Metagenome	TBZ/SUC gene expression	TBZ73/TBZ57 gene expression	TBZ109/TBZ57 gene expression	SUC73/SUC57 gene expression	SUC109/SUC57 gene expression
Urate degradation - Uni- Sym- and Antiporters - Uni- Sym-	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems - Type III secretion system, extended -	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems - Type III secretion system, extended -	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems - Type III secretion system, extended - Type III secretion system of the system of the secretion sy	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems - Type III secretion systems -	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems - Type III secretion system, extended - Type III secretion system -
tRNA sulfuration - Tricarboxylate transporter - Triacylglycerols - Transposable elements -	tRNA sulfuration - Tricarboxylate transporter - Triacylglycerols - Transposable elements -	TRNA sulfuration - Tricarboxylate transporter - Triacylglycerols - Transposable elements -	Tricarboxylate transporter - Triacylglycerols - Transposable elements -	Tricarboxylate transporter - Triacylglycerols - Transposable elements -	Tricarboxylate transporter - Tricarboxylate transporter - Transposable elements -
Translation -	Translation - Transcription - Toxins and superantigens - TidD cluster -	Translation - Transcription - Toxins and superantigens - TldD cluster -	Translation - Transcription - Toxins and superantigens - TldD cluster -	Translation - Transcription - Toxins and superantigens - TidD cluster -	Translation - Transcription - Transcription - Toxins and superantigens - TldD cluster -
Three hypotheticals linked to lipoprotein biosynthesis -	Three hypotheticals linked to lipoprotein biosynthesis - Tetrapyrroles - Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -	Three hypotheticals linked to lipoprotein biosynthesis - Tetrapyrroles - Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -	Three hypotheticals linked to lipoprotein biosynthesis - Tetrapyrroles - Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -	Three hypotheticals linked to lipoprotein biosynthesis - Tetrapyrroles - Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -	Three hypotheticals linked to lipoprotein biosynthesis - Tetrapyrroles - Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -
Sugar alcohols - Sodium lon-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores - Siderophores - Selenoproteins -	Sugar alcohols - Sodium Ion-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores - Siderophores -	Sugar alconois - Sodium Ion-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Sidenoproteins -	Sugar alconois - Sodium lon-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores - Selegoproteins -	Sugar alconois - Sodium lon-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores - Siderophores - Selepoprotains -	Sugar alconois - Sodium Ion-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Sidenonrotains -
Secretion - Sarcosine oxidase - Sarcosine oxidase - RNA processing and modification - Sarcosine oxidation - Sa	Secretion - Sarcosine oxidase - RNA processing and modification - Ribosome-related cluster -	Secretion - Sarcosine oxidase - RNA processing and modification - Ribosome-related cluster -	Secretion - Sarcosine oxidase - RNA processing and modification - Ribosome-related cluster -	Secretion - Sarcosine oxidase - RNA processing and modification - Ribosome-related cluster -	Secretion - Sarcosine oxidase - RNA processing and modification - Ribosome-related cluster -
Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD - Besistance to antibiotics and toxic compounds - Regulation of virulence -	Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD - Resistance to antibiotics and toxic compounds - Regulation of virulence -	Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD - Resistance to antibiotics and toxic compounds - Regulation of virulence -	Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD - Resistance to antibiotics and toxic compounds - Regulation of virulence -	Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD - Resistance to antibiotics and toxic compounds - Regulation of virulence -	Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD - Resistance to antibiotics and toxic compounds - Regulation of virtulence -
Quorum sensing and biofilm formation - Conference Cluster - Conference C	Quorum sensing and biofilm formation - Quinone cofactors - Pyruvate kinase associated cluster -	Quorum sensing and biofilm formation - Quinone cofactors - Pyruvate kinase associated cluster - Pyrimidines -	Quorum sensing and biofilm formation - Quinone cofactors - Quinone cofactors - Pyruvate kinase associated cluster - Pyrimidines -	Quorum sensing and biofilm formation - Quinone cofactors - Pyruvate kinase associated cluster - Pyrimidines -	Quorum sensing and biofilm formation - Quinone cofactors - Pyruvate kinase associated cluster - Pyrimidines -
Pyridoxine - Pyridoxine - Pyridoxine - Pyridoxine - Pyridoxine - Putrescine/GABA utilization cluster-temporal,to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion - Putative GGDEF domain protein related to agglutinin secretion - Putative GGDEF domain protein related to agglutinin secretion - Putative GGDEF domain protein related to agglutinin secretion - Putative GGDEF domain protein related to agglutinin secretion - Putative GGDEF domain protein related to agglutinin secretion - Pyridoxine - Pyridoxine - Pyridoxine - Pyridoxine - Pyridoxine - Pyridoxine - Putative Isoquinoline 1-oxidoreductase subunit - Putative Isoquinoline Isoquinoline 1-oxidoreductase subunit - Putative Isoquinoline Isoqu	Putrescine/GABA utilization cluster-temporal, to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion -	Putrescine/GABA utilization cluster-temporal,to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion -	Pyridoxine - Putrescine/GABA utilization cluster-temporal,to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion -	Putrescine/GABA utilization cluster-temporal,to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion -	Putrescine/GABA utilization cluster-temporal,to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion -
Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - Proteolytic pathway	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - proteosome related - Proteolytic pathway -	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - proteosome related - Proteolytic pathway -	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - proteosome related - Proteolytic pathway -	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - proteosome related - Proteolytic pathway -	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - proteosome related - Proteolytic pathway -
Protein secretion system, Type VII (Chaperone/Usher pathway, CU) - Protein secretion system, Type VI - Protein secretion system, Type VII - Protein secretion system. Type III - Protein secretion system secretion system secretion sec	Protein translocation across cytoplasmic membrane - Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) - Protein secretion system, Type VII (Chaperone/Usher pathway, CU) - Protein secretion system, Type VI - Protein secretion system, Type VI - Protein secretion system, Type III -	Protein translocation across cytoplasmic membrané - Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) - Protein secretion system, Type VII (Chaperone/Usher pathway, CU) - Protein secretion system, Type VI - Protein secretion system, Type VI - Protein secretion system, Type III -	Protein translocation across cytoplasmic membrane - Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) - Protein secretion system, Type VII (Chaperone/Usher pathway, CU) - Protein secretion system, Type VI - Protein secretion system, Type VI - Protein secretion system, Type III -	Protein translocation across cytoplasmić membrané - Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) - Protein secretion system, Type VII (Chaperone/Usher pathway, CU) - Protein secretion system, Type VI - Protein secretion system, Type III -	Protein translocation across cytoplasmic membrane - Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) - Protein secretion system, Type VII (Chaperone/Usher pathway, CU) - Protein secretion system, Type VI - Protein secretion system, Type VI - Protein secretion system. Type III -
Protein secretion system, Type II - • • • • • • • • • • • • • • • • •	Protein secretion system, Type II - Protein processing and modification - Protein folding - Protein export? -	Protein secretion system, Type II - Protein processing and modification - Protein folding - Protein export? -	Protein secretion system, Type II - Protein processing and modification - Protein folding - Protein export? -	Protein secretion system, Type II - Protein processing and modification - Protein folding - Protein export? -	Protein secretion system, Type II - Protein processing and modification - Protein folding - Protein export? -
Protein degradation - Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydroxyproline - Protein and Toxin and Toxi	Protein degradation - Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydroxyproline -	Protein degradation - Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydroxyproline - Programmed Cell Posth and Toxin antitoxin Systems	Protein degradation - Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydroxyproline - Programmed Cell Death and Toxin entitodic Systems	Protein degradation - Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydroxyrphice - Protein and Toylin and To	Protein degradation - Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydrox yproline - Proline and 4-hydrox yproline -
Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related - Polysaccharides -	Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related - Polysaccharides -	Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related - Polysaccharides -	Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related - Polysaccharides -	Programmed Cell Death and Toxin-antioxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related - Polysaccharides -	Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related - Probably GTP or GMP signaling related - Polysaccharides -
Plant-Prokaryote DOE project - • • • • • • • • • • • • • • • • • •	Plant-Prokaryote DOE project - Plant Octadecanoids - Plant Hormones - Plant Alkaloids -	Plant-Prokaryote DOE project - Plant Octadecanoids - Plant Hormones - Plant Alkaloids -	Plant-Prokaryote DOE project - Plant Octadecanoids - Plant Hormones - Plant Alkaloids -	Plant-Prokaryote DOE project - Plant Octadecanoids - Plant Hormones - Plant Alkaloids -	Plant-Prokaryote DOE project - Plant Octadecanoids - Plant Hormones - Plant Alkaloids -
Phospholipids - Phages, Prophages - Phage Host Interactions - Peripheral pathways for catabolism of aromatic compounds - Peripheral pathways for catabolism of	Phospholipids - Phages, Prophages - Phage Host Interactions - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds -	Phospholipids - Phages, Prophages - Phage Host Interactions - Periplasmic Stress - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds -	Phospholipids - Phages, Prophages - Phage Host Interactions - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds -	Phospholipids - Phages, Prophages - Phage Host Interactions - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds -	Phospholipids - Phages, Prophages - Phage Host Interactions - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds -
Pathogenicity islands - Oxidative stress - Osmotic stress - Osmotic stress - Organic sulfur assimilation - Organic sulfur assi	Pathogeniaty islands - Oxidative stress -	Pathogenicity islands - Oxidative stress - Osmotic stress - Organic sulfur assimilation - TBZperSUC.log2FC	Pathogenicity islands - Oxidative stress - Osmotic stress -	Pathogenicity islands - Oxidative stress - Osmotic stress - Organic sulfur assimilation -	Pathogenicity islands - Oxidative stress - Osmotic stress - Organic sulfur assimilation -
Organic acids - One-carbon Metabolism - One-carbon Metabolism - One-carbon Metabolism - One-carbon Metabolic cluster - One-carbon MADP - One-carbon Metabolism - One-carbon Me	Organic acids - One-carbon Metabolism - Nucleotidyl-phosphate metabolic cluster - NAD and NADP -	Organic acids - One-carbon Metabolism - Nucleotidyl-phosphate metabolic cluster - NAD and NADP -	Organic acids - One-carbon Metabolism - Nucleotidyl-phosphate metabolic cluster - NAD and NADP - NAD and NADP - 2	Nucleotidyl-phosphate metabolic cluster - SUC73perSUC57.SUC73.log2FC W	Organic acids - One-carbon Metabolism - Nucleotidyl-phosphate metabolic cluster - NAD and NADP - SUC109perSUC57.SUC109.log2FC
Monosaccharides Molybdopterin oxidoreductase Metabolism of central aromatic intermediates Lysine, threonine, methionine, and cysteine Monosaccharides Monosac	Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization - Metabolism of central aromatic intermediates - Lysine, threonine, methionine, and cysteine -	Monosaccharides - Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization - Metabolism of central aromatic intermediates - Lysine, threonine, and cysteine -	Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization - Metabolism of central aromatic intermediates - Lysine, threonine, methionine, and cysteine - Monosaccharides - Monosaccharides - Methylamine utilization - Methylamine utilizati	Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization - Methylamine utilization - Methylamine utilization - Lysine, threonine, methionine, and cysteine - Monosaccharides - Monosaccharides - Methylamine utilization - Methylamine util	Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization - Metabolism of central aromatic intermediates - Lysine, threonine, methionine, and cysteine - Monosaccharides - 4 4 6
Lysine Biosynthesis - Lipoic acid - Light-harvesting complexes - Light-har	Lysine Biosynthesis - Lipoic acid - Light-harvesting complexes - Soprepoids -	Lysine Biosynthesis - Lipoic acid - Lipoic acid - Light-harvesting complexes - Lipoic acid - L	Lysine Biosynthesis - Lipoic acid - Light-harvesting complexes - Lipone acid - Light-harvesting complexes - Light-harvesting complex	Lysiné Biosynthesis - Lipoic acid - Lipoic acid - Light-harvesting complexes - Light-harvesting complex	Lysiné Biosynthesis - Lipoic acid - Light-harvesting complexes - Soprenoids -
Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and intracellular resistance - Inorganic sulfur assimilation - Invasion and Invasion a	d/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE - Invasion and intracellular resistance - Inorganic sulfur assimilation - Hypothetical Related to Dihydroorate Dehydrogenase - Hypothetical lipase related to Phosphatidate metabolism -	Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE - Invasion and intracellular resistance - Inorganic sulfur assimilation - Hypothetical Related to Dihydroorate Dehydrogenase - Hypothetical lipase related to Phosphatidate metabolism -	Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE - Invasion and intracellular resistance - Inorganic sulfur assimilation - Hypothetical Related to Dihydroorate Dehydrogenase - Hypothetical lipase related to Phosphatidate metabolism -	Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE - Invasion and intracellular resistance - Inorganic sulfur assimilation - Hypothetical Related to Dihydroorate Dehydrogenase - Hypothetical lipase related to Phosphatidate metabolism -	Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE - Invasion and intracellular resistance - Inorganic sulfur assimilation - Hypothetical Related to Dihydroorate Dehydrogenase - Hypothetical lipase related to Phosphatidate metabolism - Hypothetical Phosphatidate Phosphatidate metabolism - Hypothetical Phosphatidate Phosphat
Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock - Heat	Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock -	Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock -	Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock -	Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock -	Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock -
Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases - Glycoside hydrola	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases - Glycoside hydrolases - Glutamine, glutamate, aspartate, asparagine; ammonia assimilation -	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases - Glycoside hydrolases - Glutamine, glutamate, aspartate, asparagine; ammonia assimilation -	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases - Glycoside hydrolases - Glutamine, glutamate, aspartate, asparagine; anmonia assimilation -	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases - Glycoside hydrolases - Glutamine, glutamate, aspartate, asparagine; ammonia assimine -	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases - Glycoside hydrolases - Glutamine, glutamate, aspartate, asparagine; amonoia assimilation -
Flagellar motility in Prokaryota - Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation -	Flagellar motility in Prokaryota - Flagella protein? - Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation -	Flagellar motility in Prokaryota - Flagellar protein? - Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation -	Flagellar motility in Prokaryota - Flagella protein? - Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation -	Flagellar motility in Prokaryota - Flagella protein? - Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation -	Flagellar motility in Prokaryota - Flagella protein? - Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation -
Fatty acids - Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron accepting reactions - Electron accepting reaction - Electron -	Fatty acids - Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron donating reactions -	Fatty acids - Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron donating reactions -	Fatty acids - Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron consting reactions -	Fatty acids - Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron donating reactions -	Fatty acids - Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron donating reactions -
DNA uptake, competence - DNA replication - DNA repair - DNA recombination - DNA recomb	DNA repair - DNA recombination -	DNA uptake, competence - DNA repair - DNA recombination -	DNA uptake, competence - DNA repair - DNA recombination -	DNA uptake, competence - DNA repair - DNA recombination -	DNA uptake, competence - DNA replication - DNA repair - DNA recombination -
DNA polymerase III epsilon cluster -	DNA polymerase III epsilon cluster - Di- and oligosaccharides - Detoxification - Detection -	DNA polymerase III epsilon cluster - Di- and oligosaccharides - Detoxification - Detection -	DNA polymerase III epsilon cluster - Di- and oligosaccharides - Detoxification - Detection -	DNA polymerase III epsilon cluster - Di- and oligosaccharides - Detoxification - Detection -	DNA polymerase III epsilon cluster - Di- and oligosaccharides - Detoxification - Detection -
Dessication stress - D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1) cluster - Cytochrome biogenesis - CRISPs - CRISPs - CRISPs - CRISPs - CRISPs - CRISPRs and associated hypotheticals -	Dessication stress - D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1) cluster - Cytochrome biogenesis - CRISPs - CRISPRs and associated hypotheticals -	Dessication stress - D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1) cluster - Cytochrome biogenesis - CRISPRs and associated hypotheticals -	Dessication stress - D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1) cluster - Cytochrome biogenesis - CRISPs - CRISPs and associated hypotheticals -	Dessication stress - D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1) cluster - Cytochrome biogenesis - CRISPs - CRISPRs and associated hypotheticals -	Dessication stress - D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1) cluster - Cytochrome biogenesis - CRISPs - CRISPs - CRISPs and associated hypotheticals -
Cold shock - Coenzyme M - Coenzyme F420 - Coenzyme A - Coenzyme A - Coenzyme A - Coenzyme A - Coenzyme	Cold shock - Coenzyme M - Coenzyme F420 - Coenzyme A -	Cold shock - Coenzyme M - Coenzyme F420 - Coenzyme A -	Cold shock - Coenzyme M - Coenzyme F420 - Coenzyme A -	Cold shock - Coenzyme M - Coenzyme F420 - Coenzyme A -	Cold shock - Coenzyme M - Coenzyme F420 - Coenzyme A -
CO2 fixation - Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradation, putative -	CO2 fixation - Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradation, putative -	CO2 fixation - Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradative - Chematavis regregation, putative -	CO2 fixation - Clustering-based subsystems - Chromosome Replication - Choline bitarrate degradation, pulative - Chomotoxic represes regulators	CO2 fixation - Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradation, property - Chomotoxic representative -	CO2 fixation - Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradation, putative - Chomotoxic representation
Chemotaxis, response regulators - Central carbohydrate metabolism - Cell wall of Mycobacteria - Cell Division - Catabolism of an unknown compound -	Chemotaxis, response regulators - Central carbohydrate metabolism - Cell wall of Mycobacteria - Cell Division - Catabolism of an unknown compound -	Chemotaxis, response regulators - Central carbohydrate metabolism - Cell wall of Mycobacteria - Cell Division - Catabolism of an unknown compound -	Chemotaxis, response regulators - Central carbohydrate metabolism - Cell wall of Mycobacteria - Cell Division - Catabolism of an unknown compound -	Chemotaxis, response regulators - Central carbohydrate metabolism - Cell wall of Mycobacteria - Cell Division - Catabolism of an unknown compound -	Chemotaxis, response regulators - Central carbohydrate metabolism - Cell wall of Mycobacteria - Cell Division - Catabolism of an unknown compound -
Carotenoid biosynthesis - Carbohydrates - Carbohydrates - Capsular and extracellular polysacchrides - Branched-chain amino acids - Biotin -	Carotenoid biosynthesis - Carbohydrates - Capsular and extracellular polysacchrides - Branched-chain amino acids -	Carotenoid biosynthesis - Carbohydrates - Carbohydrates - Capsular and extracellular polysacchrides - Branched-chain amino acids -	Carotenoid biosynthesis - Carbohydrates - Carbohydrates - Capsular and extracellular polysacchrides - Branched-chain amino acids -	Carotenoid biosynthesis - Carbohydrates - Capsular and extracellular polysacchrides - Branched-chain amino acids -	Carotenoid biosynthesis - Carbohydrates - Capsular and extracellular polysacchrides - Branched-chain amino acids -
Biosynthesis of phenylpropanoids - Biosynthesis of galactoglycans and related lipopolysacharides - Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny -	Biosynthesis of phenylpropanoids - Biosynthesis of galactoglycans and related lipopolysacharides - Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny -	Biosynthesis of phenylpropadids - Biosynthesis of galactoglycans and related lipopolysacharides - Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny -	Biosynthesis of phenylpropanoids - Biosynthesis of galactoglycans and related lipopolysacharides - Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny -	Biosynthesis of phenylpropanoids - Biosynthesis of galactoglycans and related lipopolysacharides - Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny -	Biosynthesis of phenylpropandids - Biosynthesis of galactoglycans and related lipopolysacharides - Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny -
Bacteriocins, ribosomally synthesized antibacterial peptides -	Bacteriocins, ribosomally synthesized antibacterial peptides - Bacterial cytostatics, differentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -	Bacteriocins, ribosomally synthesized antibacterial peptides - Bacterial cytostatics, differentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -	Bacteriocins, ribosomally synthesized antibacterial peptides - Bacterial cytostatics, differentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -	Bacteriocins, ribosomally synthesized antibacterial peptides - Bacterial cytostatics, differentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -	Bacteriocins, ribosomally synthesized antibacterial peptides - Bacterial cytostatics, differentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -
Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - Aminosugars - Alapine, serving and alwaise - Alapine, servin	Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - alpha-proteobacterial cluster of hypotheticals -	Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - alpha-proteobacterial cluster of hypotheticals -	Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - alpha-proteobacterial cluster of hydrogen and dycine	Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - alpha-proteobacterial cluster of hypotheticals -	Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - alpha-proteobacterial cluster of hypotheticals - Alapino, corring and alveids -
Alanine, serine, and glycine Adhesion Acid stress ABC transporters	Alanine, serine, and glycine - Adhesion - Acid stress - ABC transporters -	Alanine, serine, and glycine - Adhesion - Acid stress - ABC transporters -	Alanine, serine, and glycine - Adhesion - Acid stress - ABC transporters - ABC transporte	Alanine, serine, and glycine - Adhesion - Acid stress - ABC transporters -	Alanine, serine, and glycine - Adhesion - Acid stress - ABC transporters -
binned	binned for the phage for the p	binned a sphaga a sph	binned and binned and binned and backer and backer and backlins and backlins and backlins and backlins and backlins and backlins and backling and ba	binned by	binned bi
un wosphing ydrogenc inobacte -Sphingo	un wosphing ydrogenc iinobacte 4. Pimekt 3. Sphing ydrogeno ub_Thiok 0. Sub_S 7. Sphing vdrogeno Mesorhiz Microbact idyrhizob drogeno	un ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing ydrogophing	woosphing woosph	un ydrogenc ijnobacte ydrogenc Sphing ydrogenc Wesorhiz Mesorhiz Microba dyrhizoba ydrogenc	un yvosphing ydrogene 14 Pimek 3 Sphing ydrogene Mesorhiz Microba idyrhizob ydrogene
in_30_Nc iin_34_H Jin_34_H Jin_48_F Jin_48_F Jinout.01 1.013_sul 1.013_sul 1.013_sul 1.013_sul 1.013_sul 1.013_sul 1.013_sul 2.sub_H 3.sub_H 5.sub_H 7.sub_H 7.sub_H 7.sub_H 7.sub_H 7.sub_H 8	n_30_Nc in_34_H; iin_34_H; iin_36_S; iin_36_S; iin_48_F; iin_50_ ut.008_s; iinout.017_ it_bin12_ at_bin21_ at_bin25_ bin5_Bra	n 30 NS in 34 H NS in 36 S in	n 30	m in 30 Nc min 34 H H H h h h h h h h h h h h h h h h h	m min 30 NX m bin 34 NX m bin 36 S sub 12 Sub 15 Su
oopm_bi roopm_c groopm_t groopm_t groopm_t groopm_t maxbinou metaba metaba metaba idbin_422 bin_5222	oopm_bi roopm_bi groopm_r groopm_r groopm_r groopm_r groopm_r maxbino maxbinout inout.016 metaba metaba metaba netaba	oopm_bi roopm_bi roopm_bi groopm_ groopm_ groopm_ maxbinoux,016 maxbinoux,016 maxbinoux,016 maxbinoux,016 maxbinoux,016 illoux,016 maxbinoux,016 maxbinoux,016 maxbinoux,016 maxbinoux,016 metaba netabat lidoux,016 illoux,	oopm_bi roopm_bi roopm_bi groopm_ groopm_ maxbino metaba metabat bi metabat bi metabat bi metabat bi metabat bi	oopm_bi roopm_b groopm_b groopm_c groopm_c groopm_c groopm_c groopm_c maxbino maxbino metaba metaba metabat_bin_bi2225	oopm_bi roopm_bi groopm_maxbinou maxbinou metaba metabat lidbin_5225
bin Solid S	solidi solidi salah sala	bin	bin	bin	bin