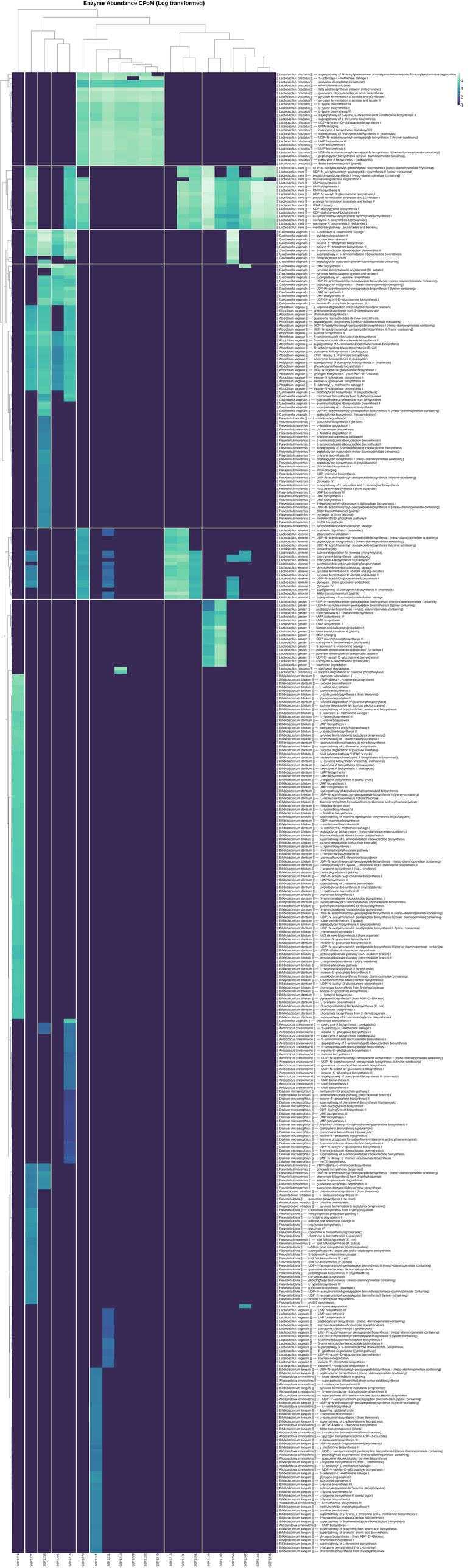
Enzyme Abundance CPoM (Log transformed)
6
4
2
0
[Lactobacillus crispatus]| -- superpathway of N-acetylglucosamine, N-acetylmanosamine and N-acetylneuraminate degradation
[Lactobacillus crispatus]| -- S-adenosyl-L-methionine salvage I
[Lactobacillus crispatus]| -- acetylene degradation (anaerobic)
[Lactobacillus crispatus]| -- ethanolamine utilization
[Lactobacillus crispatus]| -- glycolysis III (from glucose) mitiation (mitochondria)
[Lactobacillus crispatus]| -- guanosine ribonucleotides de novo biosynthesis
[Lactobacillus crispatus]| -- pyruvate fermentation to acetate and (S)-lactate I
[Lactobacillus crispatus]| -- pyruvate fermentation to acetate and lactate II
[Lactobacillus crispatus]| -- L-lysine biosynthesis III
[Lactobacillus crispatus]| -- L-lysine biosynthesis II
[Lactobacillus crispatus]| -- L-lysine biosynthesis VI
[Lactobacillus crispatus]| -- superpathway of L-threonine, L-threonine and L-methionine biosynthesis II
[Lactobacillus crispatus]| -- superpathway of L-threonine biosynthesis
[Lactobacillus crispatus]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Lactobacillus crispatus]| -- tRNA charging
[Lactobacillus crispatus]| -- coenzyme A biosynthesis II (eukaryotic)
[Lactobacillus crispatus]| -- superpathway of coenzyme A biosynthesis III (mammals)
[Lactobacillus crispatus]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Lactobacillus crispatus]| -- UMP biosynthesis III
[Lactobacillus crispatus]| -- UMP biosynthesis I
[Lactobacillus crispatus]| -- UMP biosynthesis II
[Lactobacillus crispatus]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus crispatus]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus crispatus]| -- coenzyme A biosynthesis I (prokaryotic)
[Lactobacillus crispatus]| -- folate transformations II (plants)
[Lactobacillus iners]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus iners]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Lactobacillus iners]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus iners]| -- lactose and galactose degradation I
[Lactobacillus iners]| -- UMP biosynthesis III
[Lactobacillus iners]| -- UMP biosynthesis I
[Lactobacillus iners]| -- UMP biosynthesis II
[Lactobacillus iners]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Lactobacillus iners]| -- pyruvate fermentation to acetate and (S)-lactate I
[Lactobacillus iners]| -- pyruvate fermentation to acetate and lactate II
[Lactobacillus iners]| -- tRNA charging
[Lactobacillus iners]| -- CDP-diacylglycerol biosynthesis I
[Lactobacillus iners]| -- CDP-diacylglycerol biosynthesis II
[Lactobacillus iners]| -- 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I
[Lactobacillus iners]| -- coenzyme A biosynthesis I (prokaryotic)
[Lactobacillus iners]| -- coenzyme A biosynthesis II (eukaryotic)
[Lactobacillus iners]| -- mevalonate pathway I (eukaryotes and bacteria)
[Gardnerella vaginalis]| -- S-adenosyl-L-methionine salvage I
[Gardnerella vaginalis]| -- glycogen degradation II
[Gardnerella vaginalis]| -- sucrose biosynthesis II
[Gardnerella vaginalis]| -- inosine-5'-phosphate biosynthesis I
[Gardnerella vaginalis]| -- inosine-5'-phosphate biosynthesis II
[Gardnerella vaginalis]| -- 5-aminoimidazole ribonucleotide biosynthesis II
[Gardnerella vaginalis]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Gardnerella vaginalis]| -- Bifidobacterium shunt
[Gardnerella vaginalis]| -- peptidoglycan maturation (meso-diaminopimelate containing)
[Gardnerella vaginalis]| -- UMP biosynthesis I
[Gardnerella vaginalis]| -- pyruvate fermentation to acetate and (S)-lactate I
[Gardnerella vaginalis]| -- pyruvate fermentation to acetate and lactate II
[Gardnerella vaginalis]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Gardnerella vaginalis]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Gardnerella vaginalis]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Gardnerella vaginalis]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Gardnerella vaginalis]| -- UMP biosynthesis III
[Gardnerella vaginalis]| -- UMP biosynthesis II
[Gardnerella vaginalis]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Gardnerella vaginalis]| -- inosine-5'-phosphate biosynthesis II
[Atopobium vaginae]| -- L-arginine degradation XIII (reductive Stickland reaction)
[Atopobium vaginae]| -- superpathway of NAD+ from 3-dehydroquinate
[Atopobium vaginae]| -- chorismate biosynthesis I
[Atopobium vaginae]| -- guanosine ribonucleotides de novo biosynthesis
[Atopobium vaginae]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Atopobium vaginae]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Atopobium vaginae]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Atopobium vaginae]| -- sucrose biosynthesis II
[Atopobium vaginae]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Atopobium vaginae]| -- 5-aminoimidazole ribonucleotide biosynthesis II
[Atopobium vaginae]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Atopobium vaginae]| -- O-antigen building blocks biosynthesis (E. coli)
[Atopobium vaginae]| -- coenzyme A biosynthesis I (prokaryotic)
[Atopobium vaginae]| -- dTDP-4,6dx,L-rhamnose biosynthesis
[Atopobium vaginae]| -- coenzyme A biosynthesis II (eukaryotic)
[Atopobium vaginae]| -- superpathway of coenzyme A biosynthesis III (mammals)
[Atopobium vaginae]| -- phosphopantothenate biosynthesis I
[Atopobium vaginae]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I
[Atopobium vaginae]| -- glycogen biosynthesis I (from ADP-D-Glucose)
[Atopobium vaginae]| -- inosine-5'-phosphate biosynthesis II
[Atopobium vaginae]| -- inosine-5'-phosphate biosynthesis III
[Atopobium vaginae]| -- S-adenosyl-L-methionine salvage I
[Atopobium vaginae]| -- inosine-5'-phosphate biosynthesis I
[Gardnerella vaginalis]| -- peptidoglycan biosynthesis III (mycobacteria)
[Gardnerella vaginalis]| -- superpathway of NAD+ from 3-dehydroquinate
[Gardnerella vaginalis]| -- guanosine ribonucleotides de novo biosynthesis
[Gardnerella vaginalis]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Gardnerella vaginalis]| -- superpathway of L-threonine biosynthesis
[Gardnerella vaginalis]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis III (meso-diaminopimelate containing)
[Gardnerella vaginalis]| -- peptidoglycan biosynthesis II (staphylococci)
[Prevotella buccalis]| -- L-histidine degradation I
[Prevotella buccalis]| -- superpathway of L-tryptophan I (de novo)
[Prevotella timonensis]| -- L-histidine degradation I
[Prevotella timonensis]| -- cis-vaccenate biosynthesis
[Prevotella timonensis]| -- L-histidine degradation III
[Prevotella timonensis]| -- adenine and adenosine salvage III
[Prevotella timonensis]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Prevotella timonensis]| -- 5-aminoimidazole ribonucleotide biosynthesis II
[Prevotella timonensis]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Prevotella timonensis]| -- peptidoglycan maturation (meso-diaminopimelate containing)
[Prevotella timonensis]| -- UMP biosynthesis I
[Prevotella timonensis]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Prevotella timonensis]| -- peptidoglycan biosynthesis III (mycobacteria)
[Prevotella timonensis]| -- chorismate biosynthesis I
[Prevotella timonensis]| -- tRNA charging
[Prevotella timonensis]| -- CDP-mannose biosynthesis
[Prevotella timonensis]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Prevotella timonensis]| -- L-lysine biosynthesis VI
[Prevotella timonensis]| -- superpathway of L-aspartate and L-asparagine biosynthesis
[Prevotella timonensis]| -- NAD de novo biosynthesis I (from aspartate)
[Prevotella timonensis]| -- UMP biosynthesis III
[Prevotella timonensis]| -- UMP biosynthesis I
[Prevotella timonensis]| -- UMP biosynthesis II
[Prevotella timonensis]| -- 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I
[Prevotella timonensis]| -- superpathway of L-threonine, L-threonine and L-methionine biosynthesis II (meso-diaminopimelate containing)
[Prevotella timonensis]| -- folate transformations II (plants)
[Prevotella timonensis]| -- glycolysis III (from glucose)
[Prevotella timonensis]| -- methylerythritol phosphate pathway I
[Prevotella timonensis]| -- preQ0 biosynthesis
[Prevotella timonensis]| -- pyrimidine deoxyribonucleosides salvage
[Lactobacillus jensenii]| -- acetylene degradation (anaerobic)
[Lactobacillus jensenii]| -- ethanolamine utilization
[Lactobacillus jensenii]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus jensenii]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus jensenii]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Lactobacillus jensenii]| -- UMP biosynthesis I
[Lactobacillus jensenii]| -- sucrose degradation IV (sucrose phosphorylase)
[Lactobacillus jensenii]| -- coenzyme A biosynthesis I (prokaryotic)
[Lactobacillus jensenii]| -- coenzyme A biosynthesis II (eukaryotic)
[Lactobacillus jensenii]| -- pyrimidine deoxyribonucleotide phosphorylation
[Lactobacillus jensenii]| -- pyrimidine deoxyribonucleotides salvage
[Lactobacillus jensenii]| -- pyruvate fermentation to acetate and (S)-lactate I
[Lactobacillus jensenii]| -- pyruvate fermentation to acetate and lactate II
[Lactobacillus jensenii]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Lactobacillus jensenii]| -- glycolysis I (from glucose 6-phosphate)
[Lactobacillus jensenii]| -- glycolysis IV
[Lactobacillus jensenii]| -- superpathway of coenzyme A biosynthesis III (mammals)
[Lactobacillus jensenii]| -- folate transformations II (plants)
[Lactobacillus jensenii]| -- superpathway of pyrimidine nucleobases salvage
[Lactobacillus gasseri]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus gasseri]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Lactobacillus gasseri]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus gasseri]| -- superpathway of L-threonine biosynthesis
[Lactobacillus gasseri]| -- UMP biosynthesis III
[Lactobacillus gasseri]| -- UMP biosynthesis I
[Lactobacillus gasseri]| -- UMP biosynthesis II
[Lactobacillus gasseri]| -- lactose and galactose degradation I
[Lactobacillus gasseri]| -- folate transformations II (plants)
[Lactobacillus gasseri]| -- tRNA charging
[Lactobacillus gasseri]| -- CDP-diacylglycerol biosynthesis III
[Lactobacillus gasseri]| -- coenzyme A biosynthesis II (eukaryotic)
[Lactobacillus gasseri]| -- S-adenosyl-L-methionine salvage I
[Lactobacillus gasseri]| -- pyruvate fermentation to acetate and (S)-lactate I
[Lactobacillus gasseri]| -- pyruvate fermentation to acetate and lactate II
[Lactobacillus gasseri]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Lactobacillus gasseri]| -- coenzyme A biosynthesis I (prokaryotic)
[Lactobacillus gasseri]| -- stachyose degradation
[Lactobacillus crispatus]| -- UMP biosynthesis I
[Lactobacillus crispatus]| -- sucrose degradation IV (sucrose phosphorylase)
[Bifidobacterium dentium]| -- glycogen degradation II
[Bifidobacterium bifidum]| -- dTDP-4,6dx,L-rhamnose biosynthesis
[Bifidobacterium dentium]| -- sucrose biosynthesis II
[Bifidobacterium bifidum]| -- L-valine biosynthesis
[Bifidobacterium bifidum]| -- sucrose biosynthesis II
[Bifidobacterium bifidum]| -- L-lysine biosynthesis I (from threonine)
[Bifidobacterium bifidum]| -- glycogen degradation II
[Bifidobacterium dentium]| -- sucrose degradation IV (sucrose phosphorylase)
[Bifidobacterium bifidum]| -- sucrose degradation IV (sucrose phosphorylase)
[Bifidobacterium bifidum]| -- superpathway of branched chain amino acid biosynthesis
[Bifidobacterium bifidum]| -- S-adenosyl-L-methionine salvage I
[Bifidobacterium dentium]| -- L-lysine biosynthesis III
[Bifidobacterium bifidum]| -- UMP biosynthesis I
[Bifidobacterium bifidum]| -- UMP biosynthesis II
[Bifidobacterium bifidum]| -- methylerythritol phosphate pathway I
[Bifidobacterium bifidum]| -- L-isoleucine biosynthesis III
[Bifidobacterium bifidum]| -- pyruvate fermentation to isobutanol (engineered)
[Bifidobacterium bifidum]| -- superpathway of L-isoleucine biosynthesis I
[Bifidobacterium dentium]| -- guanosine ribonucleotides de novo biosynthesis
[Bifidobacterium bifidum]| -- superpathway of L-threonine biosynthesis
[Bifidobacterium dentium]| -- sucrose degradation III (sucrose invertase)
[Bifidobacterium bifidum]| -- L-lysine biosynthesis I
[Bifidobacterium dentium]| -- superpathway of coenzyme A biosynthesis III (mammals)
[Bifidobacterium dentium]| -- L-cysteine biosynthesis VI (from L-methionine)
[Bifidobacterium dentium]| -- coenzyme A biosynthesis I (prokaryotic)
[Bifidobacterium dentium]| -- coenzyme A biosynthesis II (eukaryotic)
[Bifidobacterium dentium]| -- UMP biosynthesis I
[Bifidobacterium dentium]| -- UMP biosynthesis II
[Bifidobacterium bifidum]| -- 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (acetyl cycle)
[Bifidobacterium bifidum]| -- UMP biosynthesis I
[Bifidobacterium bifidum]| -- UMP biosynthesis III
[Bifidobacterium bifidum]| -- UMP biosynthesis II
[Bifidobacterium bifidum]| -- superpathway of branched chain amino acid biosynthesis
[Bifidobacterium bifidum]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Bifidobacterium dentium]| -- L-isoleucine biosynthesis I (from threonine)
[Bifidobacterium bifidum]| -- thiamine phosphate formation from pyrithiamine and oxythiamine (yeast)
[Bifidobacterium bifidum]| -- L-lysine biosynthesis VI
[Bifidobacterium dentium]| -- L-lysine biosynthesis VI
[Bifidobacterium bifidum]| -- L-lysine biosynthesis I
[Bifidobacterium bifidum]| -- superpathway of thiamine diphosphate biosynthesis III (eukaryotes)
[Bifidobacterium dentium]| -- CDP-mannose biosynthesis
[Bifidobacterium bifidum]| -- L-methionine biosynthesis III
[Bifidobacterium dentium]| -- S-adenosyl-L-methionine salvage I
[Bifidobacterium bifidum]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Bifidobacterium bifidum]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Bifidobacterium bifidum]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Bifidobacterium bifidum]| -- sucrose degradation III (sucrose invertase)
[Bifidobacterium bifidum]| -- L-lysine biosynthesis I
[Bifidobacterium dentium]| -- methylerythritol phosphate pathway I
[Bifidobacterium dentium]| -- L-isoleucine biosynthesis III
[Bifidobacterium dentium]| -- superpathway of L-threonine biosynthesis
[Bifidobacterium bifidum]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Bifidobacterium bifidum]| -- superpathway of L-arginine biosynthesis I (via L-ornithine)
[Bifidobacterium bifidum]| -- chitin degradation II (Vibrio)
[Bifidobacterium bifidum]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Bifidobacterium dentium]| -- UMP biosynthesis III
[Bifidobacterium bifidum]| -- superpathway of L-alanine biosynthesis
[Bifidobacterium dentium]| -- peptidoglycan biosynthesis III (mycobacteria)
[Bifidobacterium bifidum]| -- L-methionine biosynthesis II
[Bifidobacterium bifidum]| -- chorismate biosynthesis I
[Bifidobacterium dentium]| -- 5-aminoimidazole ribonucleotide biosynthesis II
[Bifidobacterium dentium]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Bifidobacterium bifidum]| -- guanosine ribonucleotides de novo biosynthesis
[Bifidobacterium bifidum]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Bifidobacterium bifidum]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (meso-diaminopimelate containing)
[Bifidobacterium dentium]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Bifidobacterium dentium]| -- folate transformations II (plants)
[Bifidobacterium bifidum]| -- superpathway of L-tryptophan I (de novo)
[Bifidobacterium dentium]| -- peptidoglycan biosynthesis III (mycobacteria)
[Bifidobacterium bifidum]| -- L-methionine biosynthesis I
[Bifidobacterium bifidum]| -- L-lysine biosynthesis VI
[Bifidobacterium bifidum]| -- superpathway of L-aspartate and L-asparagine biosynthesis
[Bifidobacterium bifidum]| -- NAD de novo biosynthesis I (from aspartate)
[Bifidobacterium bifidum]| -- inosine-5'-phosphate biosynthesis I
[Bifidobacterium bifidum]| -- inosine-5'-phosphate biosynthesis II
[Bifidobacterium bifidum]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis III (meso-diaminopimelate containing)
[Bifidobacterium bifidum]| -- pentose phosphate pathway (non-oxidative branch) I
[Bifidobacterium bifidum]| -- pentose phosphate pathway (non-oxidative branch) II
[Bifidobacterium bifidum]| -- L-arginine biosynthesis I (via L-ornithine)
[Bifidobacterium bifidum]| -- pentose phosphate pathway
[Bifidobacterium bifidum]| -- L-arginine biosynthesis II (acetyl cycle)
[Bifidobacterium bifidum]| -- inosine-5'-phosphate biosynthesis II
[Bifidobacterium bifidum]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Bifidobacterium bifidum]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Bifidobacterium bifidum]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Bifidobacterium bifidum]| -- chorismate biosynthesis from 3-dehydroquinate
[Bifidobacterium bifidum]| -- inosine-5'-phosphate biosynthesis I
[Bifidobacterium bifidum]| -- L-histidine biosynthesis
[Bifidobacterium bifidum]| -- glycogen biosynthesis I (from ADP-D-Glucose)
[Bifidobacterium dentium]| -- L-ornithine biosynthesis I
[Bifidobacterium dentium]| -- O-antigen building blocks biosynthesis (E. coli)
[Bifidobacterium dentium]| -- L-lysine biosynthesis VI
[Bifidobacterium dentium]| -- chorismate biosynthesis from 3-dehydroquinate
[Bifidobacterium dentium]| -- superpathway of L-serine and glycine biosynthesis I
[Gardnerella vaginalis]| -- chorismate biosynthesis I
[Aerococcus christensenii]| -- coenzyme A biosynthesis I (prokaryotic)
[Aerococcus christensenii]| -- S-adenosyl-L-methionine salvage I
[Aerococcus christensenii]| -- inosine-5'-phosphate biosynthesis II
[Aerococcus christensenii]| -- inosine-5'-phosphate biosynthesis I
[Aerococcus christensenii]| -- 5-aminoimidazole ribonucleotide biosynthesis II
[Aerococcus christensenii]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Aerococcus christensenii]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Aerococcus christensenii]| -- inosine-5'-phosphate biosynthesis I
[Aerococcus christensenii]| -- sucrose biosynthesis II
[Aerococcus christensenii]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Aerococcus christensenii]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Aerococcus christensenii]| -- guanosine ribonucleotides de novo biosynthesis
[Aerococcus christensenii]| -- UMP biosynthesis III
[Aerococcus christensenii]| -- inosine-5'-phosphate biosynthesis II
[Aerococcus christensenii]| -- superpathway of coenzyme A biosynthesis III (mammals)
[Aerococcus christensenii]| -- UMP biosynthesis I
[Aerococcus christensenii]| -- UMP biosynthesis II
[Aerococcus christensenii]| -- UMP biosynthesis III
[Dialister microaerophilus]| -- methylerythritol phosphate pathway I
[Dialister microaerophilus]| -- pentose phosphate pathway (non-oxidative branch) I
[Dialister microaerophilus]| -- inosine-5'-phosphate biosynthesis II
[Dialister microaerophilus]| -- superpathway of coenzyme A biosynthesis III (mammals)
[Dialister microaerophilus]| -- CDP-diacylglycerol biosynthesis I
[Dialister microaerophilus]| -- CDP-diacylglycerol biosynthesis II
[Dialister microaerophilus]| -- UMP biosynthesis III
[Dialister microaerophilus]| -- UMP biosynthesis I
[Dialister microaerophilus]| -- UMP biosynthesis II
[Dialister microaerophilus]| -- 4-amino-2-methyl-5-diphosphomethylpyrimidine biosynthesis II
[Dialister microaerophilus]| -- coenzyme A biosynthesis I (prokaryotic)
[Dialister microaerophilus]| -- coenzyme A biosynthesis II (eukaryotic)
[Dialister microaerophilus]| -- inosine-5'-phosphate biosynthesis I
[Dialister microaerophilus]| -- thiamine phosphate formation from pyrithiamine and oxythiamine (yeast)
[Dialister microaerophilus]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Dialister microaerophilus]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Dialister microaerophilus]| -- 5-aminoimidazole ribonucleotide biosynthesis II
[Dialister microaerophilus]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Dialister microaerophilus]| -- CMP-3-deoxy-D-manno-octulosonate biosynthesis
[Dialister microaerophilus]| -- preQ0 biosynthesis
[Prevotella timonensis]| -- dTDP-4,6dx,L-rhamnose biosynthesis
[Prevotella timonensis]| -- gondoate biosynthesis (anaerobic)
[Prevotella timonensis]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Prevotella timonensis]| -- chorismate biosynthesis from 3-dehydroquinate
[Prevotella timonensis]| -- L-histidine degradation I
[Prevotella timonensis]| -- guanosine nucleotides degradation III
[Prevotella timonensis]| -- guanosine ribonucleotides de novo biosynthesis
[Anaerococcus tetradius]| -- L-isoleucine biosynthesis I (from threonine)
[Anaerococcus tetradius]| -- L-isoleucine biosynthesis III
[Prevotella bivia]| -- guanosine biosynthesis I (de novo)
[Anaerococcus tetradius]| -- L-valine biosynthesis
[Prevotella bivia]| -- superpathway of L-threonine biosynthesis
[Prevotella bivia]| -- pyruvate fermentation to isobutanol (engineered)
[Prevotella bivia]| -- chorismate biosynthesis from 3-dehydroquinate
[Prevotella bivia]| -- methylerythritol phosphate pathway I
[Prevotella bivia]| -- L-histidine degradation I
[Prevotella bivia]| -- adenine and adenosine salvage III
[Prevotella bivia]| -- chorismate biosynthesis I
[Prevotella bivia]| -- glycolysis IV
[Prevotella bivia]| -- coenzyme A biosynthesis I (prokaryotic)
[Prevotella bivia]| -- coenzyme A biosynthesis II (eukaryotic)
[Prevotella bivia]| -- superpathway of L-tryptophan I (de novo)
[Prevotella timonensis]| -- lipid IVA biosynthesis (P. putida)
[Prevotella bivia]| -- NAD de novo biosynthesis I (from aspartate)
[Prevotella bivia]| -- superpathway of L-aspartate and L-asparagine biosynthesis
[Prevotella bivia]| -- S-adenosyl-L-methionine salvage I
[Prevotella bivia]| -- lipid IVA biosynthesis (E. coli)
[Prevotella bivia]| -- lipid IVA biosynthesis (P. putida)
[Prevotella bivia]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis III (meso-diaminopimelate containing)
[Prevotella bivia]| -- guanosine ribonucleotides de novo biosynthesis
[Prevotella bivia]| -- peptidoglycan biosynthesis III (mycobacteria)
[Prevotella bivia]| -- cis-vaccenate biosynthesis
[Prevotella bivia]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Prevotella bivia]| -- L-lysine biosynthesis III
[Prevotella bivia]| -- gondoate biosynthesis (anaerobic)
[Prevotella bivia]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Prevotella bivia]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Prevotella bivia]| -- L-histidine degradation I
[Prevotella bivia]| -- preQ0 biosynthesis
[Lactobacillus jensenii]| -- stachyose degradation
[Lactobacillus vaginalis]| -- UMP biosynthesis III
[Lactobacillus vaginalis]| -- UMP biosynthesis I
[Lactobacillus vaginalis]| -- UMP biosynthesis II
[Lactobacillus vaginalis]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus vaginalis]| -- sucrose degradation IV (sucrose phosphorylase)
[Lactobacillus vaginalis]| -- coenzyme A biosynthesis I (prokaryotic)
[Lactobacillus vaginalis]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Lactobacillus vaginalis]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Lactobacillus vaginalis]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Lactobacillus vaginalis]| -- 5-aminoimidazole ribonucleotide biosynthesis II
[Lactobacillus vaginalis]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Lactobacillus vaginalis]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Lactobacillus vaginalis]| -- stachyose degradation
[Lactobacillus vaginalis]| -- inosine-5'-phosphate biosynthesis I
[Lactobacillus vaginalis]| -- inosine-5'-phosphate biosynthesis II
[Bifidobacterium longum]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Bifidobacterium longum]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Alloscardovia omnicolens]| -- folate transformations II (plants)
[Alloscardovia omnicolens]| -- superpathway of branched chain amino acid biosynthesis
[Bifidobacterium longum]| -- pyruvate fermentation to isobutanol (engineered)
[Alloscardovia omnicolens]| -- 5-aminoimidazole ribonucleotide biosynthesis II
[Alloscardovia omnicolens]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Bifidobacterium longum]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)
[Alloscardovia omnicolens]| -- L-valine biosynthesis
[Alloscardovia omnicolens]| -- L-isoleucine biosynthesis I
[Bifidobacterium longum]| -- L-ornithine biosynthesis I
[Bifidobacterium longum]| -- L-isoleucine biosynthesis I (from threonine)
[Bifidobacterium longum]| -- superpathway of L-phenylalanine biosynthesis
[Alloscardovia omnicolens]| -- dTDP-4,6dx,L-rhamnose biosynthesis
[Bifidobacterium longum]| -- folate transformations II (plants)
[Alloscardovia omnicolens]| -- L-isoleucine biosynthesis I (from threonine)
[Bifidobacterium longum]| -- glycogen biosynthesis I (from ADP-D-Glucose)
[Bifidobacterium longum]| -- L-isoleucine biosynthesis III
[Bifidobacterium longum]| -- UDP-N-acetyl-D-glucosamine biosynthesis I
[Bifidobacterium longum]| -- L-methionine biosynthesis III
[Alloscardovia omnicolens]| -- UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)
[Alloscardovia omnicolens]| -- peptidoglycan biosynthesis I (meso-diaminopimelate containing)
[Alloscardovia omnicolens]| -- guanosine ribonucleotides de novo biosynthesis
[Bifidobacterium longum]| -- L-cysteine biosynthesis VI (from L-methionine)
[Alloscardovia omnicolens]| -- S-adenosyl-L-methionine salvage I
[Bifidobacterium longum]| -- L-methionine biosynthesis I
[Bifidobacterium longum]| -- S-adenosyl-L-methionine salvage I
[Bifidobacterium longum]| -- glycogen degradation II
[Bifidobacterium longum]| -- sucrose biosynthesis II
[Bifidobacterium longum]| -- L-lysine biosynthesis III
[Bifidobacterium longum]| -- sucrose degradation IV (sucrose phosphorylase)
[Bifidobacterium longum]| -- L-lysine biosynthesis VI
[Bifidobacterium longum]| -- 6-hydroxymethyl-dihydropterin diphosphate biosynthesis II (acetyl cycle)
[Bifidobacterium longum]| -- L-lysine biosynthesis I
[Alloscardovia omnicolens]| -- L-methionine biosynthesis III
[Bifidobacterium longum]| -- methylerythritol phosphate pathway I
[Bifidobacterium longum]| -- L-valine biosynthesis
[Bifidobacterium longum]| -- superpathway of L-lysine, L-threonine and L-methionine biosynthesis II
[Bifidobacterium longum]| -- 5-aminoimidazole ribonucleotide biosynthesis I
[Bifidobacterium longum]| -- superpathway of 5-aminoimidazole ribonucleotide biosynthesis
[Alloscardovia omnicolens]| -- UMP biosynthesis I
[Bifidobacterium longum]| -- superpathway of branched chain amino acid biosynthesis
[Bifidobacterium longum]| -- superpathway of aromatic amino acid biosynthesis
[Bifidobacterium longum]| -- glycogen biosynthesis I (from ADP-D-Glucose)
[Bifidobacterium longum]| -- chorismate biosynthesis I
[Bifidobacterium longum]| -- superpathway of L-threonine biosynthesis
[Bifidobacterium longum]| -- L-arginine biosynthesis I (via L-ornithine)
[Bifidobacterium longum]| -- chorismate biosynthesis from 3-dehydroquinate
SRR3191
SRR3187
SRR3256
SRR3261
SRR3275
SRR3222
SRR3231
SRR3228
SRR3240
SRR3219
SRR3171
SRR3263
SRR3138
SRR3250
SRR3207
SRR3165
SRR3246