

Supplementary Table 10

- 0: Kegg module complete
- 1: 1 block missing
- 2: 2 blocks missing
- 4: Kegg module absent

Cluster 1

- M00072: N-glycosylation by oligosaccharyltransferase
- M00036: Leucine degradation, leucine => acetoacetate + acetyl-CoA
- M00152: Cytochrome bc1 complex
- M00155: Cytochrome c oxidase, prokaryotes
- M00161: Photosystem II
- M00162: Cytochrome b6f complex
- M00163: Photosystem I
- M00177: Ribosome, eukaryotes
- M00184: RNA polymerase, archaea
- M00203: Glucose/arabinose transport system
- M00218: Fructose transport system
- M00289: RF-C complex
- M00295: BRCA1-associated genome surveillance complex (BASC)
- M00301: Mannopine transport system
- M00302: 2-Aminoethylphosphonate transport system
- M00321: Bicarbonate transport system
- M00322: Neutral amino acid transport system
- M00327: S-Layer protein transport system
- M00328: Hemophore/metalloprotease transport system
- M00343: Archaeal proteasome
- M00391: Exosome, eukaryotes
- M00400: p97-Ufd1-Npl4 complex
- M00403: HRD1/SEL1 ERAD complex
- M00423: Molybdate/tungstate transport system
- M00425: H/ACA ribonucleoprotein complex
- M00433: Lysine biosynthesis, 2-oxoglutarate => 2-oxoadipate
- M00438: Nitrate/nitrite transport system
- M00448: CsxS-CsxR (secretion stress response) two-component regulatory system
- M00462: PrrB-PrrA (intracellular multiplication) two-component regulatory system
- M00463: TrcS-TrcR two-component regulatory system
- M00464: NrsS-NrsR (nickel tolerance) two-component regulatory system
- M00466: NblS-NblR (photosynthesis) two-component regulatory system
- M00470: YxdK-YxdJ (antimicrobial peptide response) two-component regulatory system
- M00505: KinB-AlgB (alginate production) two-component regulatory system
- M00507: ChpA-ChpB/PilGH (chemosensory) two-component regulatory system
- M00512: CckA-CtrA/CpdR (cell cycle control) two-component regulatory system
- M00520: ChvG-ChvI (acidity sensing) two-component regulatory system
- M00521: CiaH-CiaR two-component regulatory system

M00584: Acetoin utilization transport system
M00592: Inositol transport system
M00601: Putative chitobiose transport system
M00604: Trehalose transport system
M00607: Glycerol transport system
M00634: Oleandomycin transport system
M00637: Anthranilate degradation, anthranilate => catechol
M00654: ParS-ParR (polymyxin-adaptive resistance) two-component regulatory system
M00655: AdeS-AdeR two-component regulatory system
M00656: VanS-VanR (VanB type vancomycin resistance) two-component regulatory system
M00663: SsrA-SsrB two-component regulatory system
M00668: Tetracycline resistance, TetA transporter
M00731: Bacitracin transport system
M00766: Streptomycin resistance, deactivating enzyme StrAB
M00044: Tyrosine degradation, tyrosine => homogentisate
M00034: Methionine salvage pathway
M00047: Creatine pathway
M00076: Dermatan sulfate degradation
M00085: Fatty acid biosynthesis, elongation, mitochondria
M00129: Ascorbate biosynthesis, animals, glucose-1P => ascorbate
M00346: Formaldehyde assimilation, serine pathway
M00356: Methanogenesis, methanol => methane
M00357: Methanogenesis, acetate => methane
M00358: Coenzyme M biosynthesis
M00374: Dicarboxylate-hydroxybutyrate cycle
M00508: PixL-PixGH (positive phototaxis) two-component regulatory system
M00529: Denitrification, nitrate => nitrogen
M00533: Homoprotocatechuate degradation, homoprotocatechuate => 2-oxohept-3-enedioate
M00540: Benzoate degradation, cyclohexanecarboxylic acid => pimeloyl-CoA
M00547: Benzene/toluene degradation, benzene => catechol / toluene => 3-methylcatechol
M00563: Methanogenesis, methylamine/dimethylamine/trimethylamine => methane
M00575: Pertussis pathogenicity signature 2, T1SS
M00639: Multidrug resistance, efflux pump MexCD-OprJ
M00641: Multidrug resistance, efflux pump MexEF-OprN
M00642: Multidrug resistance, efflux pump MexJK-OprM
M00649: Multidrug resistance, efflux pump AdeABC
M00698: Multidrug resistance, efflux pump BpeEF-OprC
M00737: Bacitracin resistance, VraDE transporter
M00136: GABA biosynthesis, prokaryotes, putrescine => GABA
M00080: Lipopolysaccharide biosynthesis, inner core => outer core => O-antigen
M00151: Cytochrome bc1 complex respiratory unit
M00186: Tungstate transport system
M00219: AI-2 transport system
M00305: PTS system, 2-O-A-mannosyl-D-glycerate-specific II component
M00319: Manganese/zinc/iron transport system
M00323: Urea transport system
M00457: TctE-TctD (tricarboxylic acid transport) two-component regulatory system
M00465: ManS-ManR (manganese homeostasis) two-component regulatory system

M00478: DegS-DegU (multicellular behavior control) two-component regulatory system
M00479: DesK-DesR (membrane lipid fluidity regulation) two-component regulatory system
M00493: AlgZ-AlgR (alginate production) two-component regulatory system
M00509: WspE-WspRF (chemosensory) two-component regulatory system
M00517: RpfC-RpfG (cell-to-cell signaling) two-component regulatory system
M00531: Assimilatory nitrate reduction, nitrate => ammonia
M00545: Trans-cinnamate degradation, trans-cinnamate => acetyl-CoA
M00551: Benzoate degradation, benzoate => catechol / methylbenzoate => methylcatechol
M00568: Catechol ortho-cleavage, catechol => 3-oxoadipate
M00587: Arginine/lysine/histidine/glutamine transport system
M00590: Erythritol transport system
M00608: 2-Oxocarboxylic acid chain extension, 2-oxoglutarate => 2-oxoadipate => 2-oxopimelate => 2-oxosuberate
M00734: BraS-BraR (bacitracin transport) two-component regulatory system

Cluster 2

M00202: Oligogalacturonide transport system
M00175: Nitrogen fixation, nitrogen => ammonia
M00205: N-Acetylglucosamine transport system
M00461: MtrB-MtrA (osmotic stress response) two-component regulatory system
M00469: BceS-BceR (bacitracin transport) two-component regulatory system
M00498: NtrY-NtrX (nitrogen regulation) two-component regulatory system
M00501: PilS-PilR (type 4 fimbriae synthesis) two-component regulatory system
M00342: Bacterial proteasome
M00290: Holo-TFIIF complex
M00518: GlnK-GlnL (glutamine utilization) two-component regulatory system
M00586: Putative amino-acid transport system
M00599: Inositol-phosphate transport system
M00600: alpha-1,4-Digalacturonate transport system
M00338: Cysteine biosynthesis, homocysteine + serine => cysteine
M00315: Uncharacterized ABC transport system
M00443: SenX3-RegX3 (phosphate starvation response) two-component regulatory system
M00610: PTS system, D-glucosamine-specific II component
M00033: Ectoine biosynthesis, aspartate => ectoine
M00013: Malonate semialdehyde pathway, propanoyl-CoA => acetyl-CoA
M00309: Non-phosphorylative Entner-Doudoroff pathway, gluconate/galactonate => glycerate
M00569: Catechol meta-cleavage, catechol => acetyl-CoA / 4-methylcatechol => propanoyl-CoA
M00643: Multidrug resistance, efflux pump MexXY-OprM
M00695: cAMP signaling
M00079: Keratan sulfate degradation
M00077: Chondroitin sulfate degradation
M00422: Acetyl-CoA pathway, CO₂ => acetyl-CoA
M00377: Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)
M00511: PleC-PleD (cell fate control) two-component regulatory system
M00467: SasA-RpaAB (circadian timing mediating) two-component regulatory system
M00620: Incomplete reductive citrate cycle, acetyl-CoA => oxoglutarate
M00538: Toluene degradation, toluene => benzoate
M00537: Xylene degradation, xylene => methylbenzoate
M00253: Sodium transport system
M00156: Cytochrome c oxidase, cbb3-type

M00442: Putative hydroxymethylpyrimidine transport system
M00460: MprB-MprA (maintenance of persistent infection) two-component regulatory system
M00220: Rhamnose transport system
M00252: Lipooligosaccharide transport system
M00244: Putative zinc/manganese transport system
M00190: Iron(III) transport system
M00281: PTS system, lactose-specific II component
M00519: YesM-YesN two-component regulatory system
M00603: Putative aldouronate transport system
M00657: VanS-VanR (VanE type vancomycin resistance) two-component regulatory system
M00216: Multiple sugar transport system
M00159: V/A-type ATPase, prokaryotes
M00245: Cobalt/nickel transport system
M00246: Nickel transport system
M00250: Lipopolysaccharide transport system
M00566: Dipeptide transport system, Firmicutes
M00332: Type III secretion system
M00224: Fluoroquinolone transport system
M00652: Vancomycin resistance, D-Ala-D-Ser type

Cluster 3

M00192: Putative thiamine transport system
M00185: Sulfate transport system
M00217: D-Allose transport system
M00225: Lysine/arginine/ornithine transport system
M00226: Histidine transport system
M00229: Arginine transport system
M00241: Vitamin B12 transport system
M00249: Capsular polysaccharide transport system
M00300: Putrescine transport system
M00324: Dipeptide transport system
M00417: Cytochrome o ubiquinol oxidase
M00435: Taurine transport system
M00444: PhoQ-PhoP (magnesium transport) two-component regulatory system
M00446: RstB-RstA two-component regulatory system
M00447: CpxA-CpxR (envelope stress response) two-component regulatory system
M00449: CreC-CreB (phosphate regulation) two-component regulatory system
M00451: BasS-BasR (antimicrobial peptide resistance) two-component regulatory system
M00452: CusS-CusR (copper tolerance) two-component regulatory system
M00453: QseC-QseB (quorum sensing) two-component regulatory system
M00455: TorS-TorR (TMAO respiration) two-component regulatory system
M00456: ArcB-ArcA (anoxic redox control) two-component regulatory system
M00473: UhpB-UhpA (hexose phosphates uptake) two-component regulatory system
M00474: RcsC-RcsD-RcsB (capsule synthesis) two-component regulatory system
M00477: EvgS-EvgA (acid and drug tolerance) two-component regulatory system
M00486: CitA-CitB (citrate fermentation) two-component regulatory system
M00488: DcuS-DcuR (C4-dicarboxylate metabolism) two-component regulatory system
M00500: AtoS-AtoC (cPHB biosynthesis) two-component regulatory system
M00502: GlrK-GlrR (amino sugar metabolism) two-component regulatory system

M00503: PgtB-PgtA (phosphoglycerate transport) two-component regulatory system
M00552: D-galactonate degradation, De Ley-Doudoroff pathway, D-galactonate => glycerate-3P
M00555: Betaine biosynthesis, choline => betaine
M00707: Multidrug resistance, SmdAB/MdlAB transporter
M00709: Macrolide resistance, MacAB-TolC transporter
M00711: Multidrug resistance, efflux pump MdtIJ
M00721: Cationic antimicrobial peptide (CAMP) resistance, arnBCADTEF operon
M00722: Cationic antimicrobial peptide (CAMP) resistance, phosphoethanolamine transferase PmrC
M00724: Cationic antimicrobial peptide (CAMP) resistance, palmitoyl transferase PagP
M00739: Cationic peptide transport system
M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone
M00040: Tyrosine biosynthesis, prephanate => pretyrosine => tyrosine
M00165: Reductive pentose phosphate cycle (Calvin cycle)
M00235: Arginine/ornithine transport system
M00314: Bacitracin transport system
M00257: Hemin transport system
M00317: Manganese/iron transport system
M00416: Cytochrome aa3-600 menaquinol oxidase
M00504: DctB-DctD (C4-dicarboxylate transport) two-component regulatory system
M00733: GraS-GraR (cationic antimicrobial peptide transport) two-component regulatory system
M00316: Manganese transport system
M00231: Octopine/nopaline transport system
M00330: Adhesin protein transport system
M00653: AauS-AauR (acidic amino acids utilization) two-component regulatory system
M00713: Fluoroquinolone resistance, efflux pump LfrA
M00714: Multidrug resistance, efflux pump QacA
M00716: ArlS-ArlR (virulence regulation) two-component regulatory system
M00723: Cationic antimicrobial peptide (CAMP) resistance, phosphoethanolamine transferase EptB
M00732: Cationic antimicrobial peptide transport system
M00744: Cationic antimicrobial peptide (CAMP) resistance, protease PgtE
M00745: Imipenem resistance, repression of porin OprD
M00746: Multidrug resistance, repression of porin OmpF
M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone
M00767: Multidrug resistance, efflux pump OqxAB
M00730: Cationic antimicrobial peptide (CAMP) resistance, VraFG transporter
M00334: Type VI secretion system
M00259: Heme transport system
M00440: Nickel transport system
M00450: BaeS-BaeR (envelope stress response) two-component regulatory system
M00701: Multidrug resistance, efflux pump EmrAB
M00223: Phosphonate transport system
M00591: Putative xylitol transport system
M00204: Trehalose/maltose transport system
M00098: Acylglycerol degradation
M00515: FlrB-FlrC (polar flagellar synthesis) two-component regulatory system
M00728: Cationic antimicrobial peptide (CAMP) resistance, envelope protein folding and degrading factors Deg
M00648: Multidrug resistance, efflux pump MdtABC
M00645: Multidrug resistance, efflux pump SmeABC

Cluster 4

M00172: C4-dicarboxylic acid cycle, NADP - malic enzyme type
M00095: C5 isoprenoid biosynthesis, mevalonate pathway
M00173: Reductive citrate cycle (Arnon-Buchanan cycle)
M00179: Ribosome, archaea
M00200: Putative sorbitol/mannitol transport system
M00206: Cellobiose transport system
M00339: RaxAB-RaxC type I secretion system
M00571: AlgE-type Mannuronan C-5-Epimerase transport system
M00573: Biotin biosynthesis, BioI pathway, long-chain-acyl-ACP => pimeloyl-ACP => biotin
M00581: Biotin transport system
M00605: Glucose/mannose transport system
M00606: N,N'-Diacetylchitobiose transport system
M00609: Cysteine biosynthesis, methionine => cysteine
M00669: gamma-Hexachlorocyclohexane transport system
M00670: Mce transport system
M00720: Multidrug resistance, efflux pump VexEF-ToIC
M00729: Fluoroquinolone resistance, gyrase-protecting protein Qnr
M00029: Urea cycle
M00585: L-Cystine transport system
M00646: Multidrug resistance, efflux pump AcrAD-ToIC
M00012: Glyoxylate cycle
M00727: Cationic antimicrobial peptide (CAMP) resistance, N-acetylmuramoyl-L-alanine amidase AmiA and AmiB
M00166: Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P
M00726: Cationic antimicrobial peptide (CAMP) resistance, lysyl-phosphatidylglycerol (L-PG) synthase MprF
M00725: Cationic antimicrobial peptide (CAMP) resistance, dltABCD operon
M00697: Multidrug resistance, efflux pump MdtEF-ToIC
M00024: Phenylalanine biosynthesis, chorismate => phenylalanine
M00008: Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate
M00025: Tyrosine biosynthesis, chorismate => tyrosine
M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate
M00060: Lipopolysaccharide biosynthesis, KDO2-lipid A
M00118: Glutathione biosynthesis, glutamate => glutathione
M00149: Succinate dehydrogenase, prokaryotes
M00150: Fumarate reductase, prokaryotes
M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => ribulose-5P
M00176: Assimilatory sulfate reduction, sulfate => H₂S
M00191: Thiamine transport system
M00194: Maltose/maltodextrin transport system
M00198: Putative sn-glycerol-phosphate transport system
M00210: Phospholipid transport system
M00215: D-Xylose transport system
M00227: Glutamine transport system
M00230: Glutamate/aspartate transport system
M00232: General L-amino acid transport system
M00272: PTS system, arbutin-, cellobiose-, and salicin-specific II component
M00279: PTS system, galactitol-specific II component
M00303: PTS system, N-acetylmuramic acid-specific II component

M00320: Lipopolysaccharide export system
M00331: Type II general secretion pathway
M00333: Type IV secretion system
M00345: Formaldehyde assimilation, ribulose monophosphate pathway
M00394: RNA degradosome
M00458: ResE-ResD (aerobic and anaerobic respiration) two-component regulatory system
M00475: BarA-UvrY (central carbon metabolism) two-component regulatory system
M00580: Pentose phosphate pathway, archaea, fructose 6P => ribose 5P
M00124: Pyridoxal biosynthesis, erythrose-4P => pyridoxal-5P
M00087: beta-Oxidation
M00530: Dissimilatory nitrate reduction, nitrate => ammonia
M00743: Aminoglycoside resistance, protease HtpX
M00572: Pimeloyl-ACP biosynthesis, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP
M00141: C1-unit interconversion, eukaryotes
M00135: GABA biosynthesis, eukaryotes, putrescine => GABA
M00197: Putative fructooligosaccharide transport system
M00325: alpha-Hemolysin/cyclolysin transport system
M00326: RTX toxin transport system
M00577: Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin
M00593: Inositol transport system
M00602: Arabinosaccharide transport system
M00741: Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA
M00361: Nucleotide sugar biosynthesis, eukaryotes
M00199: L-Arabinose/lactose transport system
M00188: NitT/TauT family transport system
M00365: C10-C20 isoprenoid biosynthesis, archaea
M00429: Competence-related DNA transformation transporter
M00122: Cobalamin biosynthesis, cobinamide => cobalamin
M00035: Methionine degradation
M00308: Semi-phosphorylative Entner-Doudoroff pathway, gluconate => glycerate-3P
M00233: Glutamate transport system
M00064: ADP-L-glycero-D-manno-heptose biosynthesis
M00053: Pyrimidine deoxyribonucleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP
M00144: NADH:quinone oxidoreductase, prokaryotes
M00211: Putative ABC transport system
M00251: Teichoic acid transport system
M00283: PTS system, ascorbate-specific II component
M00647: Multidrug resistance, efflux pump AcrAB-TolC/SmeDEF
M00742: Aminoglycoside resistance, protease FtsH
M00002: Glycolysis, core module involving three-carbon compounds
M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate
M00003: Gluconeogenesis, oxaloacetate => fructose-6P
M00004: Pentose phosphate pathway (Pentose phosphate cycle)
M00005: PRPP biosynthesis, ribose 5P => PRPP
M00006: Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P
M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P
M00009: Citrate cycle (TCA cycle, Krebs cycle)
M00010: Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate

M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate
M00015: Proline biosynthesis, glutamate => proline
M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine
M00017: Methionine biosynthesis, aspartate => homoserine => methionine
M00018: Threonine biosynthesis, aspartate => homoserine => threonine
M00019: Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine
M00020: Serine biosynthesis, glycerate-3P => serine
M00021: Cysteine biosynthesis, serine => cysteine
M00022: Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate
M00023: Tryptophan biosynthesis, chorismate => tryptophan
M00026: Histidine biosynthesis, PRPP => histidine
M00027: GABA (gamma-Aminobutyrate) shunt
M00028: Ornithine biosynthesis, glutamate => ornithine
M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP
M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP
M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP
M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP
M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP
M00061: D-Glucuronate degradation, D-glucuronate => pyruvate + D-glyceraldehyde 3P
M00063: CMP-KDO biosynthesis
M00082: Fatty acid biosynthesis, initiation
M00083: Fatty acid biosynthesis, elongation
M00086: beta-Oxidation, acyl-CoA synthesis
M00093: Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE
M00096: C5 isoprenoid biosynthesis, non-mevalonate pathway
M00115: NAD biosynthesis, aspartate => NAD
M00119: Pantothenate biosynthesis, valine/L-aspartate => pantothenate
M00120: Coenzyme A biosynthesis, pantothenate => CoA
M00123: Biotin biosynthesis, pimeloyl-ACP/CoA => biotin
M00125: Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD
M00126: Tetrahydrofolate biosynthesis, GTP => THF
M00127: Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P
M00140: C1-unit interconversion, prokaryotes
M00153: Cytochrome d ubiquinol oxidase
M00157: F-type ATPase, prokaryotes and chloroplasts
M00168: CAM (Crassulacean acid metabolism), dark
M00169: CAM (Crassulacean acid metabolism), light
M00178: Ribosome, bacteria
M00183: RNA polymerase, bacteria
M00189: Molybdate transport system
M00201: alpha-Glucoside transport system
M00207: Putative multiple sugar transport system
M00208: Glycine betaine/proline transport system
M00209: Osmoprotectant transport system
M00212: Ribose transport system
M00214: Methyl-galactoside transport system
M00221: Putative simple sugar transport system
M00222: Phosphate transport system

M00228: Putative glutamine transport system
M00234: Cystine transport system
M00236: Putative polar amino acid transport system
M00237: Branched-chain amino acid transport system
M00238: D-Methionine transport system
M00239: Peptides/nickel transport system
M00240: Iron complex transport system
M00242: Zinc transport system
M00247: Putative ABC transport system
M00254: ABC-2 type transport system
M00255: Lipoprotein-releasing system
M00256: Cell division transport system
M00258: Putative ABC transport system
M00260: DNA polymerase III complex, bacteria
M00265: PTS system, glucose-specific II component
M00266: PTS system, maltose and glucose-specific II component
M00267: PTS system, N-acetylglucosamine-specific II component
M00268: PTS system, arbutin-like II component
M00269: PTS system, sucrose-specific II component
M00270: PTS system, trehalose-specific II component
M00271: PTS system, beta-glucosides-specific II component
M00273: PTS system, fructose-specific II component
M00274: PTS system, mannitol-specific II component
M00275: PTS system, cellobiose-specific II component
M00276: PTS system, mannose-specific II component
M00280: PTS system, glucitol/sorbitol-specific II component
M00282: PTS system, D-glucosamine-specific II component
M00299: Spermidine/putrescine transport system
M00307: Pyruvate oxidation, pyruvate => acetyl-CoA
M00335: Sec (secretion) system
M00336: Twin-arginine translocation (Tat) system
M00359: Aminoacyl-tRNA biosynthesis, eukaryotes
M00360: Aminoacyl-tRNA biosynthesis, prokaryotes
M00362: Nucleotide sugar biosynthesis, prokaryotes
M00364: C10-C20 isoprenoid biosynthesis, bacteria
M00432: Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate
M00434: PhoR-PhoB (phosphate starvation response) two-component regulatory system
M00439: Oligopeptide transport system
M00454: KdpD-KdpE (potassium transport) two-component regulatory system
M00459: VicK-VicR (cell wall metabolism) two-component regulatory system
M00491: arabinogalactan oligomer/maltooligosaccharide transport system
M00495: AgrC-AgrA (exoprotein synthesis) two-component regulatory system
M00549: Nucleotide sugar biosynthesis, glucose => UDP-glucose
M00554: Nucleotide sugar biosynthesis, galactose => UDP-galactose
M00565: Trehalose biosynthesis, D-glucose 1P => trehalose
M00570: Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine
M00579: Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate
M00582: Energy-coupling factor transport system

M00589: Putative lysine transport system
M00631: D-Galacturonate degradation (bacteria), D-galacturonate => pyruvate + D-glyceraldehyde 3P
M00632: Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P
M00708: Multidrug resistance, PatAB transporter
M00298: Multidrug/hemolysin transport system
M00134: Polyamine biosynthesis, arginine => ornithine => putrescine
M00525: Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine
M00196: Raffinose/stachyose/melibiose transport system
M00526: Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine
M00527: Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine
M00535: Isoleucine biosynthesis, pyruvate => 2-oxobutanoate
M00506: CheA-CheYBV (chemotaxis) two-component regulatory system
M00090: Phosphatidylcholine (PC) biosynthesis, choline => PC
M00046: Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate
M00170: C4-dicarboxylic acid cycle, phosphoenolpyruvate carboxykinase type
M00366: C10-C20 isoprenoid biosynthesis, plants
M00367: C10-C20 isoprenoid biosynthesis, non-plant eukaryotes
M00368: Ethylene biosynthesis, methionine => ethylene
M00699: Multidrug resistance, efflux pump AmeABC
M00596: Dissimilatory sulfate reduction, sulfate => H₂S
M00089: Triacylglycerol biosynthesis
M00651: Vancomycin resistance, D-Ala-D-Lac type
M00696: Multidrug resistance, efflux pump AcrEF-TolC
M00718: Multidrug resistance, efflux pump MexAB-OprM
M00627: beta-Lactam resistance, Bla system

Cluster 5

M00145: NAD(P)H:quinone oxidoreductase, chloroplasts and cyanobacteria
M00116: Menaquinone biosynthesis, chorismate => menaquinone
M00243: Manganese/iron transport system
M00304: PTS system, fructose-specific II component
M00344: Formaldehyde assimilation, xylulose monophosphate pathway
M00700: Multidrug resistance, efflux pump AbcA
M00480: VraS-VraR (cell-wall peptidoglycan synthesis) two-component regulatory system
M00278: PTS system, sorbose-specific II component
M00628: beta-Lactam resistance, AmpC system
M00615: Nitrate assimilation
M00306: PTS system, fructose-specific II-like component
M00213: L-Arabinose transport system
M00348: Glutathione transport system
M00349: Microcin C transport system
M00445: EnvZ-OmpR (osmotic stress response) two-component regulatory system
M00471: NarX-NarL (nitrate respiration) two-component regulatory system
M00472: NarQ-NarP (nitrate respiration) two-component regulatory system
M00499: HydH-HydG (metal tolerance) two-component regulatory system
M00550: Ascorbate degradation, ascorbate => D-xylulose-5P
M00133: Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine
M00121: Heme biosynthesis, glutamate => protoheme/siroheme
M00277: PTS system, N-acetylgalactosamine-specific II component

M00193: Putative spermidine/putrescine transport system
M00287: PTS system, galactosamine-specific II component
M00436: Sulfonate transport system
M00483: NreB-NreC (dissimilatory nitrate/nitrite reduction) two-component regulatory system
M00492: LytS-LytR two-component regulatory system
M00497: GlnL-GlnG (nitrogen regulation) two-component regulatory system
M00706: Multidrug resistance, EfrAB transporter
M00712: Multidrug resistance, efflux pump YkkCD
M00481: LiaS-LiaR (cell wall stress response) two-component regulatory system
M00318: Iron/zinc/copper transport system
M00738: Bacitracin resistance, BceAB transporter
M00081: Pectin degradation
M00754: Nisin resistance, phage shock protein homolog LiaH
M00702: Multidrug resistance, efflux pump NorB
M00154: Cytochrome c oxidase
M00468: SaeS-SaeR (staphylococcal virulence regulation) two-component regulatory system
M00583: Putative peptide transport system

0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	4	4
0	4	1	4
0	4	1	4
0	4	1	4
0	4	1	4
0	4	1	4
0	4	1	4
1	4	1	4
1	4	1	4
1	4	1	4
1	4	1	4
1	4	1	4
1	4	1	4
0	4	0	4
0	4	0	4
0	4	0	4
1	4	0	4
2	4	2	4
2	4	2	4
2	4	2	4
2	4	2	4
2	4	2	4
2	4	2	4
1	4	2	4
1	4	2	4
1	4	2	4
0	4	2	4
1	4	4	2
1	4	4	2
1	4	4	2
2	4	4	2
2	4	4	2
0	4	4	1
0	4	4	1

0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	0	4	4
0	1	4	4
0	1	4	4
0	1	4	4
0	1	4	4
1	0	4	4
1	0	4	4
1	0	4	4
1	0	4	4
1	0	4	4
1	0	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	1	4	4
1	2	4	4
2	2	4	4
2	1	4	4
0	0	4	1
0	0	4	1
0	0	4	1
0	0	4	1
0	0	4	0
1	1	4	1
1	1	4	1
0	1	4	1
0	1	4	0
0	0	4	2
0	0	4	2
1	1	4	2

0	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0
0	0	1	0
0	0	1	0
0	1	0	0
0	1	0	0
0	1	0	0
0	1	0	0
0	2	1	0
2	2	2	2
2	2	2	2
2	2	2	2
2	2	2	2
2	2	2	2
2	2	2	2
2	2	2	2
2	2	2	2
2	2	2	2
1	2	2	2
1	2	2	2
1	2	2	2
1	2	2	2
1	2	2	2
0	2	2	2
1	1	1	4
1	1	1	4
1	1	1	4
1	1	1	4
1	1	1	4
1	1	1	4
1	0	1	4
1	0	1	4
0	1	1	4
0	1	1	4
0	0	1	4
0	0	1	4
0	0	1	4
0	0	1	4
0	0	1	4
0	0	1	4
0	0	1	4
0	0	1	4
0	0	1	4
0	0	1	4
0	0	2	4
0	0	2	4
0	0	0	4

0	0	0	4
0	0	0	4
0	0	0	4
0	0	0	4
0	0	0	4
0	0	0	4
0	0	0	4
0	0	0	4
1	0	0	4
1	0	0	4
1	2	2	4
1	2	2	4
2	1	1	4
4	1	4	4
4	1	4	4
4	0	4	4
4	4	0	4