

# Supplementary Table 7

0: Kegg module complete

1: 1 block missing

2: 2 blocks missing

4: Kegg module absent

## KEGG Module

### Cluster 1

M00326: RTX toxin transport system

M00325: alpha-Hemolysin/cyclolysin transport system

M00339: RaxAB-RaxC type I secretion system

M00571: AlgE-type Mannuronan C-5-Epimerase transport system

M00720: Multidrug resistance, efflux pump VexEF-TolC

M00696: Multidrug resistance, efflux pump AcrEF-TolC

M00124: Pyridoxal biosynthesis, erythrose-4P => pyridoxal-5P

M00697: Multidrug resistance, efflux pump MdtEF-TolC

M00596: Dissimilatory sulfate reduction, sulfate => H<sub>2</sub>S

M00695: cAMP signaling

M00081: Pectin degradation

M00627: beta-Lactam resistance, Bla system

M00467: SasA-RpaAB (circadian timing mediating) two-component regulatory system

M00422: Acetyl-CoA pathway, CO<sub>2</sub> => acetyl-CoA

M00643: Multidrug resistance, efflux pump MexXY-OprM

M00079: Keratan sulfate degradation

M00349: Microcin C transport system

M00243: Manganese/iron transport system

M00116: Menaquinone biosynthesis, chorismate => menaquinone

M00471: NarX-NarL (nitrate respiration) two-component regulatory system

M00572: Pimeloyl-ACP biosynthesis, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP

M00628: beta-Lactam resistance, AmpC system

M00537: Xylene degradation, xylene => methylbenzoate

M00170: C4-dicarboxylic acid cycle, phosphoenolpyruvate carboxykinase type

M00538: Toluene degradation, toluene => benzoate

M00223: Phosphonate transport system

M00472: NarQ-NarP (nitrate respiration) two-component regulatory system

M00445: EnvZ-OmpR (osmotic stress response) two-component regulatory system

M00498: NtrY-NtrX (nitrogen regulation) two-component regulatory system

M00230: Glutamate/aspartate transport system

M00304: PTS system, fructose-specific II component

M00205: N-Acetylglucosamine transport system

M00306: PTS system, fructose-specific II-like component

M00344: Formaldehyde assimilation, xylulose monophosphate pathway

M00442: Putative hydroxymethylpyrimidine transport system

M00098: Acylglycerol degradation

M00728: Cationic antimicrobial peptide (CAMP) resistance, assembly of multidrug transporters

M00173: Reductive citrate cycle (Arnon-Buchanan cycle)  
M00701: Multidrug resistance, efflux pump EmrAB  
M00122: Cobalamin biosynthesis, cobinamide => cobalamin  
M00361: Nucleotide sugar biosynthesis, eukaryotes  
M00012: Glyoxylate cycle  
M00652: Vancomycin resistance, D-Ala-D-Ser type  
M00033: Ectoine biosynthesis, aspartate => ectoine  
M00738: Bacitracin resistance, BceAB transporter  
M00469: BceS-BceR (bacitracin transport) two-component regulatory system  
M00332: Type III secretion system  
M00259: Heme transport system  
M00156: Cytochrome c oxidase, cbb3-type  
M00334: Type VI secretion system  
M00440: Nickel transport system  
M00515: FlrB-FlrC (polar flagellar synthesis) two-component regulatory system  
M00213: L-Arabinose transport system  
M00202: Oligogalacturonide transport system  
M00290: Holo-TFIIH complex  
M00348: Glutathione transport system  
M00586: Putative amino-acid transport system  
M00309: Non-phosphorylative Entner-Doudoroff pathway, gluconate/galactonate => glycerate  
M00599: Inositol-phosphate transport system  
M00175: Nitrogen fixation, nitrogen => ammonia  
M00569: Catechol meta-cleavage, catechol => acetyl-CoA / 4-methylcatechol => propanoyl-CoA  
M00501: PilS-PilR (type 4 fimbriae synthesis) two-component regulatory system  
M00499: HydH-HydG (metal tolerance) two-component regulatory system  
M00087: beta-Oxidation  
M00585: L-Cystine transport system  
M00475: BarA-UvrY (central carbon metabolism) two-component regulatory system  
M00191: Thiamine transport system  
M00593: Inositol transport system  
M00220: Rhamnose transport system  
M00204: Trehalose/maltose transport system  
M00253: Sodium transport system  
M00450: BaeS-BaeR (envelope stress response) two-component regulatory system  
M00591: Putative xylitol transport system  
M00646: Multidrug resistance, efflux pump AcrAD-TolC  
M00645: Multidrug resistance, efflux pump SmeABC  
M00648: Multidrug resistance, efflux pump MdtABC  
M00215: D-Xylose transport system  
M00460: MprB-MprA (maintenance of persistent infection) two-component regulatory system  
M00176: Assimilatory sulfate reduction, sulfate => H<sub>2</sub>S  
M00135: GABA biosynthesis, eukaryotes, putrescine => GABA  
M00046: Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate  
M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate  
M00331: Type II general secretion pathway  
M00064: ADP-L-glycero-D-manno-heptose biosynthesis

## Cluster 2

M00318: Iron/zinc/copper transport system  
M00315: Uncharacterized ABC transport system  
M00583: Putative peptide transport system  
M00712: Multidrug resistance, efflux pump YkkCD  
M00480: VraS-VraR (cell-wall peptidoglycan synthesis) two-component regulatory system  
M00461: MtrB-MtrA (osmotic stress response) two-component regulatory system  
M00600: alpha-1,4-Digalacturonate transport system  
M00550: Ascorbate degradation, ascorbate => D-xylulose-5P  
M00481: LiaS-LiaR (cell wall stress response) two-component regulatory system  
M00053: Pyrimidine deoxyribonucleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP  
M00338: Cysteine biosynthesis, homocysteine + serine => cysteine  
M00342: Bacterial proteasome  
M00443: SenX3-RegX3 (phosphate starvation response) two-component regulatory system  
M00436: Sulfonate transport system  
M00233: Glutamate transport system  
M00497: GlnL-GlnG (nitrogen regulation) two-component regulatory system  
M00232: General L-amino acid transport system  
M00189: Molybdate transport system  
M00199: L-Arabinose/lactose transport system  
M00224: Fluoroquinolone transport system  
M00250: Lipopolysaccharide transport system  
M00216: Multiple sugar transport system  
M00198: Putative sn-glycerol-phosphate transport system  
M00267: PTS system, N-acetylglucosamine-specific II component  
M00212: Ribose transport system  
M00251: Teichoic acid transport system  
M00519: YesM-YesN two-component regulatory system  
M00603: Putative aldouronate transport system  
M00188: NitT/TauT family transport system  
M00651: Vancomycin resistance, D-Ala-D-Lac type  
M00090: Phosphatidylcholine (PC) biosynthesis, choline => PC  
M00657: VanS-VanR (VanE type vancomycin resistance) two-component regulatory system  
M00190: Iron(III) transport system  
M00214: Methyl-galactoside transport system  
M00221: Putative simple sugar transport system  
M00333: Type IV secretion system  
M00506: CheA-CheYBV (chemotaxis) two-component regulatory system

### **Cluster 3**

M00367: C10-C20 isoprenoid biosynthesis, non-plant eukaryotes  
M00366: C10-C20 isoprenoid biosynthesis, plants  
M00095: C5 isoprenoid biosynthesis, mevalonate pathway  
M00726: Cationic antimicrobial peptide (CAMP) resistance, addition of lysine to phospholipids  
M00609: Cysteine biosynthesis, methionine => cysteine  
M00725: Cationic antimicrobial peptide (CAMP) resistance, addition of alanine to teichoic acids  
M00492: LytS-LytR two-component regulatory system  
M00365: C10-C20 isoprenoid biosynthesis, archaea  
M00362: Nucleotide sugar biosynthesis, prokaryotes  
M00118: Glutathione biosynthesis, glutamate => glutathione

M00089: Triacylglycerol biosynthesis  
M00615: Nitrate assimilation  
M00518: GlnK-GlnL (glutamine utilization) two-component regulatory system  
M00700: Multidrug resistance, efflux pump AbcA  
M00483: NreB-NreC (dissimilatory nitrate/nitrite reduction) two-component regulatory system  
M00530: Dissimilatory nitrate reduction, nitrate => ammonia  
M00027: GABA (gamma-Aminobutyrate) shunt  
M00281: PTS system, lactose-specific II component  
M00208: Glycine betaine/proline transport system  
M00252: Lipooligosaccharide transport system  
M00580: Pentose phosphate pathway, archaea, fructose 6P => ribose 5P  
M00525: Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine  
M00150: Fumarate reductase, prokaryotes  
M00134: Polyamine biosynthesis, arginine => ornithine => putrescine

#### **Cluster 4**

M00278: PTS system, sorbose-specific II component  
M00287: PTS system, galactosamine-specific II component  
M00610: PTS system, D-glucosamine-specific II component  
M00277: PTS system, N-acetylgalactosamine-specific II component  
M00283: PTS system, ascorbate-specific II component  
M00193: Putative spermidine/putrescine transport system  
M00589: Putative lysine transport system  
M00566: Dipeptide transport system, Firmicutes  
M00495: AgrC-AgrA (exoprotein synthesis) two-component regulatory system  
M00708: Multidrug resistance, PatAB transporter  
M00280: PTS system, glucitol/sorbitol-specific II component  
M00276: PTS system, mannose-specific II component  
M00458: ResE-ResD (aerobic and anaerobic respiration) two-component regulatory system  
M00298: Multidrug/hemolysin transport system  
M00279: PTS system, galactitol-specific II component  
M00706: Multidrug resistance, EfrAB transporter  
M00211: Putative ABC transport system  
M00209: Osmoprotectant transport system  
M00581: Biotin transport system  
M00234: Cystine transport system  
M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine  
M00246: Nickel transport system  
M00245: Cobalt/nickel transport system  
M00237: Branched-chain amino acid transport system  
M00454: KdpD-KdpE (potassium transport) two-component regulatory system  
M00266: PTS system, maltose and glucose-specific II component  
M00265: PTS system, glucose-specific II component  
M00270: PTS system, trehalose-specific II component  
M00271: PTS system, beta-glucosides-specific II component  
M00268: PTS system, arbutin-like II component  
M00303: PTS system, N-acetylmuramic acid-specific II component  
M00272: PTS system, arbutin-, cellobiose-, and salicin-specific II component  
M00282: PTS system, D-glucosamine-specific II component

M00269: PTS system, sucrose-specific II component  
M00274: PTS system, mannitol-specific II component  
M00275: PTS system, cellobiose-specific II component  
M00273: PTS system, fructose-specific II component  
M00228: Putative glutamine transport system  
M00227: Glutamine transport system  
M00247: Putative ABC transport system  
M00238: D-Methionine transport system  
M00197: Putative fructooligosaccharide transport system  
M00194: Maltose/maltodextrin transport system  
M00200: Putative sorbitol/mannitol transport system  
M00206: Cellobiose transport system  
M00602: Arabinosaccharide transport system  
M00605: Glucose/mannose transport system  
M00606: N,N'-Diacetylchitobiose transport system  
M00196: Raffinose/stachyose/melibiose transport system  
M00491: arabinogalactan oligomer/maltooligosaccharide transport system  
M00207: Putative multiple sugar transport system  
M00201: alpha-Glucoside transport system  
M00582: Energy-coupling factor transport system  
M00236: Putative polar amino acid transport system  
M00439: Oligopeptide transport system  
M00239: Peptides/nickel transport system  
M00459: VicK-VicR (cell wall metabolism) two-component regulatory system

#### **Cluster 5**

M00577: Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin  
M00573: Biotin biosynthesis, BioI pathway, long-chain-acyl-ACP => pimeloyl-ACP => biotin  
M00060: Lipopolysaccharide biosynthesis, KDO2-lipid A  
M00718: Multidrug resistance, efflux pump MexAB-OprM  
M00699: Multidrug resistance, efflux pump AmeABC  
M00172: C4-dicarboxylic acid cycle, NADP - malic enzyme type  
M00145: NAD(P)H:quinone oxidoreductase, chloroplasts and cyanobacteria  
M00647: Multidrug resistance, efflux pump AcrAB-TolC/SmeDEF  
M00009: Citrate cycle (TCA cycle, Krebs cycle)  
M00741: Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA  
M00123: Biotin biosynthesis, pimeloyl-ACP/CoA => biotin  
M00119: Pantothenate biosynthesis, valine/L-aspartate => pantothenate  
M00320: Lipopolysaccharide export system  
M00210: Phospholipid transport system  
M00669: gamma-Hexachlorocyclohexane transport system  
M00670: Mce transport system  
M00336: Twin-arginine translocation (Tat) system  
M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate  
M00063: CMP-KDO biosynthesis  
M00255: Lipoprotein-releasing system  
M00024: Phenylalanine biosynthesis, chorismate => phenylalanine  
M00025: Tyrosine biosynthesis, chorismate => tyrosine  
M00127: Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P

M00727: Cationic antimicrobial peptide (CAMP) resistance, envelope maintenance  
M00149: Succinate dehydrogenase, prokaryotes  
M00168: CAM (Crassulacean acid metabolism), dark  
M00244: Putative zinc/manganese transport system  
M00153: Cytochrome d ubiquinol oxidase  
M00008: Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate  
M00126: Tetrahydrofolate biosynthesis, GTP => THF  
M00242: Zinc transport system  
M00004: Pentose phosphate pathway (Pentose phosphate cycle)  
M00006: Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P  
M00240: Iron complex transport system

#### **Cluster 6**

M00061: D-Glucuronate degradation, D-glucuronate => pyruvate + D-glyceraldehyde 3P  
M00308: Semi-phosphorylative Entner-Doudoroff pathway, gluconate => glycerate-3P  
M00631: D-Galacturonate degradation (bacteria), D-galacturonate => pyruvate + D-glyceraldehyde  
M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => ribulose-5P  
M00359: Aminoacyl-tRNA biosynthesis, eukaryotes  
M00144: NADH:quinone oxidoreductase, prokaryotes  
M00169: CAM (Crassulacean acid metabolism), light  
M00159: V/A-type ATPase, prokaryotes  
M00368: Ethylene biosynthesis, methionine => ethylene  
M00166: Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P  
M00029: Urea cycle  
M00017: Methionine biosynthesis, aspartate => homoserine => methionine  
M00035: Methionine degradation  
M00022: Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate  
M00570: Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine  
M00019: Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine  
M00432: Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate  
M00535: Isoleucine biosynthesis, pyruvate => 2-oxobutanoate  
M00020: Serine biosynthesis, glycerate-3P => serine  
M00028: Ornithine biosynthesis, glutamate => ornithine  
M00010: Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate  
M00565: Trehalose biosynthesis, D-glucose 1P => trehalose  
M00256: Cell division transport system  
M00394: RNA degradosome  
M00179: Ribosome, archaea  
M00335: Sec (secretion) system  
M00345: Formaldehyde assimilation, ribulose monophosphate pathway  
M00729: Fluoroquinolone resistance, gyrase-protecting protein Qnr  
M00429: Competence-related DNA transformation transporter  
M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P  
M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP  
M00364: C10-C20 isoprenoid biosynthesis, bacteria  
M00260: DNA polymerase III complex, bacteria  
M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP  
M00254: ABC-2 type transport system  
M00183: RNA polymerase, bacteria

M00083: Fatty acid biosynthesis, elongation  
M00140: C1-unit interconversion, prokaryotes  
M00178: Ribosome, bacteria  
M00002: Glycolysis, core module involving three-carbon compounds  
M00258: Putative ABC transport system  
M00005: PRPP biosynthesis, ribose 5P => PRPP  
M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP  
M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP  
M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate  
M00579: Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate  
M00527: Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine  
M00526: Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine  
M00003: Gluconeogenesis, oxaloacetate => fructose-6P  
M00360: Aminoacyl-tRNA biosynthesis, prokaryotes  
M00120: Coenzyme A biosynthesis, pantothenate => CoA  
M00549: Nucleotide sugar biosynthesis, glucose => UDP-glucose  
M00093: Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE  
M00141: C1-unit interconversion, eukaryotes  
M00434: PhoR-PhoB (phosphate starvation response) two-component regulatory system  
M00021: Cysteine biosynthesis, serine => cysteine  
M00082: Fatty acid biosynthesis, initiation  
M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP  
M00015: Proline biosynthesis, glutamate => proline  
M00018: Threonine biosynthesis, aspartate => homoserine => threonine  
M00632: Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P  
M00554: Nucleotide sugar biosynthesis, galactose => UDP-galactose  
M00222: Phosphate transport system  
M00157: F-type ATPase, prokaryotes and chloroplasts  
M00307: Pyruvate oxidation, pyruvate => acetyl-CoA  
M00299: Spermidine/putrescine transport system  
M00096: C5 isoprenoid biosynthesis, non-mevalonate pathway  
M00026: Histidine biosynthesis, PRPP => histidine  
M00023: Tryptophan biosynthesis, chorismate => tryptophan  
M00115: NAD biosynthesis, aspartate => NAD  
M00125: Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD  
M00086: beta-Oxidation, acyl-CoA synthesis

***E. faecalis* KB1**

***T. muris*' YL45**

***M. schaedleri* ASF457**

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