

## SUPPLEMENT-F: DIVERSITY OF FUNCTIONAL GENES OBSERVED BY DIRECT METAGENOME ANALYSIS

TABLE 39: RELATIVE ABUNDANCE OF ORF IN FUNCTIONAL CATEGORIES

Functional Category	Number of ORF
Amino acid metabolism	16105
Biosynthesis of other secondary metabolites	1831
Carbohydrate metabolism	14713
Cellular Processes	9488
Energy metabolism	10135
Environmental Information Processing	21078
Enzyme families	5744
Genetic Information Processing	26053
Glycan biosynthesis and metabolism	3299
Human Diseases	4682
Lipid metabolism	3905
Metabolism of cofactors and vitamins	7054
Metabolism of other amino acids	3323
Metabolism of terpenoids and polyketides	2413
Nucleotide metabolism	6197
Organismal Systems	2549
Xenobiotics biodegradation and metabolism	2323
Unclassified	14927

TABLE 40: RESULTS OF RECONSTRUCTED BRITE ANALYSIS.

Genes and Proteins	Number of KEGG Ortholog
<u>Orthologs and modules</u>	
ko00001 KEGG Orthology (KO)	2579
ko00002 KEGG modules	1484
<u>Protein families: metabolism</u>	
ko01000 Enzymes	2511
ko01001 Protein kinases	70
ko01009 Protein phosphatases and associated proteins	25
ko01002 Peptidases	139
ko01003 Glycosyltransferases	59
ko01005 Lipopolysaccharide biosynthesis proteins	45
ko01004 Lipid biosynthesis proteins	34
ko01008 Polyketide biosynthesis proteins	5

ko01006 Prenyltransferases	16
ko01007 Amino acid related enzymes	70
ko00199 Cytochrome P450	2
ko00194 Photosynthesis proteins	10
<b><u>Protein families: genetic information processing</u></b>	
ko03000 Transcription factors	119
ko03021 Transcription machinery	51
ko03019 Messenger RNA biogenesis	41
ko03041 Spliceosome	9
ko03011 Ribosome	49
ko03009 Ribosome biogenesis	88
ko03016 Transfer RNA biogenesis	124
ko03012 Translation factors	30
ko03110 Chaperones and folding catalysts	57
ko04121 Ubiquitin system	38
ko03051 Proteasome	11
ko03032 DNA replication proteins	52
ko03036 Chromosome	80
ko03400 DNA repair and recombination proteins	121
ko03029 Mitochondrial biogenesis	38
<b>Protein families: signaling and cellular processes</b>	
ko02000 Transporters	550
ko02044 Secretion system	117
ko02042 bacterial toxins	6
ko02022 Two-component system	110
ko02035 bacterial motility proteins	85
ko04812 Cytoskeleton proteins	25
ko04147 Exosome	97
ko02048 Prokaryotic defense system	62
ko04030 G protein-coupled receptors	5
ko04050 Cytokine receptors	1
ko04040 Ion channels	8
ko04031 GTP-binding proteins	4
ko04052 Cytokines	1
ko04516 Cell adhesion molecules and their ligands	16
ko04090 Cellular antigens	9
ko00535 Proteoglycans	1
ko00536 Glycosaminoglycan binding proteins	12
ko00537 Glycosylphosphatidylinositol (GPI-anchored proteins )	6
ko04091 Lectins	1
ko01504 Antimicrobial resistance genes	51

TABLE 41: RECONSTRUCTED PATHWAY MODULE

Pathway module
Energy metabolism
Carbon fixation
M00165 Reductive pentose phosphate cycle (Calvin cycle) [PATH:map01200 map00710] (940) (complete)
M00166 Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P [PATH:map01200 map00710] (244) (complete)
M00167 Reductive pentose phosphate cycle, glyceraldehyde-3P => ribulose-5P [PATH:map01200 map00710] (696) (complete)
M00168 CAM (Crassulacean acid metabolism) , dark [PATH:map01200 map00710] (91) (complete)
M00169 CAM (Crassulacean acid metabolism) , light [PATH:map01200 map00710] (167) (complete)
M00172 C4-dicarboxylic acid cycle, NADP - malic enzyme type [PATH:map01200 map00710] (216) (1 block missing)
M00170 C4-dicarboxylic acid cycle, phosphoenolpyruvate carboxykinase type [PATH:map01200 map00710] (101) (2 blocks missing)
M00173 Reductive citrate cycle (Arnon-Buchanan cycle) [PATH:map01200 map00720] (1826) (1 block missing)
M00377 Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway) [PATH:map01200 map00720] (387) (complete)
M00579 Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate [PATH:map01200 map00720] (97) (complete)
M00620 Incomplete reductive citrate cycle, acetyl-CoA => oxoglutarate [PATH:map01200 map00720] (736) (2 blocks missing)
Nitrogen metabolism
M00175 Nitrogen fixation, nitrogen => ammonia [PATH:map00910] (2) (1 block missing)
M00531 Assimilatory nitrate reduction, nitrate => ammonia [PATH:map00910] (42) (complete)
M00530 Dissimilatory nitrate reduction, nitrate => ammonia [PATH:map00910] (184) (complete)
M00529 Denitrification, nitrate => nitrogen [PATH:map00910] (177) (complete)
M00804 Complete nitrification, ammonia => nitrite => nitrate [PATH:map00910] (63) (2 blocks missing)
methane metabolism
M00357 Methanogenesis, acetate => methane [PATH:map01200 map00680] (678) (2 blocks missing)
M00356 Methanogenesis, methanol => methane [PATH:map01200 map00680] (347) (2 blocks missing)
M00358 Coenzyme M biosynthesis [PATH:map00680] (28) (1 block missing)
M00608 2-Oxocarboxylic acid chain extension, 2-oxoglutarate => 2-oxoadipate => 2-oxopimelate => 2-oxosuberate [PATH:map01210 map00680] (7) (1 block missing)
M00346 Formaldehyde assimilation, serine pathway [PATH:map01200 map00680] (351) (2 blocks missing)
M00345 Formaldehyde assimilation, ribulose monophosphate pathway [PATH:map01200 map00680] (227) (complete)
M00344 Formaldehyde assimilation, xylulose monophosphate pathway [PATH:map01200 map00680] (83) (1 block missing)
M00378 F420 biosynthesis [PATH:map00680] (53) (complete)
M00422 Acetyl-CoA pathway, CO2 => acetyl-CoA [PATH:map00680] (83) (complete)
Sulfur metabolism

M00176 Assimilatory sulfate reduction, sulfate => H<sub>2</sub>S [PATH:map00920] (197) (complete)

M00596 Dissimilatory sulfate reduction, sulfate => H<sub>2</sub>S [PATH:map00920] (79) (complete)

M00595 Thiosulfate oxidation by SOX complex, thiosulfate => sulfate [PATH:map00920] (20) (1 block missing)

Carbohydrate and lipid metabolism

Central carbohydrate metabolism

M00001 Glycolysis (Embden-Meyerhof pathway) , glucose => pyruvate [PATH:map01200 map00010] (1164) (complete)

M00002 Glycolysis, core module involving three-carbon compounds [PATH:map01200 map01230 map00010] (716) (complete)

M00003 Gluconeogenesis, oxaloacetate => fructose-6P [PATH:map00010 map00020] (874) (complete)

M00307 Pyruvate oxidation, pyruvate => acetyl-CoA [PATH:map01200 map00010 map00020 map00620] (857) (complete)

M00009 Citrate cycle (TCA cycle, Krebs cycle) [PATH:map01200 map00020] (1533) (complete)

M00010 Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate [PATH:map01200 map01210 map01230 map00020] (368) (complete)

M00011 Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate [PATH:map01200 map00020] (1165) (complete)

M00004 Pentose phosphate pathway (Pentose phosphate cycle) [PATH:map01200 map00030] (610) (complete)

M00006 Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P [PATH:map01200 map00030] (136) (complete)

M00007 Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P [PATH:map01200 map01230 map00030] (392) (complete)

M00580 Pentose phosphate pathway, archaea, fructose 6P => ribose 5P [PATH:map01200 map01230 map00030] (43) (complete)

M00005 PRPP biosynthesis, ribose 5P => PRPP [PATH:map01200 map01230 map00030 map00230] (102) (complete)

M00008 Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate [PATH:map01200 map00030] (101) (complete)

M00308 Semi-phosphorylative Entner-Doudoroff pathway, gluconate => glycerate-3P [PATH:map01200 map00030] (277) (1 block missing)

M00309 Non-phosphorylative Entner-Doudoroff pathway, gluconate/galactonate => glycerate [PATH:map01200 map00030 map00052] (325) (2 blocks missing)

Other carbohydrate metabolism

M00012 Glyoxylate cycle [PATH:map01200 map00630] (367) (complete)

M00373 Ethylmalonyl pathway [PATH:map01200 map00630] (431) (1 block missing)

M00013 Malonate semialdehyde pathway, propanoyl-CoA => acetyl-CoA [PATH:map01200 map00640] (74) (1 block missing)

M00741 Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA [PATH:map01200 map00280 map00630 map00640] (292) (complete)

M00632 Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P [PATH:map00052] (277) (complete)

M00552 D-galactonate degradation, De Ley-Doudoroff pathway, D-galactonate => glycerate-3P [PATH:map00052] (233) (2 blocks missing)

M00014 Glucuronate pathway (uronate pathway) [PATH:map00040] (301) (2 blocks missing)

M00631 D-Galacturonate degradation (bacteria) [PATH:map00040 map00030] (112) (complete)

M00061 D-Glucuronate degradation [PATH:map00040 map00030] (101) (complete)

M00081 Pectin degradation [PATH:map00040] (4) (2 blocks missing)

M00565 Trehalose biosynthesis, D-glucose 1P => trehalose [PATH:map00500] (588) (complete)

M00549 Nucleotide sugar biosynthesis, glucose => UDP-glucose [PATH:map00520] (227) (complete)

M00554 Nucleotide sugar biosynthesis, galactose => UDP-galactose [PATH:map00520 map00052] (81) (complete)

M00793 dTDP-L-rhamnose biosynthesis [PATH:map00521 map00523] (241) (complete)

**Fatty acid metabolism**

M00082 Fatty acid biosynthesis, initiation [PATH:map01212 map00061] (371) (complete)

M00083 Fatty acid biosynthesis, elongation [PATH:map01212 map00061] (551) (complete)

M00085 Fatty acid biosynthesis, elongation, mitochondria [PATH:map01212 map00062] (6) (2 blocks missing)

M00086 beta-Oxidation, acyl-CoA synthesis [PATH:map01212 map00071] (308) (complete)

M00087 beta-Oxidation [PATH:map01212 map00071] (266) (complete)

M00088 Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone [PATH:map00072] (358) (complete)

**Lipid metabolism**

M00089 Triacylglycerol biosynthesis [PATH:map00561] (212) (2 blocks missing)

M00098 Acylglycerol degradation [PATH:map00561] (3) (1 block missing)

M00091 Phosphatidylcholine (PC) biosynthesis, PE => PC [PATH:map00564] (2) (complete)

M00093 Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE [PATH:map00564] (126) (complete)

M00131 Inositol phosphate metabolism, Ins (1,3,4,5) P4 => Ins (1,3,4) P3 => myo-inositol [PATH:map00562] (73) (2 blocks missing)

M00066 Lactosylceramide biosynthesis [PATH:map00600] (2) (1 block missing)

M00100 Sphingosine degradation [PATH:map00600] (2) (1 block missing)

**Lipopolysaccharide metabolism**

M00060 Lipopolysaccharide biosynthesis, KDO2-lipid A [PATH:map00540] (240) (complete)

M00063 CMP-KDO biosynthesis [PATH:map00540] (80) (complete)

M00064 ADP-L-glycero-D-manno-heptose biosynthesis [PATH:map00540] (77) (complete)

**Glycan metabolism**

M00072 N-glycosylation by oligosaccharyltransferase [PATH:map00510] (16) (1 block missing)

**Glycosaminoglycan metabolism**

M00076 Dermatan sulfate degradation [PATH:map00531] (13) (2 blocks missing)

M00077 Chondroitin sulfate degradation [PATH:map00531] (13) (1 block missing)

M00079 Keratan sulfate degradation [PATH:map00531] (21) (2 blocks missing)

**Terpenoid backbone biosynthesis**

M00095 C5 isoprenoid biosynthesis, mevalonate pathway [PATH:map00900] (385) (complete)

M00096 C5 isoprenoid biosynthesis, non-mevalonate pathway [PATH:map00900] (460) (complete)

M00364 C10-C20 isoprenoid biosynthesis, *Bacteria* [PATH:map00900] (114) (complete)

M00365 C10-C20 isoprenoid biosynthesis, *Archaea* [PATH:map00900] (70) (complete)

M00366 C10-C20 isoprenoid biosynthesis, plants [PATH:map00900] (69) (2 blocks missing)

M00367 C10-C20 isoprenoid biosynthesis, non-plant eukaryotes [PATH:map00900] (35) (2 blocks missing)

**Sterol biosynthesis**

M00107 Steroid hormone biosynthesis, cholesterol => progesterone => progesterone [PATH:map00140] (1) (1 block missing)

M00110 C19/C18-Steroid hormone biosynthesis, pregnenolone => androstenedione => estrone [PATH:map00140] (1) (2 blocks missing)

#### Other terpenoid biosynthesis

M00097 beta-Carotene biosynthesis, GGAP => beta-carotene [PATH:map00906] (45) (2 blocks missing)

#### Nucleotide and amino acid metabolism

##### Purine metabolism

M00048 Inosine monophosphate biosynthesis, PRPP + glutamine => IMP [PATH:map00230] (894) (complete)

M00049 Adenine ribonucleotide biosynthesis, IMP => ADP,ATP [PATH:map00230] (359) (complete)

M00050 Guanine ribonucleotide biosynthesis IMP => GDP,GTP [PATH:map00230] (396) (complete)

M00546 Purine degradation, xanthine => urea [PATH:map00230] (55) (1 block missing)

##### Pyrimidine metabolism

M00051 Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP [PATH:map00240] (758) (complete)

M00052 Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP [PATH:map00240] (174) (complete)

M00053 Pyrimidine deoxyribonucleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP [PATH:map00240] (452) (complete)

M00046 Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate [PATH:map00240] (72) (complete)

##### Serine and threonine metabolism

M00020 Serine biosynthesis, glycerate-3P => serine [PATH:map01200 map01230 map00260] (191) (complete)

M00018 Threonine biosynthesis, aspartate => homoserine => threonine [PATH:map01230 map00260] (448) (complete)

M00555 Betaine biosynthesis, choline => betaine [PATH:map00260] (26) (complete)

##### Cysteine and methionine metabolism

M00021 Cysteine biosynthesis, serine => cysteine [PATH:map01200 map01230 map00270] (127) (complete)

M00338 Cysteine biosynthesis, homocysteine + serine => cysteine [PATH:map01230 map00270] (34) (complete)

M00609 Cysteine biosynthesis, methionine => cysteine [PATH:map01230 map00270] (150) (complete)

M00017 Methionine biosynthesis, aspartate => homoserine => methionine [PATH:map01230 map00270] (585) (complete)

M00034 Methionine salvage pathway [PATH:map00270] (350) (complete)

M00035 Methionine degradation [PATH:map00270] (275) (complete)

M00368 Ethylene biosynthesis, methionine => ethylene [PATH:map00270] (103) (2 blocks missing)

##### Branched-chain amino acid metabolism

M00019 Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine [PATH:map01210 map01230 map00290] (513) (complete)

M00535 Isoleucine biosynthesis, pyruvate => 2-oxobutanoate [PATH:map01210 map01230 map00290] (184) (complete)

M00570 Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine [PATH:map01230 map00290] (601) (complete)

M00432 Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate [PATH:map01210 map01230 map00290] (314) (complete)

M00036 Leucine degradation, leucine => acetoacetate + acetyl-CoA [PATH:map00280] (484) (complete)

##### Lysine metabolism

M00016 Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine [PATH:map01230 map00300] (590) (complete)

M00525 Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine [PATH:map01230 map00300] (495) (complete)

M00526 Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine [PATH:map01230 map00300] (436) (complete)

M00527 Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine [PATH:map01230 map00300] (519) (complete)

M00433 Lysine biosynthesis, 2-oxoglutarate => 2-oxoadipate [PATH:map01210 map01230 map00300] (6) (1 block missing)

M00031 Lysine biosynthesis, mediated by LysW, 2-aminoadipate => lysine [PATH:map01210 map01230 map00300] (29) (1 block missing)

M00032 Lysine degradation, lysine => saccharopine => acetoacetyl-CoA [PATH:map00310] (243) (2 blocks missing)

#### Arginine and proline metabolism

M00015 Proline biosynthesis, glutamate => proline [PATH:map01230 map00330] (149) (complete)

M00028 Ornithine biosynthesis, glutamate => ornithine [PATH:map01210 map01230 map00220] (298) (complete)

M00763 Ornithine biosynthesis, mediated by LysW, glutamate => ornithine [PATH:map01230 map01210 map00220] (22) (2 blocks missing)

M00029 Urea cycle [PATH:map01230 map00220] (232) (1 block missing)

#### Histidine metabolism

M00026 Histidine biosynthesis, PRPP => histidine [PATH:map01230 map00340] (586) (complete)

M00045 Histidine degradation, histidine => N-formiminoglutamate => glutamate [PATH:map00340] (212) (complete)

#### Aromatic amino acid metabolism

M00022 Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate [PATH:map01230 map00400] (393) (complete)

M00023 Tryptophan biosynthesis, chorismate => tryptophan [PATH:map01230 map00400] (372) (complete)

M00024 Phenylalanine biosynthesis, chorismate => phenylalanine [PATH:map01230 map00400] (62) (complete)

M00025 Tyrosine biosynthesis, chorismate => tyrosine [PATH:map01230 map00400] (79) (complete)

M00040 Tyrosine biosynthesis, prephanate => pretyrosine => tyrosine [PATH:map01230 map00400] (2) (1 block missing)

M00042 Catecholamine biosynthesis, tyrosine => dopamine => noradrenaline => adrenaline [PATH:map00350] (16) (2 blocks missing)

M00044 Tyrosine degradation, tyrosine => homogentisate [PATH:map00350] (37) (2 blocks missing)

M00533 Homoprotocatechuate degradation, homoprotocatechuate => 2-oxohept-3-enedioate [PATH:map01220 map00350] (9) (1 block missing)

M00545 Trans-cinnamate degradation, trans-cinnamate => acetyl-CoA [PATH:map01220 map00360] (32) (1 block missing)

M00038 Tryptophan metabolism, tryptophan => kynurenine => 2-aminomuconate [PATH:map00380] (102) (complete)

#### Other amino acid metabolism

M00033 Ectoine biosynthesis, aspartate => ectoine [PATH:map01210 map01230 map00260] (233) (complete)

M00027 GABA (gamma-Aminobutyrate) shunt [PATH:map00250] (125) (complete)

M00047 Creatine pathway [PATH:map00330] (2) (1 block missing)

#### Cofactor and vitamin biosynthesis

M00127 Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P [PATH:map00730] (177) (complete)

M00125 Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD [PATH:map00740] (349) (complete)

M00124 Pyridoxal biosynthesis, erythrose-4P => pyridoxal-5P [PATH:map00750] (115) (1 block missing)

M00115 NAD biosynthesis, aspartate => NAD [PATH:map00760] (357) (complete)

M00119 Pantothenate biosynthesis, valine/L-aspartate => pantothenate [PATH:map00770] (250) (complete)

M00120 Coenzyme A biosynthesis, pantothenate => CoA [PATH:map00770] (210) (complete)

M00572 Pimeloyl-ACP biosynthesis, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP [PATH:map00780] (410) (complete)

M00123 Biotin biosynthesis, pimeloyl-ACP/CoA => biotin [PATH:map00780] (96) (complete)

M00573 Biotin biosynthesis, BioI pathway, long-chain-acyl-ACP => pimeloyl-ACP => biotin [PATH:map00780] (96) (1 block missing)

M00577 Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin [PATH:map00780] (99) (complete)

M00126 Tetrahydrofolate biosynthesis, GTP => THF [PATH:map00790 map00670] (394) (1 block missing)

M00121 Heme biosynthesis, glutamate => protoheme/siroheme [PATH:map00860] (803) (complete)

M00129 Ascorbate biosynthesis, animals, glucose-1P => ascorbate [PATH:map00040 map00053] (197) (1 block missing)

M00122 Cobalamin biosynthesis, cobinamide => cobalamin [PATH:map00860] (138) (complete)

M00117 Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone [PATH:map00130] (167) (1 block missing)

M00116 Menaquinone biosynthesis, chorismate => menaquinone [PATH:map00130] (157) (1 block missing)

M00118 Glutathione biosynthesis, glutamate => glutathione [PATH:map00480] (36) (complete)

M00140 C1-unit interconversion, prokaryotes [PATH:map00670] (249) (complete)

M00141 C1-unit interconversion, eukaryotes [PATH:map00670] (128) (complete)

**Polyamine biosynthesis**

M00133 Polyamine biosynthesis, arginine => agatine => putrescine => spermidine [PATH:map00330] (191) (complete)

M00134 Polyamine biosynthesis, arginine => ornithine => putrescine [PATH:map00330] (28) (complete)

M00135 GABA biosynthesis, eukaryotes, putrescine => GABA [PATH:map00330] (140) (complete)

**Secondary metabolism**

**Aromatics degradation**

M00538 Toluene degradation, toluene => benzoate [PATH:map01220 map00623] (2) (2 blocks missing)

M00537 Xylene degradation, xylene => methylbenzoate [PATH:map01220 map00622] (2) (2 blocks missing)

M00548 Benzene degradation, benzene => catechol [PATH:map01220 map00362] (4) (1 block missing)

M00551 Benzoate degradation, benzoate => catechol / methylbenzoate => methylcatechol [PATH:map01220 map00362 map00622] (2) (2 blocks missing)

M00637 Anthranilate degradation, anthranilate => catechol [PATH:map00627] (2) (1 block missing)

M00568 Catechol ortho-cleavage, catechol => 3-oxoadipate [PATH:map01220 map00362] (9) (1 block missing)

M00569 Catechol meta-cleavage, catechol => acetyl-CoA / 4-methylcatechol => propanoyl-CoA [PATH:map01220 map00362 map00622] (48) (1 block missing)

M00541 Benzoyl-CoA degradation, benzoyl-CoA => 3-hydroxypimeloyl-CoA [PATH:map01220 map00362] (11) (2 blocks missing)

M00540 Benzoate degradation, cyclohexanecarboxylic acid => pimeloyl-CoA [PATH:map01220 map00362] (5) (2 blocks missing)

M00638 Salicylate degradation, salicylate => gentisate [PATH:map00626] (3) (1 block missing)



M00623 Phthalate degradation, phthalate => protocatechuate [PATH:map01220 map00624] (2) (2 blocks missing)

Biosynthesis of secondary metabolites

M00778 Type II polyketide backbone biosynthesis, acyl-CoA + malonyl-CoA => polyketide [PATH:map01056] (1) (2 blocks missing)

Structural complex

Energy metabolism

ATP synthesis

M00144 NADH:quinone oxidoreductase, prokaryotes [PATH:map00190] (867) (1 block missing)

M00145 NAD (P) H:quinone oxidoreductase, chloroplasts and cyanobacteria [PATH:map00190] (1) (1 block missing)

M00143 NADH dehydrogenase (ubiquinone) Fe-S protein/ flavoprotein complex, mitochondria [PATH:map00190] (3) (1 block missing)

M00149 Succinate dehydrogenase, prokaryotes [PATH:map00190] (186) (complete)

M00150 Fumarate reductase, prokaryotes [PATH:map00190] (18) (1 block missing)

M00162 Cytochrome b6f complex [PATH:map00195] (6) (1 block missing)

M00151 Cytochrome bc1 complex respiratory unit [PATH:map00190] (75) (complete)

M00152 Cytochrome bc1 complex [PATH:map00190] (32) (1 block missing)

M00154 Cytochrome c oxidase [PATH:map00190] (40) (1 block missing)

M00155 Cytochrome c oxidase, prokaryotes [PATH:map00190] (256) (complete)

M00153 Cytochrome d ubiquinol oxidase [PATH:map00190] (77) (complete)

M00417 Cytochrome o ubiquinol oxidase [PATH:map00190] (5) (1 block missing)

M00156 Cytochrome c oxidase, cbb3-type [PATH:map00190] (29) (1 block missing)

M00157 F-type ATPase, prokaryotes and chloroplasts [PATH:map00190 map00195] (351) (complete)

M00158 F-type ATPase, eukaryotes [PATH:map00190] (1) (1 block missing)

M00159 V-type ATPase, prokaryotes [PATH:map00190] (206) (1 block missing)

M00160 V-type ATPase, eukaryotes [PATH:map00190] (3) (1 block missing)

Genetic information processing

DNA polymerase

M00260 DNA polymerase III complex, *Bacteria* [PATH:map03030 map03430 map03440] [BR:ko03032 ko03400] (646) (complete)

M00264 DNA polymerase II complex, *Archaea* [BR:ko03032] (32) (complete)

M00262 DNA polymerase delta complex [PATH:map03030 map03410 map03420] [BR:ko03032 ko03400] (2) (1 block missing)

Replication system

M00288 RPA complex [PATH:map03030 map03420 map03430 map03440] [BR:ko03032 ko03400] (9) (1 block missing)

Repair system

M00290 Holo-TFIIH complex [PATH:map03420] [BR:ko03021 ko03400] (23) (1 block missing)

M00295 BRCA1-associated genome surveillance complex (BASC) [PATH:map03430 map03440 map03460] [BR:ko03400] (2) (1 block missing)

M00413 FA core complex [PATH:map03460] [BR:ko03400] (12) (1 block missing)

M00414 Bloom's syndrome complex [PATH:map03460] [BR:ko03400] (1) (1 block missing)

RNA polymerase

M00183 RNA polymerase, *Bacteria* [PATH:map03020] [BR:ko03021 ko03400] (588) (complete)

M00184 RNA polymerase, *Archaea* [PATH:map03020] [BR:ko03021] (55) (1 block missing)

M00180 RNA polymerase II, eukaryotes [PATH:map03020 map05016] [BR:ko03021 ko03400] (1) (1 block missing)

Spliceosome

M00352 Spliceosome, U2-snRNP [PATH:map03040] [BR:ko03041] (1) (1 block missing)

M00354 Spliceosome, U4/U6.U5 tri-snRNP [PATH:map03040] [BR:ko03041] (2) (1 block missing)

M00355 Spliceosome, 35S U5-snRNP [PATH:map03040] [BR:ko03041] (2) (1 block missing)

M00353 Spliceosome, Prp19/CDC5L complex [PATH:map03040] [BR:ko03041] (1) (1 block missing)

RNA processing

M00425 H/ACA ribonucleoprotein complex [PATH:map03008] [BR:ko03032 ko03009] (5) (1 block missing)

M00427 Nuclear pore complex [PATH:map03013] (1) (1 block missing)

M00390 Exosome, *Archaea* [PATH:map03018] (17) (complete)

M00391 Exosome, eukaryotes [PATH:map03018] (17) (1 block missing)

M00394 RNA degradosome [PATH:map03018] (283) (complete)

Ribosome

M00178 Ribosome, *Bacteria* [PATH:map03010] [BR:ko03011] (844) (1 block missing)

M00179 Ribosome, *Archaea* [PATH:map03010] [BR:ko03011] (628) (1 block missing)

M00177 Ribosome, eukaryotes [PATH:map03010] [BR:ko03011] (30) (1 block missing)

Proteasome

M00341 Proteasome, 19S regulatory particle (PA700) [PATH:map03050] [BR:ko03051] (5) (1 block missing)

M00342 bacterial proteasome [PATH:map03050] [BR:ko03051] (41) (complete)

M00343 archaeal proteasome [PATH:map03050] [BR:ko03051] (13) (complete)

Ubiquitin system

M00389 APC/C complex [PATH:map04120 map04110 map04114 map04914 map04111 map04113] [BR:ko04121 ko03036] (3) (1 block missing)

Protein processing

M00400 p97-Ufd1-Npl4 complex [PATH:map04141] (37) (1 block missing)

M00401 Sec61 complex [PATH:map03060 map04141 map04145 map05110] [BR:ko02044] (4) (1 block missing)

M00403 HRD1/SEL1 ERAD complex [PATH:map04141] (38) (1 block missing)

M00412 ESCRT-III complex [PATH:map04144] (1) (1 block missing)

Environmental information processing

Mineral and organic ion transport system

M00185 Sulfate transport system [PATH:map02010] [BR:ko02000] (16) (complete)

M00189 Molybdate transport system [PATH:map02010] [BR:ko02000] (84) (complete)

M00423 Molybdate/tungstate transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00186 Tungstate transport system [PATH:map02010] [BR:ko02000] (67) (complete)

M00438 Nitrate/nitrite transport system [PATH:map02010] [BR:ko02000] (16) (complete)

M00188 NitT/TauT family transport system [BR:ko02000] (159) (complete)

M00436 Sulfonate transport system [PATH:map02010] [BR:ko02000] (13) (complete)

M00190 Iron (III) transport system [PATH:map02010] [BR:ko02000] (256) (complete)

M00191 Thiamine transport system [PATH:map02010] [BR:ko02000] (22) (complete)

M00299 Spermidine/putrescine transport system [PATH:map02010] [BR:ko02000] (66) (complete)

M00300 Putrescine transport system [PATH:map02010] [BR:ko02000] (14) (complete)

M00193 Putative spermidine/putrescine transport system [BR:ko02000] (58) (complete)

M00208 Glycine betaine/proline transport system [PATH:map02010] [BR:ko02000] (101) (complete)

M00209 Osmoprotectant transport system [PATH:map02010] [BR:ko02000] (114) (complete)

M00442 Putative hydroxymethylpyrimidine transport system [PATH:map02010] [BR:ko02000] (15) (complete)

Saccharide, polyol, and lipid transport system

M00194 Maltose/maltodextrin transport system [PATH:map02010] [BR:ko02000] (76) (1 block missing)

M00196 Multiple sugar transport system [PATH:map02010] [BR:ko02000] (149) (complete)

M00201 alpha-Glucoside transport system [PATH:map02010] [BR:ko02000] (103) (complete)

M00605 Glucose/mannose transport system [PATH:map02010] [BR:ko02000] (90) (complete)

M00204 Trehalose/maltose transport system [PATH:map02010] [BR:ko02000] (19) (complete)

M00604 Trehalose transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00205 N-Acetylglucosamine transport system [PATH:map02010] [BR:ko02000] (12) (complete)

M00206 Cellobiose transport system [PATH:map02010] [BR:ko02000] (100) (complete)

M00606 N,N'-Diacetylchitobiose transport system [PATH:map02010] [BR:ko02000] (77) (complete)

M00601 Putative chitobiose transport system [PATH:map02010] [BR:ko02000] (6) (complete)

M00199 L-Arabinose/lactose transport system [PATH:map02010] [BR:ko02000] (14) (complete)

M00202 Oligogalacturonide transport system [PATH:map02010] [BR:ko02000] (4) (complete)

M00600 alpha-1,4-Digalacturonate transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00603 Putative aldouronate transport system [PATH:map02010] [BR:ko02000] (98) (complete)

M00215 D-Xylose transport system [PATH:map02010] [BR:ko02000] (18) (complete)

M00216 Multiple sugar transport system [PATH:map02010] [BR:ko02000] (22) (complete)

M00218 Fructose transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00220 Rhamnose transport system [PATH:map02010] [BR:ko02000] (12) (complete)

M00212 Ribose transport system [PATH:map02010] [BR:ko02000] (184) (complete)

M00590 Erythritol transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00591 Putative xylitol transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00592 Inositol transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00593 Inositol transport system [PATH:map02010] [BR:ko02000] (3) (1 block missing)

M00599 Inositol-phosphate transport system [PATH:map02010] [BR:ko02000] (4) (complete)

M00197 Putative fructooligosaccharide transport system [BR:ko02000] (73) (1 block missing)

M00607 Glycerol transport system [PATH:map02010] [BR:ko02000] (5) (1 block missing)

M00198 Putative sn-glycerol-phosphate transport system [PATH:map02010] [BR:ko02000] (68) (complete)

M00200 Putative sorbitol/mannitol transport system [PATH:map02010] [BR:ko02000] (77) (1 block missing)

M00602 Arabinosaccharide transport system [PATH:map02010] [BR:ko02000] (83) (complete)

M00669 gamma-Hexachlorocyclohexane transport system [BR:ko02000] (101) (1 block missing)

M00210 Phospholipid transport system [PATH:map02010] [BR:ko02000] (111) (complete)

M00670 Mce transport system [BR:ko02000] (101) (1 block missing)

M00491 arabinogalactan oligomer/maltooligosaccharide transport system [PATH:map02010] [BR:ko02000] (136) (complete)

M00207 Putative multiple sugar transport system [BR:ko02000] (477) (complete)

M00221 Putative simple sugar transport system [BR:ko02000] (252) (complete)

M00211 Putative ABC transport system [BR:ko02000] (34) (complete)

#### Phosphate and amino acid transport system

M00222 Phosphate transport system [PATH:map02010] [BR:ko02000] (353) (complete)

M00223 Phosphonate transport system [PATH:map02010] [BR:ko02000] (148) (complete)

M00227 Glutamine transport system [PATH:map02010] [BR:ko02000] (13) (1 block missing)

M00230 Glutamate/aspartate transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00232 General L-amino acid transport system [PATH:map02010] [BR:ko02000] (34) (complete)

M00233 Glutamate transport system [PATH:map02010] [BR:ko02000] (3) (1 block missing)

M00234 Cystine transport system [PATH:map02010] [BR:ko02000] (13) (complete)

M00235 Arginine/ornithine transport system [PATH:map02010] [BR:ko02000] (3) (1 block missing)

M00237 Branched-chain amino acid transport system [PATH:map02010] [BR:ko02000] (705) (complete)

M00322 Neutral amino acid transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00323 Urea transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00238 D-Methionine transport system [PATH:map02010] [BR:ko02000] (56) (complete)

M00586 Putative amino-acid transport system [PATH:map02010] [BR:ko02000] (3) (1 block missing)

M00236 Putative polar amino acid transport system [BR:ko02000] (114) (complete)

#### Peptide and nickel transport system

M00439 Oligopeptide transport system [PATH:map02010] [BR:ko02000] (211) (complete)

M00324 Dipeptide transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00566 Dipeptide transport system, Firmicutes [PATH:map02010] [BR:ko02000] (16) (1 block missing)

M00440 Nickel transport system [PATH:map02010] [BR:ko02000] (18) (complete)

M00348 Glutathione transport system [PATH:map02010] [BR:ko02000] (10) (1 block missing)

M00239 Peptides/nickel transport system [PATH:map02010] [BR:ko02000] (1512) (complete)

M00349 Microcin C transport system [PATH:map02010] [BR:ko02000] (55) (complete)

#### Metallic cation, iron-siderophore and vitamin B12 transport system

M00240 Iron complex transport system [PATH:map02010] [BR:ko02000] (356) (complete)

M00242 Zinc transport system [PATH:map02010] [BR:ko02000] (128) (complete)

M00317 Manganese/iron transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00792 Manganese/zinc transport system [PATH:map02010] [BR:ko02000] (23) (complete)

M00319 Manganese/zinc/iron transport system [PATH:map02010] [BR:ko02000] (38) (complete)

M00243 Manganese/iron transport system [BR:ko02000] (5) (1 block missing)

M00245 Cobalt/nickel transport system [PATH:map02010] [BR:ko02000] (55) (1 block missing)

M00246 Nickel transport system [PATH:map02010] [BR:ko02000] (56) (complete)

M00581 Biotin transport system [PATH:map02010] [BR:ko02000] (21) (1 block missing)

M00582 Energy-coupling factor transport system [PATH:map02010] [BR:ko02000] (232) (complete)

M00244 Putative zinc/manganese transport system [BR:ko02000] (13) (1 block missing)

M00247 Putative ABC transport system [BR:ko02000] (39) (complete)

#### ABC-2 type and other transport systems

M00298 Multidrug/hemolysin transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00250 Lipopolysaccharide transport system [PATH:map02010] [BR:ko02000] (63) (complete)

M00320 Lipopolysaccharide export system [PATH:map02010] [BR:ko02000] (78) (complete)

M00251 Teichoic acid transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00252 Lipooligosaccharide transport system [PATH:map02010] [BR:ko02000] (34) (complete)

M00253 Sodium transport system [PATH:map02010] [BR:ko02000] (27) (complete)

M00762 Copper-processing system [PATH:map02010] [BR:ko02000] (16) (complete)

M00634 Oleandomycin transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00747 Bacitracin transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00314 Bacitracin transport system [PATH:map02010 map02020] [BR:ko02000] (13) (complete)

M00224 Fluoroquinolone transport system [PATH:map02010] [BR:ko02000] (27) (complete)

M00255 Lipoprotein-releasing system [PATH:map02010] [BR:ko02000] (85) (complete)

M00259 Heme transport system [PATH:map02010] [BR:ko02000] (49) (complete)

M00256 Cell division transport system [PATH:map02010] [BR:ko02000] (88) (complete)

M00315 Uncharacterized ABC transport system [PATH:map02020] [BR:ko02000] (5) (complete)

M00258 Putative ABC transport system [BR:ko02000] (656) (complete)

M00254 ABC-2 type transport system [BR:ko02000] (1107) (complete)

Drug efflux transporter/pump

M00720 Multidrug resistance, efflux pump VexEF-ToIC (56) (complete)

Phosphotransferase system (PTS)

M00265 PTS system, glucose-specific II component [PATH:map00010 map02060] [BR:ko02000] (4) (1 block missing)

M00267 PTS system, N-acetylglucosamine-specific II component [PATH:map00520 map02060] [BR:ko02000] (14) (1 block missing)

M00266 PTS system, maltose and glucose-specific II component [PATH:map00010 map00500 map02060] [BR:ko02000] (8) (complete)

M00282 PTS system, D-glucosamine-specific II component [PATH:map00520 map02060] [BR:ko02000] (33) (complete)

M00269 PTS system, sucrose-specific II component [PATH:map00500 map02060] [BR:ko02000] (18) (1 block missing)

M00271 PTS system, beta-glucosides-specific II component [PATH:map02060] [BR:ko02000] (33) (complete)

M00272 PTS system, arbutin-, cellobiose-, and salicin-specific II component [PATH:map00010 map02060] [BR:ko02000] (4) (1 block missing)

M00270 PTS system, trehalose-specific II component [PATH:map00500 map02060] [BR:ko02000] (18) (complete)

M00303 PTS system, N-acetylmuramic acid-specific II component [PATH:map02060] [BR:ko02000] (4) (1 block missing)

M00268 PTS system, arbutin-like II component [PATH:map00010 map02060] [BR:ko02000] (14) (complete)

M00273 PTS system, fructose-specific II component [PATH:map00051 map02060] [BR:ko02000] (50) (complete)

M00306 PTS system, fructose-specific II-like component [BR:ko02000] (1) (1 block missing)

M00274 PTS system, mannitol-specific II component [PATH:map00051 map02060] [BR:ko02000] (18) (complete)

M00281 PTS system, lactose-specific II component [PATH:map00052 map02060] [BR:ko02000] (2) (1 block missing)

M00275 PTS system, cellobiose-specific II component [PATH:map02060] [BR:ko02000] (7) (1 block missing)

M00280 PTS system, glucitol/sorbitol-specific II component [PATH:map00051 map02060] [BR:ko02000] (10) (1 block missing)

M00279 PTS system, galactitol-specific II component [PATH:map00052 map02060] [BR:ko02000] (9) (1 block missing)

M00276 PTS system, mannose-specific II component [PATH:map00051 map02060] [BR:ko02000] (8) (complete)

M00283 PTS system, ascorbate-specific II component [PATH:map00053 map02060] [BR:ko02000] (9) (1 block missing)

**bacterial secretion system**

M00325 alpha-Hemolysin/cyclolysin transport system [PATH:map02010 map03070] [BR:ko02044] (22) (complete)

M00326 RTX toxin transport system [BR:ko02044] (20) (1 block missing)

M00330 Adhesin protein transport system [BR:ko02044] (3) (1 block missing)

M00571 AlgE-type Mannuronan C-5-Epimerase transport system [BR:ko02044] (20) (1 block missing)

M00339 RaxAB-RaxC type I secretion system [PATH:map04626] [BR:ko02044] (24) (1 block missing)

M00331 Type II general secretion system [PATH:map03070] [BR:ko02044] (201) (complete)

M00332 Type III secretion system [PATH:map03070] [BR:ko02044] (1) (1 block missing)

M00333 Type IV secretion system [PATH:map03070] [BR:ko02044] (3) (1 block missing)

M00334 Type VI secretion system [PATH:map03070] [BR:ko02044] (105) (complete)

M00335 Sec (secretion) system [PATH:map03070] [BR:ko02044] (706) (1 block missing)

M00336 Twin-arginine translocation (Tat) system [PATH:map03070] [BR:ko02044] (47) (complete)

M00429 Competence-related DNA transformation transporter [BR:ko02044] (189) (1 block missing)

**Functional set**

**Metabolism**

**Aminoacyl tRNA**

M00360 Aminoacyl-tRNA biosynthesis, prokaryotes [PATH:map00970] (2777) (complete)

M00359 Aminoacyl-tRNA biosynthesis, eukaryotes [PATH:map00970] (2616) (complete)

**Nucleotide sugar**

M00362 Nucleotide sugar biosynthesis, prokaryotes [PATH:map00520] (679) (complete)

M00361 Nucleotide sugar biosynthesis, eukaryotes [PATH:map00520] (426) (complete)

**Environmental information processing**

**Two-component regulatory system**

M00434 PhoR-PhoB (phosphate starvation response) two-component regulatory system [PATH:map02020] [BR:ko02022] (127) (complete)

M00443 SenX3-RegX3 (phosphate starvation response) two-component regulatory system [PATH:map02020] [BR:ko02022] (10) (complete)

M00444 PhoQ-PhoP (magnesium transport) two-component regulatory system [PATH:map02020] [BR:ko02022] (10) (complete)

M00445 EnvZ-OmpR (osmotic stress response) two-component regulatory system [PATH:map02020] [BR:ko02022] (6) (complete)

M00446 RstB-RstA two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (1 block missing)

M00447 CpxA-CpxR (envelope stress response) two-component regulatory system [PATH:map02020] [BR:ko02022] (4) (complete)

M00448 CsxS-CsxR (secretion stress response) two-component regulatory system [PATH:map02020] [BR:ko02022] (17) (complete)

M00449 CreC-CreB (phosphate regulation) two-component regulatory system [PATH:map02020] [BR:ko02022] (1) (1 block missing)

M00450 BaeS-BaeR (envelope stress response) two-component regulatory system [PATH:map02020] [BR:ko02022] (16) (complete)

M00452 CusS-CusR (copper tolerance) two-component regulatory system [PATH:map02020] [BR:ko02022] (3) (complete)

M00453 QseC-QseB (quorum sensing) two-component regulatory system [PATH:map02020] [BR:ko02022] (5) (complete)

M00454 KdpD-KdpE (potassium transport) two-component regulatory system [PATH:map02020] [BR:ko02022] (45) (complete)

M00458 ResE-ResD (aerobic and anaerobic respiration) two-component regulatory system [PATH:map02020] [BR:ko02022] (22) (complete)

M00459 VicK-VicR (cell wall metabolism) two-component regulatory system [PATH:map02020] [BR:ko02022] (46) (complete)

M00460 MprB-MprA (maintenance of persistent infection) two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (complete)

M00461 MtrB-MtrA (osmotic stress response) two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (complete)

M00467 SasA-RpaAB (circadian timing mediating) two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (2 blocks missing)

M00469 BceS-BceR (bacitracin transport) two-component regulatory system [PATH:map02020] [BR:ko02022] (10) (complete)

M00471 NarX-NarL (nitrate respiration) two-component regulatory system [PATH:map02020] [BR:ko02022] (13) (complete)

M00473 UhpB-UhpA (hexose phosphates uptake) two-component regulatory system [PATH:map02020] [BR:ko02022] (1) (1 block missing)

M00475 BarA-UvrY (central carbon metabolism) two-component regulatory system [PATH:map02020] [BR:ko02022] (8) (complete)

M00476 ComP-ComA (competence) two-component regulatory system [PATH:map02020] [BR:ko02022] (1) (1 block missing)

M00478 DegS-DegU (multicellular behavior control) two-component regulatory system [PATH:map02020] [BR:ko02022] (27) (complete)

M00479 DesK-DesR (membrane lipid fluidity regulation) two-component regulatory system [PATH:map02020] [BR:ko02022] (30) (complete)

M00481 LiaS-LiaR (cell wall stress response) two-component regulatory system [PATH:map02020] [BR:ko02022] (29) (complete)

M00483 NreB-NreC (dissimilatory nitrate/nitrite reduction) two-component regulatory system [PATH:map02020] [BR:ko02022] (4) (1 block missing)

M00489 DctS-DctR (C4-dicarboxylate transport) two-component regulatory system [PATH:map02020] [BR:ko02022] (6) (complete)

M00490 MalK-MalR (malate transport) two-component regulatory system [PATH:map02020] [BR:ko02022] (3) (complete)

M00492 LytS-LytR two-component regulatory system [PATH:map02020] [BR:ko02022] (13) (complete)

M00493 AlgZ-AlgR (alginate production) two-component regulatory system [PATH:map02020] [BR:ko02022] (15) (complete)

M00497 GlnL-GlnG (nitrogen regulation) two-component regulatory system [PATH:map02020] [BR:ko02022] (32) (complete)

M00498 NtrY-NtrX (nitrogen regulation) two-component regulatory system [PATH:map02020] [BR:ko02022] (19) (complete)

M00499 HydH-HydG (metal tolerance) two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (1 block missing)

M00500 AtoS-AtoC (cPHB biosynthesis) two-component regulatory system [PATH:map02020] [BR:ko02022] (4) (1 block missing)

M00501 PilS-PilR (type 4 fimbriae synthesis) two-component regulatory system [PATH:map02020] [BR:ko02022] (22) (complete)

M00502 GlrK-GlrR (amino sugar metabolism) two-component regulatory system [PATH:map02020] [BR:ko02022] (23) (complete)

M00504 DctB-DctD (C4-dicarboxylate transport) two-component regulatory system [PATH:map02020] [BR:ko02022] (4) (complete)

M00505 KinB-AlgB (alginate production) two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (1 block missing)

M00772 HupT-HupR (hydrogenase synthesis regulation) two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (1 block missing)

M00506 CheA-CheYBV (chemotaxis) two-component regulatory system [PATH:map02020 map02030] [BR:ko02022 ko02030 ko02035] (183) (complete)

M00507 ChpA-ChpB/PilGH (chemosensory) two-component regulatory system [PATH:map02020] [BR:ko02022 ko02035] (56) (1 block missing)

M00509 WspE-WspRF (chemosensory) two-component regulatory system [PATH:map02020] [BR:ko02022] (1) (2 blocks missing)

M00511 PleC-PleD (cell fate control) two-component regulatory system [PATH:map02020 map04112] [BR:ko02022] (6) (2 blocks missing)

M00512 CckA-CtrA/CpdR (cell cycle control) two-component regulatory system [PATH:map02020 map04112] [BR:ko02022] (7) (1 block missing)

M00514 TtrS-TtrR (tetrathionate respiration) two-component regulatory system [PATH:map02020] [BR:ko02022] (6) (complete)

M00515 FlrB-FlrC (polar flagellar synthesis) two-component regulatory system [PATH:map02020 map05111] [BR:ko02022] (4) (1 block missing)

M00517 RpfC-RpfG (cell-to-cell signaling) two-component regulatory system [PATH:map02020] [BR:ko02022] (4) (complete)

M00518 GlnK-GlnL (glutamine utilization) two-component regulatory system [PATH:map02020] [BR:ko02022] (11) (complete)

M00519 YesM-YesN two-component regulatory system [PATH:map02020] [BR:ko02022] (53) (complete)

M00520 ChvG-ChvI (acidity sensing) two-component regulatory system [PATH:map02020] [BR:ko02022] (4) (complete)

M00523 RegB-RegA (redox response) two-component regulatory system [PATH:map02020] [BR:ko02022] (9) (complete)

M00524 FixL-FixJ (nitrogen fixation) two-component regulatory system [PATH:map02020] [BR:ko02022] (1) (1 block missing)

M00655 AdeS-AdeR two-component regulatory system [PATH:map01501] [BR:ko02022] (1) (1 block missing)

M00657 VanS-VanR (VanE type vancomycin resistance) two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (complete)

Drug efflux transporter/pump

M00668 Tetracycline resistance, TetA transporter (5) (1 block missing)

M00709 Macrolide resistance, MacAB-ToIC transporter (36) (complete)

M00715 Lincosamide resistance, efflux pump LmrB (9) (complete)

M00713 Fluoroquinolone resistance, efflux pump LfrA (2) (1 block missing)

M00738 Bacitracin resistance, BceAB transporter [PATH:map02020] (23) (complete)

M00645 Multidrug resistance, efflux pump SmeABC [PATH:map02020] (16) (1 block missing)

M00646 Multidrug resistance, efflux pump AcrAD-ToIC [PATH:map02020] (60) (1 block missing)

M00647 Multidrug resistance, efflux pump AcrAB-ToIC/SmeDEF (127) (complete)

M00648 Multidrug resistance, efflux pump MdtABC [PATH:map02020] (16) (1 block missing)

M00699 Multidrug resistance, efflux pump AmeABC (99) (2 blocks missing)

M00701 Multidrug resistance, efflux pump EmrAB (12) (1 block missing)

M00767 Multidrug resistance, efflux pump OqxAB (7) (2 blocks missing)

M00768 Multidrug resistance, efflux pump GesABC (4) (2 blocks missing)



## Drug resistance

M00628 beta-Lactam resistance, AmpC system [PATH:map01501] (79) (1 block missing)

M00742 Aminoglycoside resistance, protease FtsH (292) (complete)

M00743 Aminoglycoside resistance, protease HtpX (92) (complete)

M00760 Erythromycin resistance, macrolide 2'-phosphotransferase I MphA (5) (1 block missing)

M00766 Streptomycin resistance, deactivating enzyme StrAB (5) (1 block missing)

M00729 Fluoroquinolone resistance, gyrase-protecting protein Qnr (133) (1 block missing)

M00721 Cationic antimicrobial peptide (CAMP) resistance, arnBCADTEF operon [PATH:map01503] (10) (1 block missing)

M00723 Cationic antimicrobial peptide (CAMP) resistance, phosphoethanolamine transferase EptB [PATH:map01503] (10) (2 blocks missing)

M00724 Cationic antimicrobial peptide (CAMP) resistance, palmitoyl transferase PagP [PATH:map01503] (10) (1 block missing)

M00727 Cationic antimicrobial peptide (CAMP) resistance, N-acetylmuramoyl-L-alanine amidase AmiA and AmiC [PATH:map01503] (146) (complete)

M00728 Cationic antimicrobial peptide (CAMP) resistance, envelope protein folding and degrading factors DegP and DsbA [PATH:map01503] (106) (complete)

M00754 Nisin resistance, phage shock protein homolog LiaH (29) (1 block missing)

## Cell signaling

M00688 MAPK (JNK) signaling [PATH:map04010 map04013] (2) (1 block missing)

M00689 MAPK (p38) signaling [PATH:map04010 map04013] (1) (2 blocks missing)

M00690 MAPK (ERK5) signaling [PATH:map04010] (1) (2 blocks missing)

M00682 Notch signaling [PATH:map04330] (1) (2 blocks missing)

M00679 BMP signaling [PATH:map04350 map04390 map04550] (1) (2 blocks missing)

M00684 JAK-STAT signaling [PATH:map04630] (2) (1 block missing)

M00695 cAMP signaling [PATH:map04024] (14) (2 blocks missing)

## Signature module

### Gene set

#### Metabolic capacity

M00615 Nitrate assimilation (49) (complete)

#### Pathogenicity

M00575 Pertussis pathogenicity signature 2, T1SS [PATH:map05133] (22) (2 blocks missing)

#### Drug resistance

M00627 beta-Lactam resistance, Bla system [PATH:map01501] (22) (1 block missing)

M00745 Imipenem resistance, repression of porin OprD (3) (1 block missing)

M00651 Vancomycin resistance, D-Ala-D-Lac type [PATH:map01502 map02020] (27) (2 blocks missing)

M00652 Vancomycin resistance, D-Ala-D-Ser type [PATH:map01502 map02020] (3) (2 blocks missing)

M00704 Tetracycline resistance, efflux pump Tet38 (5) (1 block missing)

M00726 Cationic antimicrobial peptide (CAMP) resistance, lysyl-phosphatidylglycerol (L-PG) synthase MprF [PATH:map01503] (4) (2 blocks missing)

M00744 Cationic antimicrobial peptide (CAMP) resistance, protease PgtE (10) (1 block missing)

M00718 Multidrug resistance, efflux pump MexAB-OprM (103) (1 block missing)

M00642 Multidrug resistance, efflux pump MexJK-OprM (4) (2 blocks missing)

M00643 Multidrug resistance, efflux pump MexXY-OprM (4) (2 blocks missing)

M00649 Multidrug resistance, efflux pump AdeABC [PATH:map01501] (1) (2 blocks missing)

M00696 Multidrug resistance, efflux pump AcrEF-ToIC (20) (2 blocks missing)  
M00697 Multidrug resistance, efflux pump MdtEF-ToIC (20) (2 blocks missing)  
M00698 Multidrug resistance, efflux pump BpeEF-OprC (4) (1 block missing)  
M00700 Multidrug resistance, efflux pump AbcA (8) (1 block missing)  
M00714 Multidrug resistance, efflux pump QacA (2) (1 block missing)

TABLE 42: RESULTS OF RECONSTRUCTED PATHWAY ANALYSIS.

Pathway	Number of KEGG Ortholog
<b>Metabolism</b>	
<u>Global and overview maps</u>	
01100 Metabolic pathways	1208
01110 Biosynthesis of secondary metabolites	445
01120 Microbial metabolism in diverse environments	496
01130 Biosynthesis of antibiotics	320
01200 Carbon metabolism	220
01210 2-Oxocarboxylic acid metabolism	42
01212 Fatty acid metabolism	38
01230 Biosynthesis of amino acids	179
01220 Degradation of aromatic compounds	46
<u>Carbohydrate metabolism</u>	
00010 Glycolysis / Gluconeogenesis	68
00020 Citrate cycle (TCA cycle)	42
00030 Pentose phosphate pathway	49
00040 Pentose and glucuronate interconversions	34
00051 Fructose and mannose metabolism	67
00052 Galactose metabolism	31
00053 Ascorbate and aldarate metabolism	14
00500 Starch and sucrose metabolism	68
00520 Amino sugar and nucleotide sugar metabolism	88
00620 Pyruvate metabolism	72
00630 Glyoxylate and dicarboxylate metabolism	66
00640 Propanoate metabolism	63
00650 Butanoate metabolism	60
00660 C5-Branched dibasic acid metabolism	15
00562 Inositol phosphate metabolism	14
<u>Energy metabolism</u>	
00190 Oxidative phosphorylation	73
00195 Photosynthesis	10
00710 Carbon fixation in photosynthetic organisms	23

00720 Carbon fixation pathways in prokaryotes	66
00680 methane metabolism	116
00910 Nitrogen metabolism	39
00920 Sulfur metabolism	53
<u>Lipid metabolism</u>	
00061 Fatty acid biosynthesis	22
00062 Fatty acid elongation	2
00071 Fatty acid degradation	28
00072 Synthesis and degradation of ketone bodies	8
00073 Cutin, suberine and wax biosynthesis	1
00100 Steroid biosynthesis	4
00120 Primary bile acid biosynthesis	2
00121 Secondary bile acid biosynthesis	1
00140 Steroid hormone biosynthesis	5
00561 Glycerolipid metabolism	24
00564 Glycerophospholipid metabolism	39
00565 Ether lipid metabolism	6
00600 Sphingolipid metabolism	13
00590 Arachidonic acid metabolism	5
00591 Linoleic acid metabolism	4
00592 alpha-Linolenic acid metabolism	5
01040 Biosynthesis of unsaturated fatty acids	10
<u>Nucleotide metabolism</u>	
00230 Purine metabolism	115
00240 Pyrimidine metabolism	84
<u>Amino acid metabolism</u>	
00250 Alanine, aspartate and glutamate metabolism	43
00260 Glycine, serine and threonine metabolism	66
00270 Cysteine and methionine metabolism	65
00280 Valine, leucine and isoleucine degradation	48
00290 Valine, leucine and isoleucine biosynthesis	15
00300 Lysine biosynthesis	36
00310 Lysine degradation	25
00220 Arginine biosynthesis	33
00330 Arginine and proline metabolism	50
00340 Histidine metabolism	27
00350 Tyrosine metabolism	35
00360 Phenylalanine metabolism	38
00380 Tryptophan metabolism	24
00400 Phenylalanine, tyrosine, and tryptophan biosynthesis	39

### Metabolism of other amino acids

00410 beta-Alanine metabolism	26
00430 Taurine and hypotaurine metabolism	13
00440 Phosphonate and phosphinate metabolism	11
00450 Selenocompound metabolism	17
00460 Cyanoamino acid metabolism	8
00471 D-Glutamine and D-glutamate metabolism	5
00472 D-Arginine and D-ornithine metabolism	4
00473 D-Alanine metabolism	3
00480 Glutathione metabolism	19

### Glycan biosynthesis and metabolism

00510 N-Glycan biosynthesis	3
00513 Various types of N-glycan biosynthesis	1
00512 Mucin type O-Glycan biosynthesis	1
00514 Other types of O-glycan biosynthesis	1
00533 Glycosaminoglycan biosynthesis - keratan sulfate	1
00531 Glycosaminoglycan degradation	8
00563 Glycosylphosphatidylinositol (GPI-anchor biosynthesis )	3
00603 Glycosphingolipid biosynthesis - globo series	4
00604 Glycosphingolipid biosynthesis - ganglio series	2
00540 Lipopolysaccharide biosynthesis	25
00550 Peptidoglycan biosynthesis	25
00511 Other glycan degradation	10

### Metabolism of cofactors and vitamins

00730 Thiamine metabolism	18
00740 Riboflavin metabolism	15
00750 Vitamin B6 metabolism	9
00760 Nicotinate and nicotinamide metabolism	29
00770 Pantothenate and CoA biosynthesis	27
00780 Biotin metabolism	13
00785 Lipoic acid metabolism	3
00790 Folate biosynthesis	24
00670 One carbon pool by folate	22
00830 Retinol metabolism	6
00860 Porphyrin and chlorophyll metabolism	54
00130 Ubiquinone and other terpenoid-quinone biosynthesis	27

### Metabolism of terpenoids and polyketides

00900 Terpenoid backbone biosynthesis	29
00909 Sesquiterpenoid and triterpenoid biosynthesis	3

00904 Diterpenoid biosynthesis	1
00906 Carotenoid biosynthesis	9
00908 Zeatin biosynthesis	1
00903 Limonene and pinene degradation	6
00281 Geraniol degradation	11
01051 Biosynthesis of ansamycins	2
01057 Biosynthesis of type II polyketide products	1
00253 Tetracycline biosynthesis	6
00523 Polyketide sugar unit biosynthesis	6
01054 Nonribosomal peptide structures	1
01053 Biosynthesis of siderophore group nonribosomal peptides	4
01055 Biosynthesis of vancomycin group antibiotics	3
<u>Biosynthesis of other secondary metabolites</u>	
00940 Phenylpropanoid biosynthesis	5
00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis	1
00941 Flavonoid biosynthesis	1
00944 Flavone and flavonol biosynthesis	1
00943 Isoflavonoid biosynthesis	1
00901 Indole alkaloid biosynthesis	1
00950 Isoquinoline alkaloid biosynthesis	9
00960 Tropane, piperidine and pyridine alkaloid biosynthesis	8
00232 Caffeine metabolism	2
00965 Betalain biosynthesis	3
00311 Penicillin and cephalosporin biosynthesis	7
00332 Carbapenem biosynthesis	2
00261 Monobactam biosynthesis	11
00521 Streptomycin biosynthesis	11
00524 Butirosin and neomycin biosynthesis	2
00401 Novobiocin biosynthesis	7
00404 Staurosporine biosynthesis	1
<u>Xenobiotics biodegradation and metabolism</u>	
00362 Benzoate degradation	46
00627 Aminobenzoate degradation	25
00364 Fluorobenzoate degradation	6
00625 Chloroalkane and chloroalkene degradation	13
00361 Chlorocyclohexane and chlorobenzene degradation	13
00623 Toluene degradation	8
00622 Xylene degradation	11
00633 Nitrotoluene degradation	15
00642 Ethylbenzene degradation	1
00643 Styrene degradation	13

00791 Atrazine degradation	3
00930 Caprolactam degradation	9
00363 Bisphenol degradation	2
00621 Dioxin degradation	6
00626 Naphthalene degradation	8
00624 Polycyclic aromatic hydrocarbon degradation	6
00365 Furfural degradation	2
00984 Steroid degradation	5
00980 Metabolism of xenobiotics by cytochrome P450	6
00982 Drug metabolism - cytochrome P450	7
00983 Drug metabolism - other enzymes	15
<u>Chemical structure transformation maps</u>	
01062 Biosynthesis of terpenoids and steroids	1
<b>Genetic Information Processing</b>	
<u>Transcription</u>	
03020 RNA polymerase	13
03022 Basal transcription factors	5
03040 Spliceosome	6
<u>Translation</u>	
03010 Ribosome	49
00970 Aminoacyl-tRNA biosynthesis	36
03013 RNA transport	12
03015 mRNA surveillance pathway	8
03008 Ribosome biogenesis in eukaryotes	13
<u>Folding, sorting and degradation</u>	
03060 Protein export	17
04141 Protein processing in endoplasmic reticulum	10
04120 Ubiquitin-mediated proteolysis	9
04122 Sulfur relay system	12
03050 Proteasome	7
03018 RNA degradation	22
<u>Replication and repair</u>	
03030 DNA replication	30
03410 Base excision repair	21
03420 Nucleotide excision repair	14
03430 Mismatch repair	23
03440 Homologous recombination	27
03450 Non-homologous end-joining	3
03460 Fanconi anemia pathway	3

## Environmental Information Processing

### Membrane transport

02010 ABC transporters	250
02060 Phosphotransferase system (PTS)	41
03070 bacterial secretion system	36

### Signal transduction

02020 Two-component system	187
04014 Ras signaling pathway	11
04015 Rap1 signaling pathway	5
04010 MAPK signaling pathway	8
04011 MAPK signaling pathway - yeast	3
04012 ErbB signaling pathway	4
04310 Wnt signaling pathway	3
04330 Notch signaling pathway	4
04340 Hedgehog signaling pathway	3
04350 TGF-beta signaling pathway	2
04390 Hippo signaling pathway	5
04391 Hippo signaling pathway - fly	3
04370 VEGF signaling pathway	3
04630 Jak-STAT signaling pathway	5
04064 NF-kappa B signaling pathway	2
04668 TNF signaling pathway	5
04066 HIF-1 signaling pathway	8
04068 FoxO signaling pathway	8
04020 Calcium signaling pathway	5
04070 Phosphatidylinositol signaling system	8
04072 Phospholipase D signaling pathway	5
04071 Sphingolipid signaling pathway	9
04024 cAMP signaling pathway	9
04022 cGP-PKG signaling pathway	4
04151 PI3K-Akt signaling pathway	16
04152 AMPK signaling pathway	13
04150 mTOR signaling pathway	1
04075 Plant hormone signal transduction	1

### Signaling molecules and interaction

04080 Neuroactive ligand-receptor interaction	5
04060 Cytokine-cytokine receptor interaction	1
04512 ECM-receptor interaction	8
04514 Cell adhesion molecules (CAMs)	2

### Cellular Processes

## Transport and catabolism

04144 Endocytosis	6
04145 Phagosome	5
04142 Lysosome	15
04146 Peroxisome	23
04139 Regulation of mitophagy - yeast	1

## Cell motility

02030 bacterial chemotaxis	21
02040 Flagellar assembly	27
04810 Regulation of actin cytoskeleton	7

## Cell growth and death

04110 Cell cycle	8
04111 Cell cycle - yeast	7
04112 Cell cycle - Caulobacter	22
04113 Meiosis - yeast	7
04114 Oocyte meiosis	8
04210 Apoptosis	6
04214 Apoptosis - fly	4
04215 Apoptosis - multiple species	2
04115 p53 signaling pathway	1

## Cellular community

04510 Focal adhesion	13
04520 Adherens junction	4
04530 Tight junction	7
04540 Gap junction	1
04550 Signaling pathways regulating pluripotency of stem cells	4

## Organismal Systems

## Immune system

04640 Hematopoietic cell lineage	1
04611 Platelet activation	6
04620 Toll-like receptor signaling pathway	2
04621 NOD-like receptor signaling pathway	2
04622 RIG-I-like receptor signaling pathway	3
04650 Natural killer cell mediated cytotoxicity	1
04612 Antigen processing and presentation	2
04660 T cell receptor signaling pathway	2
04662 B cell receptor signaling pathway	2
04664 Fc epsilon RI signaling pathway	3
04666 Fc gamma R-mediated phagocytosis	4



04670 Leukocyte transendothelial migration	6
04062 Chemokine signaling pathway	5
<u>Endocrine system</u>	
04910 Insulin signaling pathway	11
04922 Glucagon signaling pathway	10
04923 Regulation of lipolysis in adipocytes	1
04920 Adipocytokine signaling pathway	7
03320 PPAR signaling pathway	7
04912 GnRH signaling pathway	5
04913 Ovarian steroidogenesis	1
04915 Estrogen signaling pathway	3
04914 Progesterone-mediated oocyte maturation	5
04917 Prolactin signaling pathway	5
04921 Oxytocin signaling pathway	6
04918 Thyroid hormone synthesis	2
04919 Thyroid hormone signaling pathway	4
04916 Melanogenesis	2
04924 Renin secretion	2
04614 Renin-angiotensin system	4
04925 Aldosterone synthesis and secretion	1
<u>Circulatory system</u>	
04260 Cardiac muscle contraction	3
04261 Adrenergic signaling in cardiomyocytes	4
04270 Vascular smooth muscle contraction	3
<u>Digestive system</u>	
04970 Salivary secretion	1
04972 Pancreatic secretion	4
04976 Bile secretion	4
04973 Carbohydrate digestion and absorption	4
04974 Protein digestion and absorption	9
04975 Fat digestion and absorption	1
04978 Mineral absorption	2
<u>Excretory system</u>	
04962 Vasopressin-regulated water reabsorption	1
04960 Aldosterone-regulated sodium reabsorption	1
04964 Proximal tubule bicarbonate reclamation	4
04966 Collecting duct acid secretion	2
<u>Nervous system</u>	
04724 Glutamatergic synapse	6
04727 GABAergic synapse	5

04725 Cholinergic synapse	4
04728 Dopaminergic synapse	8
04726 Serotonergic synapse	5
04720 Long-term potentiation	2
04730 Long-term depression	2
04723 Retrograde endocannabinoid signaling	3
04721 Synaptic vesicle cycle	5
04722 Neurotrophin signaling pathway	5
<u>Sensory system</u>	
04740 Olfactory transduction	2
04742 Taste transduction	1
04750 Inflammatory mediator regulation of TRP channels	4
<u>Development</u>	
04320 Dorso-ventral axis formation	2
04360 Axon guidance	8
04380 Osteoclast differentiation	2
<u>Aging</u>	
04211 Longevity regulating pathway	4
04212 Longevity regulating pathway - worm	9
04213 Longevity regulating pathway - multiple species	7
<u>Environmental adaptation</u>	
04710 Circadian rhythm	2
04713 Circadian entrainment	1
04626 Plant-pathogen interaction	5
<u>Human Diseases</u>	
<u>Cancers: Overview</u>	
05200 Pathways in cancer	18
05230 Central carbon metabolism in cancer	9
05231 Choline metabolism in cancer	6
05202 Transcriptional misregulation in cancer	5
05206 MicroRNAs in cancer	10
05205 Proteoglycans in cancer	10
05204 Chemical carcinogenesis	5
05203 Viral carcinogenesis	9
<u>Cancers: Specific types</u>	
05210 Colorectal cancer	3
05212 Pancreatic cancer	3
05214 Glioma	1

05216 Thyroid cancer	1
05221 Acute myeloid leukemia	3
05220 Chronic myeloid leukemia	3
05217 Basal cell carcinoma	3
05218 Melanoma	1
05211 Renal cell carcinoma	3
05219 Bladder cancer	2
05215 Prostate cancer	3
05213 Endometrial cancer	1
05222 Small cell lung cancer	5
05223 Non-small cell lung cancer	1
<u>Immune diseases</u>	
05322 Systemic lupus erythematosus	2
05323 Rheumatoid arthritis	2
05321 Inflammatory bowel disease (IBD)	2
05340 Primary immunodeficiency	3
<u>Neurodegenerative diseases</u>	
05010 Alzheimer's disease	10
05012 Parkinson's disease	8
05014 Amyotrophic lateral sclerosis (ALS)	3
05016 Huntington's disease	14
05020 Prion diseases	1
<u>Substance dependence</u>	
05030 Cocaine addiction	3
05031 Amphetamine addiction	4
05032 Morphine addiction	1
05033 Nicotine addiction	2
05034 Alcoholism	4
<u>Cardiovascular diseases</u>	
05410 Hypertrophic cardiomyopathy (HCM)	4
05412 Arrhythmogenic right ventricular cardiomyopathy (ARVC)	2
05414 Dilated cardiomyopathy	2
05416 Viral myocarditis	2
<u>Endocrine and metabolic diseases</u>	
04930 Type II diabetes mellitus	6
04940 Type I diabetes mellitus	2
04932 Non-alcoholic fatty liver disease (NAFLD)	11
04931 Insulin resistance	11
04933 AGE-RAGE signaling pathway in diabetic complications	7

**Infectious diseases: Bacterial**

05110 Vibrio cholerae infection	4
05111 Vibrio cholerae pathogenic cycle	9
05120 Epithelial cell signaling in Helicobacter pylori infection	6
05130 Pathogenic Escherichia coli infection	1
05132 Salmonella infection	9
05131 Shigellosis	2
05133 Pertussis	5
05134 Legionellosis	7
05150 Staphylococcus aureus infection	2
05152 Tuberculosis	11
05100 bacterial invasion of epithelial cells	2

**Infectious Diseases: Viral**

05166 HTLV-I infection	11
05162 Measles	6
05164 Influenza A	7
05161 Hepatitis B	8
05160 Hepatitis C	5
05168 Herpes simplex infection	9
05169 Epstein-Barr virus infection	11

**Infectious diseases: Parasitic**

05146 Amoebiasis	10
05144 Malaria	2
05145 Toxoplasmosis	6
05140 Leishmaniasis	1
05142 Chagas disease (American trypanosomiasis )	5
05143 African trypanosomiasis	3

**Drug resistance**

01501 beta-Lactam resistance	24
01502 Vancomycin resistance	11
01503 Cationic antimicrobial peptide (CAMP resistance)	13

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