Supplementary Table S1. *S. aureus* KEGG-modules.

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	53	1
M00002	Glycolysis, core module involving three-carbon compounds	53	1
M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P	53	1
M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate	53	1
M00018	Threonine biosynthesis, aspartate => homoserine => threonine	53	1
M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate	53	1
M00045	Histidine degradation, histidine => N-formiminoglutamate => glutamate	53	1
M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	53	1
M00052	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP	53	1
M00082	Fatty acid biosynthesis, initiation	53	1
M00120	Coenzyme A biosynthesis, pantothenate => CoA	53	1
M00123	Biotin biosynthesis, pimeloyl-ACP/CoA => biotin	53	1
M00140	C1-unit interconversion, prokaryotes	53	1
M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	53	1
M00345	Formaldehyde assimilation, ribulose monophosphate pathway	53	1
M00364	C10-C20 isoprenoid biosynthesis, bacteria	53	1
M00549	Nucleotide sugar biosynthesis, glucose => UDP-glucose	53	1
M00579	Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate	53	1
M00580	Pentose phosphate pathway, archaea, fructose 6P => ribose 5P	53	1
M00700	Multidrug resistance, efflux pump AbcA	53	1
M00702	Multidrug resistance, efflux pump NorB	53	1
M00726	Cationic antimicrobial peptide (CAMP) resistance, lysyl-phosphatidylglycerol (L-PG) synthase MprF	53	1
M00730	Cationic antimicrobial peptide (CAMP) resistance, VraFG transporter	53	1
M00844	Arginine biosynthesis, ornithine => arginine	53	1
M00875	Staphyloferrin B biosynthesis, L-serine => staphyloferrin B	53	1

Supplementary Table S1 (continuation). *S. aureus* KEGG-modules.

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00876	Staphyloferrin A biosynthesis, L-ornithine => staphyloferrin A	53	1
M00003	Gluconeogenesis, oxaloacetate => fructose-6P	52	0.98
M00009	Citrate cycle (TCA cycle, Krebs cycle)	52	0.98
M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate	52	0.98
M00021	Cysteine biosynthesis, serine => cysteine	52	0.98
M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	52	0.98
M00086	beta-Oxidation, acyl-CoA synthesis	52	0.98
M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	52	0.98
M00555	Betaine biosynthesis, choline => betaine	52	0.98
M00577	Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin	52	0.98
M00005	PRPP biosynthesis, ribose 5P => PRPP	51	0.96
M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	45	0.85
M00157	F-type ATPase, prokaryotes and chloroplasts	45	0.85
M00416	Cytochrome aa3-600 menaquinol oxidase	45	0.85
M00704	Tetracycline resistance, efflux pump Tet38	45	0.85
M00705	Multidrug resistance, efflux pump MepA	45	0.85
M00725	Cationic antimicrobial peptide (CAMP) resistance, dltABCD operon	45	0.85
M00083	Fatty acid biosynthesis, elongation	44	0.83
M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	44	0.83
M00530	Dissimilatory nitrate reduction, nitrate => ammonia	43	0.81
M00023	Tryptophan biosynthesis, chorismate => tryptophan	42	0.79
M00126	Tetrahydrofolate biosynthesis, GTP => THF	42	0.79
M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	41	0.77
M00019	Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine	38	0.72
M00570	Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine	38	0.72
M00627	beta-Lactam resistance, Bla system	24	0.45
M00625	Methicillin resistance	13	0.25
M00714	Multidrug resistance, efflux pump QacA	11	0.21

Supplementary Table S2. *S. aureus* KEGG-pathways.

KEGG-pathway ID	KEGG-pathway description	Genomes	Frequency
00010	Glycolysis / Gluconeogenesis	53	1
00020	Citrate cycle (TCA cycle)	53	1
00030	Pentose phosphate pathway	53	1
00040	Pentose and glucuronate interconversions	53	1
00051	Fructose and mannose metabolism	53	1
00052	Galactose metabolism	53	1
00053	Ascorbate and aldarate metabolism	53	1
00061	Fatty acid biosynthesis	53	1
00071	Fatty acid degradation	53	1
00072	Synthesis and degradation of ketone bodies	53	1
00121	Secondary bile acid biosynthesis	53	1
00130	Ubiquinone and other terpenoid-quinone biosynthesis	53	1
00190	Oxidative phosphorylation	53	1
00220	Arginine biosynthesis	53	1
00230	Purine metabolism	53	1
00240	Pyrimidine metabolism	53	1
00250	Alanine, aspartate and glutamate metabolism	53	1
00260	D-Alanine metabolism	53	1
00261	Monobactam biosynthesis	53	1
00270	Cysteine and methionine metabolism	53	1
00280	Valine, leucine and isoleucine degradation	53	1
00281	Geraniol degradation	53	1
00290	Valine, leucine and isoleucine biosynthesis	53	1
00300	Lysine biosynthesis	53	1
00310	Lysine degradation	53	1
00330	Arginine and proline metabolism	53	1
00340	Histidine metabolism	53	1
00350	Tyrosine metabolism	53	1
00360	Phenylalanine metabolism	53	1
00362	Benzoate degradation	53	1
00380	Tryptophan metabolism	53	1
00400	Phenylalanine, tyrosine and tryptophan biosynthesis	53	1
00401	Novobiocin biosynthesis	53	1
00410	beta-Alanine metabolism	53	1
00430	Taurine and hypotaurine metabolism	53	1
00440	Phosphonate and phosphinate metabolism	53	1
00450	Selenocompound metabolism	53	1
00460	Cyanoamino acid metabolism	53	1
00471	D-Glutamine and D-glutamate metabolism	53	1
00472	D-Arginine and D-ornithine metabolism	53	1

Supplementary Table S2 (continuation). *S. aureus* KEGG-pathways.

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
00473	D-Alanine metabolism	53	1
00480	Glutathione metabolism	53	1
00500	Starch and sucrose metabolism	53	1
00520	Amino sugar and nucleotide sugar metabolism	53	1
00521	Streptomycin biosynthesis	53	1
00550	Peptidoglycan biosynthesis	53	1
00561	Glycerolipid metabolism	53	1
00562	Inositol phosphate metabolism	53	1
00564	Glycerophospholipid metabolism	53	1
00590	Arachidonic acid metabolism	53	1
00592	alpha-Linolenic acid metabolism	53	1
00620	Pyruvate metabolism	53	1
00622	Xylene degradation	53	1
00625	Chloroalkane and chloroalkene degradation	53	1
00626	Naphthalene degradation	53	1
00630	Glyoxylate and dicarboxylate metabolism	53	1
00640	Propanoate metabolism	53	1
00650	Butanoate metabolism	53	1
00660	C5-Branched dibasic acid metabolism	53	1
00670	One carbon pool by folate	53	1
00680	Methane metabolism	53	1
00730	Thiamine metabolism	53	1
00740	Riboflavin metabolism	53	1
00750	Vitamin B6 metabolism	53	1
00760	Nicotinate and nicotinamide metabolism	53	1
00770	Pantothenate and CoA biosynthesis	53	1
00780	Biotin metabolism	53	1
00785	Lipoic acid metabolism	53	1
00790	Folate biosynthesis	53	1
00860	Porphyrin and chlorophyll metabolism	53	1
00900	Terpenoid backbone biosynthesis	53	1
00906	Carotenoid biosynthesis	53	1
00910	Nitrogen metabolism	53	1
00920	Sulfur metabolism	53	1
00970	Aminoacyl-tRNA biosynthesis	53	1
00998	Biosynthesis of secondary metabolites - other antibiotics	53	1
00999	Biosynthesis of secondary metabolites - unclassified	53	1
01100	Metabolic pathways	53	1
01110	Biosynthesis of secondary metabolites	53	1
01120	Microbial metabolism in diverse environments	53	1

Supplementary Table S2 (continuation). *S. aureus* KEGG-pathways.

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
01130	Biosynthesis of antibiotics	53	1
01200	Carbon metabolism	53	1
01210	2-Oxocarboxylic acid metabolism	53	1
01212	Fatty acid metabolism	53	1
01220	Degradation of aromatic compounds	53	1
01230	Biosynthesis of amino acids	53	1
01501	beta-Lactam resistance	53	1
01502	Vancomycin resistance	53	1
01503	Cationic antimicrobial peptide (CAMP) resistance	53	1
02010	ABC transporters	53	1
02020	Two-component system	53	1
02024	Quorum sensing	53	1
02060	Phosphotransferase system (PTS)	53	1
03010	Ribosome	53	1
03018	RNA degradation	53	1
03020	RNA polymerase	53	1
03030	DNA replication	53	1
03060	Protein export	53	1
03070	Bacterial secretion system	53	1
03410	Base excision repair	53	1
03420	Nucleotide excision repair	53	1
03430	Mismatch repair	53	1
03440	Homologous recombination	53	1
04122	Sulfur relay system	53	1
05150	Staphylococcus aureus infection	53	1
05100	Bacterial invasion of epithelial cells	37	0.70
00643	Styrene degradation	2	0.04
00627	Aminobenzoate degradation	1	0.02

Supplementary Table S3. *Enterobacter spp.* KEGG-modules.

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	35	1
M00002	Glycolysis, core module involving three-carbon compounds	35	1
M00003	Gluconeogenesis, oxaloacetate => fructose-6P	35	1
M00004	Pentose phosphate pathway (Pentose phosphate cycle)	35	1
M00005	PRPP biosynthesis, ribose 5P => PRPP	35	1
M00006	Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P	35	1
M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P	35	1
M00008	Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate	35	1
M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate	35	1
M00012	Glyoxylate cycle	35	1
M00015	Proline biosynthesis, glutamate => proline	35	1
M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	35	1
M00018	Threonine biosynthesis, aspartate => homoserine => threonine	35	1
M00019	Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine	35	1
M00020	Serine biosynthesis, glycerate-3P => serine	35	1
M00021	Cysteine biosynthesis, serine => cysteine	35	1
M00023	Tryptophan biosynthesis, chorismate => tryptophan	35	1
M00028	Ornithine biosynthesis, glutamate => ornithine	35	1
M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP	35	1
M00061	D-Glucuronate degradation, D-glucuronate => pyruvate + D-glyceraldehyde 3P	35	1
M00087	beta-Oxidation	35	1
M00120	Coenzyme A biosynthesis, pantothenate => CoA	35	1
M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	35	1
M00157	F-type ATPase, prokaryotes and chloroplasts	35	1
M00168	CAM (Crassulacean acid metabolism), dark	35	1
M00176	Assimilatory sulfate reduction, sulfate => H2S	35	1
M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	35	1
M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	35	1
M00549	Nucleotide sugar biosynthesis, glucose => UDP-glucose	35	1

Supplementary Table S3 (continuation). *Enterobacter spp.* KEGG-modules.

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00570	Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine	35	1
M00579	Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate	35	1
M00844	Arginine biosynthesis, ornithine => arginine	35	1
M00854	Glycogen biosynthesis, glucose-1P => glycogen/starch	35	1
M00855	Glycogen degradation, glycogen => glucose-6P	35	1
M00009	Citrate cycle (TCA cycle, Krebs cycle)	34	0.97
M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate	34	0.97
M00017	Methionine biosynthesis, apartate => homoserine => methionine	34	0.97
M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate	34	0.97
M00026	Histidine biosynthesis, PRPP => histidine	34	0.97
M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	34	0.97
M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	34	0.97
M00052	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP	34	0.97
M00083	Fatty acid biosynthesis, elongation	34	0.97
M00086	beta-Oxidation, acyl-CoA synthesis	34	0.97
M00116	Menaquinone biosynthesis, chorismate => menaquinol	34	0.97
M00118	Glutathione biosynthesis, glutamate => glutathione	34	0.97
M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	34	0.97
M00123	Biotin biosynthesis, pimeloyl-ACP/CoA => biotin	34	0.97
M00126	Tetrahydrofolate biosynthesis, GTP => THF	34	0.97
M00127	Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P	34	0.97
M00144	NADH:quinone oxidoreductase, prokaryotes	34	0.97
M00149	Succinate dehydrogenase, prokaryotes	34	0.97
M00150	Fumarate reductase, prokaryotes	34	0.97
M00530	Dissimilatory nitrate reduction, nitrate => ammonia	34	0.97
M00554	Nucleotide sugar biosynthesis, galactose => UDP-galactose	34	0.97
M00616	Sulfate-sulfur assimilation	34	0.97
M00632	Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P	34	0.97
M00024	Phenylalanine biosynthesis, chorismate => phenylalanine	33	0.94
M00025	Tyrosine biosynthesis, chorismate => tyrosine	33	0.94
M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	33	0.94

Supplementary Table S3 (continuation). *Enterobacter spp.* KEGG-modules.

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP	33	0.94
M00063	CMP-KDO biosynthesis	33	0.94
M00064	ADP-L-glycero-D-manno-heptose biosynthesis	33	0.94
M00082	Fatty acid biosynthesis, initiation	33	0.94
M00093	Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE	33	0.94
M00115	NAD biosynthesis, aspartate => NAD	33	0.94
M00117	Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone	33	0.94
M00124	Pyridoxal biosynthesis, erythrose-4P => pyridoxal-5P	33	0.94
M00364	C10-C20 isoprenoid biosynthesis, bacteria	33	0.94
M00417	Cytochrome o ubiquinol oxidase	33	0.94
M00572	Pimeloyl-ACP biosynthesis, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP	33	0.94
M00034	Methionine salvage pathway	32	0.91
M00060	KDO2-lipid A biosynthesis, Raetz pathway, LpxL-LpxM type	32	0.91
M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	32	0.91
M00121	Heme biosynthesis, plants and bacteria, glutamate => heme	32	0.91
M00846	Siroheme biosynthesis, glutamate => siroheme	32	0.91
M00045	Histidine degradation, histidine => N-formiminoglutamate => glutamate	31	0.89
M00133	Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine	31	0.89
M00338	Cysteine biosynthesis, homocysteine + serine => cysteine	31	0.89
M00631	D-Galacturonate degradation (bacteria), D-galacturonate => pyruvate + D-glyceraldehyde 3P	31	0.89
M00533	Homoprotocatechuate degradation, homoprotocatechuate => 2-oxohept-3-enedioate	31	0.89
M00550	Ascorbate degradation, ascorbate => D-xylulose-5P	30	0.86
M00153	Cytochrome bd ubiquinol oxidase	29	0.83
M00555	Betaine biosynthesis, choline => betaine	28	0.80
M00761	Undecaprenylphosphate alpha-L-Ara4N biosynthesis, UDP-GlcA => undecaprenyl phosphate alpha-L-Ara4N	27	0.77
M00696	Multidrug resistance, efflux pump AcrEF-TolC	26	0.74
M00565	Trehalose biosynthesis, D-glucose 1P => trehalose	26	0.74
M00552	D-galactonate degradation, De Ley-Doudoroff pathway, D-galactonate => glycerate-3P	25	0.71
M00793	dTDP-L-rhamnose biosynthesis	19	0.54

Supplementary Table S3 (continuation). *Enterobacter spp.* KEGG-modules.

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00136	GABA biosynthesis, prokaryotes, putrescine => GABA	16	0.46
M00851	Carbapenem resistance	11	0.31
M00122	Cobalamin biosynthesis, cobinamide => cobalamin	7	0.20
M00568	Catechol ortho-cleavage, catechol => 3-oxoadipate	5	0.14
M00551	Benzoate degradation, benzoate => catechol / methylbenzoate => methylcatechol	4	0.11
M00035	Methionine degradation	3	0.09
M00134	Polyamine biosynthesis, arginine => ornithine => putrescine	3	0.09
M00175	Nitrogen fixation, nitrogen => ammonia	3	0.09
M00545	Trans-cinnamate degradation, trans-cinnamate => acetyl-CoA	2	0.06
M00345	Formaldehyde assimilation, ribulose monophosphate pathway	2	0.06
M00580	Pentose phosphate pathway, archaea, fructose 6P => ribose 5P	2	0.06
M00046	Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate	2	0.06
M00746	Multidrug resistance, repression of porin OmpF	1	0.03
M00027	GABA (gamma-Aminobutyrate) shunt	1	0.03

Supplementary Table S4. *Enterobacter spp.* KEGG-pathways.

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
00010	Glycolysis / Gluconeogenesis	35	1
00020	Citrate cycle (TCA cycle)	35	1
00030	Pentose phosphate pathway	35	1
00040	Pentose and glucuronate interconversions	35	1
00051	Fructose and mannose metabolism	35	1
00052	Galactose metabolism	35	1
00053	Ascorbate and aldarate metabolism	35	1
00061	Fatty acid biosynthesis	35	1
00071	Fatty acid degradation	35	1
00130	Ubiquinone and other terpenoid-quinone biosynthesis	35	1
00190	Oxidative phosphorylation	35	1
00220	Arginine biosynthesis	35	1
00230	Purine metabolism	35	1
00240	Pyrimidine metabolism	35	1
00250	Alanine, aspartate and glutamate metabolism	35	1
00260	Glycine, serine and threonine metabolism	35	1
00261	Monobactam biosynthesis	35	1
00270	Cysteine and methionine metabolism	35	1
00280	Valine, leucine and isoleucine degradation	35	1
00281	Geraniol degradation	35	1
00290	Valine, leucine and isoleucine biosynthesis	35	1
00300	Lysine biosynthesis	35	1
00310	Lysine degradation	35	1
00330	Arginine and proline metabolism	35	1
00332	Carbapenem biosynthesis	35	1
00340	Histidine metabolism	35	1
00350	Tyrosine metabolism	35	1
00360	Phenylalanine metabolism	35	1
00362	Benzoate degradation	35	1
00380	Tryptophan metabolism	35	1
00400	Phenylalanine, tyrosine and tryptophan biosynthesis	35	1
00401	Novobiocin biosynthesis	35	1
00410	beta-Alanine metabolism	35	1
00430	Taurine and hypotaurine metabolism	35	1
00440	Phosphonate and phosphinate metabolism	35	1
00450	Selenocompound metabolism	35	1
00460	Cyanoamino acid metabolism	35	1
00471	D-Glutamine and D-glutamate metabolism	35	1
00473	D-Alanine metabolism	35	1
00480	Glutathione metabolism	35	1

Supplementary Table S4 (continuation). *Enterobacter spp.* KEGG-pathways.

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
00500	Starch and sucrose metabolism	35	1
00511	Other glycan degradation	35	1
00520	Amino sugar and nucleotide sugar metabolism	35	1
00521	Streptomycin biosynthesis	35	1
00523	Polyketide sugar unit biosynthesis	35	1
00540	Lipopolysaccharide biosynthesis	35	1
00550	Peptidoglycan biosynthesis	35	1
00561	Glycerolipid metabolism	35	1
00562	Inositol phosphate metabolism	35	1
00564	Glycerophospholipid metabolism	35	1
00565	Ether lipid metabolism	35	1
00590	Arachidonic acid metabolism	35	1
00592	alpha-Linolenic acid metabolism	35	1
00620	Pyruvate metabolism	35	1
00625	Chloroalkane and chloroalkene degradation	35	1
00626	Naphthalene degradation	35	1
00627	Aminobenzoate degradation	35	1
00630	Glyoxylate and dicarboxylate metabolism	35	1
00633	Nitrotoluene degradation	35	1
00640	Propanoate metabolism	35	1
00650	Butanoate metabolism	35	1
00660	C5-Branched dibasic acid metabolism	35	1
00670	One carbon pool by folate	35	1
00680	Methane metabolism	35	1
00730	Thiamine metabolism	35	1
00740	Riboflavin metabolism	35	1
00750	Vitamin B6 metabolism	35	1
00760	Nicotinate and nicotinamide metabolism	35	1
00770	Pantothenate and CoA biosynthesis	35	1
00780	Biotin metabolism	35	1
00785	Lipoic acid metabolism	35	1
00790	Folate biosynthesis	35	1
00860	Porphyrin and chlorophyll metabolism	35	1
00900	Terpenoid backbone biosynthesis	35	1
00903	Limonene and pinene degradation	35	1
00910	Nitrogen metabolism	35	1
00920	Sulfur metabolism	35	1
00930	Caprolactam degradation	35	1
00970	Aminoacyl-tRNA biosynthesis	35	1
01040	Biosynthesis of unsaturated fatty acids	35	1

Supplementary Table S4 (continuation). *Enterobacter spp.* KEGG-pathways.

KEGG-pathway ID	KEGG-pathway description	Genomes	Frequency
01053	Biosynthesis of siderophore group nonribosomal peptides	35	1
01100	Metabolic pathways	35	1
01110	Biosynthesis of secondary metabolites	35	1
01120	Microbial metabolism in diverse environments	35	1
01130	Biosynthesis of antibiotics	35	1
01200	Carbon metabolism	35	1
01210	2-Oxocarboxylic acid metabolism	35	1
01212	Fatty acid metabolism	35	1
01220	Degradation of aromatic compounds	35	1
01230	Biosynthesis of amino acids	35	1
01501	beta-Lactam resistance	35	1
01502	Vancomycin resistance	35	1
01503	Cationic antimicrobial peptide (CAMP) resistance	35	1
02010	ABC transporters	35	1
02020	Two-component system	35	1
02024	Quorum sensing	35	1
02030	Bacterial chemotaxis	35	1
02060	Phosphotransferase system (PTS)	35	1
03010	Ribosome	35	1
03018	RNA degradation	35	1
03020	RNA polymerase	35	1
03030	DNA replication	35	1
03060	Protein export	35	1
03070	Bacterial secretion system	35	1
03410	Base excision repair	35	1
03420	Nucleotide excision repair	35	1
03430	Mismatch repair	35	1
03440	Homologous recombination	35	1
04122	Sulfur relay system	35	1
00361	Chlorocyclohexane and chlorobenzene degradation	34	0.97
00364	Fluorobenzoate degradation	34	0.97
00623	Toluene degradation	34	0.97
02040	Flagellar assembly	34	0.97
00525	Acarbose and validamycin biosynthesis	32	0.91
00600	Sphingolipid metabolism	25	0.71
00072	Synthesis and degradation of ketone bodies	18	0.51
00791	Atrazine degradation	12	0.34
00405	Phenazine biosynthesis	10	0.29
00643	Styrene degradation	9	0.26
01054	Nonribosomal peptide structures	5	0.14

Supplementary Table S4 (continuation). *Enterobacter spp.* KEGG-pathways.

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
00622	Xylene degradation	5	0.14
00621	Dioxin degradation	3	0.09
00591	Linoleic acid metabolism	2	0.06
00472	D-Arginine and D-ornithine metabolism	2	0.06
00121	Secondary bile acid biosynthesis	1	0.03

Supplementary Table S5. *P. aeruginosa KEGG-modules*

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00002	Glycolysis, core module involving three-carbon compounds	21	1
M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P	21	1
M00008	Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate	21	1
M00009	Citrate cycle (TCA cycle, Krebs cycle)	21	1
M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate	21	1
M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate	21	1
M00015	Proline biosynthesis, glutamate => proline	21	1
M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	21	1
M00018	Threonine biosynthesis, aspartate => homoserine => threonine	21	1
M00019	Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine	21	1
M00020	Serine biosynthesis, glycerate-3P => serine	21	1
M00021	Cysteine biosynthesis, serine => cysteine	21	1
M00023	Tryptophan biosynthesis, chorismate => tryptophan	21	1
M00024	Phenylalanine biosynthesis, chorismate => phenylalanine	21	1
M00028	Ornithine biosynthesis, glutamate => ornithine	21	1
M00045	Histidine degradation, histidine => N-formiminoglutamate => glutamate	21	1
M00046	Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate	21	1
M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	21	1
M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	21	1
M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	21	1
M00052	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP	21	1
M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP	21	1
M00063	CMP-KDO biosynthesis	21	1
M00064	ADP-L-glycero-D-manno-heptose biosynthesis	21	1
M00082	Fatty acid biosynthesis, initiation	21	1
M00083	Fatty acid biosynthesis, elongation	21	1
M00086	beta-Oxidation, acyl-CoA synthesis	21	1
M00087	beta-Oxidation	21	1

Supplementary Table S5 (continuation). *P. aeruginosa KEGG-modules*

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00093	Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE	21	1
M00115	NAD biosynthesis, aspartate => NAD	21	1
M00118	Glutathione biosynthesis, glutamate => glutathione	21	1
M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	21	1
M00120	Coenzyme A biosynthesis, pantothenate => CoA	21	1
M00122	Cobalamin biosynthesis, cobinamide => cobalamin	21	1
M00123	Biotin biosynthesis, pimeloyl-ACP/CoA => biotin	21	1
M00124	Pyridoxal biosynthesis, erythrose-4P => pyridoxal-5P	21	1
M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	21	1
M00126	Tetrahydrofolate biosynthesis, GTP => THF	21	1
M00135	GABA biosynthesis, eukaryotes, putrescine => GABA	21	1
M00144	NADH:quinone oxidoreductase, prokaryotes	21	1
M00149	Succinate dehydrogenase, prokaryotes	21	1
M00151	Cytochrome bc1 complex respiratory unit	21	1
M00155	Cytochrome c oxidase, prokaryotes	21	1
M00157	F-type ATPase, prokaryotes and chloroplasts	21	1
M00176	Assimilatory sulfate reduction, sulfate => H2S	21	1
M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	21	1
M00338	Cysteine biosynthesis, homocysteine + serine => cysteine	21	1
M00417	Cytochrome o ubiquinol oxidase	21	1
M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	21	1
M00529	Denitrification, nitrate => nitrogen	21	1
M00551	Benzoate degradation, benzoate => catechol / methylbenzoate => methylcatechol	21	1
M00555	Betaine biosynthesis, choline => betaine	21	1
M00568	Catechol ortho-cleavage, catechol => 3-oxoadipate	21	1
M00570	Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine	21	1
M00572	Pimeloyl-ACP biosynthesis, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP	21	1
M00579	Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate	21	1
M00616	Sulfate-sulfur assimilation	21	1
M00637	Anthranilate degradation, anthranilate => catechol	21	1
M00639	Multidrug resistance, efflux pump MexCD-OprJ	21	1
M00642	Multidrug resistance, efflux pump MexJK-OprM	21	1
M00761	Undecaprenylphosphate alpha-L-Ara4N biosynthesis, UDP-GlcA => undecaprenyl phosphate alpha-L-Ara4N	21	1

Supplementary Table S5 (continuation). *P. aeruginosa KEGG-modules*

KEGG-module ID	**KEGG-module description**	**Genomes**	**Frequency**
M00793	dTDP-L-rhamnose biosynthesis	21	1
M00844	Arginine biosynthesis, ornithine => arginine	21	1
M00846	Siroheme biosynthesis, glutamate => siroheme	21	1
M00003	Gluconeogenesis, oxaloacetate => fructose-6P	20	0.95
M00005	PRPP biosynthesis, ribose 5P => PRPP	20	0.95
M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	20	0.95
M00530	Dissimilatory nitrate reduction, nitrate => ammonia	20	0.95
M00533	Homoprotocatechuate degradation, homoprotocatechuate => 2-oxohept-3-enedioate	20	0.95
M00718	Multidrug resistance, efflux pump MexAB-OprM	20	0.95
M00745	Imipenem resistance, repression of porin OprD	20	0.95
M00835	Pyocyanine biosynthesis, chorismate => pyocyanine	20	0.95
M00156	Cytochrome c oxidase, cbb3-type	19	0.90
M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate	18	0.86
M00641	Multidrug resistance, efflux pump MexEF-OprN	17	0.81
M00769	Multidrug resistance, efflux pump MexPQ-OpmE	17	0.81
M00643	Multidrug resistance, efflux pump MexXY-OprM	16	0.76
M00035	Methionine degradation	8	0.38
M00026	Histidine biosynthesis, PRPP => histidine	4	0.19
M00851	Carbapenem resistance	3	0.14

Supplementary Table S6. *P. aeruginosa KEGG-pathways*

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
00010	Glycolysis / Gluconeogenesis	21	1
00020	Citrate cycle (TCA cycle)	21	1
00030	Pentose phosphate pathway	21	1
00040	Pentose and glucuronate interconversions	21	1
00051	Fructose and mannose metabolism	21	1
00052	Galactose metabolism	21	1
00053	Ascorbate and aldarate metabolism	21	1
00061	Fatty acid biosynthesis	21	1
00071	Fatty acid degradation	21	1
00130	Ubiquinone and other terpenoid-quinone biosynthesis	21	1
00190	Oxidative phosphorylation	21	1
00220	Arginine biosynthesis	21	1
00230	Purine metabolism	21	1
00240	Pyrimidine metabolism	21	1
00250	Alanine, aspartate and glutamate metabolism	21	1
00260	Glycine, serine and threonine metabolism	21	1
00261	Monobactam biosynthesis	21	1
00270	Cysteine and methionine metabolism	21	1
00280	Valine, leucine and isoleucine degradation	21	1
00281	Geraniol degradation	21	1
00290	Valine, leucine and isoleucine biosynthesis	21	1
00300	Lysine biosynthesis	21	1
00310	Lysine degradation	21	1
00330	Arginine and proline metabolism	21	1
00332	Carbapenem biosynthesis	21	1
00340	Histidine metabolism	21	1
00350	Tyrosine metabolism	21	1
00360	Phenylalanine metabolism	21	1
00361	Chlorocyclohexane and chlorobenzene degradation	21	1
00362	Benzoate degradation	21	1
00364	Fluorobenzoate degradation	21	1
00380	Tryptophan metabolism	21	1
00400	Phenylalanine, tyrosine and tryptophan biosynthesis	21	1
00401	Novobiocin biosynthesis	21	1
00405	Phenazine biosynthesis	21	1
00410	beta-Alanine metabolism	21	1
00430	Taurine and hypotaurine metabolism	21	1
00440	Phosphonate and phosphinate metabolism	21	1
00450	Selenocompound metabolism	21	1
00460	Cyanoamino acid metabolism	21	1

Supplementary Table S6 (continuation). *P. aeruginosa KEGG-pathways*

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
00471	D-Glutamine and D-glutamate metabolism	21	1
00472	D-Arginine and D-ornithine metabolism	21	1
00473	D-Alanine metabolism	21	1
00480	Glutathione metabolism	21	1
00500	Starch and sucrose metabolism	21	1
00520	Amino sugar and nucleotide sugar metabolism	21	1
00521	Streptomycin biosynthesis	21	1
00523	Polyketide sugar unit biosynthesis	21	1
00525	Acarbose and validamycin biosynthesis	21	1
00540	Lipopolysaccharide biosynthesis	21	1
00550	Peptidoglycan biosynthesis	21	1
00561	Glycerolipid metabolism	21	1
00562	Inositol phosphate metabolism	21	1
00564	Glycerophospholipid metabolism	21	1
00565	Ether lipid metabolism	21	1
00590	Arachidonic acid metabolism	21	1
00592	alpha-Linolenic acid metabolism	21	1
00600	Sphingolipid metabolism	21	1
00620	Pyruvate metabolism	21	1
00622	Xylene degradation	21	1
00623	Toluene degradation	21	1
00625	Chloroalkane and chloroalkene degradation	21	1
00626	Naphthalene degradation	21	1
00627	Aminobenzoate degradation	21	1
00630	Glyoxylate and dicarboxylate metabolism	21	1
00633	Nitrotoluene degradation	21	1
00640	Propanoate metabolism	21	1
00643	Styrene degradation	21	1
00650	Butanoate metabolism	21	1
00660	C5-Branched dibasic acid metabolism	21	1
00670	One carbon pool by folate	21	1
00680	Methane metabolism	21	1
00730	Thiamine metabolism	21	1
00740	Riboflavin metabolism	21	1
00750	Vitamin B6 metabolism	21	1
00760	Nicotinate and nicotinamide metabolism	21	1
00770	Pantothenate and CoA biosynthesis	21	1
00780	Biotin metabolism	21	1
00785	Lipoic acid metabolism	21	1
00790	Folate biosynthesis	21	1

Supplementary Table S6 (continuation). *P. aeruginosa KEGG-pathways*

KEGG-pathway ID	KEGG-pathway description	Genomes	Frequency
00860	Porphyrin and chlorophyll metabolism	21	1
00900	Terpenoid backbone biosynthesis	21	1
00903	Limonene and pinene degradation	21	1
00910	Nitrogen metabolism	21	1
00920	Sulfur metabolism	21	1
00930	Caprolactam degradation	21	1
00970	Aminoacyl-tRNA biosynthesis	21	1
01040	Biosynthesis of unsaturated fatty acids	21	1
01053	Biosynthesis of siderophore group nonribosomal peptides	21	1
01100	Metabolic pathways	21	1
01110	Biosynthesis of secondary metabolites	21	1
01120	Microbial metabolism in diverse environments	21	1
01130	Biosynthesis of antibiotics	21	1
01200	Carbon metabolism	21	1
01210	2-Oxocarboxylic acid metabolism	21	1
01212	Fatty acid metabolism	21	1
01220	Degradation of aromatic compounds	21	1
01230	Biosynthesis of amino acids	21	1
01501	beta-Lactam resistance	21	1
01502	Vancomycin resistance	21	1
01503	Cationic antimicrobial peptide (CAMP) resistance	21	1
02010	ABC transporters	21	1
02020	Two-component system	21	1
02024	Quorum sensing	21	1
02025	Biofilm formation - Pseudomonas aeruginosa	21	1
02030	Bacterial chemotaxis	21	1
02040	Flagellar assembly	21	1
02060	Phosphotransferase system (PTS)	21	1
03010	Ribosome	21	1
03018	RNA degradation	21	1
03020	RNA polymerase	21	1
03030	DNA replication	21	1
03060	Protein export	21	1
03070	Bacterial secretion system	21	1
03410	Base excision repair	21	1
03420	Nucleotide excision repair	21	1
03430	Mismatch repair	21	1
03440	Homologous recombinatio	21	1
03450	Non-homologous end-joining	21	1

Supplementary Table S6 (continuation). *P. aeruginosa KEGG-pathways*

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
04122	Sulfur relay system	21	1
00072	Synthesis and degradation of ketone bodies	20	0.95

Supplementary Table S7. *Mycopalsma spp. KEGG-modules*

KEGG-module ID	KEGG-module description	Genomes	Frequency
M00005	PRPP biosynthesis, ribose 5P => PRPP	93	1
M00157	F-type ATPase, prokaryotes and chloroplasts	91	0.98
M00002	Glycolysis, core module involving three-carbon compounds	89	0.96
M00579	Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate	72	0.77
M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	70	0.75
M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	31	0.33
M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	23	0.25
M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	12	0.13
M00549	Nucleotide sugar biosynthesis, glucose => UDP-glucose	8	0.09
M00120	Coenzyme A biosynthesis, pantothenate => CoA	4	0.04
M00140	C1-unit interconversion, prokaryotes	1	0.01
M00854	Glycogen biosynthesis, glucose-1P => glycogen/starch	1	0.01
M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	1	0.01

Supplementary Table S8. *Mycopalsma spp. KEGG-pathways*

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
00010	Glycolysis / Gluconeogenesis	93	1
00030	Pentose phosphate pathway	93	1
00051	Fructose and mannose metabolism	93	1
00190	Oxidative phosphorylation	93	1
00230	Purine metabolism	93	1
00240	Pyrimidine metabolism	93	1
00270	Cysteine and methionine metabolism	93	1
00450	Selenocompound metabolism	93	1
00480	Glutathione metabolism	93	1
00564	Glycerophospholipid metabolism	93	1
00620	Pyruvate metabolism	93	1
00680	Methane metabolism	93	1
00760	Nicotinate and nicotinamide metabolism	93	1
00970	Aminoacyl-tRNA biosynthesis	93	1
01100	Metabolic pathways	93	1
01110	Biosynthesis of secondary metabolites	93	1
01120	Microbial metabolism in diverse environments	93	1
01130	Biosynthesis of antibiotics	93	1
01200	Carbon metabolism	93	1
01230	Biosynthesis of amino acids	93	1
02010	ABC transporters	93	1
02024	Quorum sensing	93	1
03010	Ribosome	93	1
03018	RNA degradation	93	1
03030	DNA replication	93	1
03060	Protein export	93	1
03070	Bacterial secretion system	93	1
03410	Base excision repair	93	1
03420	Nucleotide excision repair	93	1
03430	Mismatch repair	93	1
03440	Homologous recombination	93	1
03020	RNA polymerase	92	0.99
00500	Starch and sucrose metabolism	89	0.96
00260	Glycine, serine and threonine metabolism	86	0.92
00520	Amino sugar and nucleotide sugar metabolism	86	0.92
00640	Propanoate metabolism	84	0.90
00561	Glycerolipid metabolism	83	0.89
00730	Thiamine metabolism	83	0.89
02060	Phosphotransferase system (PTS)	83	0.89
00020	Citrate cycle (TCA cycle)	74	0.80

Supplementary Table S8 (contonuation). *Mycopalsma spp. KEGG-pathways*

KEGG-pathway ID	**KEGG-pathway description**	**Genomes**	**Frequency**
00630	Glyoxylate and dicarboxylate metabolism	73	0.78
00670	One carbon pool by folate	73	0.78
00280	Valine, leucine and isoleucine degradation	72	0.77
00430	Taurine and hypotaurine metabolism	72	0.77
00740	Riboflavin metabolism	70	0.75
00770	Pantothenate and CoA biosynthesis	65	0.70
00052	Galactose metabolism	62	0.67
00040	Pentose and glucuronate interconversions	56	0.60
02020	Two-component system	53	0.57
00460	Cyanoamino acid metabolism	52	0.56
04122	Sulfur relay system	51	0.55
00625	Chloroalkane and chloroalkene degradation	39	0.42
00790	Folate biosynthesis	38	0.41
00053	Ascorbate and aldarate metabolism	35	0.38
00250	Alanine, aspartate and glutamate metabolism	27	0.29
00330	Arginine and proline metabolism	27	0.29
00380	Tryptophan metabolism	26	0.28
00220	Arginine biosynthesis	25	0.27
00310	Lysine degradation	25	0.27
00626	Naphthalene degradation	21	0.23
01220	Degradation of aromatic compounds	21	0.23
00900	Terpenoid backbone biosynthesis	15	0.16
00521	Streptomycin biosynthesis	15	0.16
00660	C5-Branched dibasic acid metabolism	13	0.14
00511	Other glycan degradation	9	0.10
00071	Fatty acid degradation	8	0.09
00562	Inositol phosphate metabolism	7	0.08
00650	Butanoate metabolism	3	0.03
00400	Phenylalanine, tyrosine and tryptophan biosynthesis	2	0.02
00590	Arachidonic acid metabolism	1	0.01
00860	Porphyrin and chlorophyll metabolism	1	0.01
00600	Sphingolipid metabolism	1	0.01
00340	Histidine metabolism	1	0.01