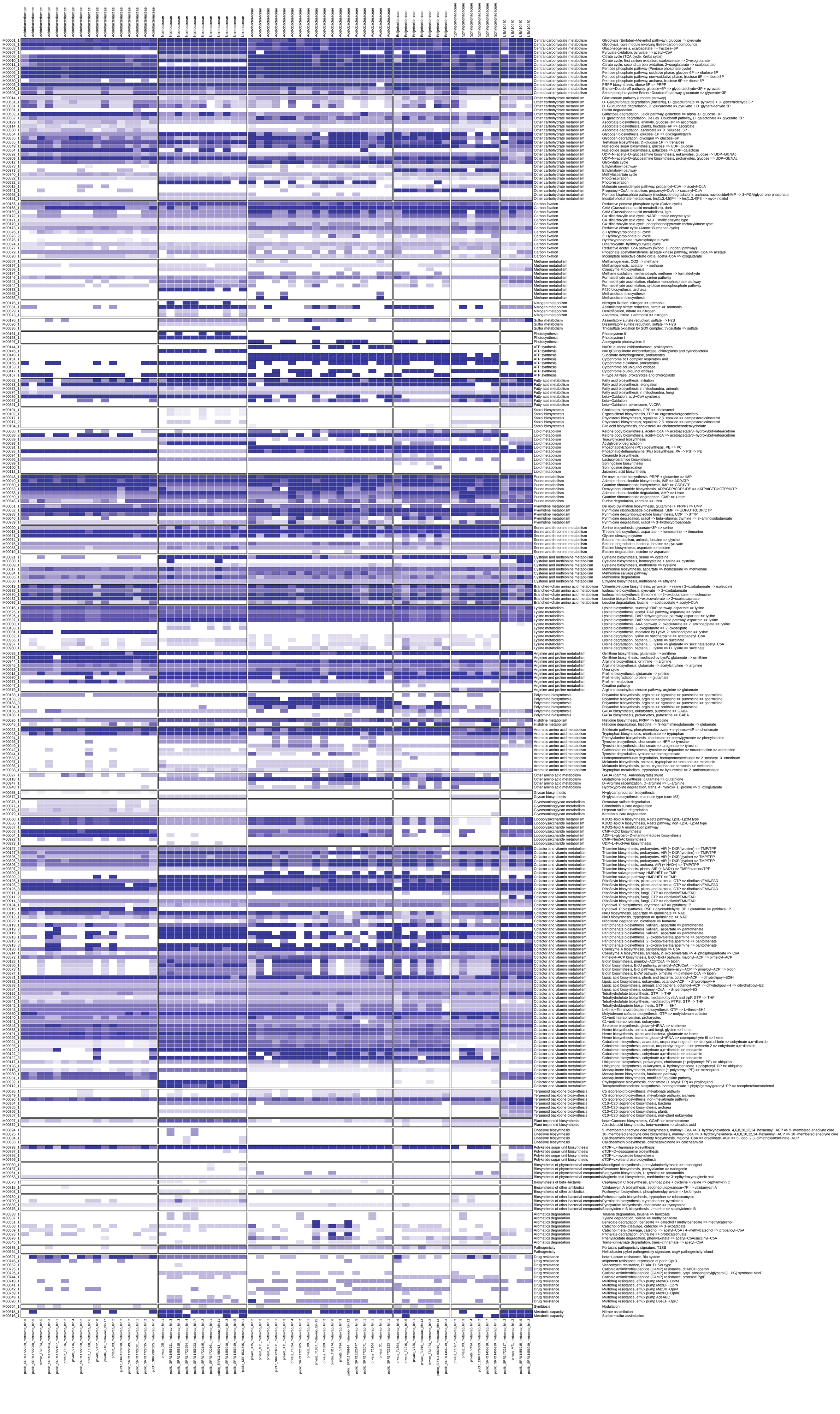
Module completeness
1
0.5
0
M00001_1 Central carbohydrate metabolism Glycolysis (Embden−Meyerhof pathway), glucose => pyruvate
M00002_1 Central carbohydrate metabolism Glycolysis, core module involving three−carbon compounds
M00003_1 Central carbohydrate metabolism Gluconeogenesis, oxaloacetate => fructose−6P
M00307_1 Central carbohydrate metabolism Pyruvate oxidation, pyruvate => acetyl−CoA
M00009_1 Central carbohydrate metabolism Citrate cycle (TCA cycle, Krebs cycle)
M00010_1 Central carbohydrate metabolism Citrate cycle, first carbon oxidation, oxaloacetate => 2−oxoglutarate
M00011_1 Central carbohydrate metabolism Citrate cycle, second carbon oxidation, 2−oxoglutarate => oxaloacetate
M00004_1 Central carbohydrate metabolism Pentose phosphate pathway (Pentose phosphate cycle)
M00006_1 Central carbohydrate metabolism Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P
M00007_1 Central carbohydrate metabolism Pentose phosphate pathway, non−oxidative phase, fructose 6P => ribose 5P
M00580_1 Central carbohydrate metabolism Pentose phosphate pathway, archaea, fructose 6P => ribose 5P
M00005_1 Central carbohydrate metabolism PRPP biosynthesis, ribose 5P => PRPP
M00008_1 Central carbohydrate metabolism Entner−Doudoroff pathway, glucose−6P => glyceraldehyde−3P + pyruvate
M00308_1 Central carbohydrate metabolism Semi−phosphorylative Entner−Doudoroff pathway, gluconate => glycerate−3P
M00014_1 Other carbohydrate metabolism Glucuronate pathway (uronate pathway)
M00631_1 Other carbohydrate metabolism D−Galacturonate degradation (bacteria), D−galacturonate => pyruvate + D−glyceraldehyde 3P
M00061_1 Other carbohydrate metabolism D−Glucuronate degradation, D−glucuronate => pyruvate + D−glyceraldehyde 3P
M00081_1 Other carbohydrate metabolism Pectin degradation
M00632_1 Other carbohydrate metabolism Galactose degradation, Leloir pathway, galactose => alpha−D−glucose−1P
M00552_1 Other carbohydrate metabolism D−galactonate degradation, De Ley−Doudoroff pathway, D−galactonate => glycerate−3P
M00129_1 Other carbohydrate metabolism Ascorbate biosynthesis, animals, glucose−1P => ascorbate
M00114_1 Other carbohydrate metabolism Ascorbate biosynthesis, plants, fructose−6P => ascorbate
M00550_1 Other carbohydrate metabolism Ascorbate degradation, ascorbate => D−xylulose−5P
M00854_1 Other carbohydrate metabolism Glycogen biosynthesis, glucose−1P => glycogen/starch
M00855_1 Other carbohydrate metabolism Glycogen degradation, glycogen => glucose−6P
M00565_1 Other carbohydrate metabolism Trehalose biosynthesis, D−glucose 1P => trehalose
M00549_1 Other carbohydrate metabolism Nucleotide sugar biosynthesis, glucose => UDP−glucose
M00554_1 Other carbohydrate metabolism Nucleotide sugar biosynthesis, galactose => UDP−galactose
M00892_1 Other carbohydrate metabolism UDP−N−acetyl−D−glucosamine biosynthesis, eukaryotes, glucose => UDP−GlcNAc
M00909_1 Other carbohydrate metabolism UDP−N−acetyl−D−glucosamine biosynthesis, prokaryotes, glucose => UDP−GlcNAc
M00012_1 Other carbohydrate metabolism Glyoxylate cycle
M00373_1 Other carbohydrate metabolism Ethylmalonyl pathway
M00373_2 Other carbohydrate metabolism Ethylmalonyl pathway
M00740_1 Other carbohydrate metabolism Methylaspartate cycle
M00532_1 Other carbohydrate metabolism Photorespiration
M00532_2 Other carbohydrate metabolism Photorespiration
M00013_1 Other carbohydrate metabolism Malonate semialdehyde pathway, propanoyl−CoA => acetyl−CoA
M00741_1 Other carbohydrate metabolism Propanoyl−CoA metabolism, propanoyl−CoA => succinyl−CoA
M00968_1 Other carbohydrate metabolism Pentose bisphosphate pathway (nucleoside degradation), archaea, nucleoside/NMP => 3−PGA/glycerone phosphate
M00131_1 Other carbohydrate metabolism Inositol phosphate metabolism, Ins(1,3,4,5)P4 => Ins(1,3,4)P3 => myo−inositol
M00165_1 Carbon fixation Reductive pentose phosphate cycle (Calvin cycle)
M00168_1 Carbon fixation CAM (Crassulacean acid metabolism), dark
M00169_1 Carbon fixation CAM (Crassulacean acid metabolism), light
M00172_1 Carbon fixation C4−dicarboxylic acid cycle, NADP − malic enzyme type
M00171_1 Carbon fixation C4−dicarboxylic acid cycle, NAD − malic enzyme type
M00170_1 Carbon fixation C4−dicarboxylic acid cycle, phosphoenolpyruvate carboxykinase type
M00173_1 Carbon fixation Reductive citrate cycle (Arnon−Buchanan cycle)
M00376_1 Carbon fixation 3−Hydroxypropionate bi−cycle
M00376_2 Carbon fixation 3−Hydroxypropionate bi−cycle
M00375_1 Carbon fixation Hydroxypropionate−hydroxybutylate cycle
M00374_1 Carbon fixation Dicarboxylate−hydroxybutyrate cycle
M00377_1 Carbon fixation Reductive acetyl−CoA pathway (Wood−Ljungdahl pathway)
M00579_1 Carbon fixation Phosphate acetyltransferase−acetate kinase pathway, acetyl−CoA => acetate
M00620_1 Carbon fixation Incomplete reductive citrate cycle, acetyl−CoA => oxoglutarate
M00567_1 Methane metabolism Methanogenesis, CO2 => methane
M00357_1 Methane metabolism Methanogenesis, acetate => methane
M00358_1 Methane metabolism Coenzyme M biosynthesis
M00174_1 Methane metabolism Methane oxidation, methanotroph, methane => formaldehyde
M00346_1 Methane metabolism Formaldehyde assimilation, serine pathway
M00345_1 Methane metabolism Formaldehyde assimilation, ribulose monophosphate pathway
M00344_1 Methane metabolism Formaldehyde assimilation, xylulose monophosphate pathway
M00378_1 Methane metabolism F420 biosynthesis, archaea
M00935_1 Methane metabolism Methanofuran biosynthesis
M00935_3 Methane metabolism Methanofuran biosynthesis
M00175_1 Nitrogen metabolism Nitrogen fixation, nitrogen => ammonia
M00531_1 Nitrogen metabolism Assimilatory nitrate reduction, nitrate => ammonia
M00529_1 Nitrogen metabolism Denitrification, nitrate => nitrogen
M00973_1 Nitrogen metabolism Anammox, nitrite + ammonia => nitrogen
M00176_1 Sulfur metabolism Assimilatory sulfate reduction, sulfate => H2S
M00596_1 Sulfur metabolism Dissimilatory sulfate reduction, sulfate => H2S
M00595_1 Sulfur metabolism Thiosulfate oxidation by SOX complex, thiosulfate => sulfate
M00161_1 Photosynthesis Photosystem II
M00163_1 Photosynthesis Photosystem I
M00597_1 Photosynthesis Anoxygenic photosystem II
M00144_1 ATP synthesis NADH:quinone oxidoreductase, prokaryotes
M00145_1 ATP synthesis NAD(P)H:quinone oxidoreductase, chloroplasts and cyanobacteria
M00149_1 ATP synthesis Succinate dehydrogenase, prokaryotes
M00151_1 ATP synthesis Cytochrome bc1 complex respiratory unit
M00155_1 ATP synthesis Cytochrome c oxidase, prokaryotes
M00153_1 ATP synthesis Cytochrome bd ubiquinol oxidase
M00417_1 ATP synthesis Cytochrome o ubiquinol oxidase
M00157_1 ATP synthesis F−type ATPase, prokaryotes and chloroplasts
M00082_1 Fatty acid metabolism Fatty acid biosynthesis, initiation
M00083_1 Fatty acid metabolism Fatty acid biosynthesis, elongation
M00873_1 Fatty acid metabolism Fatty acid biosynthesis in mitochondria, animals
M00874_1 Fatty acid metabolism Fatty acid biosynthesis in mitochondria, fungi
M00086_1 Fatty acid metabolism beta−Oxidation, acyl−CoA synthesis
M00087_1 Fatty acid metabolism beta−Oxidation
M00861_1 Fatty acid metabolism beta−Oxidation, peroxisome, VLCFA
M00101_1 Sterol biosynthesis Cholesterol biosynthesis, FPP => cholesterol
M00102_1 Sterol biosynthesis Ergocalciferol biosynthesis, FPP => ergosterol/ergocalciferol
M00917_1 Sterol biosynthesis Phytosterol biosynthesis, squalene 2,3−epoxide => campesterol/sitosterol
M00917_2 Sterol biosynthesis Phytosterol biosynthesis, squalene 2,3−epoxide => campesterol/sitosterol
M00104_1 Sterol biosynthesis Bile acid biosynthesis, cholesterol => cholate/chenodeoxycholate
M00088_1 Lipid metabolism Ketone body biosynthesis, acetyl−CoA => acetoacetate/3−hydroxybutyrate/acetone
M00088_2 Lipid metabolism Ketone body biosynthesis, acetyl−CoA => acetoacetate/3−hydroxybutyrate/acetone
M00089_1 Lipid metabolism Triacylglycerol biosynthesis
M00098_1 Lipid metabolism Acylglycerol degradation
M00091_1 Lipid metabolism Phosphatidylcholine (PC) biosynthesis, PE => PC
M00093_1 Lipid metabolism Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE
M00094_1 Lipid metabolism Ceramide biosynthesis
M00066_1 Lipid metabolism Lactosylceramide biosynthesis
M00099_1 Lipid metabolism Sphingosine biosynthesis
M00100_1 Lipid metabolism Sphingosine degradation
M00113_1 Lipid metabolism Jasmonic acid biosynthesis
M00048_1 Purine metabolism De novo purine biosynthesis, PRPP + glutamine => IMP
M00049_1 Purine metabolism Adenine ribonucleotide biosynthesis, IMP => ADP,ATP
M00050_1 Purine metabolism Guanine ribonucleotide biosynthesis, IMP => GDP,GTP
M00053_1 Purine metabolism Deoxyribonucleotide biosynthesis, ADP/GDP/CDP/UDP => dATP/dGTP/dCTP/dUTP
M00958_1 Purine metabolism Adenine ribonucleotide degradation, AMP => Urate
M00959_1 Purine metabolism Guanine ribonucleotide degradation, GMP => Urate
M00546_1 Purine metabolism Purine degradation, xanthine => urea
M00051_1 Pyrimidine metabolism De novo pyrimidine biosynthesis, glutamine (+ PRPP) => UMP
M00052_1 Pyrimidine metabolism Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP
M00938_1 Pyrimidine metabolism Pyrimidine deoxyribonucleotide biosynthesis, UDP => dTTP
M00046_1 Pyrimidine metabolism Pyrimidine degradation, uracil => beta−alanine, thymine => 3−aminoisobutanoate
M00939_1 Pyrimidine metabolism Pyrimidine degradation, uracil => 3−hydroxypropanoate
M00020_1 Serine and threonine metabolism Serine biosynthesis, glycerate−3P => serine
M00018_1 Serine and threonine metabolism Threonine biosynthesis, aspartate => homoserine => threonine
M00621_1 Serine and threonine metabolism Glycine cleavage system
M00974_1 Serine and threonine metabolism Betaine metabolism, animals, betaine => glycine
M00975_1 Serine and threonine metabolism Betaine degradation, bacteria, betaine => pyruvate
M00033_1 Serine and threonine metabolism Ectoine biosynthesis, aspartate => ectoine
M00919_1 Serine and threonine metabolism Ectoine degradation, ectoine => aspartate
M00021_1 Cysteine and methionine metabolism Cysteine biosynthesis, serine => cysteine
M00338_1 Cysteine and methionine metabolism Cysteine biosynthesis, homocysteine + serine => cysteine
M00609_1 Cysteine and methionine metabolism Cysteine biosynthesis, methionine => cysteine
M00017_1 Cysteine and methionine metabolism Methionine biosynthesis, aspartate => homoserine => methionine
M00034_1 Cysteine and methionine metabolism Methionine salvage pathway
M00035_1 Cysteine and methionine metabolism Methionine degradation
M00368_1 Cysteine and methionine metabolism Ethylene biosynthesis, methionine => ethylene
M00019_1 Branched−chain amino acid metabolism Valine/isoleucine biosynthesis, pyruvate => valine / 2−oxobutanoate => isoleucine
M00535_1 Branched−chain amino acid metabolism Isoleucine biosynthesis, pyruvate => 2−oxobutanoate
M00570_1 Branched−chain amino acid metabolism Isoleucine biosynthesis, threonine => 2−oxobutanoate => isoleucine
M00432_1 Branched−chain amino acid metabolism Leucine biosynthesis, 2−oxoisovalerate => 2−oxoisocaproate
M00036_1 Branched−chain amino acid metabolism Leucine degradation, leucine => acetoacetate + acetyl−CoA
M00016_1 Lysine metabolism Lysine biosynthesis, succinyl−DAP pathway, aspartate => lysine
M00525_1 Lysine metabolism Lysine biosynthesis, acetyl−DAP pathway, aspartate => lysine
M00526_1 Lysine metabolism Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine
M00527_1 Lysine metabolism Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine
M00030_1 Lysine metabolism Lysine biosynthesis, AAA pathway, 2−oxoglutarate => 2−aminoadipate => lysine
M00433_1 Lysine metabolism Lysine biosynthesis, 2−oxoglutarate => 2−oxoadipate
M00031_1 Lysine metabolism Lysine biosynthesis, mediated by LysW, 2−aminoadipate => lysine
M00032_1 Lysine metabolism Lysine degradation, lysine => saccharopine => acetoacetyl−CoA
M00956_1 Lysine metabolism Lysine degradation, bacteria, L−lysine => succinate
M00957_1 Lysine metabolism Lysine degradation, bacteria, L−lysine => glutarate => succinate/acetyl−CoA
M00960_1 Lysine metabolism Lysine degradation, bacteria, L−lysine => D−lysine => succinate
M00028_1 Arginine and proline metabolism Ornithine biosynthesis, glutamate => ornithine
M00763_1 Arginine and proline metabolism Ornithine biosynthesis, mediated by LysW, glutamate => ornithine
M00844_1 Arginine and proline metabolism Arginine biosynthesis, ornithine => arginine
M00845_1 Arginine and proline metabolism Arginine biosynthesis, glutamate => acetylcitrulline => arginine
M00029_1 Arginine and proline metabolism Urea cycle
M00015_1 Arginine and proline metabolism Proline biosynthesis, glutamate => proline
M00970_1 Arginine and proline metabolism Proline degradation, proline => glutamate
M00972_1 Arginine and proline metabolism Proline metabolism
M00047_1 Arginine and proline metabolism Creatine pathway
M00879_1 Arginine and proline metabolism Arginine succinyltransferase pathway, arginine => glutamate
M00133_1 Polyamine biosynthesis Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine
M00133_2 Polyamine biosynthesis Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine
M00133_3 Polyamine biosynthesis Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine
M00134_1 Polyamine biosynthesis Polyamine biosynthesis, arginine => ornithine => putrescine
M00135_1 Polyamine biosynthesis GABA biosynthesis, eukaryotes, putrescine => GABA
M00136_1 Polyamine biosynthesis GABA biosynthesis, prokaryotes, putrescine => GABA
M00026_1 Histidine metabolism Histidine biosynthesis, PRPP => histidine
M00045_1 Histidine metabolism Histidine degradation, histidine => N−formiminoglutamate => glutamate
M00022_1 Aromatic amino acid metabolism Shikimate pathway, phosphoenolpyruvate + erythrose−4P => chorismate
M00023_1 Aromatic amino acid metabolism Tryptophan biosynthesis, chorismate => tryptophan
M00024_1 Aromatic amino acid metabolism Phenylalanine biosynthesis, chorismate => phenylpyruvate => phenylalanine
M00025_1 Aromatic amino acid metabolism Tyrosine biosynthesis, chorismate => HPP => tyrosine
M00040_1 Aromatic amino acid metabolism Tyrosine biosynthesis, chorismate => arogenate => tyrosine
M00042_1 Aromatic amino acid metabolism Catecholamine biosynthesis, tyrosine => dopamine => noradrenaline => adrenaline
M00044_1 Aromatic amino acid metabolism Tyrosine degradation, tyrosine => homogentisate
M00533_1 Aromatic amino acid metabolism Homoprotocatechuate degradation, homoprotocatechuate => 2−oxohept−3−enedioate
M00037_1 Aromatic amino acid metabolism Melatonin biosynthesis, animals, tryptophan => serotonin => melatonin
M00936_1 Aromatic amino acid metabolism Melatonin biosynthesis, plants, tryptophan => serotonin => melatonin
M00038_1 Aromatic amino acid metabolism Tryptophan metabolism, tryptophan => kynurenine => 2−aminomuconate
M00027_1 Other amino acid metabolism GABA (gamma−Aminobutyrate) shunt
M00118_1 Other amino acid metabolism Glutathione biosynthesis, glutamate => glutathione
M00947_1 Other amino acid metabolism D−Arginine racemization, D−arginine => L−arginine
M00948_1 Other amino acid metabolism Hydroxyproline degradation, trans−4−hydroxy−L−proline => 2−oxoglutarate
M00055_1 Glycan biosynthesis N−glycan precursor biosynthesis
M00872_1 Glycan biosynthesis O−glycan biosynthesis, mannose type (core M3)
M00076_1 Glycosaminoglycan metabolism Dermatan sulfate degradation
M00077_1 Glycosaminoglycan metabolism Chondroitin sulfate degradation
M00078_1 Glycosaminoglycan metabolism Heparan sulfate degradation
M00079_1 Glycosaminoglycan metabolism Keratan sulfate degradation
M00060_1 Lipopolysaccharide metabolism KDO2−lipid A biosynthesis, Raetz pathway, LpxL−LpxM type
M00866_1 Lipopolysaccharide metabolism KDO2−lipid A biosynthesis, Raetz pathway, non−LpxL−LpxM type
M00867_1 Lipopolysaccharide metabolism KDO2−lipid A modification pathway
M00063_1 Lipopolysaccharide metabolism CMP−KDO biosynthesis
M00064_1 Lipopolysaccharide metabolism ADP−L−glycero−D−manno−heptose biosynthesis
M00922_1 Lipopolysaccharide metabolism CMP−Neu5Ac biosynthesis
M00923_1 Lipopolysaccharide metabolism UDP−L−FucNAm biosynthesis
M00127_2 Cofactor and vitamin metabolism Thiamine biosynthesis, prokaryotes, AIR (+ DXP/tyrosine) => TMP/TPP
M00127_3 Cofactor and vitamin metabolism Thiamine biosynthesis, prokaryotes, AIR (+ DXP/tyrosine) => TMP/TPP
M00895_2 Cofactor and vitamin metabolism Thiamine biosynthesis, prokaryotes, AIR (+ DXP/glycine) => TMP/TPP
M00895_3 Cofactor and vitamin metabolism Thiamine biosynthesis, prokaryotes, AIR (+ DXP/glycine) => TMP/TPP
M00896_2 Cofactor and vitamin metabolism Thiamine biosynthesis, archaea, AIR (+ NAD+) => TMP/TPP
M00897_2 Cofactor and vitamin metabolism Thiamine biosynthesis, plants, AIR (+ NAD+) => TMP/thiamine/TPP
M00899_1 Cofactor and vitamin metabolism Thiamine salvage pathway, HMP/HET => TMP
M00899_2 Cofactor and vitamin metabolism Thiamine salvage pathway, HMP/HET => TMP
M00125_1 Cofactor and vitamin metabolism Riboflavin biosynthesis, plants and bacteria, GTP => riboflavin/FMN/FAD
M00125_2 Cofactor and vitamin metabolism Riboflavin biosynthesis, plants and bacteria, GTP => riboflavin/FMN/FAD
M00125_3 Cofactor and vitamin metabolism Riboflavin biosynthesis, plants and bacteria, GTP => riboflavin/FMN/FAD
M00911_1 Cofactor and vitamin metabolism Riboflavin biosynthesis, fungi, GTP => riboflavin/FMN/FAD
M00911_2 Cofactor and vitamin metabolism Riboflavin biosynthesis, fungi, GTP => riboflavin/FMN/FAD
M00911_3 Cofactor and vitamin metabolism Riboflavin biosynthesis, fungi, GTP => riboflavin/FMN/FAD
M00124_1 Cofactor and vitamin metabolism Pyridoxal−P biosynthesis, erythrose−4P => pyridoxal−P
M00916_1 Cofactor and vitamin metabolism Pyridoxal−P biosynthesis, R5P + glyceraldehyde−3P + glutamine => pyridoxal−P
M00115_1 Cofactor and vitamin metabolism NAD biosynthesis, aspartate => quinolinate => NAD
M00912_1 Cofactor and vitamin metabolism NAD biosynthesis, tryptophan => quinolinate => NAD
M00622_1 Cofactor and vitamin metabolism Nicotinate degradation, nicotinate => fumarate
M00119_1 Cofactor and vitamin metabolism Pantothenate biosynthesis, valine/L−aspartate => pantothenate
M00119_2 Cofactor and vitamin metabolism Pantothenate biosynthesis, valine/L−aspartate => pantothenate
M00119_3 Cofactor and vitamin metabolism Pantothenate biosynthesis, valine/L−aspartate => pantothenate
M00913_1 Cofactor and vitamin metabolism Pantothenate biosynthesis, 2−oxoisovalerate/spermine => pantothenate
M00913_2 Cofactor and vitamin metabolism Pantothenate biosynthesis, 2−oxoisovalerate/spermine => pantothenate
M00913_3 Cofactor and vitamin metabolism Pantothenate biosynthesis, 2−oxoisovalerate/spermine => pantothenate
M00120_1 Cofactor and vitamin metabolism Coenzyme A biosynthesis, pantothenate => CoA
M00914_1 Cofactor and vitamin metabolism Coenzyme A biosynthesis, archaea, 2−oxoisovalerate => 4−phosphopantoate => CoA
M00572_1 Cofactor and vitamin metabolism Pimeloyl−ACP biosynthesis, BioC−BioH pathway, malonyl−ACP => pimeloyl−ACP
M00123_1 Cofactor and vitamin metabolism Biotin biosynthesis, pimeloyl−ACP/CoA => biotin
M00950_1 Cofactor and vitamin metabolism Biotin biosynthesis, BioU pathway, pimeloyl−ACP/CoA => biotin
M00573_1 Cofactor and vitamin metabolism Biotin biosynthesis, BioI pathway, long−chain−acyl−ACP => pimeloyl−ACP => biotin
M00577_1 Cofactor and vitamin metabolism Biotin biosynthesis, BioW pathway, pimelate => pimeloyl−CoA => biotin
M00881_1 Cofactor and vitamin metabolism Lipoic acid biosynthesis, plants and bacteria, octanoyl−ACP => dihydrolipoyl−E2/H
M00882_1 Cofactor and vitamin metabolism Lipoic acid biosynthesis, eukaryotes, octanoyl−ACP => dihydrolipoyl−H
M00883_1 Cofactor and vitamin metabolism Lipoic acid biosynthesis, animals and bacteria, octanoyl−ACP => dihydrolipoyl−H => dihydrolipoyl−E2
M00884_1 Cofactor and vitamin metabolism Lipoic acid biosynthesis, octanoyl−CoA => dihydrolipoyl−E2
M00126_1 Cofactor and vitamin metabolism Tetrahydrofolate biosynthesis, GTP => THF
M00840_1 Cofactor and vitamin metabolism Tetrahydrofolate biosynthesis, mediated by ribA and trpF, GTP => THF
M00841_1 Cofactor and vitamin metabolism Tetrahydrofolate biosynthesis, mediated by PTPS, GTP => THF
M00842_1 Cofactor and vitamin metabolism Tetrahydrobiopterin biosynthesis, GTP => BH4
M00843_1 Cofactor and vitamin metabolism L−threo−Tetrahydrobiopterin biosynthesis, GTP => L−threo−BH4
M00880_1 Cofactor and vitamin metabolism Molybdenum cofactor biosynthesis, GTP => molybdenum cofactor
M00140_1 Cofactor and vitamin metabolism C1−unit interconversion, prokaryotes
M00141_1 Cofactor and vitamin metabolism C1−unit interconversion, eukaryotes
M00846_1 Cofactor and vitamin metabolism Siroheme biosynthesis, glutamyl−tRNA => siroheme
M00868_1 Cofactor and vitamin metabolism Heme biosynthesis, animals and fungi, glycine => heme
M00121_1 Cofactor and vitamin metabolism Heme biosynthesis, plants and bacteria, glutamate => heme
M00926_1 Cofactor and vitamin metabolism Heme biosynthesis, bacteria, glutamyl−tRNA => coproporphyrin III => heme
M00924_1 Cofactor and vitamin metabolism Cobalamin biosynthesis, anaerobic, uroporphyrinogen III => sirohydrochlorin => cobyrinate a,c−diamide
M00925_1 Cofactor and vitamin metabolism Cobalamin biosynthesis, aerobic, uroporphyrinogen III => precorrin 2 => cobyrinate a,c−diamide
M00122_1 Cofactor and vitamin metabolism Cobalamin biosynthesis, cobyrinate a,c−diamide => cobalamin
M00122_2 Cofactor and vitamin metabolism Cobalamin biosynthesis, cobyrinate a,c−diamide => cobalamin
M00122_3 Cofactor and vitamin metabolism Cobalamin biosynthesis, cobyrinate a,c−diamide => cobalamin
M00117_1 Cofactor and vitamin metabolism Ubiquinone biosynthesis, prokaryotes, chorismate (+ polyprenyl−PP) => ubiquinol
M00128_1 Cofactor and vitamin metabolism Ubiquinone biosynthesis, eukaryotes, 4−hydroxybenzoate + polyprenyl−PP => ubiquinol
M00116_1 Cofactor and vitamin metabolism Menaquinone biosynthesis, chorismate (+ polyprenyl−PP) => menaquinol
M00930_1 Cofactor and vitamin metabolism Menaquinone biosynthesis, futalosine pathway
M00931_1 Cofactor and vitamin metabolism Menaquinone biosynthesis, modified futalosine pathway
M00932_1 Cofactor and vitamin metabolism Phylloquinone biosynthesis, chorismate (+ phytyl−PP) => phylloquinol
M00112_1 Cofactor and vitamin metabolism Tocopherol/tocotorienol biosynthesis, homogentisate + phytyl/geranylgeranyl−PP => tocopherol/tocotorienol
M00095_1 Terpenoid backbone biosynthesis C5 isoprenoid biosynthesis, mevalonate pathway
M00849_1 Terpenoid backbone biosynthesis C5 isoprenoid biosynthesis, mevalonate pathway, archaea
M00096_1 Terpenoid backbone biosynthesis C5 isoprenoid biosynthesis, non−mevalonate pathway
M00364_1 Terpenoid backbone biosynthesis C10−C20 isoprenoid biosynthesis, bacteria
M00365_1 Terpenoid backbone biosynthesis C10−C20 isoprenoid biosynthesis, archaea
M00366_1 Terpenoid backbone biosynthesis C10−C20 isoprenoid biosynthesis, plants
M00367_1 Terpenoid backbone biosynthesis C10−C20 isoprenoid biosynthesis, non−plant eukaryotes
M00097_1 Plant terpenoid biosynthesis beta−Carotene biosynthesis, GGAP => beta−carotene
M00372_1 Plant terpenoid biosynthesis Abscisic acid biosynthesis, beta−carotene => abscisic acid
M00824_1 Enediyne biosynthesis 9−membered enediyne core biosynthesis, malonyl−CoA => 3−hydroxyhexadeca−4,6,8,10,12,14−hexaenoyl−ACP => 9−membered enediyne core
M00825_1 Enediyne biosynthesis 10−membered enediyne core biosynthesis, malonyl−CoA => 3−hydroxyhexadeca−4,6,8,10,12,14−hexaenoyl−ACP => 10−membered enediyne core
M00834_1 Enediyne biosynthesis Calicheamicin orsellinate moiety biosynthesis, malonyl−CoA => orsellinate−ACP => 5−iodo−2,3−dimethoxyorsellinate−ACP
M00833_1 Enediyne biosynthesis Calicheamicin biosynthesis, calicheamicinone => calicheamicin
M00793_1 Polyketide sugar unit biosynthesis dTDP−L−rhamnose biosynthesis
M00797_1 Polyketide sugar unit biosynthesis dTDP−D−desosamine biosynthesis
M00798_1 Polyketide sugar unit biosynthesis dTDP−L−mycarose biosynthesis
M00799_1 Polyketide sugar unit biosynthesis dTDP−L−oleandrose biosynthesis
M00039_1 Biosynthesis of phytochemical compounds Monolignol biosynthesis, phenylalanine/tyrosine => monolignol
M00137_1 Biosynthesis of phytochemical compounds Flavanone biosynthesis, phenylalanine => naringenin
M00961_1 Biosynthesis of phytochemical compounds Betacyanin biosynthesis, L−tyrosine => amaranthin
M00953_1 Biosynthesis of phytochemical compounds Mugineic acid biosynthesis, methionine => 3−epihydroxymugineic acid
M00673_1 Biosynthesis of beta−lactams Cephamycin C biosynthesis, aminoadipate + cysteine + valine => cephamycin C
M00815_1 Biosynthesis of other antibiotics Validamycin A biosynthesis, sedoheptulopyranose−7P => validamycin A
M00903_1 Biosynthesis of other antibiotics Fosfomycin biosynthesis, phosphoenolpyruvate => fosfomycin
M00789_1 Biosynthesis of other bacterial compounds Rebeccamycin biosynthesis, tryptophan => rebeccamycin
M00790_1 Biosynthesis of other bacterial compounds Pyrrolnitrin biosynthesis, tryptophan => pyrrolnitrin
M00835_1 Biosynthesis of other bacterial compounds Pyocyanine biosynthesis, chorismate => pyocyanine
M00875_1 Biosynthesis of other bacterial compounds Staphyloferrin B biosynthesis, L−serine => staphyloferrin B
M00538_1 Aromatics degradation Toluene degradation, toluene => benzoate
M00537_1 Aromatics degradation Xylene degradation, xylene => methylbenzoate
M00551_1 Aromatics degradation Benzoate degradation, benzoate => catechol / methylbenzoate => methylcatechol
M00568_1 Aromatics degradation Catechol ortho−cleavage, catechol => 3−oxoadipate
M00569_1 Aromatics degradation Catechol meta−cleavage, catechol => acetyl−CoA / 4−methylcatechol => propanoyl−CoA
M00623_1 Aromatics degradation Phthalate degradation, phthalate => protocatechuate
M00878_1 Aromatics degradation Phenylacetate degradation, phenylaxetate => acetyl−CoA/succinyl−CoA
M00545_1 Aromatics degradation Trans−cinnamate degradation, trans−cinnamate => acetyl−CoA
M00575_1 Pathogenicity Pertussis pathogenicity signature, T1SS
M00564_1 Pathogenicity Helicobacter pylori pathogenicity signature, cagA pathogenicity island
M00627_1 Drug resistance beta−Lactam resistance, Bla system
M00745_1 Drug resistance Imipenem resistance, repression of porin OprD
M00652_1 Drug resistance Vancomycin resistance, D−Ala−D−Ser type
M00725_1 Drug resistance Cationic antimicrobial peptide (CAMP) resistance, dltABCD operon
M00726_1 Drug resistance Cationic antimicrobial peptide (CAMP) resistance, lysyl−phosphatidylglycerol (L−PG) synthase MprF
M00744_1 Drug resistance Cationic antimicrobial peptide (CAMP) resistance, protease PgtE
M00718_1 Drug resistance Multidrug resistance, efflux pump MexAB−OprM
M00641_1 Drug resistance Multidrug resistance, efflux pump MexEF−OprN
M00642_1 Drug resistance Multidrug resistance, efflux pump MexJK−OprM
M00769_1 Drug resistance Multidrug resistance, efflux pump MexPQ−OpmE
M00649_1 Drug resistance Multidrug resistance, efflux pump AdeABC
M00698_1 Drug resistance Multidrug resistance, efflux pump BpeEF−OprC
M00664_1 Symbiosis Nodulation
M00615_1 Metabolic capacity Nitrate assimilation
M00616_1 Metabolic capacity Sulfate−sulfur assimilation
Acidobacteriaceae
Nostocaceae
Acetobacteraceae
Beijerinckiaceae
Sphingomonadaceae
UBA10450
public_SRR14722229_metawrap_bin.6
public_SRR14722088_metawrap_bin.5
private_TS1974_metawrap_bin.5
public_SRR14722154_metawrap_bin.3
public_SRR14722157_metawrap_bin.1
private_T1916_metawrap_bin.2
private_VT16_metawrap_bin.4
public_SRR14722050_metawrap_bin.2
private_T1888_metawrap_bin.6
private_VT22_metawrap_bin.8
private_X16_metawrap_bin.17
private_X3_metawrap_bin.2
public_ERR4179390_metawrap_bin.2
public_SRR14722049_metawrap_bin.2
public_SRR14722081_metawrap_bin.1
public_SRR14722095_metawrap_bin.2
public_SRR2387885_metawrap_bin.6
private_X5_metawrap_bin.1
public_SRR11456921_metawrap_bin.3
public_SRR11456915_metawrap_bin.3
public_SRR14721994_metawrap_bin.4
public_SRR11456923_metawrap_bin.7
public_SRR14722145_metawrap_bin.2
public_SRR14722161_metawrap_bin.1
public_SRR11456913_metawrap_bin.11
public_SRR11456918_metawrap_bin.3
public_SRR11456919_metawrap_bin.5
public_SRR1531545_metawrap_bin.1
private_X15_metawrap_bin.2
private_VT1_metawrap_bin.3
private_VT1_metawrap_bin.1
public_SRR7232211_metawrap_bin.1
private_X11_metawrap_bin.3
private_T1894_metawrap_bin.4
public_SRR14721985_metawrap_bin.2
private_X9_metawrap_bin.1
private_T1887_metawrap_bin.15
private_T1889_metawrap_bin.2
private_TS1974_metawrap_bin.6
private_VT34_metawrap_bin.3
public_SRR11456914_metawrap_bin.12
public_SRR13125477_metawrap_bin.5
public_SRR14722071_metawrap_bin.1
private_T1904_metawrap_bin.1
private_X1_metawrap_bin.1
public_SRR14722123_metawrap_bin.1
private_T1894_metawrap_bin.9
private_T1916_metawrap_bin.6
private_VT26_metawrap_bin.1
private_T1916_metawrap_bin.13
private_TS1974_metawrap_bin.3
public_SRR11456918_metawrap_bin.13
public_SRR11456919_metawrap_bin.3
private_T1887_metawrap_bin.3
private_X3_metawrap_bin.3
private_VT34_metawrap_bin.4
public_ERR4179389_metawrap_bin.2
public_SRR11456918_metawrap_bin.7
public_SRR11456919_metawrap_bin.1
public_SRR14722117_metawrap_bin.2
private_VT1_metawrap_bin.2
public_SRR11456915_metawrap_bin.9
public_SRR11456919_metawrap_bin.2