ZZ_gjo_need_homes - Zinc_resistance -						•	TBZ/SUC gene expression ZZ_gjo_need_homes				
Zinc_regulated_enzymes - YbbK - Xylose_utilization - Widespread_colonization_island - Valine_degradation -			•		•	•	Zinc_resistance - Zinc_regulated_enzymes - YbbK - YbbK - Xylose_utilization - Widespread_colonization_island - Valine_degradation - Val				
Utilization_of_glutathione_as_a_sulphur_source - USS-DB-7 - USS-DB-6 - Urea_decomposition - Universal_stress_protein_family - Universal_GTPases -											
UDP-N-acetylmuramate_from_Fructose-6-phosphate_Biosynthesis - Ubiquinone_Menaquinone-cytochrome_c_reductase_complexes - Ubiquinone_Biosynthesis - Type_VI_secretion_systems - Type_IV_pilus -			•			•	UDP-N-acetylmuramate_from_Fructose-6-phosphate_Biosynthesis - Ubiquinone_Menaquinone-cytochrome_c_reductase_complexes - Ubiquinone_Biosynthesis - Type_VI_secretion_systems - Type_IV_pilus - Type_IV_pilus - UDP-N-acetylmuramate_from_Fructose-6-phosphate_Biosynthesis - Ubiquinone_Menaquinone-cytochrome_c_reductase_complexes - Ubiquinone_Biosynthesis - Ubiquinone_Menaquinone-cytochrome_c_reductase_complexes - Ubiquinone_Menaquinone-cytochrome_c_reductase_complexes - Ubiquinone_Biosynthesis - Ubiquinone_Menaquinone-cytochrome_c_reductase_complexes - Ubiquinone_Menaquinone-cytochrome_c_reductase_complexes - Ubiquinone_Biosynthesis - Ubiqui				•
Type_4_secretion_and_conjugative_transfer - Two_cell_division_clusters_relating_to_chromosome_partitioning - Twin-arginine_translocation_system - Tryptophan_synthesis - tRNAs - tRNA_processing -						•	Type_4_secretion_and_conjugative_transfer - Two_cell_division_clusters_relating_to_chromosome_partitioning - Twin-arginine_translocation_system - Tryptophan_synthesis - tRNAs - tRNA_processing -				
tRNA_nucleotidyltransferase - tRNA_modification_Archaea - tRNA_aminoacylation,_ Val - tRNA_aminoacylation,_ Tyr - tRNA_aminoacylation,_ Trp - tRNA_aminoacylation,_ Thr -						•	tRNA_nucleotidyltransferase - tRNA_modification_Archaea - tRNA_aminoacylation,_Val - tRNA_aminoacylation,_Tyr - tRNA_aminoacylation,_Trp - tRNA_aminoacylation,_Thr -				
tRNA_aminoacylation,_Ser - tRNA_aminoacylation,_Pro - tRNA_aminoacylation,_Phe - tRNA_aminoacylation,_Met - tRNA_aminoacylation,_Lys -							tRNA_aminoacylation,_Ser - tRNA_aminoacylation,_Pro - tRNA_aminoacylation,_Phe - tRNA_aminoacylation,_Met - tRNA_aminoacylation,_Lys -				
tRNA_aminoacylation,_Leu - tRNA_aminoacylation,_lle - tRNA_aminoacylation,_His - tRNA_aminoacylation,_Gly - tRNA_aminoacylation,_Glu_and_Gln - tRNA_aminoacylation,_Asp_and_Asn -							tRNA_aminoacylation,_Leu tRNA_aminoacylation,_Leu tRNA_aminoacylation,_lle tRNA_aminoacylation,_lle tRNA_aminoacylation,_His tRNA_aminoacylation,_Gly tRNA_aminoacylation,_Glu_and_Gln tRNA_aminoacylation,_Asp_and_Asn				
tRNA_aminoacylation,_Arg - tRNA_aminoacylation,_Arg - tRNA_aminoacylation,_Ala - Triacylglycerol_metabolism - Transport_of_Zinc - Transport_of_Iron -		•					tRNA_aminoacylation,_Arg - tRNA_aminoacylation,_Ala - tRNA_aminoacylation,_Ala - Triacylglycerol_metabolism - Transport_of_Zinc - Transport_of_Iron -				
Translation_termination_factors_bacterial - Translation_initiation_factors_bacterial - Translation_elongation_factors_bacterial - Transcription_initiation,_bacterial_sigma_factors - Transcription_factors_bacterial - Transcription_factors_bacterial - Trans-envelope_signaling_system_VreARI_in_Pseudomonas -	* :		• •	•	• • •	• •	Translation_termination_factors_bacterial - Translation_initiation_factors_bacterial - Translation_elongation_factors_bacterial - Transcription_initiation,_bacterial_sigma_factors - Transcription_factors_bacterial - Transcription_factors_bacterial - Transcription_system_VreARl_in_Pseudomonas - Transcription_factors_bacterial - Transcription_fac		• •		•
Ton_and_Tol_transport_systems - Tolerance_to_colicin_E2 - Threonine_and_Homoserine_Biosynthesis - Thioredoxin-disulfide_reductase - Thiamin_biosynthesis -			•		•	•	Ton_and_Tol_transport_systems - Ton_and_Tol_transport_systems - Tolerance_to_colicin_E2 - Threonine_and_Homoserine_Biosynthesis - Thioredoxin-disulfide_reductase - Thiamin_biosynthesis - Thiamin_biosynthesi				
The_Chv_regulatory_system_of_Alphaproteobacteria - Terminal_cytochrome_O_ubiquinol_oxidase - Terminal_cytochrome_C_oxidases - TCA_Cycle - Synthesis_of_osmoregulated_periplasmic_glucans - Synechocystis_experimental -	•		•			• •	The_Chv_regulatory_system_of_Alphaproteobacteria				• •
Sulfur_oxidation - Sucrose_utilization - Streptococcal_Hyaluronic_Acid_Capsule - Staphylococcal_phi-Mu50B-like_prophages - Soluble_methane_monooxygenase_(sMMO) -			•			• •	Sulfur_oxidation - Sucrose_utilization - Sucrose_utilization - Streptococcal_Hyaluronic_Acid_Capsule - Staphylococcal_phi-Mu50B-like_prophages - Soluble_methane_monooxygenase_(sMMO) - Sulfur_oxidation - Sucrose_utilization - Sucrose_utilizati		•	•	•
Soluble_cytochromes_and_functionally_related_electron_carriers - Signal_peptidase - SigmaB_stress_responce_regulation - Siderophore_Pyoverdine - Siderophore_assembly_kit - Sialic Acid Metabolism -							Soluble_cytochromes_and_functionally_related_electron_carriers - Signal_peptidase - SigmaB_stress_responce_regulation - Siderophore_Pyoverdine - Siderophore_assembly_kit - Sialic Acid Metabolism -				
Serine-glyoxylate_cycle - Serine_endopeptidase_(EC_3.4.21) - Serine_Biosynthesis - SeqA_and_Co-occurring_Genes - Selenoprotein_O - Salicylate_and_gentisate_catabolism -	• •				•	• •	Serine-glyoxylate_cycle - Serine_endopeptidase_(EC_3.4.21) - Serine_Biosynthesis - SeqA_and_Co-occurring_Genes - Selenoprotein_O - Salicylate_and_gentisate_catabolism - Selenoprotein_O				
RuvABC_plus_a_hypothetical - RNA_processing_and_degradation,_bacterial - RNA_polymerase_bacterial - Ribosome_SSU_bacterial - Ribosome_LSU_bacterial -	\bullet					• •	RuvABC_plus_a_hypothetical - RNA_processing_and_degradation,_bacterial - RNA_polymerase_bacterial - Ribosome_SSU_bacterial - Ribosome_LSU_bacterial -				
Ribosome_biogenesis_bacterial - Ribosome_activity_modulation - Ribosomal_protein_S5p_acylation - Ribosomal_protein_S12p_Asp_methylthiotransferase - Ribonucleotide_reduction - Riboflavin,_FMN_and_FAD_metabolism -						•	Ribosome_biogenesis_bacterial - Ribosome_activity_modulation -				•
Ribotiavin, FMin_and_FAD_metabolism - Rhamnose_containing_glycans - Respiratory_dehydrogenases_1 - Respiratory_Complex_I - Resistance_to_fluoroquinolones - Redox-dependent_regulation_of_nucleus_processes -			•			•	Ribotiavin, FMN_and_FAD_metabolism - Rhamnose_containing_glycans - Respiratory_dehydrogenases_1 - Respiratory_Complex_I - Resistance_to_fluoroquinolones - Redox-dependent_regulation_of_nucleus_processes - Redox-dependent_regulation_processes - Redox-dependent_regulation_of_nucleus_processes - Redox-dependent_regulation_processes - Redox-dependent_regulation_processes - Redox-dependent_regulation_processes - Redox-dependent_regulation_processes - Redox-dependent_regulation_processes - Redox-dependent_regulation_processes - Redox-dependent_re				•
Recycling_of_Peptidoglycan_Amino_Acids - Queuosine-Archaeosine_Biosynthesis - Pyruvate_metabolism_II:_acetyl-CoA,_acetogenesis_from_pyruvate - Pyruvate_metabolism_I:_anaplerotic_reactions,_PEP - Pyruvate_Alanine_Serine_Interconversions -			•				Recycling_of_Peptidoglycan_Amino_Acids - Queuosine-Archaeosine_Biosynthesis - Pyruvate_metabolism_II:_acetyl-CoA,_acetogenesis_from_pyruvate - Pyruvate_metabolism_I:_anaplerotic_reactions,_PEP - Pyruvate_Alanine_Serine_Interconversions -				
Pyrroloquinoline_Quinone_biosynthesis - Pyrimidine_utilization - pyrimidine_conversions - Pyridoxin_(Vitamin_B6)_Biosynthesis - Putrescine_utilization_pathways - Putative_TIdE-TIdD_proteolytic_complex -						•	Pyrroloquinoline_Quinone_biosynthesis - Pyrimidine_utilization - pyrimidine_conversions - Pyridoxin_(Vitamin_B6)_Biosynthesis - Putrescine_utilization_pathways - Putative_TldE-TldD_proteolytic_complex -	•			•••
Purine_Utilization - Purine_conversions - Pterin_metabolism_3 - Pterin_biosynthesis - Proton-dependent_Peptide_Transporters -							Purine_Utilization - Purine_conversions - Pterin_metabolism_3 - Pterin_biosynthesis - Proton-dependent_Peptide_Transporters -	•			
Proteolysis_in_bacteria,_ATP-dependent - Protein_degradation - Protein_chaperones - Proteasome_bacterial - Propionyl-CoA_to_Succinyl-CoA_Module - Propionate-CoA_to_Succinate_Module -							Proteolysis_in_bacteria,_ATP-dependent - Protein_degradation - Protein_chaperones - Proteasome_bacterial - Propionyl-CoA_to_Succinyl-CoA_Module - Propionate-CoA_to_Succinate_Module -				
Proline,_4-hydroxyproline_uptake_and_utilization - Programmed_frameshift - Predicted_carbohydrate_hydrolases - Potassium_homeostasis - Polyhydroxybutyrate_metabolism -					•	•	Proline,_4-hydroxyproline_uptake_and_utilization - Programmed_frameshift - Predicted_carbohydrate_hydrolases - Potassium_homeostasis - Polyhydroxybutyrate_metabolism -				
Polyamine_Metabolism - Polyadenylation_bacterial - Photosystem_II-type_photosynthetic_reaction_center - Photorespiration_(oxidative_C2_cycle) - Phosphate_metabolism - Phenylpropanoid_compound_degradation -					•		Polyamine_Metabolism Polyadenylation_bacterial Photosystem_II-type_photosynthetic_reaction_center Photorespiration_(oxidative_C2_cycle) Phosphate_metabolism Phenylpropanoid_compound_degradation				••
Phenylalanine_and_Tyrosine_Branches_from_Chorismate - Phage_shock_protein_(psp)_operon - Periplasmic_Stress_Response - Periplasmic_disulfide_interchange - Peptidyl-prolyl_cis-trans_isomerase -			•			•	Phenylalanine_and_Tyrosine_Branches_from_Chorismate - Phage_shock_protein_(psp)_operon - Periplasmic_Stress_Response - Periplasmic_disulfide_interchange - Peptidyl-prolyl_cis-trans_isomerase -				
Peptidoglycan_Crosslinking_of_Peptide_Stems - Peptidoglycan_biosynthesisgjo - Peptidoglycan_Biosynthesis - Peptide_methionine_sulfoxide_reductase - Pentose_phosphate_pathway - Oxidative_stress -						•	Peptidoglycan_Crosslinking_of_Peptide_Stems - Peptidoglycan_biosynthesisgjo - Peptidoglycan_Biosynthesis - Peptidoglycan_Biosynthesis - Peptide_methionine_sulfoxide_reductase - Pentose_phosphate_pathway - Oxidative_stress - Oxidative_stres				
Outer_membrane - Osmoregulation - Orphan_regulatory_proteins - One-carbon_metabolism_by_tetrahydropterines - Nudix_proteins_(nucleoside_triphosphate_hydrolases) -	•						Outer_membrane - Osmoregulation - Orphan_regulatory_proteins - One-carbon_metabolism_by_tetrahydropterines - Nudix_proteins_(nucleoside_triphosphate_hydrolases) -				
Nitric_oxide_synthase - NAD_and_NADP_cofactor_biosynthesis_global - N-heterocyclic_aromatic_compound_degradation - Murein_Hydrolases - Murein_hydrolase_regulation_and_cell_death - Multidrug_Resistance_Efflux_Pumps -							Nitric_oxide_synthase				
Molybdopterin_cytosine_dinucleotide - Molybdenum_cofactor_biosynthesis - Methylglyoxal_Metabolism - Methylcitrate_cycle - Methionine_Biosynthesis -	•				•	•	Molybdopterin_cytosine_dinucleotide - Molybdenum_cofactor_biosynthesis - Methylglyoxal_Metabolism - Methylcitrate_cycle - Methionine_Biosynthesis -				•
Mercury_resistance_operon - Mediator_of_hyperadherence_YidE_in_Enterobacteria_and_its_conserved_region - Mannose_Metabolism - Maltose_and_Maltodextrin_Utilization - Malonate_decarboxylase - Major_Outer_Membrane_Proteins -							Mercury_resistance_operon Mediator_of_hyperadherence_YidE_in_Enterobacteria_and_its_conserved_region Mannose_Metabolism Maltose_and_Maltodextrin_Utilization Malonate_decarboxylase Major_Outer_Membrane_Proteins				
Lysine_degradation - Lysine_Biosynthesis_DAP_Pathway - Lipoprotein_sorting_system - Lipopolysaccharide_assembly - Leucine_Degradation_and_HMG-CoA_Metabolism -						•	Lysine_degradation Lysine_Biosynthesis_DAP_Pathway Lipoprotein_sorting_system Lipopolysaccharide_assembly Leucine_Degradation_and_HMG-CoA_Metabolism				•
Lactate_utilization - L-fucose_utilization_temp - KDO2-Lipid_A_biosynthesis - Isoprenoid_Biosynthesis - Isoleucine_degradation - Iron_acquisition_in_Streptococcus -			•				Lactate_utilization				
lojap - Inositol_catabolism - Inorganic_Sulfur_Assimilation - Inner_membrane_protein_YhjD_and_conserved_cluster_involved_in_LPS_biosynthesis - Hypothetical_Related_to_Dihydroorotate_dehydrogenase - HtrA_and_Sec_secretion -					•	•	lojap - Inositol_catabolism - Inorganic_Sulfur_Assimilation - Inner_membrane_protein_YhjD_and_conserved_cluster_involved_in_LPS_biosynthesis - Hypothetical_Related_to_Dihydroorotate_dehydrogenase - HtrA_and_Sec_secretion				
Homogentisate_pathway_of_aromatic_compound_degradation - Histidine_Biosynthesis - Hfl_operon - Hemin_transport_system - Heme_and_Siroheme_Biosynthesis -						•	Homogentisate_pathway_of_aromatic_compound_degradation - Histidine_Biosynthesis - Hfl_operon - Hemin_transport_system - Heme_and_Siroheme_Biosynthesis -				•
Heat_shock_dnaK_gene_cluster_extended - GroEL_GroES - Glyoxylate_bypass - Glycolysis_and_Gluconeogenesis - Glycolate,_glyoxylate_interconversions - Glycogen_metabolism -			• •	•			Heat_shock_dnaK_gene_cluster_extended GroEL_GroES Glyoxylate_bypass Glycolysis_and_Gluconeogenesis Glycolate,_glyoxylate_interconversions Glycogen_metabolism				
Glycine_Biosynthesis - Glycine_and_Serine_Utilization - Glycerolipid_and_Glycerophospholipid_Metabolism_in_Bacteria - Glycerol_and_Glycerol-3-phosphate_Uptake_and_Utilization - Glycerate_metabolism -		•	•		•	•	Glycine_Biosynthesis - Glycine_and_Serine_Utilization - Glycerolipid_and_Glycerophospholipid_Metabolism_in_Bacteria - Glycerol_and_Glycerol-3-phosphate_Uptake_and_Utilization - Glycerate_metabolism -		•		
Glutathione:_Redox_cycle - Glutathione:_Non-redox_reactions - Glutathione:_Biosynthesis_and_gamma-glutamyl_cycle - Glutathione-regulated_potassium-efflux_system_and_associated_functions - Glutathione-dependent_pathway_of_formaldehyde_detoxification - Glutaredoxins -						•	Glutathione:_Redox_cycle - Glutathione:_Non-redox_reactions - Glutathione:_Biosynthesis_and_gamma-glutamyl_cycle - Glutathione-regulated_potassium-efflux_system_and_associated_functions - Glutathione-dependent_pathway_of_formaldehyde_detoxification - Glutaredoxins - Glutathione:_Redox_cycle - Glutathione:_Redox_cycle - Glutathione:_Redox_cycle - Glutathione:_Non-redox_reactions - Glut			•	•
Glutamine,_Glutamate,_Aspartate_and_Asparagine_Biosynthesis - General_Secretion_Pathway - Fructose_utilization - Formate_hydrogenase - Formaldehyde_assimilation:_Ribulose_monophosphate_pathway - Folate_Biosynthesis -					•	•	Glutamine,_Glutamate,_Aspartate_and_Asparagine_Biosynthesis - General_Secretion_Pathway - Fructose_utilization - Formate_hydrogenase - Formaldehyde_assimilation:_Ribulose_monophosphate_pathway - Folate_Biosynthesis - Glutamine,_Glutamate,_Aspartate_and_Asparagine_Biosynthesis - Glutamate,_Aspartate_and_Asparagine_Biosynthesis - Glutamate,_Aspartate,_Aspartate_and_Asparagine_Biosynthesis - Glutamate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,_Aspartate,				
Flagellum_in_Campylobacter - Flagellum - Flagellar_motility - Fermentations:_Mixed_acid - Fatty_acid_degradation_regulons -						•	Flagellum_in_Campylobacter - Flagellum - F	•			•
Fatty_Acid_Biosynthesis_FASII - F0F1-type_ATP_synthase - Exopolysaccharide_Biosynthesis - Entner-Doudoroff_Pathway - DNA-replication - DNA structural proteins, bacterial -	• •			•			Fatty_Acid_Biosynthesis_FASII F0F1-type_ATP_synthase Exopolysaccharide_Biosynthesis Entner-Doudoroff_Pathway DNA-replication DNA_structural_proteins,_bacterial			•	
DNA_repair,_UvrABC_system - DNA_repair,_bacterial_UvrD_and_related_helicases - DNA_repair,_bacterial_UmuCD_system - DNA_repair,_bacterial_RecFOR_pathway - DNA_repair,_bacterial_RecBCD_pathway -		•				•	DNA_repair,_UvrABC_system - DNA_repair,_bacterial_UvrD_and_related_helicases - DNA_repair,_bacterial_UmuCD_system - DNA_repair,_bacterial_RecFOR_pathway - DNA_repair,_bacterial_RecBCD_pathway -	•			
DNA_repair,_bacterial_MutL-MutS_system - DNA_repair,_bacterial - DNA_Repair_Base_Excision - DNA_processing_cluster - Dehydrogenase_complexes - De_Novo_Pyrimidine_Synthesis -						• •	DNA_repair,_bacterial_MutL-MutS_system - DNA_repair,_bacterial - DNA_Repair_Base_Excision - DNA_processing_cluster - Dehydrogenase_complexes - De_Novo_Pyrimidine_Synthesis -		••		8
De_Novo_Purine_Biosynthesis - D-ribose_utilization - D-Galacturonate_and_D-Glucuronate_Utilization - D-galactonate_catabolism - Cysteine_Biosynthesis -		•					De_Novo_Purine_Biosynthesis - D-ribose_utilization - D-Galacturonate_and_D-Glucuronate_Utilization - D-galactonate_catabolism - Cysteine_Biosynthesis -				•
Cyanobacterial_Circadian_Clock - Cresol_degradation - Creatine_and_Creatinine_Degradation - Copper_homeostasis - Conserved_gene_cluster_possibly_involved_in_RNA_metabolism - Conserved_gene_cluster_associated_with_Met-tRNA_formyltransferase -	•		•			•					
Common_Pathway_For_Synthesis_of_Aromatic_Compounds_(DAHP_synthase_to_chorismate) - Cold_shock,_CspA_family_of_proteins - COG2363 - Coenzyme_B12_biosynthesis - Coenzyme_A_Biosynthesis - Cobalt-zinc-cadmium_resistance -				•		•	Common_Pathway_For_Synthesis_of_Aromatic_Compounds_(DAHP_synthase_to_chorismate) - Cold_shock, CspA_family_of_proteins - COG2363 - Coenzyme_B12_biosynthesis - Coenzyme_A_Biosynthesis - Coenzyme_Biosynthesis				
CO2_uptake,_carboxysome - CO_Dehydrogenase - Chorismate:_Intermediate_for_synthesis_of_PAPA_antibiotics,_PABA,_anthranilate,_3-hydroxyanthranilate_and_more Chorismate_Synthesis - Choline_and_Betaine_Uptake_and_Betaine_Biosynthesis -				•	•	• •	CO2_uptake,_carboxysome - CO_Dehydrogenase - Chorismate:_Intermediate_for_synthesis_of_PAPA_antibiotics,_PABA,_anthranilate,_3-hydroxyanthranilate_and_more Chorismate_Synthesis - Choline_and_Betaine_Uptake_and_Betaine_Biosynthesis -				
Cholesterol_catabolic_operon_in_Mycobacteria - Chlorophyll_Biosynthesis - Chitin_and_N-acetylglucosamine_utilization - Central_meta-cleavage_pathway_of_aromatic_compound_degradation - CBSS-87626.3.peg.3639 - CBSS-84588.1.peg.1247 -			•				Cholesterol_catabolic_operon_in_Mycobacteria - Chlorophyll_Biosynthesis - Chitin_and_N-acetylglucosamine_utilization - Central_meta-cleavage_pathway_of_aromatic_compound_degradation - CBSS-87626.3.peg.3639 - CBSS-84588.1.peg.1247 -				
CBSS-83331.1.peg.3039 - CBSS-49338.1.peg.459 - CBSS-354.1.peg.2917 - CBSS-316407.3.peg.2816 - CBSS-316273.3.peg.2378 -					•		CBSS-83331.1.peg.3039 - CBSS-49338.1.peg.459 - CBSS-354.1.peg.2917 - CBSS-316407.3.peg.2816 - CBSS-316273.3.peg.2378 - CBSS-316273.2.peg.2378 - CBSS-316273.2.peg.2378 - CBSS-316273.2.peg.2378 - CBSS-316278 - CBSS-3				
CBSS-316057.3.peg.1308 - CBSS-312309.3.peg.1965 - CBSS-291331.3.peg.3674 - CBSS-290633.1.peg.1906 - CBSS-288000.5.peg.1793 - CBSS-281090.3.peg.464 -							CBSS-316057.3.peg.1308 - CBSS-312309.3.peg.1965 - CBSS-291331.3.peg.3674 - CBSS-290633.1.peg.1906 - CBSS-288000.5.peg.1793 - CBSS-281090.3.peg.464 - CBSS-281090.3.peg.464 - CBSS-281090.3.peg.464 - CBSS-281090.3.peg.464				
CBSS-265072.7.peg.546 - CBSS-258594.1.peg.3339 - CBSS-246196.1.peg.364 - CBSS-224911.1.peg.435 - CBSS-203122.12.peg.188 -							CBSS-265072.7.peg.546 - CBSS-258594.1.peg.3339 - CBSS-246196.1.peg.364 - CBSS-224911.1.peg.435 - CBSS-203122.12.peg.188 - CBSS-203122.peg.188 - CBSS-203122.p				
CBSS-196164.1.peg.1690 -							CBSS-196164.1.peg.1690 - CBSS-188.1.peg.9880 - CBSS-176279.3.peg.868 - CBSS-160492.1.peg.550 - CBSS-138119.3.peg.2719 - Catechol_branch_of_beta-ketoadipate_pathway - CBSS-188119.3.peg.2719 - Catechol_branch_of_beta-ketoadipate_pathway - Catechol_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_branch_of_br	•			
Carotenoids - Carbon_monoxide_dehydrogenase_maturation_factors - carbazol_degradation_cluster - Capsular_Polysaccharides_Biosynthesis_and_Assembly - Capsular_heptose_biosynthesis -							Carotenoids - Carbon_monoxide_dehydrogenase_maturation_factors - carbazol_degradation_cluster - Capsular_Polysaccharides_Biosynthesis_and_Assembly - Capsular_heptose_biosynthesis - Capsular_				
cAMP_signaling_in_bacteria - Calvin-Benson_cycle - Branched-Chain_Amino_Acid_Biosynthesis - BlaR1_Family_Regulatory_Sensor-transducer_Disambiguation - Biphenyl_Degradation - Biotin_biosynthesis -				•			cAMP_signaling_in_bacteria - Calvin-Benson_cycle - Branched-Chain_Amino_Acid_Biosynthesis - BlaR1_Family_Regulatory_Sensor-transducer_Disambiguation - Biphenyl_Degradation - Biotin_biosynthesis -				• • • •
Biogenesis_of_cytochrome_c_oxidases - Biogenesis_of_c-type_cytochromes - Biflavanoid_biosynthesis - Beta-lactamase - Beta-Glucoside_Metabolism -							Biogenesis_of_cytochrome_c_oxidases - Biogenesis_of_c-type_cytochromes - Biflavanoid_biosynthesis - Beta-lactamase - Beta-Glucoside_Metabolism -				
Benzoate_transport_and_degradation_cluster - Benzoate_catabolism - Bacteriorhodopsin - Bacterial_RNA-metabolizing_Zn-dependent_hydrolases - Bacterial_hemoglobins - Bacterial_Cytoskeleton -							Benzoate_transport_and_degradation_cluster - Benzoate_catabolism - Bacteriorhodopsin - Bacterial_RNA-metabolizing_Zn-dependent_hydrolases - Bacterial_hemoglobins - Bacterial_Cytoskeleton - Bacterial_Otytoskeleton - Bacterial_O				
Bacterial_Chemotaxis - Bacterial_Cell_Division - ATP-dependent_RNA_helicases,_bacterial - Aromatic_amino_acid_degradation - Aromatic_Amin_Catabolism -						•	Bacterial_Chemotaxis - Bacterial_Cell_Division - ATP-dependent_RNA_helicases,_bacterial - Aromatic_amino_acid_degradation - Aromatic_Amin_Catabolism -				
Arginine_Biosynthesis_extended - Arginine_and_Ornithine_Degradation - Anaerobic_respiratory_reductases - Ammonia_assimilation - Aminopeptidases_(EC_3.4.11) - Alpha-Amylase_locus_in_Streptocococcus -					•	•	Arginine_Biosynthesis_extended - Arginine_and_Ornithine_Degradation - Anaerobic_respiratory_reductases - Ammonia_assimilation - Aminopeptidases_(EC_3.4.11) - Alpha-Amylase_locus_in_Streptocococcus -				
Alkanesulfonate_assimilation - Alkaloid_biosynthesis_from_L-lysine - Alanine_biosynthesis - Acyl_Homoserine_Lactone_(AHL)_Autoinducer_Quorum_Sensing Acyclic_terpenes_utilization -							Alkanesulfonate_assimilation - Alkaloid_biosynthesis_from_L-lysine - Alanine_biosynthesis - Acyl_Homoserine_Lactone_(AHL)_Autoinducer_Quorum_Sensing Acyclic_terpenes_utilization -				
Acetyl-CoA_fermentation_to_Butyrate - ABC_transporter_peptide_(TC_3.A.1.5.5) - ABC_transporter_oligopeptide_(TC_3.A.1.5.1) - ABC_transporter_dipeptide_(TC_3.A.1.5.2) - ABC_transporter_branched-chain_amino_acid_(TC_3.A.1.4.1) - ABC_transporter_alkylphosphonate_(TC_3.A.1.9.1) -				•		•	Acetyl-CoA_fermentation_to_Butyrate - ABC_transporter_peptide_(TC_3.A.1.5.5) - ABC_transporter_oligopeptide_(TC_3.A.1.5.1) - ABC_transporter_dipeptide_(TC_3.A.1.5.2) - ABC_transporter_branched-chain_amino_acid_(TC_3.A.1.4.1) - ABC_transporter_alkylphosphonate_(TC_3.A.1.9.1) - ABC_transporter_alkylphosphonate_ABC_transporter_alkylphosphonate_ABC_transporter_alkylphosphonate_ABC_transporter_alkylphosphonate_ABC_transporter_alkylphosphonate_ABC_transporter_alkylphosphonate_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC_transporter_ABC				•••
A_Hypothetical_Protein_Related_to_Proline_Metabolism - 5-FCL-like_protein -	vinned -	aceae - bium - onas -	adillus • ninella • opyxis •	obium -	erium -	obium -	A_Hypothetical_Protein_Related_to_Proline_Metabolism 5-FCL-like_protein = ## ## ## ## ## ## ## ## ## ## ## ## #	aceae - pyxis- bium - onas-	adillus-inella -	bium -	terium - aceae - obium - obium - obium - obium - obium - obia obium -
	unk 0_Novosphingc	36_Sinobacter 36_Sinobacter 3in_43_Sphing(48_Hyphomicrc _50_Sphingom	008_sub_Thiob out.010_sub_SP 3_sub_Sphingc b_Hydrogenop	.017_Mesorhizd in12_Flavobact	bin21_sub_Fili. in25_Microbac. ;_Bradyrhizobia	_sub_Bradyrhiz _sub_Hydrogenop	unbi 2_Novosphingo 4_Hydrogenopl	36_Sinobacter oin_43_Sphingo 48_Hyphomicrc 50_Sphingom	308_sub_Thiob out.010_sub_Sh 3_sub_Sphingc	sub_Hydrogeno .017_Mesorhizc in12_Flavobact in21_sub_Filim	Juliz Juliz
	groopm_bin_3	groopm_bin_ groopm_k groopm_bin_ groopm_bin_	maxbinout.00 maxbinout.013 maxbinout.013	maxbinout. metabat_bi	metabat_ metabat_b metabat_bin5	solidbin_4270_ Nidbin_5229_su	groopm_bin_3(groopm_bin_ groopm_k groopm_bin_ groopm_bin_	maxbinout.(maxbino ma	naxbinout.U16_s maxbinout. metabat_bi metabat_bi	metabat_k metabat_bin; solidbin_4270_ lidbin_5229_su
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