Urate degradation Uni- Sym- and Antiporters Type III, Type IV, Type VI, ESAT secretion systems Type III secretion system, extended Two related proteases tRNA sulfuration Tricarboxylate transporter Triacylglycerols Transposable elements Translation Transcription Toxins and superantigens TldD cluster Three hypotheticals linked to lipoprotein biosynthesis Tetrapyrroles Superinfection Exclusion Sulfatases and sulfatase modifying factor 1 (and a hypothetical) Sugar Phosphotransferase Systems, PTS Sugar alcohols Spore DNA protection Sodium Ion-Coupled Energetics Social motility and nonflagellar swimming in bacteria Signal transduction in Eukaryotes Siderophores Shiga toxin cluster Selenoproteins Secretion Sarcosine oxidase RNA processing and modification Ribosome-related cluster Ribosomal Protein L28P relates to a set of uncharacterized proteins Riboflavin, FMN, FAD Resistance to antibiotics and toxic compounds Related to Menaquinone-cytochrome C reductase Regulation of virulence recX and regulatory cluster Recombination related cluster Quorum sensing and biofilm formation Quinone cofactors Pyruvate kinase associated cluster **Pyrimidines** Pyridoxine Putrescine/GABA utilization cluster-temporal,to add to SSs Putative GGDEF domain protein related to agglutinin secretion Putative asociate of RNA polymerase sigma-54 factor rpoN **Purines** proteosome related Proteolytic pathway Protein translocation across cytoplasmic membrane cretion 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 secretion system, Type II Protein processing and modification Protein folding Protein export? Protein degradation Protein biosynthesis Protein and nucleoprotein secretion system, Type IV Proteasome related clusters Proline and 4-hydroxyproline Programmed Cell Death and Toxin-antitoxin Systems Probably Ybbk-related hypothetical membrane proteins Probably Pyrimidine biosynthesis-related Probably organic hydroperoxide resistance related hypothetical protein Probably GTP or GMP signaling related Polysaccharides Plasmid related functions Plant-Prokaryote DOE project Plant Octadecanoids Plant Hormones Plant Alkaloids Pigment biosynthesis Phospholipids Phages, Prophages Phage Host Interactions Phage family-specific subsystems Periplasmic Stress Peripheral pathways for catabolism of aromatic compounds Pathogenicity islands Oxidative stress Osmotic stress Organic sulfur assimilation Organic acids One-carbon Metabolism Nucleotidyl-phosphate metabolic cluster NAD and NADP Monosaccharides Molybdopterin oxidoreductase Methylamine utilization Metabolism of central aromatic intermediates Membrane-bound hydrogenase Lysine, threonine, methionine, and cysteine Lysine Biosynthesis Lipoic acid Light-harvesting complexes Isoprenoids osynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE Invasion and intracellular resistance Inorganic sulfur assimilation Hypothetical Related to Dihydroorate Dehydrogenase Hypothetical protein possible functionally linked with Alanyl-tRNA synthetase Hypothetical lipase related to Phosphatidate metabolism 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 Glutamine, glutamate, aspartate, asparagine; ammonia assimilation Folate and pterines 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 donating reactions Electron accepting reactions DNA uptake, competence DNA replication DNA repair DNA recombination DNA polymerase III epsilon cluster DNA metabolism Di- and oligosaccharides Detoxification Detection Dessication stress D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-) cluster Cytochrome biogenesis **CRISPs** CRISPRs and associated hypotheticals Cold shock Coenzyme M Coenzyme F420 Coenzyme B Coenzyme A CO₂ fixation Clustering-based subsystems Chromosome Replication Choline bitartrate degradation, putative Chemotaxis, response regulators Central carbohydrate metabolism Cell wall of Mycobacteria Cell Division Catabolism of an unknown compound Carbohydrates Capsular and extracellular polysacchrides Branched-chain amino acids **Biotin** Biosynthesis of phenylpropanoids Biosynthesis of galactoglycans and related lipopolysacharides Biologically active compounds in metazoan cell defence and differentiation Bacteriophage structural proteins Bacteriophage integration/excision/lysogeny 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 alpha-proteobacterial cluster of hypotheticals Alanine, serine, and glycine Adhesion Acid stress ABC transporters -2 2 Median Effect Size (Log₂) absolute