

## Supplementary Table 9

0: Kegg module complete

1: 1 block missing

2: 2 blocks missing

4: Kegg module absent

### Cluster 1

M00136: GABA biosynthesis, prokaryotes, putrescine => GABA

M00013: Malonate semialdehyde pathway, propanoyl-CoA => acetyl-CoA

M00540: Benzoate degradation, cyclohexanecarboxylic acid => pimeloyl-CoA

M00568: Catechol ortho-cleavage, catechol => 3-oxoadipate

M00301: Mannopine transport system

M00766: Streptomycin resistance, deactivating enzyme StrAB

M00663: SsrA-SsrB two-component regulatory system

M00641: Multidrug resistance, efflux pump MexEF-OprN

M00642: Multidrug resistance, efflux pump MexJK-OprM

M00639: Multidrug resistance, efflux pump MexCD-OprJ

M00768: Multidrug resistance, efflux pump GesABC

M00643: Multidrug resistance, efflux pump MexXY-OprM

M00698: Multidrug resistance, efflux pump BpeEF-OprC

M00361: Nucleotide sugar biosynthesis, eukaryotes

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

M00173: Reductive citrate cycle (Arnon-Buchanan cycle)

M00241: Vitamin B12 transport system

M00117: Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone

M00711: Multidrug resistance, efflux pump MdtIJ

M00080: Lipopolysaccharide biosynthesis, inner core => outer core => O-antigen

M00723: Cationic antimicrobial peptide (CAMP) resistance, phosphoethanolamine tra

M00746: Multidrug resistance, repression of porin OmpF

M00655: AdeS-AdeR two-component regulatory system

M00249: Capsular polysaccharide transport system

M00649: Multidrug resistance, efflux pump AdeABC

M00644: Vanadium resistance, efflux pump MexGHI-OpmD

M00170: C4-dicarboxylic acid cycle, phosphoenolpyruvate carboxykinase type

M00710: Multidrug resistance, efflux pump EbrAB

M00330: Adhesin protein transport system

M00451: BasS-BasR (antimicrobial peptide resistance) two-component regulatory sys

M00722: Cationic antimicrobial peptide (CAMP) resistance, phosphoethanolamine tr

M00165: Reductive pentose phosphate cycle (Calvin cycle)

M00503: PgtB-PgtA (phosphoglycerate transport) two-component regulatory system

M00133: Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine

M00761: Undecaprenylphosphate alpha-L-Ara4N biosynthesis, UDP-GlcA => undeca

M00302: 2-Aminoethylphosphonate transport system

M00219: AI-2 transport system

M00213: L-Arabinose transport system

M00552: D-galactonate degradation, De Ley-Doudoroff pathway, D-galactonate => gly

M00456: ArcB-ArcA (anoxic redox control) two-component regulatory system  
M00720: Multidrug resistance, efflux pump VexEF-TolC  
M00571: AlgE-type Mannuronan C-5-Epimerase transport system  
M00124: Pyridoxal biosynthesis, erythrose-4P => pyridoxal-5P  
M00474: RcsC-RcsD-RcsB (capsule synthesis) two-component regulatory system  
M00339: RaxAB-RaxC type I secretion system  
M00326: RTX toxin transport system  
M00455: TorS-TorR (TMAO respiration) two-component regulatory system  
M00696: Multidrug resistance, efflux pump AcrEF-TolC  
M00697: Multidrug resistance, efflux pump MdtEF-TolC  
M00699: Multidrug resistance, efflux pump AmeABC  
M00718: Multidrug resistance, efflux pump MexAB-OprM  
M00628: beta-Lactam resistance, AmpC system  
M00063: CMP-KDO biosynthesis  
M00336: Twin-arginine translocation (Tat) system  
M00060: Lipopolysaccharide biosynthesis, KDO2-lipid A  
M00577: Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin  
M00573: Biotin biosynthesis, BioI pathway, long-chain-acyl-ACP => pimeloyl-ACP => t  
M00081: Pectin degradation  
M00145: NAD(P)H:quinone oxidoreductase, chloroplasts and cyanobacteria  
M00116: Menaquinone biosynthesis, chorismate => menaquinone  
M00695: cAMP signaling  
M00172: C4-dicarboxylic acid cycle, NADP - malic enzyme type  
M00079: Keratan sulfate degradation  
M00077: Chondroitin sulfate degradation  
M00403: HRD1/SEL1 ERAD complex  
M00400: p97-Ufd1-Npl4 complex  
M00653: AauS-AauR (acidic amino acids utilization) two-component regulatory system  
M00514: TtrS-TtrR (tetrathionate respiration) two-component regulatory system  
M00668: Tetracycline resistance, TetA transporter  
M00520: ChvG-ChvI (acidity sensing) two-component regulatory system  
M00486: CitA-CitB (citrate fermentation) two-component regulatory system  
M00417: Cytochrome o ubiquinol oxidase  
M00473: UhpB-UhpA (hexose phosphates uptake) two-component regulatory system  
M00739: Cationic peptide transport system  
M00615: Nitrate assimilation  
M00472: NarQ-NarP (nitrate respiration) two-component regulatory system  
M00053: Pyrimidine deoxyribonucleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP  
M00259: Heme transport system  
M00121: Heme biosynthesis, glutamate => protoheme/siroheme  
M00334: Type VI secretion system  
M00367: C10-C20 isoprenoid biosynthesis, non-plant eukaryotes  
M00366: C10-C20 isoprenoid biosynthesis, plants  
M00701: Multidrug resistance, efflux pump EmrAB  
M00027: GABA (gamma-Aminobutyrate) shunt  
M00530: Dissimilatory nitrate reduction, nitrate => ammonia  
M00482: DevS-DevR (redox response) two-component regulatory system  
M00177: Ribosome, eukaryotes

M00583: Putative peptide transport system  
M00714: Multidrug resistance, efflux pump QacA  
M00713: Fluoroquinolone resistance, efflux pump LfrA  
M00480: VraS-VraR (cell-wall peptidoglycan synthesis) two-component regulatory sys  
M00712: Multidrug resistance, efflux pump YkkCD  
M00257: Hemin transport system  
M00715: Lincosamide resistance, efflux pump LmrB  
M00095: C5 isoprenoid biosynthesis, mevalonate pathway  
M00707: Multidrug resistance, SmdAB/MdlAB transporter  
M00609: Cysteine biosynthesis, methionine => cysteine  
M00118: Glutathione biosynthesis, glutamate => glutathione  
M00208: Glycine betaine/proline transport system  
M00490: MalK-MalR (malate transport) two-component regulatory system  
M00488: DcuS-DcuR (C4-dicarboxylate metabolism) two-component regulatory syste  
M00487: CitS-CitT (magnesium-citrate transport) two-component regulatory system  
M00489: DctS-DctR (C4-dicarboxylate transport) two-component regulatory system  
M00555: Betaine biosynthesis, choline => betaine  
M00318: Iron/zinc/manganese/copper transport system  
M00316: Manganese transport system  
M00317: Manganese/iron transport system  
M00319: Manganese/zinc/iron transport system  
M00243: Manganese/iron transport system  
M00287: PTS system, galactosamine-specific II component  
M00306: PTS system, fructose-specific II-like component  
M00610: PTS system, D-glucosaminatate-specific II component  
M00305: PTS system, 2-O-A-mannosyl-D-glycerate-specific II component  
M00281: PTS system, lactose-specific II component  
M00277: PTS system, N-acetylgalactosamine-specific II component  
M00276: PTS system, mannose-specific II component  
M00550: Ascorbate degradation, ascorbate => D-xylulose-5P  
M00304: PTS system, fructose-specific II component  
M00278: PTS system, sorbose-specific II component  
M00283: PTS system, ascorbate-specific II component  
M00754: Nisin resistance, phage shock protein homolog LiaH  
M00481: LiaS-LiaR (cell wall stress response) two-component regulatory system  
M00483: NreB-NreC (dissimilatory nitrate/nitrite reduction) two-component regulatory  
M00478: DegS-DegU (multicellular behavior control) two-component regulatory syste  
M00226: Histidine transport system  
M00225: Lysine/arginine/ornithine transport system  
M00231: Octopine/nopaline transport system  
M00585: L-Cystine transport system  
M00586: Putative amino-acid transport system  
M00744: Cationic antimicrobial peptide (CAMP) resistance, protease PgtE  
M00709: Macrolide resistance, MacAB-TolC transporter  
M00724: Cationic antimicrobial peptide (CAMP) resistance, palmitoyl transferase Pag  
M00444: PhoQ-PhoP (magnesium transport) two-component regulatory system  
M00279: PTS system, galactitol-specific II component  
M00235: Arginine/ornithine transport system

M00479: DesK-DesR (membrane lipid fluidity regulation) two-component regulatory system  
M00229: Arginine transport system  
M00230: Glutamate/aspartate transport system  
M00471: NarX-NarL (nitrate respiration) two-component regulatory system  
M00325: alpha-Hemolysin/cyclolysin transport system

## Cluster 2

M00368: Ethylene biosynthesis, methionine => ethylene  
M00166: Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P  
M00745: Imipenem resistance, repression of porin OprD  
M00728: Cationic antimicrobial peptide (CAMP) resistance, envelope protein folding  
M00727: Cationic antimicrobial peptide (CAMP) resistance, N-acetylmuramoyl-L-ala  
M00721: Cationic antimicrobial peptide (CAMP) resistance, arnBCADTEF operon  
M00743: Aminoglycoside resistance, protease HtpX  
M00647: Multidrug resistance, efflux pump AcrAB-TolC/SmeDEF  
M00445: EnvZ-OmpR (osmotic stress response) two-component regulatory system  
M00320: Lipopolysaccharide export system  
M00515: FlrB-FlrC (polar flagellar synthesis) two-component regulatory system  
M00501: PilS-PilR (type 4 fimbriae synthesis) two-component regulatory system  
M00499: HydH-HydG (metal tolerance) two-component regulatory system  
M00497: GlnL-GlnG (nitrogen regulation) two-component regulatory system  
M00502: GlrK-GlrR (amino sugar metabolism) two-component regulatory system  
M00500: AtoS-AtoC (cPHB biosynthesis) two-component regulatory system  
M00670: Mce transport system  
M00669: gamma-Hexachlorocyclohexane transport system  
M00210: Phospholipid transport system  
M00572: Pimeloyl-ACP biosynthesis, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP  
M00504: DctB-DctD (C4-dicarboxylate transport) two-component regulatory system  
M00498: NtrY-NtrX (nitrogen regulation) two-component regulatory system  
M00505: KinB-AlgB (alginate production) two-component regulatory system  
M00741: Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA  
M00477: EvgS-EvgA (acid and drug tolerance) two-component regulatory system  
M00506: CheA-CheYBV (chemotaxis) two-component regulatory system  
M00475: BarA-UvrY (central carbon metabolism) two-component regulatory system  
M00332: Type III secretion system  
M00300: Putrescine transport system  
M00648: Multidrug resistance, efflux pump MdtABC  
M00646: Multidrug resistance, efflux pump AcrAD-TolC  
M00645: Multidrug resistance, efflux pump SmeABC  
M00450: BaeS-BaeR (envelope stress response) two-component regulatory system  
M00035: Methionine degradation  
M00447: CpxA-CpxR (envelope stress response) two-component regulatory system  
M00123: Biotin biosynthesis, pimeloyl-ACP/CoA => biotin  
M00119: Pantothenate biosynthesis, valine/L-aspartate => pantothenate  
M00011: Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate  
M00009: Citrate cycle (TCA cycle, Krebs cycle)  
M00533: Homoprotocatechuate degradation, homoprotocatechuate => 2-oxohept-3-er  
M00122: Cobalamin biosynthesis, cobinamide => cobalamin  
M00349: Microcin C transport system

M00149: Succinate dehydrogenase, prokaryotes  
M00324: Dipeptide transport system  
M00046: Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoic acid  
M00135: GABA biosynthesis, eukaryotes, putrescine => GABA  
M00440: Nickel transport system  
M00348: Glutathione transport system  
M00176: Assimilatory sulfate reduction, sulfate => H<sub>2</sub>S  
M00012: Glyoxylate cycle  
M00087: beta-Oxidation  
M00220: Rhamnose transport system  
M00590: Erythritol transport system  
M00591: Putative xylitol transport system  
M00215: D-Xylose transport system  
M00098: Acylglycerol degradation  
M00593: Inositol transport system  
M00214: Methyl-galactoside transport system  
M00199: L-Arabinose/lactose transport system  
M00198: Putative sn-glycerol-phosphate transport system  
M00449: CreC-CreB (phosphate regulation) two-component regulatory system  
M00465: ManS-ManR (manganese homeostasis) two-component regulatory system  
M00457: TctE-TctD (tricarboxylic acid transport) two-component regulatory system  
M00362: Nucleotide sugar biosynthesis, prokaryotes  
M00232: General L-amino acid transport system  
M00150: Fumarate reductase, prokaryotes  
M00338: Cysteine biosynthesis, homocysteine + serine => cysteine  
M00587: Arginine/lysine/histidine/glutamine transport system  
M00453: QseC-QseB (quorum sensing) two-component regulatory system  
M00064: ADP-L-glycero-D-manno-heptose biosynthesis  
M00134: Polyamine biosynthesis, arginine => ornithine => putrescine  
M00435: Taurine transport system  
M00040: Tyrosine biosynthesis, prephenate => pretyrosine => tyrosine  
M00191: Thiamine transport system  
M00190: Iron(III) transport system  
M00654: ParS-ParR (polymyxin-adaptive resistance) two-component regulatory system  
M00280: PTS system, glucitol/sorbitol-specific II component  
M00446: RstB-RstA two-component regulatory system

### **Cluster 3**

M00620: Incomplete reductive citrate cycle, acetyl-CoA => oxoglutarate  
M00563: Methanogenesis, methylamine/dimethylamine/trimethylamine => methane  
M00356: Methanogenesis, methanol => methane  
M00548: Benzene degradation, benzene => catechol  
M00494: NatK-NatR (sodium extrusion) two-component regulatory system  
M00513: LuxQN/CqsS-LuxU-LuxO (quorum sensing) two-component regulatory system  
M00033: Ectoine biosynthesis, aspartate => ectoine  
M00569: Catechol meta-cleavage, catechol => acetyl-CoA / 4-methylcatechol => propionyl-CoA  
M00464: NrsS-NrsR (nickel tolerance) two-component regulatory system  
M00156: Cytochrome c oxidase, cbb3-type  
M00151: Cytochrome bc<sub>1</sub> complex respiratory unit

M00162: Cytochrome b6f complex  
M00163: Photosystem I  
M00391: Exosome, eukaryotes  
M00076: Dermatan sulfate degradation  
M00551: Benzoate degradation, benzoate => catechol / methylbenzoate => methylcat  
M00702: Multidrug resistance, efflux pump NorB  
M00154: Cytochrome c oxidase  
M00416: Cytochrome aa3-600 menaquinol oxidase  
M00584: Acetoin utilization transport system  
M00155: Cytochrome c oxidase, prokaryotes  
M00607: Glycerol transport system  
M00604: Trehalose transport system  
M00518: GlnK-GlnL (glutamine utilization) two-component regulatory system  
M00088: Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/ac  
M00423: Molybdate/tungstate transport system  
M00192: Putative thiamine transport system  
M00217: D-Allose transport system  
M00592: Inositol transport system  
M00438: Nitrate/nitrite transport system  
M00309: Non-phosphorylative Entner-Doudoroff pathway, gluconate/galactonate => gl  
M00342: Bacterial proteasome  
M00322: Neutral amino acid transport system  
M00343: Archaeal proteasome  
M00218: Fructose transport system  
M00175: Nitrogen fixation, nitrogen => ammonia  
M00321: Bicarbonate transport system  
M00377: Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)  
M00186: Tungstate transport system  
M00422: Acetyl-CoA pathway, CO2 => acetyl-CoA  
M00484: YdfH-YdfI two-component regulatory system  
M00524: FixL-FixJ (nitrogen fixation) two-component regulatory system  
M00485: KinABCDE-Spo0FA (sporulation control) two-component regulatory system  
M00512: CckA-CtrA/CpdR (cell cycle control) two-component regulatory system  
M00719: Ihk-Irr (virulence regulation) two-component regulatory system  
M00205: N-Acetylglucosamine transport system  
M00511: PleC-PleD (cell fate control) two-component regulatory system  
M00507: ChpA-ChpB/PilGH (chemosensory) two-component regulatory system  
M00662: Hk1-Rrp1 (glycerol uptake and utilization) two-component regulatory system  
M00531: Assimilatory nitrate reduction, nitrate => ammonia  
M00522: SalK-SalR two-component regulatory system  
M00652: Vancomycin resistance, D-Ala-D-Ser type  
M00538: Toluene degradation, toluene => benzoate  
M00537: Xylene degradation, xylene => methylbenzoate  
M00767: Multidrug resistance, efflux pump OqxAB  
M00204: Trehalose/maltose transport system  
M00509: WspE-WspRF (chemosensory) two-component regulatory system  
M00344: Formaldehyde assimilation, xylulose monophosphate pathway  
M00090: Phosphatidylcholine (PC) biosynthesis, choline => PC

M00433: Lysine biosynthesis, 2-oxoglutarate => 2-oxoadipate  
M00608: 2-Oxocarboxylic acid chain extension, 2-oxoglutarate => 2-oxoadipate => 2-oxo-3-oxoadipate  
M00601: Putative chitobiose transport system  
M00625: Methicillin resistance  
M00290: Holo-TFIIH complex  
M00600: alpha-1,4-Digalacturonate transport system  
M00202: Oligogalacturonide transport system  
M00603: Putative aldouronate transport system  
M00656: VanS-VanR (VanB type vancomycin resistance) two-component regulatory system  
M00467: SasA-RpaAB (circadian timing mediating) two-component regulatory system  
M00737: Bacitracin resistance, VraDE transporter  
M00634: Oleandomycin transport system  
M00442: Putative hydroxymethylpyrimidine transport system  
M00253: Sodium transport system  
M00091: Phosphatidylcholine (PC) biosynthesis, PE => PC  
M00462: PrrB-PrrA (intracellular multiplication) two-component regulatory system  
M00045: Histidine degradation, histidine => N-formiminoglutamate => glutamate  
M00700: Multidrug resistance, efflux pump AbcA  
M00496: ComD-ComE (competence) two-component regulatory system  
M00466: NblS-NblR (photosynthesis) two-component regulatory system  
M00216: Multiple sugar transport system  
M00463: TrcS-TrcR two-component regulatory system  
M00223: Phosphonate transport system  
M00298: Multidrug/hemolysin transport system  
M00599: Inositol-phosphate transport system  
M00708: Multidrug resistance, PatAB transporter  
M00448: CssS-CssR (secretion stress response) two-component regulatory system  
M00517: RpfC-RpfG (cell-to-cell signaling) two-component regulatory system  
M00159: V/A-type ATPase, prokaryotes

#### **Cluster 4**

M00019: Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine  
M00432: Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate  
M00570: Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine  
M00028: Ornithine biosynthesis, glutamate => ornithine  
M00022: Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate  
M00026: Histidine biosynthesis, PRPP => histidine  
M00535: Isoleucine biosynthesis, pyruvate => 2-oxobutanoate  
M00096: C5 isoprenoid biosynthesis, non-mevalonate pathway  
M00144: NADH:quinone oxidoreductase, prokaryotes  
M00169: CAM (Crassulacean acid metabolism), light  
M00454: KdpD-KdpE (potassium transport) two-component regulatory system  
M00519: YesM-YesN two-component regulatory system  
M00359: Aminoacyl-tRNA biosynthesis, eukaryotes  
M00493: AlgZ-AlgR (alginate production) two-component regulatory system  
M00061: D-Glucuronate degradation, D-glucuronate => pyruvate + D-glyceraldehyde  
M00308: Semi-phosphorylative Entner-Doudoroff pathway, gluconate => glycerate-3P  
M00631: D-Galacturonate degradation (bacteria), D-galacturonate => pyruvate + D-glucose  
M00212: Ribose transport system

M00492: LytS-LytR two-component regulatory system  
M00017: Methionine biosynthesis, aspartate => homoserine => methionine  
M00605: Glucose/mannose transport system  
M00200: Putative sorbitol/mannitol transport system  
M00606: N,N'-Diacetylchitobiose transport system  
M00197: Putative fructooligosaccharide transport system  
M00602: Arabinosaccharide transport system  
M00206: Cellobiose transport system  
M00194: Maltose/maltodextrin transport system  
M00491: arabinogalactan oligomer/maltooligosaccharide transport system  
M00201: alpha-Glucoside transport system  
M00196: Raffinose/stachyose/melibiose transport system  
M00207: Putative multiple sugar transport system  
M00565: Trehalose biosynthesis, D-glucose 1P => trehalose  
M00256: Cell division transport system  
M00025: Tyrosine biosynthesis, chorismate => tyrosine  
M00024: Phenylalanine biosynthesis, chorismate => phenylalanine  
M00016: Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine  
M00526: Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine  
M00443: SenX3-RegX3 (phosphate starvation response) two-component regulatory s  
M00527: Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine  
M00020: Serine biosynthesis, glycerate-3P => serine  
M00018: Threonine biosynthesis, aspartate => homoserine => threonine  
M00082: Fatty acid biosynthesis, initiation  
M00048: Inosine monophosphate biosynthesis, PRPP + glutamine => IMP  
M00429: Competence-related DNA transformation transporter  
M00364: C10-C20 isoprenoid biosynthesis, bacteria  
M00549: Nucleotide sugar biosynthesis, glucose => UDP-glucose  
M00002: Glycolysis, core module involving three-carbon compounds  
M00049: Adenine ribonucleotide biosynthesis, IMP => ADP,ATP  
M00005: PRPP biosynthesis, ribose 5P => PRPP  
M00178: Ribosome, bacteria  
M00258: Putative ABC transport system  
M00360: Aminoacyl-tRNA biosynthesis, prokaryotes  
M00434: PhoR-PhoB (phosphate starvation response) two-component regulatory sys  
M00050: Guanine ribonucleotide biosynthesis IMP => GDP,GTP  
M00254: ABC-2 type transport system  
M00458: ResE-ResD (aerobic and anaerobic respiration) two-component regulatory s  
M00459: VicK-VicR (cell wall metabolism) two-component regulatory system  
M00307: Pyruvate oxidation, pyruvate => acetyl-CoA  
M00120: Coenzyme A biosynthesis, pantothenate => CoA  
M00140: C1-unit interconversion, prokaryotes  
M00183: RNA polymerase, bacteria  
M00260: DNA polymerase III complex, bacteria  
M00052: Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP  
M00335: Sec (secretion) system  
M00003: Gluconeogenesis, oxaloacetate => fructose-6P  
M00007: Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P



M00083: Fatty acid biosynthesis, elongation  
M00051: Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP  
M00222: Phosphate transport system  
M00015: Proline biosynthesis, glutamate => proline  
M00394: RNA degradosome  
M00742: Aminoglycoside resistance, protease FtsH  
M00179: Ribosome, archaea  
M00460: MprB-MprA (maintenance of persistent infection) two-component regulatory  
M00729: Fluoroquinolone resistance, gyrase-protecting protein Qnr  
M00345: Formaldehyde assimilation, ribulose monophosphate pathway  
M00167: Reductive pentose phosphate cycle, glyceraldehyde-3P => ribulose-5P  
M00141: C1-unit interconversion, eukaryotes  
M00255: Lipoprotein-releasing system  
M00168: CAM (Crassulacean acid metabolism), dark  
M00093: Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE  
M00452: CusS-CusR (copper tolerance) two-component regulatory system  
M00299: Spermidine/putrescine transport system  
M00021: Cysteine biosynthesis, serine => cysteine  
M00242: Zinc transport system  
M00554: Nucleotide sugar biosynthesis, galactose => UDP-galactose  
M00632: Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P  
M00001: Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate  
M00579: Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate  
M00240: Iron complex transport system  
M00157: F-type ATPase, prokaryotes and chloroplasts  
M00227: Glutamine transport system  
M00582: Energy-coupling factor transport system  
M00236: Putative polar amino acid transport system  
M00439: Oligopeptide transport system  
M00239: Peptides/nickel transport system  
M00333: Type IV secretion system  
M00221: Putative simple sugar transport system  
M00436: Sulfonate transport system  
M00188: NitT/TauT family transport system  
M00251: Teichoic acid transport system  
M00250: Lipopolysaccharide transport system  
M00237: Branched-chain amino acid transport system  
M00246: Nickel transport system  
M00245: Cobalt/nickel transport system

#### **Cluster 5**

M00733: GraS-GraR (cationic antimicrobial peptide transport) two-component regulat  
M00469: BceS-BceR (bacitracin transport) two-component regulatory system  
M00734: BraS-BraR (bacitracin transport) two-component regulatory system  
M00730: Cationic antimicrobial peptide (CAMP) resistance, VraFG transporter  
M00738: Bacitracin resistance, BceAB transporter  
M00725: Cationic antimicrobial peptide (CAMP) resistance, dltABCD operon  
M00726: Cationic antimicrobial peptide (CAMP) resistance, lysyl-phosphatidylglycero  
M00731: Bacitracin transport system

M00470: YxdK-YxdJ (antimicrobial peptide response) two-component regulatory syst  
M00224: Fluoroquinolone transport system  
M00651: Vancomycin resistance, D-Ala-D-Lac type  
M00521: CiaH-CiaR two-component regulatory system  
M00252: Lipooligosaccharide transport system  
M00716: ArlS-ArlR (virulence regulation) two-component regulatory system  
M00717: Multidrug resistance, efflux pump NorA  
M00089: Triacylglycerol biosynthesis  
M00627: beta-Lactam resistance, Bla system  
M00495: AgrC-AgrA (exoprotein synthesis) two-component regulatory system  
M00315: Uncharacterized ABC transport system  
M00314: Bacitracin transport system  
M00732: Cationic antimicrobial peptide transport system  
M00468: SaeS-SaeR (staphylococcal virulence regulation) two-component regulatory  
M00525: Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine  
M00461: MtrB-MtrA (osmotic stress response) two-component regulatory system  
M00029: Urea cycle  
M00581: Biotin transport system  
M00657: VanS-VanR (VanE type vancomycin resistance) two-component regulatory s  
M00706: Multidrug resistance, EfrAB transporter

#### **Cluster 6**

M00282: PTS system, D-glucosamine-specific II component  
M00270: PTS system, trehalose-specific II component  
M00265: PTS system, glucose-specific II component  
M00266: PTS system, maltose and glucose-specific II component  
M00303: PTS system, N-acetylmuramic acid-specific II component  
M00268: PTS system, arbutin-like II component  
M00272: PTS system, arbutin-, cellobiose-, and salicin-specific II component  
M00271: PTS system, beta-glucosides-specific II component  
M00269: PTS system, sucrose-specific II component  
M00274: PTS system, mannitol-specific II component  
M00267: PTS system, N-acetylglucosamine-specific II component  
M00275: PTS system, cellobiose-specific II component  
M00331: Type II general secretion pathway  
M00193: Putative spermidine/putrescine transport system  
M00185: Sulfate transport system  
M00589: Putative lysine transport system  
M00566: Dipeptide transport system, Firmicutes  
M00273: PTS system, fructose-specific II component  
M00006: Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P  
M00004: Pentose phosphate pathway (Pentose phosphate cycle)  
M00008: Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate  
M00580: Pentose phosphate pathway, archaea, fructose 6P => ribose 5P  
M00234: Cystine transport system  
M00228: Putative glutamine transport system  
M00233: Glutamate transport system  
M00238: D-Methionine transport system  
M00211: Putative ABC transport system

M00209: Osmoprotectant transport system  
M00365: C10-C20 isoprenoid biosynthesis, archaea  
M00153: Cytochrome d ubiquinol oxidase  
M00126: Tetrahydrofolate biosynthesis, GTP => THF  
M00244: Putative zinc/manganese transport system  
M00127: Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P  
M00023: Tryptophan biosynthesis, chorismate => tryptophan  
M00115: NAD biosynthesis, aspartate => NAD  
M00125: Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD  
M00010: Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate  
M00189: Molybdate transport system  
M00086: beta-Oxidation, acyl-CoA synthesis  
M00793: dTDP-L-rhamnose biosynthesis  
M00247: Putative ABC transport system

***E. coli* Mt1B1**

***S. Typhimurium* SL1344**

***S. xylosus* 33-ERD13C**

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

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

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

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

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

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

4  
1  
1  
0  
0  
0  
1  
1  
0  
1  
4  
4  
0  
0  
0  
0  
1  
1  
1  
0  
4  
4  
4  
4  
4  
4  
4  
4  
0  
1  
0  
0  
1  
1  
0  
0  
4  
4  
4  
4  
0  
4

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







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



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

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

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

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

0  
1  
0  
0  
4  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
4

0  
1  
0  
1  
4  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
4

0  
1  
0  
0  
1  
1  
0  
4  
0  
0  
0  
0  
4  
4







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



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

4  
4  
4  
4  
4  
1  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
4  
2  
1  
4  
4  
1  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4

4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
1  
2  
1  
1  
1  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4

4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	1
4	4	2
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
2	4	4
4	2	2
4	2	2
4	4	4
4	4	4
4	4	4
4	4	4
2	4	4
2	4	4

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

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

4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
4  
4  
4  
4  
4  
1  
4  
4  
4  
4  
4  
4  
4  
4  
4  
  
4  
4  
4  
4  
4  
4  
4  
4  
1  
4  
2  
4  
4  
4  
4  
4



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

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

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

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

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

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



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

0  
1  
4  
4  
1  
4  
4  
4  
4  
4  
4  
4  
0  
4  
0

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





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

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

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



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

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

4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
4  
4  
4  
1  
4  
1  
1  
1  
4  
1  
4  
4  
1  
4  
1  
1  
1  
0  
0  
0  
1  
0  
0  
0  
0  
0  
0  
0  
0  
0  
1  
0  
0  
0  
0  
1  
0  
1





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

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

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

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

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

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

4  
0  
0  
0  
1  
1  
0  
0  
0  
0  
1  
0  
0  
0  
4



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

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

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



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

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

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







4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
0  
0  
1  
1  
0  
0  
0  
0  
0  
1  
0  
0  
0  
1  
0  
1  
1  
1  
1  
0  
1

4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
0  
0  
0  
1  
0  
0  
1  
1  
0  
1  
1  
0  
0  
1  
1  
1  
0  
1

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



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

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

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

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

4  
0  
0  
0  
1  
1  
0  
0  
0  
0  
0  
1  
0  
0  
0  
4

4  
1  
0  
0  
1  
1  
0  
0  
0  
4  
1  
0  
0  
0  
4

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









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

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

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

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



4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
1  
  
0  
0  
0  
0  
0  
0  
0  
1  
1  
1  
1  
1  
1  
4  
4  
4  
4  
4  
4  
4

4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
0  
0  
0  
0  
0  
0  
0  
1  
1  
0  
0  
0  
1  
0  
4  
4  
4  
4  
4  
4



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

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



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

4  
4  
2  
4  
4  
4  
4  
2  
2  
4  
4  
4  
4  
4  
1  
1  
2  
4  
4  
4  
  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
1  
1  
4  
1  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
4

4  
4  
4  
2  
4  
2  
4  
4  
0  
0  
0  
0  
0  
0

1  
4  
0  
0  
1  
0  
0  
0  
0  
4  
4  
1  
4

***Clostridium* spp. ASF356**

***B. longum* YL2**

***C. clostridioforme* YL32**

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

4	4	1
4	4	4
4	4	4
4	4	4
4	4	2
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	1
4	4	4
4	4	4
2	4	4
4	4	4
4	4	4
4	4	4
4	1	4
4	1	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	1
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	1	4
4	4	4
4	4	4
4	1	4
4	2	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	2	4
2	4	2
2	4	2
4	4	4
1	4	4

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

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



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



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

1	1	0
0	0	0
1	1	1
1	1	1
1	1	1
1	1	0
1	1	1
1	1	1
1	1	1
1	0	0
0	0	0
0	0	0
1	0	0
1	1	0
0	0	0
1	1	1
1	1	1
2	0	1
0	1	0
1	0	0
0	0	0
1	0	0
0	0	1
0	1	0
0	0	1
1	1	1
1	1	1
0	0	1
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
1	0	0
0	0	0
0	1	0
0	1	0
0	1	0
0	0	0
0	0	0
1	2	1
1	1	1
1	2	0
0	0	0

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

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

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

***C. innocuum* I46**

***B. coccoides* YL58**

***Clostridium* spp. ASF502**

4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
2	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	1
4	4	4	2
4	4	4	2
4	1	4	4
4	2	4	4
4	2	4	2
4	4	4	4
4	4	4	4
4	4	4	4
4	4	4	4
2	4	4	4



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



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





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

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

0  
1  
1  
1  
1  
1  
0  
0  
1  
1  
0  
0  
0  
1  
1  
0  
0  
0  
0  
1  
0  
1  
1  
1  
1  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
1  
0  
0  
1  
0  
0  
0

0  
0  
1  
1  
1  
1  
1  
1  
1  
1  
0  
0  
0  
0  
0  
0  
1  
1  
0  
0  
0  
0  
1  
1  
0  
1  
1  
1  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
0  
1  
0  
0  
0  
1  
0  
0  
0

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

0  
0  
0  
0  
1  
1  
1  
0  
1  
1  
1  
1  
1  
1  
0  
0  
0  
0  
1  
0  
0  
0  
0  
0  
0  
0  
0  
0  
1  
0  
0  
0  
0  
0  
1  
0  
0  
0  
1  
0  
0  
0  
0  
0  
0  
1  
1  
1  
1

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

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

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

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

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

4  
4  
4  
0  
4  
1  
0  
0  
4  
0  
0  
0  
0  
0  
4

0  
4  
4  
0  
4  
2  
0  
0  
0  
0  
0  
0  
0  
0  
4





4	4	4
4	4	4
4	4	4
4	4	4
2	4	4
4	4	4
1	4	4
1	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
2	4	4
2	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	2
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	1
4	1	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
2	4	4
4	4	4
4	4	4
4	4	4

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

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

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

4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
1	4	4
1	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	1
4	4	1
4	4	4
4	4	4
4	4	4
2	4	4
4	4	4
4	4	4
4	4	4
4	4	4
4	4	2
4	1	4
4	4	4
4	2	4
4	2	4
1	4	4
1	4	4
1	4	4
2	2	1
4	4	2
4	4	2
2	2	4
4	4	4
4	2	4
4	4	4
4	2	4
4	4	4
2	2	4

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





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

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

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







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

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



4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
4  
1  
4  
4  
4  
4  
4  
4  
1  
2  
1  
4  
4  
4  
2  
4  
4  
2  
4  
2  
2  
2  
2

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



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

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

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