylglycerol biosynthesis II | 2100599.12 |
| starch degradation V | 34051427.17 | L-isoleucine biosynthesis III | 32366604.71 | CDP-diacylglycerol biosynthesis I | 2100599.12 |
| guanosine deoxyribonucleotides de novo biosynthesis II | 33696318.85 | adenosine deoxyribonucleotides de novo biosynthesis II | 31948746.12 | pentose phosphate pathway (non-oxidative branch) | 2090619.61 |
| adenosine deoxyribonucleotides de novo biosynthesis II | 33696318.85 | guanosine deoxyribonucleotides de novo biosynthesis II | 31948746.12 | superpathway of branched amino acid biosynthesis | 2055294.89 |
| superpathway of L-isoleucine biosynthesis I | 33623938.23 | superpathway of polyamine biosynthesis I | 31898110.50 | fatty acid salvage | 1993050.79 |
| phosphatidylglycerol biosynthesis II (non-plastidic) | 32704959.97 | hexitol fermentation to lactate, formate, ethanol and acetate | 31862604.60 | superpathway of phospholipid biosynthesis I (bacteria) | 1991151.37 |
| phosphatidylglycerol biosynthesis I (plastidic) | 32704959.97 | dTDP-N-acetylthomosamine biosynthesis | 31861896.87 | superpathway of sulfate assimilation and cysteine biosynthesis | 1965566.64 |
| superpathway of adenosine nucleotides de novo biosynthesis II | 32681382.85 | superpathway of L-isoleucine biosynthesis I | 31801573.14 | L-isoleucine biosynthesis III | 1920492.83 |
| superpathway of polyamine biosynthesis I | 32545588.40 | superpathway of L-methionine biosynthesis (transsulfuration) | 31406712.49 | urate biosynthesis/inosine 5'-phosphate degradation | 1915638.53 |
| L-lysine biosynthesis III | 32515917.24 | superpathway of adenosine nucleotides de novo biosynthesis II | 30965700.29 | 8-amino-7-oxononanoate biosynthesis I | 1899244.13 |
| superpathway of L-methionine biosynthesis (transsulfuration) | 32509176.89 | phosphatidylglycerol biosynthesis I (plastidic) | 30824987.37 | sulfate reduction I (assimilatory) | 1899170.77 |
| dTDP-N-acetylthomosamine biosynthesis | 32439110.11 | phosphatidylglycerol biosynthesis II (non-plastidic) | 30824987.37 | peptidoglycan maturation (meso-diaminopimelate containing) | 1893845.34 |
| superpathway of L-phenylalanine biosynthesis | 32293766.33 | L-lysine biosynthesis III | 30802845.50 | superpathway of adenosine nucleotides de novo biosynthesis I | 1886912.51 |
| hexitol fermentation to lactate, formate, ethanol and acetate | 32203966.13 | superpathway of L-phenylalanine biosynthesis | 30605213.63 | superpathway of aromatic amino acid biosynthesis | 1875420.51 |
| superpathway of aromatic amino acid biosynthesis | 32099236.00 | superpathway of aromatic amino acid biosynthesis | 30294257.64 | adenosine nucleotides degradation II | 1872747.82 |
| adenosine ribonucleotides de novo biosynthesis | 31961687.87 | adenosine ribonucleotides de novo biosynthesis | 30267223.17 | adenosine ribonucleotides de novo biosynthesis | 1818091.95 |
| superpathway of L-threonine biosynthesis | 31441703.48 | superpathway of S-adenosyl-L-methionine biosynthesis | 29998284.26 | L-ornithine biosynthesis | 1816330.01 |
| superpathway of sulfate assimilation and cysteine biosynthesis | 31352065.17 | superpathway of L-threonine biosynthesis | 29747849.01 | superpathway of L-isoleucine biosynthesis I | 1807255.35 |
| L-lysine biosynthesis VI | 31289898.57 | L-lysine biosynthesis VI | 29601843.57 | superpathway of pyrimidine nucleobases salvage | 1805908.17 |
| (5Z)-dodec-5-enoate biosynthesis | 31108328.54 | pentose phosphate pathway | 29487678.54 | superpathway of adenosine nucleotides de novo biosynthesis II | 1801338.89 |
| superpathway of S-adenosyl-L-methionine biosynthesis | 31027213.88 | superpathway of sulfate assimilation and cysteine biosynthesis | 29426944.10 | phosphatidylglycerol biosynthesis II (non-plastidic) | 1795570.66 |
| pentose phosphate pathway | 30935480.25 | (5Z)-dodec-5-enoate biosynthesis | 28847314.59 | phosphatidylglycerol biosynthesis I (plastidic) | 1795570.66 |
| CDP-diacylglycerol biosynthesis I | 30770471.63 | Calvin-Benson-Bassham cycle | 28791652.39 | guanosine deoxyribonucleotides de novo biosynthesis II | 1792788.90 |
| CDP-diacylglycerol biosynthesis II | 30770471.63 | CDP-diacylglycerol biosynthesis I | 28786700.73 | adenosine deoxyribonucleotides de novo biosynthesis II | 1792788.90 |
| Calvin-Benson-Bassham cycle | 30498292.42 | CDP-diacylglycerol biosynthesis II | 28786700.73 | superpathway of L-phenylalanine biosynthesis | 1791887.85 |
| oleate biosynthesis IV (anaerobic) | 30481054.76 | superpathway of L-tyrosine biosynthesis | 28766389.69 | 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I | 1788718.11 |
| superpathway of pyrimidine ribonucleotides de novo biosynthesis | 30396449.54 | superpathway of pyrimidine ribonucleotides de novo biosynthesis | 28757753.53 | chorismate biosynthesis I | 1782192.79 |
| UMP biosynthesis | 30386901.67 | UMP biosynthesis | 28757062.69 | pentose phosphate pathway | 1767618.38 |
| superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis | 30344463.97 | superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis | 28754597.13 | 6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia) | 1763006.03 |
| pyrimidine deoxyribonucleotides de novo biosynthesis I | 30324754.94 | pyrimidine deoxyribonucleotides de novo biosynthesis I | 28753471.76 | biotin biosynthesis I | 1757257.67 |
| gondoate biosynthesis (anaerobic) | 30317421.69 | urate biosynthesis/inosine 5'-phosphate degradation | 28709393.78 | L-lysine biosynthesis III | 1740422.02 |
| superpathway of L-tyrosine biosynthesis | 30209415.04 | NAD salvage pathway II | 28698740.81 | N10-formyl-tetrahydrofolate biosynthesis | 1732478.87 |
| urate biosynthesis/inosine 5'-phosphate degradation | 30174248.09 | L-methionine biosynthesis I | 28682255.87 | superpathway of L-alanine biosynthesis | 1721570.94 |
| fatty acid elongation -- saturated | 30039748.21 | guanosine nucleotides degradation III | 28680424.66 | L-lysine biosynthesis I | 1716513.17 |
| L-lysine biosynthesis I | 29837496.16 | L-lysine biosynthesis I | 28145100.75 | chorismate biosynthesis from 3-dehydroquinate | 1711292.73 |
| guanosine nucleotides degradation III | 29825959.11 | superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis | 28125469.74 | GDP-mannose biosynthesis | 1705992.36 |
| chorismate biosynthesis I | 29708709.39 | oleate biosynthesis IV (anaerobic) | 28070065.47 | 5-aminoimidazole ribonucleotide biosynthesis I | 1698698.59 |
| superpathway of fatty acid biosynthesis initiation (E. coli) | 29703076.79 | superpathway of L-lysine, L-threonine and L-methionine biosynthesis I | 28048540.98 | TCA cycle VIII (helicobacter) | 1692403.07 |
| superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis | 29424738.59 | chorismate biosynthesis I | 27986164.76 | superpathway of pyrimidine ribonucleotides de novo biosynthesis | 1686024.92 |
| superpathway of L-lysine, L-threonine and L-methionine biosynthesis I | 29422849.98 | TCA cycle VI (obligate autotrophs) | 27814305.44 | UMP biosynthesis | 1678562.25 |
| palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate) | 29415694.50 | superpathway of arginine and polyamine biosynthesis | 27700552.05 | superpathway of guanosine nucleotides de novo biosynthesis I | 1675266.35 |
| L-methionine biosynthesis I | 29346721.25 | superpathway of fatty acid biosynthesis initiation (E. coli) | 27698062.04 | superpathway of purine nucleotides de novo biosynthesis I | 1674256.91 |
| TCA cycle VI (obligate autotrophs) | 29180799.58 | gondoate biosynthesis (anaerobic) | 27538483.69 | L-lysine biosynthesis VI | 1673514.97 |
| superpathway of pyrimidine nucleobases salvage | 29177690.85 | fatty acid elongation -- saturated | 27514472.15 | superpathway of tetrahydrofolate biosynthesis and salvage | 1672168.03 |
| NAD salvage pathway II | 29164987.10 | superpathway of purine nucleotides de novo biosynthesis I | 27510861.29 | L-tryptophan biosynthesis | 1660746.30 |
| superpathway of purine nucleotides de novo biosynthesis I | 29115480.48 | superpathway of (R,R)-butanediol biosynthesis | 27458908.18 | superpathway of L-threonine biosynthesis | 1660048.17 |
| cis-vaccenate biosynthesis | 29074982.63 | superpathway of pyrimidine nucleobases salvage | 27405373.44 | TCA cycle VII (acetate-producers) | 1654706.53 |
| superpathway of guanosine nucleotides de novo biosynthesis I | 29042221.88 | superpathway of guanosine nucleotides de novo biosynthesis I | 27404539.40 | Calvin-Benson-Bassham cycle | 1650334.55 |
| heme biosynthesis II (anaerobic) | 28967307.23 | heme biosynthesis II (anaerobic) | 27389254.84 | ubiquinol-9 biosynthesis (prokaryotic) | 1648238.64 |
| biotin biosynthesis I | 28772378.12 | CMP-3-deoxy-D-manno-octulosonate biosynthesis I | 27381199.75 | ubiquinol-7 biosynthesis (prokaryotic) | 1648238.64 |
| CMP-3-deoxy-D-manno-octulosonate biosynthesis I | 28726911.82 | S-adenosyl-L-methionine cycle I | 27337388.74 | ubiquinol-10 biosynthesis (prokaryotic) | 1648238.64 |
| superpathway of arginine and polyamine biosynthesis | 28719613.77 | galactose degradation I (Leloir pathway) | 27335657.16 | ubiquinol-8 biosynthesis (prokaryotic) | 1648238.64 |
| tRNA charging | 28694271.48 | tRNA charging | 27196590.34 | superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis | 1645113.29 |
| glycolysis I (from glucose 6-phosphate) | 28501957.26 | palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate) | 27067628.73 | heme biosynthesis II (anaerobic) | 1645069.90 |
| stearate biosynthesis II (bacteria and plants) | 28484116.86 | superpathway of histidine, purine, and pyrimidine biosynthesis | 27004277.60 | pyrimidine deoxyribonucleotides de novo biosynthesis I | 1639549.13 |
| 8-amino-7-oxononanoate biosynthesis I | 28464849.07 | glycolysis I (from glucose 6-phosphate) | 26992626.97 | superpathway of guanosine nucleotides de novo biosynthesis II | 1631784.06 |
| superpathway of guanosine nucleotides de novo biosynthesis II | 28448441.95 | glycolysis II (from fructose 6-phosphate) | 26990561.26 | dTDP-L-rhamnose biosynthesis I | 1622084.50 |
| glycolysis II (from fructose 6-phosphate) | 28427056.25 | biotin biosynthesis I | 26902808.06 | superpathway of glyoxylate bypass and TCA | 1617282.81 |
| chorismate biosynthesis from 3-dehydroquinate | 28334829.03 | superpathway of guanosine nucleotides de novo biosynthesis II | 26853645.72 | L-arginine biosynthesis III (via N-acetyl-L-citrulline) | 1589952.81 |
| superpathway of histidine, purine, and pyrimidine biosynthesis | 28257956.76 | cis-vaccenate biosynthesis | 26733019.56 | superpathway of ubiquinol-8 biosynthesis (prokaryotic) | 1576415.89 |
| 5-aminoimidazole ribonucleotide biosynthesis I | 28253586.53 | superpathway of purine nucleotides de novo biosynthesis II | 26666681.70 | L-methionine biosynthesis III | 1572213.94 |
| superpathway of tetrahydrofolate biosynthesis and salvage | 28213123.23 | chorismate biosynthesis from 3-dehydroquinate | 26653388.02 | flavin biosynthesis I (bacteria and plants) | 1569144.37 |
| L-tryptophan biosynthesis | 28199536.90 | L-tryptophan biosynthesis | 26630593.75 | superpathway of 5-aminoimidazole ribonucleotide biosynthesis | 1565594.12 |
| ubiquinol-9 biosynthesis (prokaryotic) | 28147672.17 | 5-aminoimidazole ribonucleotide biosynthesis I | 26629574.21 | 5-aminoimidazole ribonucleotide biosynthesis II | 1565594.12 |
| ubiquinol-8 biosynthesis (prokaryotic) | 28147672.17 | ubiquinol-8 biosynthesis (prokaryotic) | 26628253.66 | superpathway of L-methionine biosynthesis (by sulfhydrylation) | 1546307.28 |
| ubiquinol-10 biosynthesis (prokaryotic) | 28147672.17 | ubiquinol-10 biosynthesis (prokaryotic) | 26628253.66 | gluconeogenesis I | 1538930.26 |
| ubiquinol-7 biosynthesis (prokaryotic) | 28147672.17 | ubiquinol-7 biosynthesis (prokaryotic) | 26628253.66 | guanosine ribonucleotides de novo biosynthesis | 1531589.65 |
| galactose degradation I (Leloir pathway) | 28095706.40 | ubiquinol-9 biosynthesis (prokaryotic) | 26628253.66 | superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli) | 1529641.72 |
| S-adenosyl-L-methionine cycle I | 28085486.66 | ppGpp biosynthesis | 26597016.52 | tRNA charging | 1527081.35 |
| superpathway of purine nucleotides de novo biosynthesis II | 27957351.79 | superpathway of tetrahydrofolate biosynthesis and salvage | 26559226.31 | L-histidine biosynthesis | 1524609.78 |
| ppGpp biosynthesis | 27950385.69 | 8-amino-7-oxononanoate biosynthesis I | 26441193.47 | superpathway of tetrahydrofolate biosynthesis | 1519688.67 |
| superpathway of ubiquinol-8 biosynthesis (prokaryotic) | 27615298.88 | stearate biosynthesis II (bacteria and plants) | 26237925.39 | phosphopantothenate biosynthesis I | 1517172.53 |
| superpathway of (R,R)-butanediol biosynthesis | 27582781.67 | superpathway of ubiquinol-8 biosynthesis (prokaryotic) | 26143469.87 | TCA cycle VI (obligate autotrophs) | 1495061.48 |
| superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli) | 27350869.14 | superpathway of heme biosynthesis from uroporphyrinogen-III | 26114558.70 | tetrapyrrole biosynthesis II (from glycine) | 1484309.12 |
| homolactic fermentation | 27241308.15 | homolactic fermentation | 25980844.05 | glucose and glucose-1-phosphate degradation | 1479154.38 |
| glycolysis III (from glucose) | 26926703.57 | superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli) | 25906704.27 | tetrapyrrole biosynthesis I (from glutamate) | 1477736.38 |
| superpathway of heme biosynthesis from uroporphyrinogen-III | 26884319.83 | superpathway of pyrimidine ribonucleosides salvage | 25790352.82 | preQ0 biosynthesis | 1475919.08 |
| superpathway of pyrimidine ribonucleosides salvage | 26831198.69 | enterobacterial common antigen biosynthesis | 25607199.27 | UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) | 1473651.55 |
| L-arginine biosynthesis III (via N-acetyl-L-citrulline) | 26787371.51 | glycolysis III (from glucose) | 25409600.33 | polyisoprenoid biosynthesis (E. coli) | 1468431.51 |
| L-arginine biosynthesis II (acetyl cycle) | 26712561.68 | L-arginine biosynthesis III (via N-acetyl-L-citrulline) | 25244139.87 | peptidoglycan biosynthesis I (meso-diaminopimelate containing) | 1462407.75 |
| gluconeogenesis I | 26176704.39 | L-arginine biosynthesis II (acetyl cycle) | 25240077.19 | O-antigen building blocks biosynthesis (E. coli) | 1457381.12 |
| superpathway of tetrahydrofolate biosynthesis | 26049504.25 | gluconeogenesis I | 24778685.11 | inosine-5'-phosphate biosynthesis I | 1456660.45 |
| L-arginine biosynthesis I (via L-ornithine) | 25916800.94 | superpathway of tetrahydrofolate biosynthesis | 24492498.86 | peptidoglycan biosynthesis III (mycobacteria) | 1454049.12 |
| enterobacterial common antigen biosynthesis | 25848117.84 | L-arginine biosynthesis I (via L-ornithine) | 24485217.47 | pantothenate and coenzyme A biosynthesis I | 1451983.63 |
| L-arginine biosynthesis IV (archaebacteria) | 25835928.76 | L-arginine biosynthesis IV (archaebacteria) | 24410341.76 | superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis | 1449878.85 |
| superpathway of L-serine and glycine biosynthesis I | 25831424.59 | superpathway of (Kdo)2-lipid A biosynthesis | 24298339.88 | L-arginine biosynthesis II (acetyl cycle) | 1448847.86 |
| 6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia) | 25801984.15 | superpathway of L-serine and glycine biosynthesis I | 24001902.24 | superpathway of glycolysis and Entner-Doudoroff | 1448580.23 |
| 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I | 25776990.19 | 6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia) | 23999166.30 | inosine-5'-phosphate biosynthesis III | 1447741.35 |
| L-ornithine biosynthesis | 25664588.81 | L-ornithine biosynthesis | 23993759.11 | UDP-N-acetyl-D-glucosamine biosynthesis I | 1435789.46 |
| N10-formyl-tetrahydrofolate biosynthesis | 25526302.99 | 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I | 23988302.09 | thiamin salvage II | 1434588.36 |
| flavin biosynthesis I (bacteria and plants) | 25507102.84 | guanosine ribonucleotides de novo biosynthesis | 23985676.10 | mixed acid fermentation | 1429159.01 |
| L-histidine biosynthesis | 25487915.05 | UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) | 23978846.51 | superpathway of L-tyrosine biosynthesis | 1427164.50 |
| guanosine ribonucleotides de novo biosynthesis | 25480246.04 | phosphopantothenate biosynthesis I | 23978476.58 | coenzyme A biosynthesis I | 1426925.52 |
| 5-aminoimidazole ribonucleotide biosynthesis II | 25454865.89 | L-histidine biosynthesis | 23977408.66 | L-arginine biosynthesis I (via L-ornithine) | 1419986.02 |
| superpathway of 5-aminoimidazole ribonucleotide biosynthesis | 25454865.89 | N10-formyl-tetrahydrofolate biosynthesis | 23977120.52 | pyrimidine deoxyribonucleotide phosphorylation | 1418120.45 |
| phosphopantothenate biosynthesis I | 25438489.81 | peptidoglycan biosynthesis I (meso-diaminopimelate containing) | 23976238.41 | glycolysis I (from glucose 6-phosphate) | 1417493.90 |
| tetrapyrrole biosynthesis II (from glycine) | 25433106.95 | peptidoglycan biosynthesis III (mycobacteria) | 23975915.00 | guanosine nucleotides degradation III | 1416378.83 |
| tetrapyrrole biosynthesis I (from glutamate) | 25426161.14 | UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing) | 23973204.28 | L-arginine biosynthesis IV (archaebacteria) | 1414890.30 |
| polyisoprenoid biosynthesis (E. coli) | 25418724.58 | lipid IVA biosynthesis | 23972409.31 | superpathay of heme biosynthesis from glutamate | 1400908.80 |
| UDP-N-acetyl-D-glucosamine biosynthesis I | 25402010.06 | flavin biosynthesis I (bacteria and plants) | 23971904.74 | TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase) | 1385738.62 |
| UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) | 25392293.69 | pantothenate and coenzyme A biosynthesis I | 23970654.30 | methylerythritol phosphate pathway I | 1378910.50 |
| thiamin salvage II | 25386776.57 | polyisoprenoid biosynthesis (E. coli) | 23968578.93 | methylerythritol phosphate pathway II | 1378910.50 |
| peptidoglycan biosynthesis I (meso-diaminopimelate containing) | 25383501.75 | superpathway of pyridoxal 5'-phosphate biosynthesis and salvage | 23968556.94 | NAD biosynthesis I (from aspartate) | 1377078.41 |
| superpathway of (Kdo)2-lipid A biosynthesis | 25375436.03 | sucrose degradation III (sucrose invertase) | 23967812.21 | queuosine biosynthesis | 1360244.44 |
| peptidoglycan biosynthesis III (mycobacteria) | 25374181.52 | superpathway of L-aspartate and L-asparagine biosynthesis | 23967527.12 | anhydromuropeptides recycling | 1355188.61 |
| pantothenate and coenzyme A biosynthesis I | 25371461.52 | 5-aminoimidazole ribonucleotide biosynthesis II | 23967487.58 | glycolysis III (from glucose) | 1352794.02 |
| inosine-5'-phosphate biosynthesis I | 25360325.75 | superpathway of 5-aminoimidazole ribonucleotide biosynthesis | 23967487.58 | CMP-3-deoxy-D-manno-octulosonate biosynthesis I | 1350812.20 |
| superpathay of heme biosynthesis from glutamate | 25358257.19 | UDP-N-acetyl-D-glucosamine biosynthesis I | 23967429.46 | superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass | 1346370.53 |
| coenzyme A biosynthesis I | 25356349.21 | tetrapyrrole biosynthesis I (from glutamate) | 23966124.40 | lipid IVA biosynthesis | 1340041.31 |
| pyrimidine deoxyribonucleotide phosphorylation | 25347851.62 | inosine-5'-phosphate biosynthesis I | 23965948.74 | L-histidine degradation I | 1337848.47 |
| inosine-5'-phosphate biosynthesis III | 25345059.59 | coenzyme A biosynthesis I | 23965941.30 | heme biosynthesis I (aerobic) | 1331500.89 |
| preQ0 biosynthesis | 25343141.83 | pyrimidine deoxyribonucleotide phosphorylation | 23965936.30 | Kdo transfer to lipid IVA III (Chlamydia) | 1329049.15 |
| methylerythritol phosphate pathway I | 25309963.03 | queuosine biosynthesis | 23965931.05 | NAD salvage pathway I | 1321542.82 |
| methylerythritol phosphate pathway II | 25309963.03 | tetrapyrrole biosynthesis II (from glycine) | 23965925.90 | UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing) | 1310352.90 |
| lipid IVA biosynthesis | 25282881.10 | methylerythritol phosphate pathway II | 23965692.21 | starch degradation V | 1307176.70 |
| heme biosynthesis I (aerobic) | 25279287.78 | methylerythritol phosphate pathway I | 23965692.21 | L-leucine degradation I | 1302184.64 |
| UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing) | 25264571.37 | thiamin salvage II | 23965478.34 | colanic acid building blocks biosynthesis | 1297836.97 |
| queuosine biosynthesis | 25263453.52 | inosine-5'-phosphate biosynthesis III | 23963672.40 | TCA cycle IV (2-oxoglutarate decarboxylase) | 1289513.91 |
| Kdo transfer to lipid IVA III (Chlamydia) | 25256738.74 | superpathay of heme biosynthesis from glutamate | 23962965.91 | glycogen degradation I (bacterial) | 1280006.69 |
| pyridoxal 5'-phosphate biosynthesis I | 25155979.96 | sucrose degradation IV (sucrose phosphorylase) | 23962117.38 | sucrose degradation III (sucrose invertase) | 1268622.21 |
| tRNA processing | 25144834.86 | preQ0 biosynthesis | 23959581.91 | glycolysis II (from fructose 6-phosphate) | 1247604.23 |
| NAD salvage pathway I | 25139624.62 | pyridoxal 5'-phosphate biosynthesis I | 23959450.64 | glyoxylate cycle | 1244866.85 |
| glucose and glucose-1-phosphate degradation | 25105384.65 | Kdo transfer to lipid IVA III (Chlamydia) | 23959373.30 | sucrose degradation IV (sucrose phosphorylase) | 1241862.55 |
| L-histidine degradation I | 25094346.11 | pyrimidine deoxyribonucleotides de novo biosynthesis II | 23958463.83 | myo-, chiro- and scillo-inositol degradation | 1237748.00 |
| pyrimidine deoxyribonucleotides de novo biosynthesis II | 25070601.69 | heme biosynthesis I (aerobic) | 23958311.60 | L-tyrosine degradation I | 1232757.27 |
| NAD biosynthesis I (from aspartate) | 25041819.23 | tRNA processing | 23957274.30 | superpathway of L-lysine, L-threonine and L-methionine biosynthesis I | 1224874.75 |
| superpathway of L-aspartate and L-asparagine biosynthesis | 25021269.22 | ADP-L-glycero-beta-D-manno-heptose biosynthesis | 23953922.28 | superpathway of purine nucleotides de novo biosynthesis II | 1216860.31 |
| superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP) | 24997914.80 | glucose and glucose-1-phosphate degradation | 23952373.56 | superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP) | 1205693.06 |
| superpathway of pyrimidine deoxyribonucleoside salvage | 24990739.52 | NAD salvage pathway I | 23947997.30 | protocatechuate degradation II (ortho-cleavage pathway) | 1203744.06 |
| sucrose degradation III (sucrose invertase) | 24945147.88 | NAD biosynthesis I (from aspartate) | 23945251.45 | superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis | 1195809.12 |
| sucrose degradation IV (sucrose phosphorylase) | 24939670.80 | superpathway of pyrimidine deoxyribonucleoside salvage | 23944590.58 | pyridoxal 5'-phosphate biosynthesis I | 1187376.36 |
| L-histidine degradation II | 24897354.57 | superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP) | 23944249.60 | ppGpp biosynthesis | 1165424.35 |
| glycogen biosynthesis I (from ADP-D-Glucose) | 24891584.95 | L-arginine degradation II (AST pathway) | 23940081.84 | aromatic biogenic amine degradation (bacteria) | 1158789.27 |
| superpathway of pyridoxal 5'-phosphate biosynthesis and salvage | 24833716.35 | glycogen biosynthesis I (from ADP-D-Glucose) | 23936543.80 | aspartate superpathway | 1153959.10 |
| ADP-L-glycero-beta-D-manno-heptose biosynthesis | 24820709.20 | adenine and adenosine salvage III | 23932901.34 | superpathway of histidine, purine, and pyrimidine biosynthesis | 1153856.34 |
| L-arginine degradation II (AST pathway) | 24812899.51 | pyrimidine deoxyribonucleosides salvage | 23916697.58 | homolactic fermentation | 1122318.48 |
| pyrimidine deoxyribonucleosides salvage | 24686908.94 | superpathway of purine deoxyribonucleosides degradation | 23911938.45 | L-histidine degradation II | 1122177.33 |
| adenine and adenosine salvage III | 24648232.43 | purine ribonucleosides degradation | 23909568.30 | superpathway of S-adenosyl-L-methionine biosynthesis | 1118586.46 |
| superpathway of purine deoxyribonucleosides degradation | 24384954.18 | superpathway of pyrimidine deoxyribonucleosides degradation | 23905427.90 | glycogen biosynthesis I (from ADP-D-Glucose) | 1107734.80 |
| purine ribonucleosides degradation | 24375553.97 | L-histidine degradation I | 23902883.41 | superpathway of pyridoxal 5'-phosphate biosynthesis and salvage | 1104357.73 |
| myo-, chiro- and scillo-inositol degradation | 24298657.40 | polymyxin resistance | 23891141.03 | pyrimidine deoxyribonucleotides de novo biosynthesis II | 1086968.33 |
| superpathway of pyrimidine deoxyribonucleosides degradation | 24284896.34 | L-histidine degradation II | 23874033.46 | 4-aminobutanoate degradation V | 1058892.68 |
| polymyxin resistance | 24101107.45 | myo-, chiro- and scillo-inositol degradation | 23819744.19 | tRNA processing | 1023574.90 |
| myo-inositol degradation I | 24076853.32 | myo-inositol degradation I | 23809125.02 | superpathway of L-aspartate and L-asparagine biosynthesis | 1020373.89 |
| mycolate biosynthesis | 21720070.26 | mycolate biosynthesis | 5738706.71 | L-arginine degradation II (AST pathway) | 998638.51 |
| aerobic respiration I (cytochrome c) | 6933686.11 | aspartate superpathway | 2122932.23 | octane oxidation | 969820.92 |
| aspartate superpathway | 6922308.30 | TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase) | 1706762.09 | superpathway of L-methionine biosynthesis (transsulfuration) | 964719.85 |
| TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase) | 5912238.40 | TCA cycle IV (2-oxoglutarate decarboxylase) | 1363203.83 | D-fructuronate degradation | 954887.04 |
| TCA cycle IV (2-oxoglutarate decarboxylase) | 4970531.64 | purine nucleotides degradation II (aerobic) | 1070024.52 | superpathway of pyrimidine deoxyribonucleoside salvage | 942331.17 |
| purine nucleotides degradation II (aerobic) | 4352285.65 | superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass | 1021092.32 | superpathway of arginine and polyamine biosynthesis | 938373.10 |
| superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass | 4201422.72 | superpathway of thiamin diphosphate biosynthesis I | 891081.79 | ADP-L-glycero-beta-D-manno-heptose biosynthesis | 923714.40 |
| O-antigen building blocks biosynthesis (E. coli) | 3704121.53 | superpathway of glycolysis and Entner-Doudoroff | 854172.44 | superpathway of pyrimidine ribonucleosides salvage | 880002.53 |
| adenosine nucleotides degradation II | 3691285.73 | O-antigen building blocks biosynthesis (E. coli) | 755316.45 | purine nucleotides degradation II (aerobic) | 875995.87 |
| superpathway of glycolysis and Entner-Doudoroff | 3568012.38 | superpathway of thiamin diphosphate biosynthesis II | 745538.54 | 2-methylcitrate cycle II | 874787.22 |
| superpathway of glyoxylate bypass and TCA | 3376744.23 | adenosine nucleotides degradation II | 664703.63 | L-methionine biosynthesis I | 867217.77 |
| fatty acid salvage | 3237602.70 | superpathway of glyoxylate bypass and TCA | 656457.55 | adenosylcobalamin salvage from cobinamide I | 862764.52 |
| superpathway of L-methionine biosynthesis (by sulfhydrylation) | 3215722.84 | superpathway of hexitol degradation (bacteria) | 575494.90 | superpathway of ornithine degradation | 854178.69 |
| TCA cycle VIII (helicobacter) | 3054784.37 | aerobic respiration I (cytochrome c) | 530149.64 | L-isoleucine biosynthesis IV | 853190.91 |
| dTDP-L-rhamnose biosynthesis I | 3025719.10 | dTDP-L-rhamnose biosynthesis I | 412240.42 | superpathway of thiamin diphosphate biosynthesis I | 845791.38 |
| taxadiene biosynthesis (engineered) | 2568682.73 | superpathway of L-methionine biosynthesis (by sulfhydrylation) | 372338.83 | adenosylcobalamin salvage from cobinamide II | 839994.58 |
| GDP-mannose biosynthesis | 2133301.34 | glyoxylate cycle | 330174.84 | adenosylcobalamin biosynthesis from cobyrinate a,c-diamide I | 835299.05 |
| glyoxylate cycle | 2036644.30 | L-glutamate and L-glutamine biosynthesis | 325667.00 | acetylene degradation | 745316.61 |
| superpathway of thiamin diphosphate biosynthesis I | 1906670.51 | L-isoleucine biosynthesis IV | 312825.30 | taxadiene biosynthesis (engineered) | 743507.11 |
| colanic acid building blocks biosynthesis | 1876490.54 | superpathway of N-acetylneuraminate degradation | 310843.06 | myo-inositol degradation I | 742860.48 |
| L-methionine biosynthesis III | 1671119.44 | taxadiene biosynthesis (engineered) | 308685.28 | superpathway of (Kdo)2-lipid A biosynthesis | 742596.25 |
| L-leucine degradation I | 1592390.21 | colanic acid building blocks biosynthesis | 302882.85 | pyrimidine deoxyribonucleosides salvage | 741218.41 |
| L-isoleucine biosynthesis IV | 1523089.32 | thiazole biosynthesis I (E. coli) | 300165.64 | superpathway of polyamine biosynthesis I | 728372.99 |
| superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis | 1504909.49 | superpathway of chorismate metabolism | 292323.55 | superpathway of thiamin diphosphate biosynthesis II | 711609.69 |
| superpathway of polyamine biosynthesis II | 1466224.35 | enterobactin biosynthesis | 288797.33 | S-adenosyl-L-methionine cycle I | 698768.53 |
| superpathway of thiamin diphosphate biosynthesis II | 1453011.29 | GDP-mannose biosynthesis | 267136.82 | superpathway of polyamine biosynthesis II | 686150.01 |
| 4-aminobutanoate degradation V | 1410424.83 | D-fructuronate degradation | 263085.80 | galactose degradation I (Leloir pathway) | 683709.52 |
| L-glutamate and L-glutamine biosynthesis | 1378310.70 | acetylene degradation | 255927.97 | 2-methylcitrate cycle I | 657152.90 |
| 2-methylcitrate cycle II | 1312051.21 | superpathway of L-tryptophan biosynthesis | 242557.64 | cob(II)yrinate a,c-diamide biosynthesis II (late cobalt incorporation) | 651517.47 |
| L-tyrosine degradation I | 1211573.55 | superpathway of L-arginine and L-ornithine degradation | 242090.62 | D-galacturonate degradation I | 649308.09 |
| 2-methylcitrate cycle I | 1061545.22 | superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation | 242090.62 | superpathway of beta-D-glucuronide and D-glucuronate degradation | 645227.36 |
| adenosylcobalamin salvage from cobinamide I | 951692.19 | thiazole biosynthesis II (Bacillus) | 241283.57 | methylphosphonate degradation I | 628987.92 |
| octane oxidation | 925092.10 | L-1,2-propanediol degradation | 235588.41 | adenine and adenosine salvage III | 624024.87 |
| superpathway of hexitol degradation (bacteria) | 892975.93 | superpathway of methylglyoxal degradation | 215234.91 | Bifidobacterium shunt | 618759.28 |
| D-fructuronate degradation | 887222.97 | fatty acid salvage | 208410.62 | aromatic compounds degradation via beta-ketoadipate | 606034.34 |
| adenosylcobalamin salvage from cobinamide II | 879408.16 | superpathway of menaquinol-8 biosynthesis I | 197893.04 | catechol degradation III (ortho-cleavage pathway) | 606034.34 |
| acetylene degradation | 876238.55 | superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis | 191370.03 | 4-deoxy-L-threo-hex-4-enopyranuronate degradation | 579292.08 |
| adenosylcobalamin biosynthesis from cobyrinate a,c-diamide I | 870234.12 | superpathway of glucose and xylose degradation | 190660.30 | dTDP-N-acetylthomosamine biosynthesis | 578731.54 |
| arginine, ornithine and proline interconversion | 830520.01 | superpathway of menaquinol-12 biosynthesis | 186475.12 | palmitate biosynthesis II (bacteria and plants) | 578283.99 |
| protocatechuate degradation II (ortho-cleavage pathway) | 815998.22 | superpathway of menaquinol-11 biosynthesis | 186475.12 | catechol degradation to beta-ketoadipate | 575284.60 |
| superpathway of chorismate metabolism | 721583.31 | superpathway of menaquinol-13 biosynthesis | 186475.12 | arginine, ornithine and proline interconversion | 574582.81 |
| enterobactin biosynthesis | 717081.43 | superpathway of menaquinol-9 biosynthesis | 184757.12 | polymyxin resistance | 552955.68 |
| thiazole biosynthesis I (E. coli) | 683525.29 | superpathway of menaquinol-7 biosynthesis | 184757.12 | superpathway of purine deoxyribonucleosides degradation | 513319.40 |
| superpathway of glucose and xylose degradation | 679169.27 | superpathway of menaquinol-10 biosynthesis | 184757.12 | superpathway of heme biosynthesis from uroporphyrinogen-III | 501973.19 |
| allantoin degradation to glyoxylate III | 644142.29 | superpathway of menaquinol-6 biosynthesis I | 184757.12 | urea cycle | 501835.75 |
| aromatic biogenic amine degradation (bacteria) | 625116.79 | superpathway of polyamine biosynthesis II | 178985.95 | superpathway of chorismate metabolism | 489570.43 |
| superpathway of ornithine degradation | 623512.60 | 2-methylcitrate cycle II | 175721.88 | 4-hydroxyphenylacetate degradation | 469135.46 |
| superpathway of N-acetylneuraminate degradation | 623408.81 | superpathway of ornithine degradation | 174202.37 | superpathway of salicylate degradation | 465360.83 |
| superpathway of menaquinol-8 biosynthesis I | 583460.97 | superpathway of beta-D-glucuronide and D-glucuronate degradation | 169127.02 | superpathway of pyrimidine deoxyribonucleosides degradation | 449312.07 |
| D-galacturonate degradation I | 566085.62 | adenosylcobalamin salvage from cobinamide I | 167116.22 | 4-methylcatechol degradation (ortho cleavage) | 443094.12 |
| glucose degradation (oxidative) | 564732.27 | D-galacturonate degradation I | 162998.92 | purine ribonucleosides degradation | 441197.77 |
| incomplete reductive TCA cycle | 555104.54 | 4-deoxy-L-threo-hex-4-enopyranuronate degradation | 161488.88 | superpathway of L-tryptophan biosynthesis | 429963.02 |
| superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation | 549924.97 | TCA cycle VIII (helicobacter) | 161107.74 | toluene degradation III (aerobic) (via p-cresol) | 419854.43 |
| superpathway of L-arginine and L-ornithine degradation | 549924.97 | 2-methylcitrate cycle I | 157772.56 | superpathway of glucose and xylose degradation | 418209.75 |
| superpathway of menaquinol-13 biosynthesis | 545501.13 | superpathway of hexuronide and hexuronate degradation | 149590.13 | enterobactin biosynthesis | 401801.46 |
| superpathway of menaquinol-12 biosynthesis | 545501.13 | superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation | 144041.46 | NAD salvage pathway II | 396318.02 |
| superpathway of menaquinol-11 biosynthesis | 545501.13 | superpathway of demethylmenaquinol-8 biosynthesis | 141182.56 | toluene degradation II (aerobic) (via 4-methylcatechol) | 394794.43 |
| superpathway of menaquinol-7 biosynthesis | 522555.82 | pyruvate fermentation to acetate and lactate II | 133954.61 | toluene degradation I (aerobic) (via o-cresol) | 394794.43 |
| superpathway of beta-D-glucuronide and D-glucuronate degradation | 515627.87 | L-rhamnose degradation I | 131833.52 | superpathway of N-acetylneuraminate degradation | 391076.27 |
| ectoine biosynthesis | 514230.82 | superpathway of demethylmenaquinol-9 biosynthesis | 131435.03 | thiazole biosynthesis I (E. coli) | 388819.06 |
| superpathway of menaquinol-6 biosynthesis I | 503319.69 | superpathway of demethylmenaquinol-6 biosynthesis I | 131435.03 | superpathway of menaquinol-8 biosynthesis I | 377794.75 |
| superpathway of menaquinol-9 biosynthesis | 503319.69 | arginine, ornithine and proline interconversion | 126845.40 | pyruvate fermentation to propanoate I | 377231.12 |
| superpathway of menaquinol-10 biosynthesis | 503319.69 | 1,4-dihydroxy-2-naphthoate biosynthesis I | 122469.54 | superpathway of hexuronide and hexuronate degradation | 369090.26 |
| toluene degradation III (aerobic) (via p-cresol) | 494031.15 | 4-aminobutanoate degradation V | 122005.59 | superpathway of menaquinol-13 biosynthesis | 362881.36 |
| cob(II)yrinate a,c-diamide biosynthesis II (late cobalt incorporation) | 480199.13 | superpathway of phylloquinol biosynthesis | 121890.58 | superpathway of menaquinol-11 biosynthesis | 362881.36 |
| thiazole biosynthesis II (Bacillus) | 471335.17 | L-methionine biosynthesis III | 116798.64 | superpathway of menaquinol-12 biosynthesis | 362881.36 |
| pyruvate fermentation to acetate and lactate II | 471119.73 | D-galactarate degradation I | 113903.91 | superpathway of lipopolysaccharide biosynthesis | 361570.75 |
| superpathway of methylglyoxal degradation | 470523.04 | D-glucarate degradation I | 113903.91 | phenylacetate degradation I (aerobic) | 353517.13 |
| 4-deoxy-L-threo-hex-4-enopyranuronate degradation | 463578.61 | superpathway of D-glucarate and D-galactarate degradation | 113903.91 | superpathway of menaquinol-7 biosynthesis | 348260.71 |
| superpathway of hexuronide and hexuronate degradation | 452135.17 | superpathway of lipopolysaccharide biosynthesis | 98435.31 | ectoine biosynthesis | 344604.05 |
| urea cycle | 423049.36 | superpathway of fucose and rhamnose degradation | 91187.58 | superpathway of menaquinol-6 biosynthesis I | 335277.65 |
| Bifidobacterium shunt | 421146.13 | adenosylcobalamin salvage from cobinamide II | 87664.34 | superpathway of menaquinol-10 biosynthesis | 335277.65 |
| superpathway of demethylmenaquinol-8 biosynthesis | 417560.28 | L-leucine degradation I | 87512.94 | superpathway of menaquinol-9 biosynthesis | 335277.65 |
| pyruvate fermentation to propanoate I | 388011.57 | allantoin degradation to glyoxylate III | 86613.59 | L-glutamate and L-glutamine biosynthesis | 333038.12 |
| superpathway of 2,3-butanediol biosynthesis | 378164.88 | superpathway of glycol metabolism and degradation | 85706.74 | superpathway of hexitol degradation (bacteria) | 332967.15 |
| superpathway of heme biosynthesis from glycine | 374302.33 | ectoine biosynthesis | 84448.54 | incomplete reductive TCA cycle | 332702.14 |
| superpathway of lipopolysaccharide biosynthesis | 366574.00 | 4-hydroxyphenylacetate degradation | 83223.62 | superpathway of heme biosynthesis from glycine | 306803.80 |
| superpathway of demethylmenaquinol-6 biosynthesis I | 358586.76 | adenosylcobalamin biosynthesis from cobyrinate a,c-diamide I | 81880.74 | NAD biosynthesis II (from tryptophan) | 306344.48 |
| superpathway of demethylmenaquinol-9 biosynthesis | 358586.76 | fucose degradation | 75786.89 | nitrate reduction I (denitrification) | 299087.75 |
| L-rhamnose degradation I | 354743.71 | octane oxidation | 74303.69 | enterobacterial common antigen biosynthesis | 298172.27 |
| superpathway of phylloquinol biosynthesis | 342535.94 | sulfoglycolysis | 71450.90 | superpathway of demethylmenaquinol-8 biosynthesis | 292993.60 |
| superpathway of L-tryptophan biosynthesis | 342130.26 | superpathway of 2,3-butanediol biosynthesis | 69693.76 | superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation | 291692.52 |
| ketogluconate metabolism | 335885.04 | methylphosphonate degradation I | 69496.72 | superpathway of L-arginine and L-ornithine degradation | 291692.52 |
| NAD biosynthesis II (from tryptophan) | 334191.54 | incomplete reductive TCA cycle | 64680.91 | formaldehyde assimilation II (RuMP Cycle) | 291321.77 |
| reductive TCA cycle I | 328431.14 | ketogluconate metabolism | 63976.81 | thiazole biosynthesis II (Bacillus) | 287775.74 |
| D-glucarate degradation I | 328243.48 | allantoin degradation IV (anaerobic) | 58380.18 | superpathway of phylloquinol biosynthesis | 273660.04 |
| 1,4-dihydroxy-2-naphthoate biosynthesis I | 326151.45 | methylgallate degradation | 45422.20 | D-glucarate degradation I | 271982.88 |
| D-galactarate degradation I | 316546.37 | L-tyrosine degradation I | 41109.12 | L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde | 267629.68 |
| superpathway of D-glucarate and D-galactarate degradation | 316546.37 | gallate degradation I | 36742.85 | hexitol fermentation to lactate, formate, ethanol and acetate | 264725.51 |
| methylphosphonate degradation I | 302391.73 | gallate degradation II | 36742.85 | L-rhamnose degradation I | 262449.15 |
| norspermidine biosynthesis | 296982.48 | glucose degradation (oxidative) | 35386.78 | superpathway of D-glucarate and D-galactarate degradation | 260475.82 |
| L-1,2-propanediol degradation | 294362.22 | reductive TCA cycle I | 31343.43 | D-galactarate degradation I | 260475.82 |
| toluene degradation II (aerobic) (via 4-methylcatechol) | 288274.32 | protocatechuate degradation II (ortho-cleavage pathway) | 30161.85 | superpathway of demethylmenaquinol-6 biosynthesis I | 256841.29 |
| toluene degradation I (aerobic) (via o-cresol) | 288274.32 | syringate degradation | 29033.89 | superpathway of demethylmenaquinol-9 biosynthesis | 256841.29 |
| formaldehyde assimilation II (RuMP Cycle) | 288147.88 | norspermidine biosynthesis | 21934.95 | 1,4-dihydroxy-2-naphthoate biosynthesis I | 256399.99 |
| L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde | 281208.16 | toluene degradation III (aerobic) (via p-cresol) | 21386.47 | 2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate | 256368.32 |
| superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation | 278628.68 | aromatic biogenic amine degradation (bacteria) | 20624.44 | 2-nitrobenzoate degradation I | 253982.29 |
| palmitate biosynthesis II (bacteria and plants) | 262847.15 | cob(II)yrinate a,c-diamide biosynthesis II (late cobalt incorporation) | 19717.21 | allantoin degradation to glyoxylate III | 247075.98 |
| 2-nitrobenzoate degradation I | 255936.26 | 4-methylcatechol degradation (ortho cleavage) | 18197.21 | photorespiration | 241047.41 |
| 2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate | 255882.34 | cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion) | 18181.92 | pyruvate fermentation to acetate and lactate II | 238359.60 |
| phenylacetate degradation I (aerobic) | 249474.01 | catechol degradation III (ortho-cleavage pathway) | 17493.76 | formaldehyde oxidation I | 232151.64 |
| formaldehyde oxidation I | 217696.09 | aromatic compounds degradation via beta-ketoadipate | 17493.76 | catechol degradation I (meta-cleavage pathway) | 220523.03 |
| 4-hydroxyphenylacetate degradation | 213570.77 | phenylacetate degradation I (aerobic) | 17404.48 | androstenedione degradation | 219403.71 |
| photorespiration | 212062.60 | superpathway of salicylate degradation | 17028.56 | reductive TCA cycle I | 217974.77 |
| heterolactic fermentation | 210297.90 | vanillin and vanillate degradation II | 16534.21 | ketogluconate metabolism | 206696.80 |
| adenosylcobalamin biosynthesis II (late cobalt incorporation) | 206611.49 | superpathway of phenylethylamine degradation | 16498.96 | glucose degradation (oxidative) | 202129.32 |
| aromatic compounds degradation via beta-ketoadipate | 204228.04 | catechol degradation to beta-ketoadipate | 16153.41 | superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation | 195285.76 |
| catechol degradation III (ortho-cleavage pathway) | 204228.04 | protocatechuate degradation I (meta-cleavage pathway) | 15970.15 | superpathway of 2,3-butanediol biosynthesis | 174655.71 |
| catechol degradation to beta-ketoadipate | 182336.51 | acetyl-CoA fermentation to butanoate II | 15911.54 | superpathway of phenylethylamine degradation | 173546.26 |
| superpathway of glycol metabolism and degradation | 181466.66 | Bifidobacterium shunt | 14986.58 | heterolactic fermentation | 162472.00 |
| superpathway of salicylate degradation | 177351.60 | adenosylcobalamin biosynthesis II (late cobalt incorporation) | 14939.85 | norspermidine biosynthesis | 141078.48 |
| superpathway of fucose and rhamnose degradation | 173320.53 | superpathway of L-threonine metabolism | 14803.31 | superpathway of fucose and rhamnose degradation | 140098.17 |
| syringate degradation | 166930.95 | vanillin and vanillate degradation I | 14738.42 | catechol degradation II (meta-cleavage pathway) | 137741.91 |
| 4-methylcatechol degradation (ortho cleavage) | 165391.99 | superpathway of vanillin and vanillate degradation | 14738.42 | superpathway of (R,R)-butanediol biosynthesis | 133808.28 |
| methylgallate degradation | 154074.78 | urea cycle | 14194.95 | 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation | 132106.28 |
| catechol degradation I (meta-cleavage pathway) | 144767.50 | glycerol degradation to butanol | 12444.59 | superpathway of UDP-N-acetylglucosamine-derived O-antigen building blocks biosynthesis | 129627.10 |
| superpathway of UDP-N-acetylglucosamine-derived O-antigen building blocks biosynthesis | 141023.30 | 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation | 11056.29 | creatinine degradation I | 124242.03 |
| 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation | 137767.63 | superpathway of glycerol degradation to 1,3-propanediol | 10686.06 | superpathway of glycol metabolism and degradation | 122677.51 |
| gallate degradation I | 130792.80 | pyruvate fermentation to propanoate I | 10605.46 | acetyl-CoA fermentation to butanoate II | 122183.13 |
| gallate degradation II | 125838.14 | heterolactic fermentation | 10565.62 | methyl ketone biosynthesis | 107123.91 |
| acetyl-CoA fermentation to butanoate II | 122334.95 | adenosylcobalamin biosynthesis I (early cobalt insertion) | 10551.33 | meta cleavage pathway of aromatic compounds | 106058.75 |
| fucose degradation | 118169.37 | formaldehyde assimilation II (RuMP Cycle) | 8869.44 | fucose degradation | 103358.46 |
| superpathway of phenylethylamine degradation | 112628.67 | NAD biosynthesis II (from tryptophan) | 8608.85 | p-cymene degradation | 102704.27 |
| peptidoglycan biosynthesis IV (Enterococcus faecium) | 110126.98 | methyl ketone biosynthesis | 8295.24 | p-cumate degradation | 102704.27 |
| methyl ketone biosynthesis | 109111.36 | formaldehyde oxidation I | 6658.51 | toluene degradation IV (aerobic) (via catechol) | 101941.17 |
| mono-trans, poly-cis decaprenyl phosphate biosynthesis | 104827.67 | 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate | 6578.55 | catechol degradation to 2-oxopent-4-enoate II | 100967.29 |
| creatinine degradation I | 103297.64 | cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate | 6578.55 | mono-trans, poly-cis decaprenyl phosphate biosynthesis | 95669.59 |
| sulfoglycolysis | 93528.09 | L-tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde | 5783.00 | UDP-2,3-diacetamido-2,3-dideoxy-alpha-D-mannuronate biosynthesis | 93856.35 |
| glycogen degradation II (eukaryotic) | 86958.64 | pyruvate fermentation to acetone | 5528.20 | sulfoglycolysis | 89236.13 |
| catechol degradation II (meta-cleavage pathway) | 86709.95 | pyrimidine deoxyribonucleotides de novo biosynthesis III | 5369.54 | peptidoglycan biosynthesis IV (Enterococcus faecium) | 87427.03 |
| UDP-2,3-diacetamido-2,3-dideoxy-alpha-D-mannuronate biosynthesis | 83310.31 | 2-nitrobenzoate degradation I | 4162.09 | L-arabinose degradation IV | 78859.16 |
| cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate | 80528.56 | 2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate | 4133.07 | cinnamate and 3-hydroxycinnamate degradation to 2-oxopent-4-enoate | 75578.25 |
| 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate | 80528.56 | photorespiration | 3353.30 | 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-oxopent-4-enoate | 75578.25 |
| 3-phenylpropanoate degradation | 79279.96 | nicotinate degradation I | 2433.13 | glycerol degradation to butanol | 74184.01 |
| catechol degradation to 2-oxopent-4-enoate II | 78547.28 | 3-phenylpropanoate degradation | 1323.89 | glycogen degradation II (eukaryotic) | 73616.68 |
| L-arabinose degradation IV | 74892.05 | androstenedione degradation | 903.12 | 3-phenylpropanoate degradation | 72818.29 |
| allantoin degradation IV (anaerobic) | 72441.32 | starch degradation III | 885.67 | methanol oxidation to carbon dioxide | 72616.66 |
| adenosylcobalamin biosynthesis I (early cobalt insertion) | 66990.23 | methylaspartate cycle | 528.99 | methylgallate degradation | 70353.58 |
| vanillin and vanillate degradation II | 66811.15 | formaldehyde assimilation I (serine pathway) | 351.13 | nicotinate degradation I | 69569.46 |
| protocatechuate degradation I (meta-cleavage pathway) | 66126.02 | aerobactin biosynthesis | 319.23 | L-tryptophan degradation IX | 68898.81 |
| glycine betaine degradation I | 65482.37 | glycogen degradation II (eukaryotic) | 186.98 | gallate degradation I | 62856.43 |
| superpathway of vanillin and vanillate degradation | 59779.88 | sucrose biosynthesis I (from photosynthesis) | 114.83 | gallate degradation II | 59382.19 |
| vanillin and vanillate degradation I | 59779.88 | L-lysine fermentation to acetate and butanoate | 55.65 | glycine betaine degradation I | 55709.13 |
| meta cleavage pathway of aromatic compounds | 58100.42 | sucrose biosynthesis III | 34.49 | superpathway of menaquinol-8 biosynthesis II | 55363.19 |
| cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion) | 57700.26 | CMP-legionaminate biosynthesis I | 9.34 | L-tryptophan degradation XII (Geobacillus) | 54452.46 |
| androstenedione degradation | 56887.74 |  | 0.00 | pyrimidine deoxyribonucleotides de novo biosynthesis III | 49641.14 |
| superpathway of menaquinol-8 biosynthesis II | 53537.47 |  | 0.00 | superpathway of aerobic toluene degradation | 48730.67 |
| superpathway of L-threonine metabolism | 53082.01 |  | 0.00 | syringate degradation | 48462.51 |
| L-tryptophan degradation IX | 52286.56 |  | 0.00 | adenosylcobalamin biosynthesis II (late cobalt incorporation) | 48036.81 |
| pyrimidine deoxyribonucleotides de novo biosynthesis III | 49248.63 |  | 0.00 | pyruvate fermentation to acetone | 47516.84 |
| methanol oxidation to carbon dioxide | 48671.56 |  | 0.00 | 2-aminophenol degradation | 44294.97 |
| nicotinate degradation I | 48028.13 |  | 0.00 | mycothiol biosynthesis | 43511.76 |
| L-lysine biosynthesis II | 47354.97 |  | 0.00 | superpathway of L-threonine metabolism | 42772.40 |
| glycerol degradation to butanol | 41964.13 |  | 0.00 | teichoic acid (poly-glycerol) biosynthesis | 38167.54 |
| teichoic acid (poly-glycerol) biosynthesis | 38147.22 |  | 0.00 | superpathway of methylglyoxal degradation | 36171.81 |
| mycothiol biosynthesis | 38120.44 |  | 0.00 | 1,4-dihydroxy-6-naphthoate biosynthesis II | 35466.72 |
| 1,4-dihydroxy-6-naphthoate biosynthesis II | 35099.11 |  | 0.00 | 1,4-dihydroxy-6-naphthoate biosynthesis I | 35196.21 |
| 1,4-dihydroxy-6-naphthoate biosynthesis I | 34972.95 |  | 0.00 | aerobactin biosynthesis | 34964.10 |
| L-tryptophan degradation XII (Geobacillus) | 32317.87 |  | 0.00 | CMP-legionaminate biosynthesis I | 31010.97 |
| superpathway of sulfur oxidation (Acidianus ambivalens) | 31970.45 |  | 0.00 | superpathway of sulfur oxidation (Acidianus ambivalens) | 30736.86 |
| pyruvate fermentation to acetone | 31288.29 |  | 0.00 | L-lysine biosynthesis II | 28058.87 |
| nitrate reduction I (denitrification) | 29872.77 |  | 0.00 | cob(II)yrinate a,c-diamide biosynthesis I (early cobalt insertion) | 26645.37 |
| L-rhamnose degradation II | 28961.54 |  | 0.00 | GDP-D-glycero-alpha-D-manno-heptose biosynthesis | 25270.54 |
| S-methyl-5-thio-alpha-D-ribose 1-phosphate degradation | 25809.72 |  | 0.00 | protocatechuate degradation I (meta-cleavage pathway) | 23861.99 |
| toluene degradation IV (aerobic) (via catechol) | 23481.13 |  | 0.00 | sucrose biosynthesis I (from photosynthesis) | 23341.66 |
| 2-aminophenol degradation | 23401.80 |  | 0.00 | isopropanol biosynthesis | 21636.23 |
| methylaspartate cycle | 22929.65 |  | 0.00 | chlorosalicylate degradation | 21414.61 |
| L-methionine salvage cycle III | 22785.83 |  | 0.00 | superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate) | 20879.39 |
| isopropanol biosynthesis | 22342.09 |  | 0.00 | formaldehyde assimilation I (serine pathway) | 20812.37 |
| 1,5-anhydrofructose degradation | 20891.46 |  | 0.00 | vanillin and vanillate degradation II | 20430.21 |
| formaldehyde assimilation I (serine pathway) | 19719.74 |  | 0.00 | 1,5-anhydrofructose degradation | 20210.18 |
| superpathway of glycerol degradation to 1,3-propanediol | 18398.76 |  | 0.00 | superpathway of vanillin and vanillate degradation | 18273.57 |
| superpathway of aerobic toluene degradation | 16324.11 |  | 0.00 | vanillin and vanillate degradation I | 18273.57 |
| mannan degradation | 15635.15 |  | 0.00 | mannan degradation | 17480.94 |
| ethylmalonyl-CoA pathway | 14171.61 |  | 0.00 | allantoin degradation IV (anaerobic) | 15500.07 |
| sucrose biosynthesis I (from photosynthesis) | 12348.99 |  | 0.00 | superpathway of C1 compounds oxidation to CO2 | 15247.81 |
| chlorosalicylate degradation | 12225.17 |  | 0.00 | mevalonate pathway I | 14827.76 |
| benzoyl-CoA degradation I (aerobic) | 11507.71 |  | 0.00 | S-methyl-5-thio-alpha-D-ribose 1-phosphate degradation | 14768.11 |
| purine nucleobases degradation I (anaerobic) | 9204.93 |  | 0.00 | ethylmalonyl-CoA pathway | 13777.21 |
| biotin biosynthesis II | 8618.67 |  | 0.00 | adenosylcobalamin biosynthesis I (early cobalt insertion) | 13536.16 |
| peptidoglycan biosynthesis II (staphylococci) | 8413.62 |  | 0.00 | L-rhamnose degradation II | 12651.67 |
| chlorophyllide a biosynthesis III (aerobic, light independent) | 8179.43 |  | 0.00 | creatinine degradation II | 11237.15 |
| chlorophyllide a biosynthesis II (anaerobic) | 8179.43 |  | 0.00 | methylaspartate cycle | 10503.26 |
| naphthalene degradation to acetyl-CoA | 8054.27 |  | 0.00 | benzoyl-CoA degradation I (aerobic) | 10351.90 |
| ergothioneine biosynthesis I (bacteria) | 7563.52 |  | 0.00 | purine nucleobases degradation I (anaerobic) | 9879.50 |
| GDP-D-glycero-alpha-D-manno-heptose biosynthesis | 7259.13 |  | 0.00 | ergothioneine biosynthesis I (bacteria) | 9743.10 |
| superpathway of Clostridium acetobutylicum acidogenic fermentation | 7202.99 |  | 0.00 | chlorophyllide a biosynthesis III (aerobic, light independent) | 9657.74 |
| nitrate reduction VI (assimilatory) | 6521.02 |  | 0.00 | chlorophyllide a biosynthesis II (anaerobic) | 9657.74 |
| superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate) | 6144.57 |  | 0.00 | superpathway of sulfolactate degradation | 9222.46 |
| CMP-legionaminate biosynthesis I | 6043.83 |  | 0.00 | L-1,2-propanediol degradation | 9097.92 |
| aerobactin biosynthesis | 6042.77 |  | 0.00 | L-methionine salvage cycle III | 8375.62 |
| coenzyme B biosynthesis | 5660.64 |  | 0.00 | superpathway of taurine degradation | 8370.99 |
| pyruvate fermentation to butanoate | 5612.07 |  | 0.00 | mandelate degradation to acetyl-CoA | 8233.71 |
| naphthalene degradation (aerobic) | 5427.88 |  | 0.00 | sucrose biosynthesis III | 7717.00 |
| L-lysine fermentation to acetate and butanoate | 4783.98 |  | 0.00 | superpathway of Clostridium acetobutylicum acidogenic fermentation | 7621.56 |
| mevalonate pathway I | 4345.36 |  | 0.00 | nitrate reduction VI (assimilatory) | 7360.13 |
| peptidoglycan biosynthesis V (beta-lactam resistance) | 3732.31 |  | 0.00 | coenzyme B biosynthesis | 6339.60 |
| sucrose biosynthesis III | 3721.24 |  | 0.00 | pyrimidine deoxyribonucleotides biosynthesis from CTP | 6075.73 |
| superpathway of bacteriochlorophyll a biosynthesis | 3166.87 |  | 0.00 | pyruvate fermentation to butanoate | 6072.69 |
| superpathway of sulfolactate degradation | 3144.03 |  | 0.00 | starch degradation III | 5572.58 |
| superpathway of C1 compounds oxidation to CO2 | 2923.03 |  | 0.00 | biotin biosynthesis II | 5519.46 |
| chlorophyllide a biosynthesis I (aerobic, light-dependent) | 2056.81 |  | 0.00 | naphthalene degradation to acetyl-CoA | 5180.23 |
| sucrose degradation II (sucrose synthase) | 1853.60 |  | 0.00 | sucrose degradation II (sucrose synthase) | 4799.84 |
| superpathway of mycolyl-arabinogalactan-peptidoglycan complex biosynthesis | 1763.74 |  | 0.00 | isoprene biosynthesis II (engineered) | 4702.37 |
| L-glutamate degradation VIII (to propanoate) | 1606.50 |  | 0.00 | peptidoglycan biosynthesis V (beta-lactam resistance) | 4096.08 |
| mandelate degradation to acetyl-CoA | 1457.43 |  | 0.00 | L-lysine fermentation to acetate and butanoate | 3721.26 |
| starch degradation III | 1426.97 |  | 0.00 | peptidoglycan biosynthesis II (staphylococci) | 3585.70 |
| superpathway of taurine degradation | 1329.14 |  | 0.00 | superpathway of bacteriochlorophyll a biosynthesis | 3365.77 |
| lactose and galactose degradation I | 1294.59 |  | 0.00 | naphthalene degradation (aerobic) | 3244.04 |
| creatinine degradation II | 820.34 |  | 0.00 | nylon-6 oligomer degradation | 2844.79 |
| coenzyme M biosynthesis I | 750.55 |  | 0.00 | chorismate biosynthesis II (archaea) | 2631.21 |
| mycolyl-arabinogalactan-peptidoglycan complex biosynthesis | 743.96 |  | 0.00 | mandelate degradation I | 2592.79 |
| 4-coumarate degradation (anaerobic) | 587.89 |  | 0.00 | chlorophyllide a biosynthesis I (aerobic, light-dependent) | 2410.51 |
| sitosterol degradation to androstenedione | 571.32 |  | 0.00 | L-valine degradation I | 1980.08 |
| phospholipases | 492.05 |  | 0.00 | phospholipases | 1608.81 |
| reductive TCA cycle II | 488.81 |  | 0.00 | superpathway of mycolyl-arabinogalactan-peptidoglycan complex biosynthesis | 1586.25 |
| starch biosynthesis | 431.52 |  | 0.00 | reductive acetyl coenzyme A pathway | 1474.16 |
| 4-hydroxyacetophenone degradation | 409.76 |  | 0.00 | lactose and galactose degradation I | 1204.87 |
| mandelate degradation I | 391.12 |  | 0.00 | mycolyl-arabinogalactan-peptidoglycan complex biosynthesis | 768.13 |
| nylon-6 oligomer degradation | 359.12 |  | 0.00 | superpathway of glycerol degradation to 1,3-propanediol | 736.81 |
| succinate fermentation to butanoate | 351.63 |  | 0.00 | coenzyme M biosynthesis I | 700.95 |
| chitin derivatives degradation | 317.38 |  | 0.00 | succinate fermentation to butanoate | 642.27 |
| reductive acetyl coenzyme A pathway | 313.73 |  | 0.00 | L-glutamate degradation V (via hydroxyglutarate) | 598.07 |
| isoprene biosynthesis II (engineered) | 310.79 |  | 0.00 | sitosterol degradation to androstenedione | 486.81 |
| L-glutamate degradation V (via hydroxyglutarate) | 306.55 |  | 0.00 | glycolysis V (Pyrococcus) | 484.83 |
| nitrifier denitrification | 291.83 |  | 0.00 | superpathway of the 3-hydroxypropanoate cycle | 410.56 |
| mannosylglycerate biosynthesis I | 249.13 |  | 0.00 | superpathway of demethylmenaquinol-6 biosynthesis II | 408.14 |
| L-valine degradation I | 248.04 |  | 0.00 | vitamin B6 degradation | 404.50 |
| glutaryl-CoA degradation | 186.96 |  | 0.00 | glutaryl-CoA degradation | 366.26 |
| chondroitin sulfate degradation I (bacterial) | 128.67 |  | 0.00 | 3-hydroxypropanoate cycle | 365.09 |
| Entner-Doudoroff pathway III (semi-phosphorylative) | 103.40 |  | 0.00 | glyoxylate assimilation | 309.64 |
| glycolysis V (Pyrococcus) | 97.45 |  | 0.00 | 4-coumarate degradation (anaerobic) | 298.94 |
| dTDP-N-acetylviosamine biosynthesis | 80.99 |  | 0.00 | mannosylglycerate biosynthesis I | 297.28 |
| methanogenesis from acetate | 63.15 |  | 0.00 | chitin derivatives degradation | 276.10 |
| dTDP-D-desosamine biosynthesis | 60.75 |  | 0.00 | nitrifier denitrification | 247.43 |
| (5R)-carbapenem carboxylate biosynthesis | 58.66 |  | 0.00 | starch biosynthesis | 236.79 |
| superpathway of erythromycin biosynthesis | 53.46 |  | 0.00 | 4-hydroxyacetophenone degradation | 221.80 |
| superpathway of megalomicin A biosynthesis | 53.46 |  | 0.00 | L-glutamate degradation VIII (to propanoate) | 211.67 |
| erythromycin D biosynthesis | 48.60 |  | 0.00 | reductive TCA cycle II | 198.71 |
| superpathway of erythromycin biosynthesis (without sugar biosynthesis) | 46.73 |  | 0.00 | beta-alanine biosynthesis II | 190.85 |
| vitamin B6 degradation | 42.00 |  | 0.00 | D-galacturonate degradation II | 167.03 |
| superpathway of the 3-hydroxypropanoate cycle | 37.43 |  | 0.00 | chondroitin sulfate degradation I (bacterial) | 151.46 |
| beta-alanine biosynthesis II | 37.17 |  | 0.00 | toluene degradation V (aerobic) (via toluene-cis-diol) | 128.71 |
| 3-hydroxypropanoate cycle | 33.84 |  | 0.00 | Entner-Doudoroff pathway III (semi-phosphorylative) | 103.21 |
| coumarins biosynthesis (engineered) | 29.63 |  | 0.00 | methanogenesis from acetate | 87.76 |
| D-galacturonate degradation II | 27.75 |  | 0.00 | (5R)-carbapenem carboxylate biosynthesis | 57.46 |
| glyoxylate assimilation | 26.74 |  | 0.00 | neopentalenoketolactone and pentalenate biosynthesis | 56.96 |
| neopentalenoketolactone and pentalenate biosynthesis | 25.37 |  | 0.00 | UTP and CTP dephosphorylation I | 32.79 |
| pyrimidine deoxyribonucleotides biosynthesis from CTP | 25.00 |  | 0.00 | pyrimidine deoxyribonucleotides de novo biosynthesis IV | 31.34 |
| mevalonate pathway II (archaea) | 21.31 |  | 0.00 | dTDP-N-acetylviosamine biosynthesis | 25.81 |
| pentalenolactone biosynthesis | 18.21 |  | 0.00 | biphenyl degradation | 22.89 |
| pyrimidine deoxyribonucleotides de novo biosynthesis IV | 17.50 |  | 0.00 | dTDP-D-desosamine biosynthesis | 19.43 |
| toluene degradation V (aerobic) (via toluene-cis-diol) | 11.89 |  | 0.00 | pentalenolactone biosynthesis | 18.98 |
| chorismate biosynthesis II (archaea) | 8.00 |  | 0.00 | superpathway of megalomicin A biosynthesis | 17.13 |
| superpathway of demethylmenaquinol-6 biosynthesis II | 6.70 |  | 0.00 | superpathway of erythromycin biosynthesis | 17.13 |
| biphenyl degradation | 6.21 |  | 0.00 | erythromycin D biosynthesis | 15.60 |
| spirilloxanthin and 2,2'-diketo-spirilloxanthin biosynthesis | 3.00 |  | 0.00 | superpathway of erythromycin biosynthesis (without sugar biosynthesis) | 15.00 |
| paromamine biosynthesis I | 1.00 |  | 0.00 | mevalonate pathway II (archaea) | 12.25 |
| benzoyl-CoA degradation II (anaerobic) | 0.64 |  | 0.00 | benzoyl-CoA degradation II (anaerobic) | 1.87 |
|  | 0.00 |  | 0.00 | paromamine biosynthesis I | 1.00 |