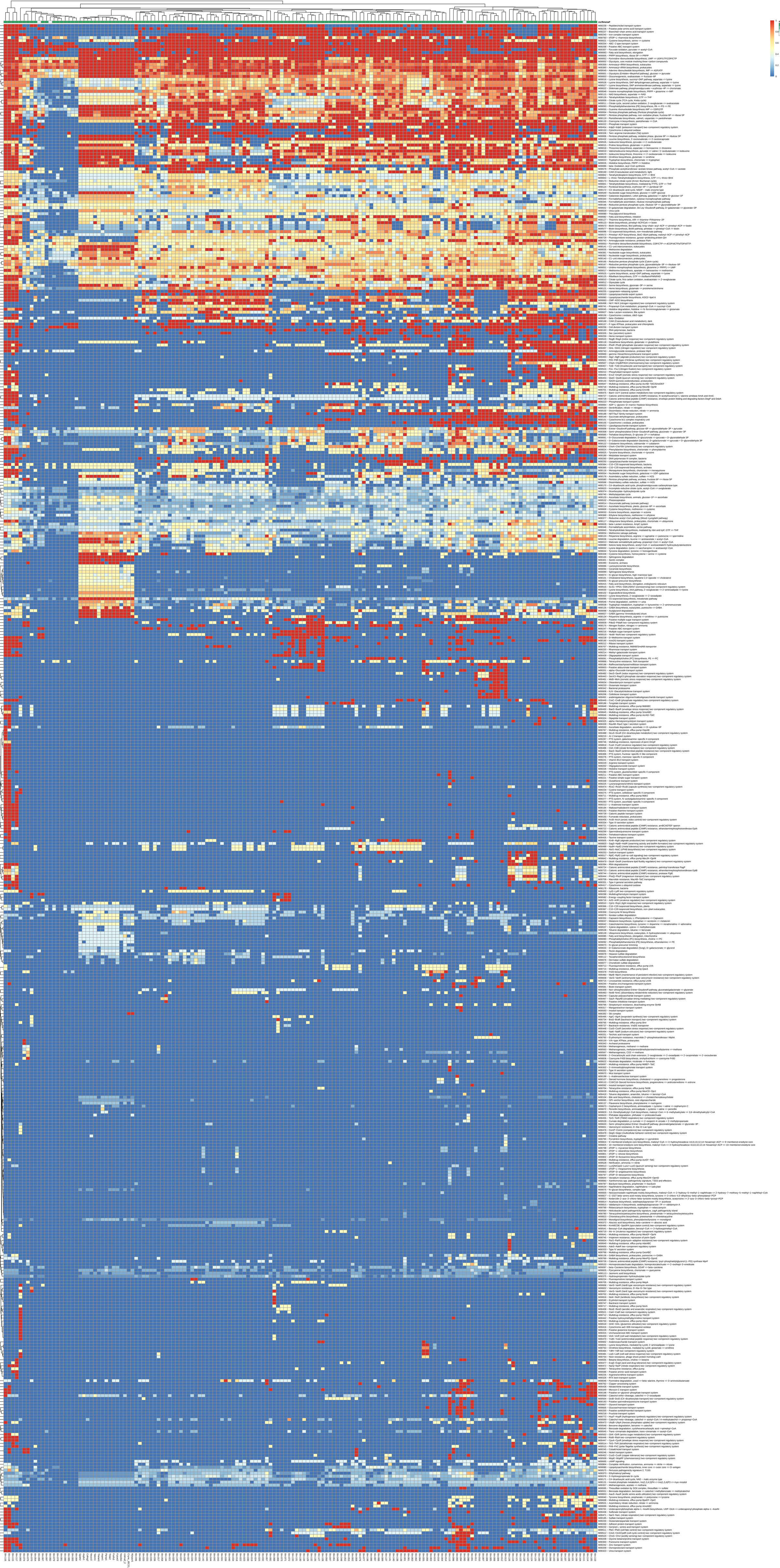
mcfbinsqrt
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M00236 - Paralogous/orthologous transport system
M00236 - Putative polar amino acid transport system
M00237 - Branched-chain amino acid transport system
M00240 - Iron complex transport system
M00241 - Cobalt/nickel transport system
M00321 - Cysteine biosynthesis, serine => cysteine
M00254 - ABC-2 type transport system
M00255 - Fatty acid/phospholipid synthesis
M00257 - Pyruvate oxidation, pyruvate => acetyl-CoA
M00083 - Fatty acid biosynthesis, elongation
M00087 - Ceramide biosynthesis, serine palmitoyltr pathway
M00332 - Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP/CDP/CTP
M00002 - Glycolysis, core module involving three-carbon compounds
M00307 - Pyruvate oxidation, pyruvate => acetyl-CoA
M00282 - Aminoacyl-tRNA biosynthesis, prokaryotes
M00048 - Adenine ribonucleotide biosynthesis, IMP => ADP,ATP
M00049 - Guanine ribonucleotide biosynthesis, IMP => GDP,GTP
M00003 - Gluconeogenesis, oxaloacetate => fructose-6P
M00018 - Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine
M00526 - Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine
M00527 - Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine
M00019 - Threonine biosynthesis, aspartate => homoserine => threonine
M00040 - Inosine monophosphate biosynthesis, PRPP + glutamine => IMP
M00115 - NAD biosynthesis, aspartate => NAD
M00051 - Purine nucleotide interconversion, IMP => ITP
M00009 - Citrate cycle (TCA cycle, Krebs cycle)
M00010 - Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate
M00011 - Citrate cycle, succinyl-CoA synthesis, succinate => CoA => ATP
M00012 - Guanine ribonucleotide biosynthesis, IMP => GDP,GTP
M00004 - Pentose phosphate pathway (Pentose phosphate cycle)
M00005 - Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P
M00120 - Pantothenate biosynthesis, valine/L-aspartate => pantothenate
M00122 - Coenzyme A biosynthesis, pantothenate => CoA
M00123 - Biotin biosynthesis
M00207 - ABC2-type(Type IV) transport two-component regulatory system
M00153 - Cytochrome c oxidase
M00154 - Cytochrome bc1 complex respiratory unit
M00155 - Cytochrome bc1 complex respiratory unit
M00156 - Pentose phosphate pathway, initiation phase, glucose 6P => ribulose 5P
M00157 - Leucine biosynthesis, 2-oxoisovalerate => 2-isopropylmalate
M00158 - Pyruvate oxidation, pyruvate => acetaldehyde
M00159 - Proline biosynthesis, glutamate => L-proline
M00033 - Threonine biosynthesis, aspartate => homoserine => threonine
M00034 - Valine/isoleucine biosynthesis, pyruvate => valine 2-oxobutanoate => isoleucine
M00035 - Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine
M00036 - Leucine biosynthesis, 2-oxoisovalerate => leucine
M00037 - Tryptophan biosynthesis, chorismate => tryptophan
M00038 - Histidine biosynthesis, PRPP => histidine
M00039 - Serine biosynthesis, glycerate => serine
M00579 - Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate
M00169 - CAM (Crassulacean acid metabolism), light
M00170 - CAM (Crassulacean acid metabolism), dark
M00341 - L-Ribose / 5deoxyribulose biosynthesis, CTP => L-ribose-dRu5
M00173 - Reductive citrate cycle (Arnon-Buchanan cycle)
M00174 - Methane monooxygenase, soluble form, methane, O2, CTP => THF
M00176 - Purine biosynthesis, xanthosine-MP => guanosine-5P
M00172 - C4-dicarboxylic acid cycle, NAD# - malic enzyme type
M00177 - Reductive pentose phosphate cycle, glyceraldehyde-3P => ribulose-5P
M00178 - Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P
M00344 - Formaldehyde assimilation, xylulose monophosphate pathway
M00346 - Formaldehyde assimilation, ribulose monophosphate pathway
M00180 - Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P
M00182 - D-galactarate degradation, De-Ley-Doudoroff pathway, D-galactonate => glycerate-3P
M00029 - Urea cycle
M00095 - Triacylglycerol biosynthesis
M00307 - Pyruvate oxidation, oxidation
M00127 - Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P
M00123 - Biotin biosynthesis, pimeloyl-ACP/CoA => biotin
M00577 - Biotin biosynthesis, BioW pathway, pimeloyl-ACP => pimeloyl-ACP => biotin
M00577 - Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin
M00096 - C5 isoprenoid biosynthesis, non-mevalonate pathway
M00578 - Biotin biosynthesis, BioC pathway, malonyl-ACP => pimeloyl-ACP => pimeloyl-ACP
M00728 - Fluoroquinolone resistance, gyrase-protecting protein Qnr
M00742 - Aminoglycoside resistance, protease Pseo
M00743 - Aminoglycoside resistance, aminoglycosidase, CDP/CTP => dCDP/dCTP/UTP/dTTP
M00744 - C1 unit interconversion, eukaryotes
M00035 - Methionine degradation
M00745 - C1 unit interconversion, eukaryotes
M00182 - Nucleotide sugar biosynthesis, prokaryotes
M00180 - C1 unit interconversion, prokaryotes
M00177 - Reductive pentose phosphate cycle (Calvin cycle)
M00177 - Reductive pentose phosphate cycle, glyceraldehyde-3P => ribulose-5P
M00051 - Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP
M00018 - Methionine biosynthesis, aspartate => homoserine => methionine
M00018 - Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine
M00018 - Lysine biosynthesis, AKB pathway, aspartate => lysine
M00009 - Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate
M00022 - Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate
M00033 - Threonine biosynthesis, glycerate-3P => serine
M00015 - Serine biosynthesis, glycerate => phosphoserine
M00525 - Lipoprotein releasing system
M00526 - Lipoprotein releasing system
M00083 - Lipopolysaccharide biosynthesis, KDO-lipid A
M00063 - CMP-KDO biosynthesis
M00437 - Two-component system(unknown) two-component regulatory system
M00004 - Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA
M00046 - Histidine degradation, histidine => N-formiminoglutamate => glutamate
M00047 - Proline degradation, proline => glutamate
M00048 - Cytochrome c oxidase, cbb3-type
M00097 - Beta-Oxidation
M00154 - Cytochrome bc1 complex respiratory unit
M00167 - F-type ATPase, prokaryotes and chloroplasts
M00552 - Cell division transport system
M00553 - Cell division transport system
M00555 - Sec translocon system
M00556 - Tat translocon system
M00557 - Rcs(P-R)(P-S)(R)(S) response two-component regulatory system
M00558 - Glutathione biosynthesis, glutamate => gamma-Glu-Cys
M00559 - Cpx(A-E)(R-P)(R-M) response two-component regulatory system
M00560 - Cpx(L-O)(H-D) sensor-regulator(-two-component regulatory system
M00561 - Aminoglycoside resistance, protease Hpd
M00562 - Aminoglycoside resistance, aminoglycosidase
M00563 - AgE (AgeR) digenic production two-component regulatory system
M00564 - PhS-PhR (type A fimbriae synthesis) two-component regulatory system
M00565 - Cpx(A-E)(R-P)(R-M)(H-D) response two-component regulatory system
M00567 - TolE-TolD (bacteriocin, acid transport) two-component regulatory system
M00624 - FeL-FeLI (nitrogen fixation) two-component regulatory system
M00625 - Cpx(A-E)(R-P)(R-M) response system
M00640 - EnvZ-OmpR (osmotic stress response) two-component regulatory system
M00643 - QseC-QseB (quorum sensing) two-component regulatory system
M00644 - Multidrug resistance, efflux pump AcrAB-TolC
M00645 - Multidrug resistance, efflux pump AcrAB-TolC/TesAB/EnvZ
M00718 - Multidrug resistance, efflux pump MexAB-OprM
M00719 - Multidrug resistance, efflux pump MexEF-OprN
M00721 - BacA-UhpT (cationic antimicrobial peptide) two-component regulatory system
M00722 - Cationic antimicrobial peptide (CAMP) resistance, N-acylhydroxamyl L-alanine amidase NmlA and AmiC
M00723 - Cationic antimicrobial peptide (CAMP) resistance, envelope protein folding and degrading factors DsrA and DsbA
M00222 - Phosphonate transport system
M00223 - Phosphate/phosphonate/phosphite transporter
M00224 - Dendrobactin, siderophore
M00225 - Dissimilatory nitrate reduction, nitrate => ammonia
M00226 - Nitrite reductase, ferredoxin
M00227 - Succinate dehydrogenase, prokaryotes
M00151 - Cytochrome bc1 complex respiratory unit
M00152 - Cytochrome bc1 complex respiratory unit
M00227 - Lipoolygosaccharide transport system
M00008 - Entner-Doudoroff pathway, glucose 6P => glyceraldehyde-3P + pyruvate
M00009 - Citrate cycle (TCA cycle, Krebs cycle), oxaloacetate => 2-oxoglutarate => succinyl-CoA
M00010 - Tetrahydro biopterin, D-glucose 2P => tetrahydro
M00061 - D-Glucuronate degradation, D-glucuronate => pyruvate + D-glyceraldehyde 3P
M00062 - Ascorbate degradation, ascorbate => D-glucuronate => pyruvate + D-glyceraldehyde 3P
M00122 - Cobalamin biosynthesis, cobinamide => cobalamin
M00188 - Chuk-Chr1/Rh1 (chemotaxis) two-component regulatory system
M00189 - Tyrosine biosynthesis, chorismate => tyrosine
M00190 - Tyrosine biosynthesis, chorismate => tyrosine
M00189 - Molybdate transport system
M00190 - DNA polymerase III complex, bacteria
M00192 - Lipopolysaccharide transport system
M00193 - Cell division protein complex, bacteria
M00194 - C10-C16 isoprenoid biosynthesis, archaea
M00195 - Menaquinone biosynthesis, chorismate => menaquinone
M00196 - Coenzyme F420 biosynthesis, 7,8-dihydro-6-hydroxymethylpterine
M00197 - Assimilatory sulfate reduction, sulfate => H2S
M00198 - Pentose phosphate pathway, archaea, fructose 6P => ribose 5P
M00199 - Pentose phosphate pathway, archaea, ribose 5P
M00200 - C4-dicarboxylic acid cycle, phosphoenolpyruvate carboxylase type
M00202 - Incomplete reductive citrate cycle, acetyl-CoA => oxoglutarate
M00203 - Incomplete reductive citrate cycle
M00204 - Methylaspartate cycle
M00205 - Ascorbate biosynthesis, animals, glucose 1P => ascorbate
M00206 - Ascorbate biosynthesis
M00207 - Glucuronate pathway (uronate pathway)
M00214 - Ascorbate biosynthesis, plants, glucose-6P => ascorbate
M00215 - Ascorbate biosynthesis, plants, mannose
M00216 - Erythrose biosynthesis, aspartate => erythrose
M00217 - Ethylene biosynthesis, methionine => ethylene
M00218 - Methylerythritol-CoA pathway (MEP-CoA pathway)
M00219 - Sesquiterpene biosynthesis, prenyl-ester, chromatin => alpha/gamma
M00220 - Formaldehyde assimilation, serine pathway
M00221 - Formaldehyde assimilation, serine pathway
M00222 - Tetrahydrobiopterin biosynthesis, mediated by rfbA and bpf, GTP => THF
M00223 - Polyamine biosynthesis, arginine
M00224 - Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine
M00225 - Leucine degradation, leucine => acetoacetate + acetyl-CoA
M00226 - Ketone body biosynthesis, acetyl-CoA => acetoacetyl-CoA
M00227 - Ketone body biosynthesis, acetyl-CoA => acetoacetyl-CoA-hydroxybutyrylacetone
M00232 - Lysine degradation, lysine => saccharopine => aminoacetyl-CoA
M00233 - Lysine degradation, lysine => cadaverine
M00234 - Cysteine biosynthesis, homocysteine + serine => cysteine
M00235 - Sphingosine degradation
M00236 - Sphingosine
M00237 - Exosome, archaea
M00238 - Lactosylceramide biosynthesis
M00239 - Ceramide biosynthesis
M00240 - Sphingosine biosynthesis
M00241 - N-glycan biosynthesis, high mannose type
M00242 - Bile acid biosynthesis, cholesterol => cholestenol
M00243 - N-glycan precursor biosynthesis
M00243 - Fatty acid biosynthesis, elongation, endoplasmic reticulum
M00244 - (LN)-(HTS)-(SSK-DNAF) (nematocyte) two-component regulatory system
M00245 - Lysine biosynthesis, AAA pathway, 2-oxoglutarate => 2-aminoadipate => lysine
M00246 - Glycosaminoglycan biosynthesis
M00247 - Lysine biosynthesis, 2-oxoglutarate => 2-isopropylmalate
M00248 - CS suppressed biosynthesis, mevalonate pathway
M00249 - Dissimilatory sulfate reduction, sulfite => H2S
M00250 - Tryptophan metabolism, tryptophan => kynurenine => 2-aminomuconate
M00251 - GABA biosynthesis, eukaryotes, putrescine => GABA
M00252 - Arginine degradation, AGDI pathway
M00253 - GABA (gamma-Aminobutyrate) shunt
M00254 - Polyamine biosynthesis, arginine => ornithine => putrescine
M00255 - Polyamine biosynthesis, ornithine => putrescine
M00256 - Fdx(I)-Rhd(I) two-component regulatory system
M00257 - Nitrogen fixation, nitrogen => ammonia
M00258 - Urea cycle, arginine => ornithine
M00259 - Multidrug resistance, efflux pump MdtABC-TolC
M00260 - Iron(III) transport system
M00261 - Iron(III) transport system
M00262 - Iron(II) transport system
M00263 - Ribose transport system
M00264 - Multidrug resistance, MdtABCD-TolC transporter
M00265 - Maltose transport system
M00266 - Maltose/maltotriose transport system
M00267 - Oligopeptide transport system
M00268 - Phosphatidylcholine (PC) biosynthesis, PE => PC
M00269 - Phosphate transport system
M00270 - Raffinose/stachyose/melibiose transport system
M00271 - Putative aldouronate transport system
M00272 - Putative xylan transport system
M00273 - OxrD-OxrR (redox response) two-component regulatory system
M00443 - SenC0-RegC0 (phosphate starvation response) two-component regulatory system
M00444 - ZraS-ZraR (zinc/zinc response) two-component regulatory system
M00445 - Oligopeptide transport system
M00275 - Glutamate transport system
M00276 - Glutamate transport system
M00277 - N,N'-Diacetylchitobiose transport system
M00278 - Cellobiose transport system
M00279 - Cellobiose/cellotriose/cellotetraose/cellopentaose/cellohexaose transport system
M00446 - CusC-CusB (copper regulation) two-component regulatory system
M00280 - Tungstate transport system
M00281 - Multidrug resistance, efflux pump MdtABC
M00450 - BaeS-BaeR (envelope stress response) two-component regulatory system
M00451 - Multidrug resistance, efflux pump SmeABC
M00284 - Multidrug resistance, efflux pump AcrAD-TolC
M00285 - Dipeptide transport system
M00286 - Putative ribose transport system
M00287 - RavA-RavC ayu-1 secretion system
M00350 - Ascorbate degradation, ascorbate => D-tyrulose-5P
M00351 - Ascorbate degradation, ascorbate => D-xylulose
M00455 - CusS-CusR (Cr-obstructive resistance) two-component regulatory system
M00353 - Ar-2 transport system
M00354 - Multidrug resistance, repressor-of-porin OmpF
M00354 - FusK-FusR (cerulenin resistance) two-component regulatory system
M00355 - BaeS-BaeR (aminoglycoside resistance) two-component regulatory system
M00356 - BaeS-BaeR (antimicrobial peptide resistance) two-component regulatory system
M00356 - PTS system, fructose-specific IIc component
M00357 - PTS system, fructose-specific IIB component
M00358 - Vitamin B12 transport system
M00359 - Arginine transport system
M00360 - Histidine transport system
M00360 - Histidine transport system
M00361 - PTS system, glucitol/sorbitol-specific II component
M00362 - Putative HBC transport system
M00363 - Putative simple sugar transport system
M00364 - Putative ribose transport system
M00365 - Lysine/arginine/ornithine transport system
M00474 - RcsC-RcsD (capsule synthesis) two-component regulatory system
M00366 - PTS system, cellobiose-specific II component
M00367 - PTS system, cellobiose-specific A component
M00111 - Multidrug resistance, efflux pump MdtEJ
M00368 - PTS system, mannose-specific II component
M00369 - PTS system, ascorbate-specific II component
M00113 - L-Arabinose transport system
M00370 - Putative D-xylose transport system
M00371 - Putative rhamnose transport system
M00372 - Cationic peptide transport system
M00373 - Ectoine/hydroxyectoine transport system
M00374 - ArcB-ArcA (aerobic redox control) two-component regulatory system
M00324 - Type VI secretion system
M00375 - Cationic antimicrobial peptide (CAMP) resistance, arnBCADTEF operon
M00376 - Cationic antimicrobial peptide (CAMP) resistance, ethanolamine/phosphoethanolamine EptA
M00299 - Spermidine/putrescine transport system
M00377 - Tetrahydromethanopterin biosynthesis
M00378 - Sulfate transport system
M00505 - NarX-NarL (nitrate-sensing/response) two-component regulatory system
M00379 - Sag(I-Hpt)R (metal tolerance) two-component regulatory system
M00380 - Hpt-HpdS (metal tolerance) two-component regulatory system
M00381 - Sag(I-Hpt)S (metal tolerance) two-component regulatory system
M00382 - Sodium transport system
M00383 - MgRC-MgRS (cell-to-cell signaling) two-component regulatory system
M00384 - Multidrug resistance, efflux pump MdtABC-TolC
M00476 - OxsR-OxsS (hydrogen peroxide stress response) two-component regulatory system
M00384 - RNA degradosome
M00385 - Cationic antimicrobial peptide (CAMP) resistance, palmitoyl transferase PagP
M00386 - Cationic antimicrobial peptide (CAMP) resistance, ethanolamine/phosphoethanolamine EptB
M00387 - Cationic antimicrobial peptide (CAMP) resistance, protease PgtE
M00388 - Cationic antimicrobial peptide (CAMP) resistance, lipid A 4-amino-4-deoxyarabinose
M00389 - Macrolide resistance, MacAB-TolC transporter
M00390 - Type II general secretion pathway
M00391 - Type II general secretion pathway
M00392 - Rhizopsins, bacteria
M00482 - LytS-LytR two-component regulatory system
M00393 - Anion/cation/amino acid transport system
M00394 - Multidrug resistance, efflux pump MdtGH
M00395 - Cpx(A-E)(R-P)(R-M) response two-component regulatory system
M00396 - CpxS-YfcZ (Cpx response) two-component regulatory system
M00398 - C10-C16 isoprenoid biosynthesis, plants
M00399 - Cobalamin biosynthesis, anaerobic, non-plant eukaryotes
M00400 - Coenzyme M biosynthesis
M00075 - Keratan sulfate degradation
M00401 - Methanol oxidation, methylene-H4F/methylene => Calvacin
M00402 - Melatonin biosynthesis, tryptophan => serotonin => melatonin
M00403 - Catecholamine biosynthesis, tyrosine => dopamine => noradrenaline => adrenaline
M00404 - Dopamine degradation, dopamine => homovanillate
M00405 - Toluene degradation, toluene => benzoate
M00406 - Ubiquinone biosynthesis, eukaryotes, 4-hydroxybenzoate => ubiquinone
M00407 - Phosphatidylcholine (PC) biosynthesis, choline => PC
M00408 - Phosphatidylethanolamine (PE) biosynthesis, ethanolamine => PE
M00409 - Trehalose biosynthesis, eukaryotes
M00410 - D-Galactonate degradation (Dahms pathway), D-galactonate => glycerol
M00411 - Pectin degradation
M00412 - Rubredoxin-NAD+ reductase
M00413 - Nicotinamide/nicotinate degradation
M00414 - Dermatan sulfate degradation
M00415 - Chondroitin sulfate degradation
M00416 - Fluoroquinolone resistance, efflux pump LfrA
M00417 - Multidrug resistance, efflux pump CmeB
M00418 - FAD biosynthesis
M00485 - MprB-MprA (maintenance of persistent infection) two-component regulatory system
M00419 - Commu(Rv0081-Rv0082) two-component regulatory system
M00420 - Linezolid resistance, efflux pump LsaB
M00244 - Putative zinc/manganese transport system
M00421 - Tetracycline resistance
M00422 - Non-phosphorylative Entner-Doudoroff pathway, gluconate/galactonate => glycerate
M00423 - NmR-NmC (rhizobitoxine/rhizobitoxine reduction) two-component regulatory system
M00424 - Alkylphosphonate utilization, PhnJ complex
M00427 - DaeH-RaeR (cinnamic response) two-component regulatory system
M00428 - Putative chlorite/cation transport system
M00429 - Cobalt/nickel transport system, ATP-binding enzyme SnhB
M00431 - Manganese/iron transport system
M00432 - Iron(II) transport system
M00433 - Iron(III) transport system
M00486 - AgC-AgA (bacteriocin synthesis) two-component regulatory system
M00434 - BvgS-BvgR (bacitracin transport) two-component regulatory system
M00435 - Multidrug resistance, efflux pump BmrA
M00437 - Bacitracin resistance, YkbDE transporter
M00438 - ZraS-ZraR (zinc/zinc response) two-component regulatory system
M00439 - NaeR-NaeS (sodium exclusion) two-component regulatory system
M00251 - Technic acid transport system
M00440 - Phosphonate degradation, methylene 2'-phosphoferulamine / MpnA
M00441 - UA-type ATPase, prokaryotes
M00243 - Archaea proteasome
M00442 - Methanogenesis, methanol => methane
M00443 - Methanogenesis, methylamine/dimethylamine/trimethylamine => methane
M00567 - Methanogenesis, CO2 => methane
M00444 - Propionate degradation, methylcitrate, 2-oxobutanoate => 2-oxoadipate => 2-oxoglutarate => 2-oxosuccinate
M00445 - Coenzyme F420 biosynthesis, dihydroxyfolate => coenzyme F420
M00502 - Nicotinate degradation, nicotinate => furanate
M00446 - Methanogenic heterodisulfide reductase, HdrABC
M00447 - 2-Aminoethylphosphonate transport system
M00232 - Type III secretion system
M00448 - Type III secretion system
M00449 - L- / D-arginine/lysine transport system
M00450 - Steroid hormone biosynthesis, cholesterol => progenerolone => progenerolone
M00451 - C10-C16 isoprenoid biosynthesis, progenerolone => androstenedione => estrone
M00452 - Cell wall biosynthesis, bacteria
M00454 - Tetracycline resistance, efflux pump TetB
M00455 - Multidrug resistance, efflux pump MexCD-OprJ
M00454 - Toluene degradation, anaerobic, toluene => benzoyl-CoA
M00456 - Cell wall biosynthesis, peptidoglycan, undecaprenyl-diphosphate
M00457 - OPI anchor biosynthesis, core oligosaccharide
M00137 - Flavanone biosynthesis, phenylalanine => naringenin
M00458 - Cationic antimicrobial peptide (CAMP) resistance, colistin => colistin => colistin-nonapeptide C
M00459 - Penicillin biosynthesis, aminoadipate + cysteine + valine => penicillin
M00460 - 3,8- Dimethylsulacylyl-CoA biosynthesis, malonyl-CoA => 6-methylsalicylate => 3,8-dimethylsalicylyl-CoA
M00461 - Cell wall biosynthesis, peptidoglycan, undecaprenyl-diphosphate
M00462 - SsrS-SsrR (T4SS) response) two-component regulatory system
M00463 - Curcuate degradation, p-curcuate => 2-oxopent-4-enoate + 2-methylpropanoate
M00464 - Glycerol-3P transport system, glycerol-3P => glycerol + glycerol-3P
M00465 - Vancomycin resistance, D-Ala-D-Lac type
M00466 - CzrsR-CzrsK (compatens) two-component regulatory system
M00467 - Cell wall biosynthesis, peptidoglycan, bacterial cell division
M00468 - Cinnamate pathway
M00782 - Pyrimidine biosynthesis, tryptophan => pyrimidine
M00469 - Ubiquinone biosynthesis, 4-hydroxybenzoyl-CoA => 2-hydroxyhexaprenyl-4-HCP => 9-membered enedyne core
M00470 - 12-membered enedyne core biosynthesis, malonyl-CoA => 2-hydroxyhexaprenyl-4-HCP => 12-membered enedyne core
M00471 - dTDP-L-rhamnose biosynthesis
M00472 - dTDP-L-rhamnose biosynthesis
M00473 - dTDP-L-rhamnose biosynthesis
M00802 - Multidrug resistance, efflux pump AcrAD-TolC
M00474 - Multidrug resistance, efflux pump AcrEF-TolC
M00475 - Methylation, ammonia => nitrite
M00476 - Cell wall biosynthesis, peptidoglycan, bacterial two-component regulatory system
M00477 - dTDP-L-rhamnose biosynthesis
M00478 - dTDP-D-ongiosaccharose biosynthesis
M00479 - GlcNAc-6P deacetylase, bacteria
M00480 - Vancomycin resistance, efflux pump MexCDR-OprJD
M00481 - Xanthomonas spp. pathogenicity signature, T3SS and effectors
M00482 - Cell wall biosynthesis, peptidoglycan, archaea
M00483 - Naphthalene degradation, naphthalene => salicylate
M00575 - N-glycan biosynthesis, complex type
M00484 - Polyketide sugar unit biosynthesis, malonyl-CoA => 2-hydroxy-3-methyl-1-naphthoate => 2-hydroxy-7-methyl-3-methyl-1-naphthoyl-CoA
M00485 - C2-C3/C7 beta-series acid moiety biosynthesis, tyrosine => 3-chloro-4,5-dihydroxy-beta-phenylalanine
M00486 - Kedarcidin C: aza-3-chloro-beta-tyrosine moiety biosynthesis, azatyrosine => 2-aza-3-chloro-beta-tyrosyl-PCP
M00487 - Kedarcidin C: 2-aminopropanamide moiety biosynthesis
M00488 - Valdiazen A biosynthesis, anthranilyl-coenzyme-TP => valdiazen A
M00489 - Relecarcinyn biosynthesis, tryptophan => relecarcinyn
M00490 - Helicobacter pylori pathogenicity signature, cagA pathogenicity island
M00491 - Tetracycline/oxytetracycline biosynthesis, gentisoyl-CoA => tetracycline/oxytetracycline
M00492 - Chlorophyll biosynthesis, protoporphyrin IX => chlorophyll a
M00493 - Monoterpenoid biosynthesis, phenylalanine/tyrosine => monoterpenoid
M00377 - Abscisic acid biosynthesis, beta-carotene => abscisic acid
M00494 - Anthracycline biosynthesis, polyketide backbone => anthracycline
M00495 - Benzoyl-CoA degradation, benzoyl-CoA => 3-hydroxypimeyl-CoA
M00719 - Rk-W (virulence regulator) two-component regulatory system
M00496 - Multidrug resistance, efflux pump MdtABC-TolC
M00497 - Imipenem resistance, repressor-of-porin OpmD
M00554 - PprS-PprR (polymyxin adaptive resistance) two-component regulatory system
M00498 - Multidrug resistance, efflux pump MdtH
M00499 - AdeS-AdeR two-component regulatory system
M00500 - Type VI secretion system
M00501 - Multidrug resistance, efflux pump CmeABC
M00502 - GABA biosynthesis, prokaryotes, putrescine => GABA
M00768 - Multidrug resistance, efflux pump MexPQ-OpmE
M00503 - Methylerythritol-4P biosynthesis, deoxyxylulose-5P => 1-hydroxyethylidenyl-diphosphate
M00504 - Homoprotocatechuate degradation, homoprotocatechuate => 2-oxohept-3-enedioate
M00507 - beta-Carotene biosynthesis, GGAP => beta-carotene
M00508 - Pyrazinamide biosynthesis, chorismate => pyrazinamide
M00511 - Jasmonic acid biosynthesis
M00512 - Phosphatidylinositol (PI) biosynthesis cycle
M00513 - Fluoroquinolone transport system
M00705 - Multidrug resistance, efflux pump MdtpA
M00514 - Vancomycin resistance, D-Ala-D-Ser type
M00515 - Vancomycin resistance, D-Ala-D-Ser type
M00516 - VanS-VanR (VanE type vancomycin resistance) two-component regulatory system
M00517 - VanS-VanR (VanG type vancomycin resistance) two-component regulatory system
M00518 - Erythrose-4P/PEP => DAHP
M00519 - VanS-VanR (VanB/vanD) two-component regulatory system
M00520 - Erythritol transport system
M00521 - Multidrug resistance, efflux pump NorA
M00522 - Multidrug resistance, efflux pump NorA
M00524 - RcsC-RcsD (arsenite and arsenitic respiration) two-component regulatory system
M00525 - Multidrug resistance, efflux pump HsrA
M00526 - Multidrug resistance, efflux pump HsrA
M00542 - Putative hydroxymethylpyrimidine transport system
M00543 - Putative 2-aminoethanol transport system
M00544 - GlnK-GlnL (glutamine utilization) two-component regulatory system
M00543 - Cytochrome a/a3-600 menaquinol oxidase
M00545 - Cytochrome c oxidase, prokaryotes
M00546 - Uncharacterized ABC transport system
M00549 - VisR-VisW (cell wall metabolism) two-component regulatory system
M00550 - YvdE-YvdJ (antimicrobial peptide response) two-component regulatory system
M00552 - Arabinosylacetate transport system
M00553 - Cationic amino acid transport system, Lysw, D-aminoadipate => lysine
M00554 - Ornithine biosynthesis, mediated by LysW, glutamate => ornithine
M00555 - YdfH-YdfI two-component regulatory system
M00556 - Multidrug resistance, efflux pump MdtABC two-component regulatory system
M00557 - Nisin resistance, phage shock protein homolog LiaH
M00558 - Betaine biosynthesis, choline => betaine
M00559 - Cell wall biosynthesis, peptidoglycan, bacterial cell division two-component regulatory system
M00560 - Tetracycline resistance, efflux pump
M00561 - Tetracycline resistance, efflux pump
M00562 - Arginine/ornithine transport system
M00563 - RTX toxin transport system
M00564 - Putative D-alanine/D-serine/glycine => beta-alanine, thymine => 3-aminoisobutanoate
M00565 - Copper scrounging system
M00566 - Nitrobenzene transport system
M00567 - Methane => methanol
M00568 - Putative cis-glycerol phosphate transport system
M00569 - Catechol ortho-cleavage, catechol => 3-oxoadipate
M00570 - DcuB-DcuS (C4-dicarboxylate transport) two-component regulatory system
M00571 - Putative spermidine/putrescine transport system
M00572 - Putative D-allose transport system
M00573 - Oligosaccharide transport system
M00574 - Putative sorbitol/mannitol transport system
M00575 - Putative D-glucose transport system
M00576 - FeuQ-FeuP (hydroxycinnamic synthesis regulator) two-component regulatory system
M00577 - Catechol meta-cleavage, catechol => acetyl-CoA / 4-methylpyrocatechol => propanoyl-CoA
M00578 - Chemosensory system, methyl-accepting chemotaxis protein, bacteria
M00579 - Benzene degradation, benzene => catechol
M00580 - Benzoate degradation, cyclohexanecarboxylic acid => pimeloyl-CoA
M00581 - Cell wall biosynthesis, peptidoglycan, bacterial cell division
M00582 - GlnK-GlnR (gamma-sugar metabolism) two-component regulatory system
M00583 - RstB-RstA two-component regulatory system
M00584 - Cell wall biosynthesis, peptidoglycan, bacterial cell division two-component regulatory system
M00585 - TctS-TctR (betaine/choline/carnitine) two-component regulatory system
M00586 - FrlB-FrlC (phase flagellar synthesis) two-component regulatory system
M00587 - Tetracycline resistance, efflux pump
M00588 - Nickel transport system
M00589 - CusS-CusR (copper tolerance) two-component regulatory system
M00590 - CpxR-YeiE (chemosensory) two-component regulatory system
M00591 - Lysine transport system
M00592 - Complete nitrification, comammox, ammonia => nitrite => nitrate
M00593 - Lipopolysaccharide biosynthesis, inner core => outer core => O-antigen
M00594 - Pertussis pathogenicity signature 2, T3SS
M00595 - Cellulose transport system
M00596 - 2-Hydroxycyclohexane-1-one cycle
M00597 - C4-dicarboxylic acid cycle, NAD - malic enzyme type
M00598 - Methylaspartate cycle, glutamate => 3-methylaspartate => mesa,3,4dP3 => myo-inositol
M00599 - Methanogenesis, acetate => methane
M00600 - Thiosulfate oxidation by SOX complex, thiosulfate => sulfate
M00601 - Methylaspartate cycle, 3-methylaspartate => mesaconate => 2-methylsuccinate
M00602 - AauS-AauR (acidic amino acids utilization) two-component regulatory system
M00604 - Tyrosine biosynthesis, prephenate => prehydrotate => tyrosine
M00605 - Multidrug resistance, efflux pump MdtABC
M00606 - Asparagine/aspartate transport system
M00608 - Multidrug resistance, efflux pump AmeABC
M00609 - Cell wall biosynthesis, peptidoglycan, O-Ala/O-Gly biosynthesis, UDP-GlcA => undecaprenyl phosphate alpha-L-Ara4N
M00610 - Sulfonate transport system
M00611 - NarX-NarL (nitrate response) two-component regulatory system
M00612 - Nitrate transport system
M00613 - Glycerophosphodiester transport system
M00614 - Adhesin protein transport system
M00615 - General L-amino acid transport system
M00616 - PilG-PilH (pili field control) two-component regulatory system
M00617 - Cell wall biosynthesis, peptidoglycan, bacterial cell division two-component regulatory system
M00618 - ChvG-ChvI (acidity sensing) two-component regulatory system
M00619 - Glycine betainyl/choline transport system
M00620 - Zinc transport system
M00621 - Zinc transport system
M00622 - Chemoprotectant transport system
M00623 - Urea transport system