MGA_71083 NA / NA / NA / NA MGA_53686 NA / NA / NA / NA MGA⁻53720 NA / NA / NA / NA MGA_49617 Motility and Chemotaxis / Flagellar motility in Prokaryota / Flagellum / RNA polymerase sigma-54 factor RpoN MGA 7139 Stress Response / Oxidative stress / Oxidative stress / transcriptional regulator, Fur family MGA_53721 NA / NA / NA / NA MGA_94559 / / / NOT FOUND MGA 6844 Metabolism of Aromatic Compounds / Metabolism of central aromatic intermediates / Catechol branch of beta-ketoadipate pathway / mandelate racemase/muconate lactonizing enzyme family protein MGA⁻53638 NA / NA / NA / NA MGA_53620 Carbohydrates / Monosaccharides / D-Galacturonate_and_D-Glucuronate_Utilization / Intracellular alpha-amylase (EC 3.2.1.1) MGA_66867 NA / NA / NA / NA MGA 94469 / / / NOT FOUND MGA_22821 Regulation and Cell signaling / Programmed Cell Death and Toxin-antitoxin Systems / Toxin-antitoxin_systems_(other_than_RelBE_and_MazEF) / Antitoxin YgiT MGA_29482 NA / NA / NA / NA MGA_42227 NA / NA / NA / NA MGA_22482 NA / NA / NA / NA MGA_42209 Carbohydrates / Organic acids / Glycerate_metabolism / Pyruvate kinase (EC 2.7.1.40)
MGA_53408 Carbohydrates / Fermentation / Acetyl-CoA_fermentation_to_Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-) MGA_53335 NA / NA / NA / NA MGA-46758 Stress Response / Detoxification / Uptake of selenate and selenite / Outer membrane porin protein NmpC precursor MGA²0072 / / NOT FOUND MGA_29586 Respiration / ATP synthases / F0F1-type_ATP_synthase / ATP synthase protein I MGA 7539 NA / NA / NA / NA MGA 42166 Clustering-based subsystems / Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE / CBSS-83331.1.peg.3039 / Penicillin-binding protein 3 MGA_19762 Metabolism of Aromatic Compounds / Peripheral pathways for catabolism of aromatic compounds / Phenylpropanoid_compound_degradation / vannilate transporter VanK MGA⁻29723 NA / NA / NA / NA MGA⁻6904 NA / NA / NA / NA MGA_53308 Miscellaneous / Plant-Prokaryote DOE project / Iojap / Nicotinamidase (EC 3.5.1.19) MGA²0107 NA / NA / NA / NA MGA 6869 Fatty Acids, Lipids, and Isoprenoids / Isoprenoids / Acyclic terpenes utilization / Geranyl-CoA carboxylase biotin-containing subunit MGA_38403 NA / NA / NA / NA MGA_42239 Amino Acids and Derivatives / Arginine; urea cycle, polyamines / Arginine_and_Ornithine_Degradation / Arginine utilization protein RocB MGA_42203 Miscellaneous / Plant-Prokaryote DOE project / At3g21300 / Transcription regulator [contains diacylglycerol kinase catalytic domain] MGA_38537 Clustering-based subsystems / / EC49-61 / DNA polymerase II (EC 2.7.7.7) MGA_53317 NA / NA / NA / NA MGA_38612 NA / NA / NA / NA MGA_7000 Stress Response / Oxidative stress / Glutaredoxins / Uncharacterized monothiol glutaredoxin ycf64-like MGA_22746 NA / NA / NA / NA MGA_29490 NA / NA / NA / NA MGA_29584 / / / NOT FOUND MGA 49622 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper homeostasis / Transcriptional activator protein CopR MGA_20071 Amino Acids and Derivatives / Arginine; urea cycle, polyamines / Putrescine_utilization_pathways / Uncharacterized protein in putrescine utilization cluster MGA_7212 NA / NA / NA / NA MGA 71050 / / NOT FOUND MGA_42250 Stress Response / Oxidative stress / Oxidative_stress / transcriptional regulator, Fur family MGA_49632 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper_homeostasis / Transcriptional activator protein CopR MGA_50043 Regulation and Cell signaling / / Orphan_regulatory_proteins / Two-component system response regulator QseB MGA_49621 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper_homeostasis / Transcriptional activator protein CopR MGA_28708 Stress ponse / / Bacterial_Hemoslobins / diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) MGA 22475 Nitrogen Metabolism / / Ammonia assimilation / ammonium/methylammonium permease MGA 22256 Respiration / Electron accepting reactions / Terminal cytochrome d ubiquinol oxidases / putative Cytochrome bd2, subunit II MGA⁻38620 NA [']/ NA / NA / NA MGA 20073 Carbohydrates / Central carbohydrate metabolism / Pyruvate Alanine Serine Interconversions / Valine--pyruvate aminotransferase (EC 2.6.1.66) MGA⁻53302 NA / NA / NA / NA MGA_7290 Clustering-based subsystems / Three hypotheticals linked to lipoprotein biosynthesis / CBSS-188.1.peg.9880 / FIG018229: hypothetical protein MGA_29483 Amino Acids and Derivatives / Lysine, threonine, methionine, and cysteine / Methionine_Biosynthesis / Predicted regulator of methionine metabolism, ArsR family MGA_20079 Carbohydrates / Central carbohydrate metabolism / Dehydrogenase_complexes / Enoyl-CoA hydratase [branched-chain amino acid degradation] (EC 4.2.1.17) MGA_19922 / / / NOT FOUND MGA_7603 NA / NA / NA / NA MGA_20078 Carbohydrates / Central carbohydrate metabolism / Dehydrogenase_complexes / Enoyl-CoA hydratase [branched-chain amino acid degradation] (EC 4.2.1.17) MGA 53353 Iron acquisition and metabolism / / Iron_acquisition_in_Vibrio / Vulnibactin utilization protein VuuB 42315 Amino Acids and Derivatives / Arginine; urea cycle, polyamines / Arginine_Biosynthesis_extended / Predicted arginine uptake transporter MGA_28589 NA / NA / NA / NA MGA_7043 Nitrogen Metabolism / Nitrate_and_nitrite_ammonification / Response regulator NasT MGA_22689 NA / NA / NA / NA MGA 50117 NA / NA / NA / NA MGA_53666 Respiration / / Formate_hydrogenase / tungsten-containing formate dehydrogenase beta subunit MGA_22533 DNA Metabolism / DNA replication / DNA-replication / Transcription-repair coupling factor MGA 29605 Amino Acids and Derivatives / Branched-chain amino acids / Branched-Chain Amino acids / Branched-chain amino acid transport system MGA 7640 NA / NA / NA / NA MGA_42290 Regulation and Cell signaling / / The_Chv_regulatory_system_of_Alphaproteobacteria / Phosphocarrier protein, nitrogen regulation associated MGA_19923 Virulence / Type III, Type IV, Type VI, ESAT secretion systems / Type_4_secretion_and_conjugative_transfer / Ynd MGA_38389 NA / NA / NA / NA MGA 28426 Amino Acids and Derivatives / Proline and 4-hydroxyproline / Proline, 4-hydroxyproline uptake and utilization / putPA fragment of control region MGA_22474 NA / NA / NA / NA MGA_75215 / / / NOT FOUND MGA_38501 Sulfur Metabolism / Organic sulfur assimilation / Alkanesulfonate_assimilation / Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17) MGA_42233 Protein Metabolism / Protein biosynthesis / Universal_GTPases / Translation initiation factor 2 MGA_53671 Stress Response / Oxidative stress / Oxidative_stress / transcriptional regulator, Fur family MGA_49744 NA / NA / NA / NA MGA_53366 / / NOT FOUND

MGA 72162 NA / NA / NA / NA

MGA 34225 NA / NA / NA / NA

MGA_9795 NA / NA / NA / NA

MGA 11576 / / NOT FOUND MGA⁻14852 NA / NA / NA / NA

MGA_36593 NA / NA / NA / NA MGA 16892 NA / NA / NA / NA MGA 31147 NA / NA / NA / NA

MGA_57985 NA / NA / NA / NA MGA 48214 NA / NA / NA / NA

MGA_33139 / '/ / NOT FOUND MGA⁻25751 NA / NA / NA / NA MGA⁻25752 NA / NA / NA / NA

MGA⁻36507 NA [']/ NA / NA / NA MGA⁻36450 NA / NA / NA / NA MGA 36679 NA / NA / NA / NA MGA_36594 NA / NA / NA / NA MGA 11028 / / NOT FOUND

MGA_55877 NA / NA / NA / NA MGA 36506 NA / NA / NA / NA MGA⁻10715 NA / NA / NA / NA

MGA 10637 NA / NA / NA / NA

MGA_25904 NA / NA / NA / NA MGA 25758 NA / NA / NA / NA MGA²⁵⁷⁰³ NA / NA / NA / NA MGA_36424 NA / NA / NA / NA MGA 36423 Membrane Transport /

MGA²⁵⁷⁴¹ NA / NA / NA / NA MGA_10287 NA / NA / NA / NA MGA 25917 NA / NA / NA / NA

MGA_55909 NA / NA / NA / NA

MGA 49845 NA / NA / NA / NA MGA 49844 NA / NA / NA / NA

MGA⁻56324 NA / NA / NA / NA MGA_56330 NA / NA / NA / NA MGA 15041 NA / NA / NA / NA

MGA_54082 / / NOT FOUND MGA⁻54080 / / NOT FOUND

MGA_49912 NA / NA / NA / NA MGA_48135 NA / NA / NA / NA

MGA⁻49922 / / NOT FOUND

MGA 49681 NA / NA / NA / NA

MGA_29698 NA / NA / NA / NA MGA_7602 NA / NA / NA / NA MGA_22599 NA / NA / NA / NA

MGA 49733 / / NOT FOUND

MGA 49631 NA / NA / NA / NA

MGA_19800 NA / NA / NA / NA MGA_22822 NA / NA / NA / NA MGA_53605 / / / NOT FOUND

MGA 33979 NA / NA / NA / NA

MGA_22588 NA / NA / NA / NA

MGA⁻6890 NA / NA / NA / NA

MGA 6887 NA / NA / NA / NA ^{*} MGA_50058 NA / NA / NA / NA MGA_28509 / / / NOT FOUND

MGA⁻42867 NA / NA / NA / NA

MGA⁻7267 NA / NA / NA / NA MGA_22586 NA / NA / NA / NA

MGA 29722 NA / NA / NA / NA 🌣

MGA 50134 NA / NA / NA / NA

MGA⁻41476 / / NOT FOUND

MGA 10781 / / NOT FOUND

MGA 14697 / / NOT FOUND

MGA⁻14676 NA / NA / NA / NA

MGA_97166 NA / NA / NA / NA MGA_97372 NA / NA / NA / NA

MGA_42977 NA / NA / NA / NA

MGA_53381 NA / NA / NA / NA

MGA⁻49625 NA / NA / NA / NA

MGA 19987 NA / NA / NA / NA

MGA_53606 / / / NOT FOUND

MGA_29583 / / / NOT FOUND

MGA_28603 NA / NA / NA / NA MGA_6910 NA / NA / NA / NA

MGA⁻22664 NA [']/ NA / NA / NA

MGA_29670 / / NOT FOUND MGA_53291 / / NOT FOUND

MGA 7614 NA / NÁ / NA / NA

MGA⁻42920 / / NOT FOUND

MGA 80647 / / NOT FOUND

MGA_42351 NA / NA / NA / NA

MGA 22723 NA / NA / NA / NA

MGA 22711 NA / NA / NA / NA

MGA_22546 NA / NA / NA / NA MGA_38376 NA / NA / NA / NA

MGA 7582 NA / NA / NA / NA

MGA_42316 / / / NOT FOUND

MGA⁻7100 / / NOT FOUND MGA 7588 NA / NA / NA / NA

MGA 38572 NA / NA / NA / NA

MGA_50133 Protein Metabolism / P MGA_42344 NA / NA / NA / NA MGA_22255 NA / NA / NA / NA MGA_42948 NA / NA / NA / NA MGA_29699 NA / NA / NA / NA MGA_29623 NA / NA / NA / NA MGA_22690 NA / NA / NA / NA

MGA_7198 NA / NA / NA / NA MGA 38613 NA / NA / NA / NA MGA 38568 NA / NA / NA / NA

MGA 42240 NA / NA / NA / NA

MGA 28653 / / NOT FOUND

MGA_22729 NA / NA / NA / NA MGA_71065 NA / NA / NA / NA MGA_19977 NA / NA / NA / NA MGA 20164 NA / NA / NA / NA MGA_20165 NA / NA / NA / NA MGA 19978 NA / NA / NA / NA

MGA 7457 NA / NA / NA / NA

MGA_7541 NA / NA / NA / NA MGA_7542 NA / NA / NA / NA MGA_28654 / / / NOT FOUND MGA_42113 NA / NA / NA / NA MGA 22694 NA / NA / NA / NA MGA_20166 NA / NA / NA / NA

MGA_22539 / / / NOT FOUND MGA 20237 / / NOT FOUND MGA 53726 NA / NA / NA / NA

MGA 7621 NA / NA / NA / NA MGA 53725 NA / NA / NA / NA

MGA 7529 NA / NA / NA / NA

MGA_50107 NA / NA / NA / NA MGA 91426 / / / NOT FOUND MGA_20187 NA / NA / NA / NA

MGA⁻89935 NA / NA / NA / NA

MGA_53354 NA / NA / NA / NA MGA_29635 _/ / NOT FOUND

MGA⁻42127 NA / NA / NA / NA

MGA⁻20260 NA / NA / NA / NA

MGA 49611 / / NOT FOUND

|MGA_7083 NA / NA / NA / NA

MGA_7622 NA / NA / NA / NA MGA_42244 / / / NOT FOUND

MGA_19988 NA / NA / NA / NA

MGA_42245 / / 1/ NOT FOUND

MGA_22536 NA / NA / NA / NA MGA_22535 / / NOT FOUND MGA_29557 NA / NA / NA / NA MGA_53603 NA / NA / NA / NA

MGA_29746 / / NOT FOUND

MGA_22530 NA / NA / NA / NA

MGA_29491 NA / NA / NA / NA MGA_28436 / / / NOT FOUND

MGA_97468 / / / NOT FOUND MGA_95506 NA / NA / NA / NA

MGA 71080 NA / NA / NA / NA

MGA_7177 NA / NA / NA / NA MGA_42252 NA / NA / NA / NA MGA 29585 / / / NOT FOUND MGA_53316 NA / NA / NA / NA

MGA⁻22174 NA / NA / NA / NA ⁻ MGA_70587 / / NOT FOUND

MGA_42871 NA / NA / NA / NA MGA_38382 NA / NA / NA / NA MGA⁻29463 NA / NA / NA / NA

MGA_7629 NA / NA / NA / NA

MGA 20169 NA / NA / NA / NA MGA_95861 NA / NA / NA / NA

MGA⁻85749 NA / NA / NA / NA

MGA_85748 / / NOT FOUND

MGA⁻7468 NA / NA / NA / NA MGA_19985 NA / NA / NA / NA

TBZ109_c_vs_TBZ.57_mean_TBZ109_a_vs_TBZ.57_mean_ITBZ109_a_vs_TBZ.57_mean_ItBZ73_c_vs_TBZ.57_mean_ItBZ73_a_vs_TBZ.57_mean_ItBZ57_a_vs_TBZ.57_mean_ItBZ57_c_vs_TBZ.57_mean_ItBZ57_c_vs_TBZ.57_mean_ItBZ57_b_vs_TBZ.57_mean_ItBZ5

NA / NA / NA

20026 Membrane Transport /

MGA_72164 Carbohydrates / One-carbon Metabolism / Serine-glyoxylate_cycle / putative isobutyryl-CoA mutase, chain B

MGA_34226 Carbohydrates / One-carbon Metabolism / Serine-glyoxylate_cycle / putative isobutyryl-CoA mutase, chain B

MGA_55913 Carbohydrates / One-carbon Metabolism / Serine-glyoxylate_cycle / putative isobutyryl-CoA mutase, chain B MGA_36527 Regulation and Cell signaling / / Orphan_regulatory_proteins / Two-component system response regulator QseB MGA_36550 Stress Response / / Universal_stress_protein_family / Universal stress protein family

MGA_14821 Cell Division and Cell Cycle / / Cyanobacterial_Circadian_Clock / Group 2 RNA polymerase sigma factor

MGA_14820 Cell Division and Cell Cycle / / Cyanobacterial_Circadian_Clock / Group 2 RNA polymerase sigma factor

MGA_10484 Respiration / Electron donating reactions / Respiratory_Complex_I / Putative subunit of NAD(P)H:quinone oxidoreductase

MGA 15115 Carbohydrates / Monosaccharides / D-Galacturonate and D-Glucuronate Utilization / Intracellular alpha-amylase (EC 3.2.1.1)

MGA 55908 Stress Response / Oxidative stress / Glutathione: Non-redox reactions / Uncharacterized glutathione S-transferase-like protein

MGA_10288 Respiration / / Soluble_cytochromes_and_functionally_related_electron_carriers / soluble [2Fe-2S] ferredoxin

MGA_36658 Nucleosides and Nucleotides / Pyrimidines / Pyrimidine_utilization / Uracil permease

MGA_14945 Membrane Transport / / Transport_of_Zinc / Zinc-regulated outer membrane porin

MGA_20011 Cell Division and Cell Cycle / / Bacterial_Cytoskeleton / Cell-shape determining protein MreBH

MGA 42271 Protein Metabolism / Protein biosynthesis / Ribosome SSU bacterial / SSU ribosomal protein Thx

MGA_6889 Metabolism of Aromatic Compounds / / p-cymene_degradation / HOMODA hydrolase (CmtE) (EC 3.7.1.-)

MGA 50052 Clustering-based subsystems / / Bacterial Cell Division / rRNA small subunit methyltransferase H

MGA_14923 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p MGA_14924 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p MGA_10478 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p MGA_10478 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p

MGA_14971 Protein Metabolism / Protein biosynthesis / Ribosome_SSU_bacterial / SSU ribosomal protein Thx

MGA 14665 Protein Metabolism / Protein biosynthesis / Ribosome SSU bacterial / SSU ribosomal protein Thx

MGA_10681 Metabolism of Aromatic Compounds / Peripheral pathways for catabolism of alomatic compounds / Diphenyl_Dogradation.

MGA_6884 NA / NA / NA / NA

MGA_96276 NA / NA / NA / NA

MGA_6883 Metabolism of Aromatic Compounds / / Aromatic_Amin_Catabolism / Phenylacetaldehyde dehydrogenase (EC 1.2.1.39)

MGA_7174 NA / NA / NA / NA

MGA_38619 NA / NA / NA / NA

MGA_38619 NA / NA / NA / NA

MGA_28699 NA / NA / NA / NA

MGA_2204 NA / NA / NA / NA

MGA_42204 NA / NA / NA / NA

MGA_422077 NA / NA / NA / NA

MGA_7431 Carbohydrates / Monosaccharides / L-fucose_utilization_temp / dehydrogenase clustered with L-fuconate utilization genes

MGA 29700 Protein Metabolism / Protein biosynthesis / Translation initiation factors bacterial / Translation initiation factor SUI1-related protein

MGA_50095 Protein Metabolism / Protein biosynthesis / Ribosome_activity_modulation / Ribosomal subunit interface protein MGA_22301 Respiration / / Soluble_cytochromes_and_functionally_related_electron_carriers / soluble [2Fe-2S] ferredoxin

MGA_22634 Carbohydrates / One-carbon Metabolism / Serine-glyoxylate_cycle / putative isobutyryl-CoA mutase, chain B

MGA_14643 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p MGA_14653 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p 4649 Protein Metabolism / Protein biosynthesis / Ribosome LSU bacterial / LSU ribosomal protein L36 MGA_14651 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p MGA_14652 Protein Metabolism / Protein biosynthesis / Ribosome_SSU_bacterial / SSU ribosomal protein Thx MGA 14650 Protein Metabolism / Protein biosynthesis / Ribosome LSU bacterial / LSU ribosomal protein L36p MGA_14654 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p MGA_14928 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p

MGA_14647 Protein Metabolism / Protein biosynthesis / Ribosome_SSU_bacterial / SSU ribosomal protein Thx
MGA_14658 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p
MGA_14655 Protein Metabolism / Protein biosynthesis / Ribosome_SSU_bacterial / SSU ribosomal protein Thx

MGA_14656 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p MGA_14657 Protein Metabolism / Protein biosynthesis / Ribosome_SSU_bacterial / SSU ribosomal protein Thx MGA_10944 Protein Metabolism / Protein biosynthesis / Ribosome_SSU_bacterial / SSU ribosomal protein Thx MGA_14648 Protein Metabolism / Protein biosynthesis / Ribosome_SSU_bacterial / SSU ribosomal protein Thx MGA_14648 Protein Metabolism / Protein biosynthesis / Ribosome_SSU_bacterial / SSU ribosomal protein Thx

MGA_14660 Protein Metabolism / Protein biosynthesis / Ribosome_LSU_bacterial / LSU ribosomal protein L36p

MGA_42989 DNA Metabolism / DNA repair / DNA_repair,_bacterial_UmuCD_system / Error-prone repair protein UmuD

MGA_28432 Protein Metabolism / Protein biosynthesis / Ribosome_biogenesis_bacterial / Ribonuclease E (EC 3.1.26.12)

MGA 50133 Protein Metabolism / Protein degradation / Proteolysis in bacteria, ATP-dependent / ATPase, AFG1 family

MGA_50137 Nucleosides and Nucleotides / Purines / Purine_conversions / putative Adenosine kinase (EC 2.7.1.20)

MGA_20082 Nitrogen Metabolism / / Nitrate_and_nitrite_ammonification / Response regulator NasT

MGA 28576 Carbohydrates / Monosaccharides / Mannose Metabolism / Beta-mannosidase Man2

MGA_19937 Motility and Chemotaxis / Flagellar motility in Prokaryota / Flagellum / RNA polymerase sigma-54 factor RpoN_

MGA_53601 Carbohydrates / One-carbon Metabolism / Serine-glyoxylate_cycle / putative isobutyryl-CoA mutase, chain B

MGA_7523 Regulation and Cell signaling / / Orphan_regulatory_proteins / Two-component system response regulator QseB

MGA_22502 Protein Metabolism / Protein biosynthesis / Universal_GTPases / Translation initiation factor 2
MGA_22473 Phosphorus Metabolism / / Phosphate_metabolism / secreted alkaline phosphatase

MGA_42099 / / NOT FOUND
MGA_7140 Stress Response / Oxidative stress / Oxidative_stress / transcriptional regulator, Fur family

MGA_29748 Stress Response / Oxidative stress / Glutathione:_Non-redox_reactions / Uncharacterized glutathione S-transferase-like protein

MGA_28692 Clustering-based subsystems / / CBSS-83333.1.peg.946 / Helicase IV (EC 3.6.1.-)
MGA_22455 Carbohydrates / Di- and oligosaccharides / Maltose_and_Maltodextrin_Utilization / Maltodextrin glycosyltransferase MmtA

MGA 22381 Carbohydrates / Monosaccharides / Lfucose utilization temp / dehydrogenase clustered with Lfuconate utilization genes

MGA 7433 Carbohydrates / Di- and oligosaccharides / Bela-Glúcoside Metabolism / Predicted aldo/keto reductase in CelR regulon, COG4989

MGA_28652 Miscellaneous / / ZZ_gjo_need_homes / Virulence factor MviM

MGA_28538 Miscellaneous / / ZZ_gjo_need_homes / Virulence factor MviM MGA_19849 / / NOT FOUND

MGA_7455 Miscellaneous / / ZZ_gjo_need_homes / Virulence factor MviM

MGA 38381 Regulation and Cell signaling / / Zinc_regulated_enzymes / Zinc uptake regulation protein ZUR

MGA-49616 Sulfur Metabolism / / Thioredoxin-disulfide reductase / Thioredoxin reductase (EC 1.8.1.9)

MGA_14576 Respiration / ATP synthases / F0F1-type_ATP_synthase / ATP synthase protein I MGA_11010 Respiration / ATP synthases / F0F1-type_ATP_synthase / ATP synthase protein I MGA_11011 Respiration / ATP synthases / F0F1-type_ATP_synthase / ATP synthase protein I MGA_97325 NA / NA / NA / NA MGA_10809 NA / NA / NA / NA MGA_14698 / / NOT FOUND

MGA 6917 Clustering-based subsystems / / CBSS-316407.3.peg.2816 / Lysine efflux permease

MGA_42235 Clustering-based subsystems / / CBSS-290633.1.peg.1906 / Mlr7403 protein

MGA_10326 Miscellaneous / Plant-Prokaryote DOE project / COG2363 / Predicted thiazole transporter ThiU

MGA 7893 Sulfur Metabolism / / Sulfur oxidation / cytochrome c subunit of flavocytochrome c sulfide dehydrogenase MGA_7894 Sulfur Metabolism / / Sulfur_oxidation / cytochrome c subunit of flavocytochrome c sulfide dehydrogenase

MGA_49846 Cofactors, Vitamins, Prosthetic Groups, Pigments / Biotin / Biotin_biosynthesis / predicted biotin regulatory protein BioR (GntR family)

MGA_56179 Cofactors, Vitamins, Prosthetic Groups, Pigments / Biotin / Biotin_biosynthesis / predicted biotin regulatory protein BioR (GntR family)
MGA_31156 Virulence / Type III, Type IV, Type VI, ESAT secretion systems / Type_4_secretion_and_conjugative_transfer / Ynd

MGA_28514 Cofactors, Vitamins, Prosthetic Groups, Pigments / Biotin / Biotin_biosynthesis / predicted biotin regulatory protein BioR (GntR family)

MGA 53429 RNA Metabolism / Transcription / Transcription_initiation,_bacterial_sigma_factors / RNA polymerase sigma-70 factor

MGA 7175 DNA Metabolism / DNA repair / DNA repair, bacterial / G:T/U mismatch-specific uracil/thymine DNA-glycosylase

MGA 53372 RNA Metabolism / Transcription / Transcription initiation, bacterial sigma factors / RNA polymerase sigma-70 factor

MGA_46723 Carbohydrates / Monosaccharides / Xylose_utilization / Acetyl xylan esterase XylU (EC 3.1.1.41)

MGA_31028 Respiration / ATP synthases / F0F1-type_ATP_synthase / ATP synthase protein I

MGA_22073 Carbohydrates / Central carbohydrate metabolism / Pyruvate_metabolism_I:_anaplerotic_reactions,_PEP / Two-component sensor histidine kinase, malate (EC 2.7.3.-)
MGA_7500 Clustering-based subsystems / Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE / CBSS-83331.1.peg.3039 / Penicillin-binding protein 3
MGA_38557 Stress Response / / Hfl_operon / GTP-binding protein related to HfIX
MGA_222863 NA / NA / NA / NA
MGA_50010 NA / NA / NA / NA MGA_50057 Miscellaneous / / ZZ_gjo_need_homes / Virulence factor MviM MGA_7151 NA / NA / NA / NA MGA_49623 / / NOT FOUND MGA 42253 Phosphorus Metabolism / / Phosphate metabolism / secreted alkaline phosphatase MGA_49680 NA / NA / NA / NA MGA_38563 NA / NA / NA / NA MGA_49618 NA / NA / NA / NA MGA_7337 Membrane Transport / / Ton_and_Tol_transport_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins MGA_53653 Cell Wall and Capsule / Capsular and extracellular polysacchrides / Streptococcal_Hyaluronic_Acid_Capsule / UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) MGA_20050 Carbohydrates / Central carbohydrate metabolism / Methylglyoxal_Metabolism / NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase) MGA_22787 NA / NA / NA / NA / NA Methylamine utilization / CBSS-265072.7.peg.546 / Bacillolysin (EC 3.4.24.28) MGA 29706 DNA Metabolism / DNÁ repair / DNÁ repair, bacterial RecFOR pathway / Single-stranded-DNA-specific exonuclease RecJ, cyanobacterial paralog MGA_6938 NA / NA / NA / NA MGA_42350 Phages, Prophages, Transposable elements, Plasmids / Phages, Prophages / Phage_packaging_machinery / Phage terminase, small subunit MGA_19982 NA / NA / NA / NA MGA_28570 Cofactors, Vitamins, Prosthetic Groups, Pigments / Folate and pterines / Pterin_metabolism_3 / Dihydropteroate synthase (EC 2.5.1.15) MGA_50040 NA / NA / NA / NA MGA_6990 / / / NOT FOUND MGA_28595 NA / NA / NA / NA MGA 7507 NA / NA / NA / NA MGA⁻28571 Membrane Transport / / Ton and Tol transport systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins MGA_22833 NA / NA / NA / NA MGA_7137 NA / NA / NA / NA MGA⁻71048 NA / NA / NA / NA MGA_28668 Clustering-based subsystems / Methylamine utilization / CBSS-265072.7.peg.546 / Bacillolysin (EC 3.4.24.28)
MGA_93449 Carbohydrates / Central carbohydrate metabolism / Methylglyoxal_Metabolism / NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase)
MGA_22266 Carbohydrates / Monosaccharides / Fructose_utilization / Phosphotransferase system, phosphocarrier protein HPr

MGA_7162 NA / NA / NA / NA MGA 53322 DNA Metabolism / / DNA structural proteins, bacterial / Chromosome partition protein MukF MGA 42957 Carbohydrates / CO2 fixation / CO2 uptake, carboxysome / ribulose 1,5-bisphosphate carboxylase/oxygenase activase MGA_7524 NA / NA / NA / NA MGA_7641 NA / NA / NA / NA MGA 22372 Sulfur Metabolism / / Galactosylceramide and Sulfatide metabolism / probable beta-D-galactosidase MGA_50031 NA / NA / NA / NA MGA⁻19822 NA / NA / NA / NA MGA_53665 Respiration / / Formate_hydrogenase / tungsten-containing formate dehydrogenase beta subunit
MGA_7059 Protein Metabolism / Protein folding / Periplasmic_disulfide_interchange / Thiol:disulfide interchange protein DsbG precursor
MGA_49666 Regulation and Cell signaling / Programmed Cell Death and Toxin-antitoxin Systems / Toxin-antitoxin_systems_(other_than_RelBE_and_MazEF) / Antitoxin YgiT |MGA⁻20197 NA / NA / NA / NA` MGA_7628 NA / NA / NA / NA MGA 28531 Stress Response / / Bacterial hemoglobins / diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) MGA_2228 NA / NA / NA / NA MGA_22697 NA / NA / NA / NA MGA_53301 NA / NA / NA / NA

MGA_29747 Metabolism of Aromatic Compounds / Metabolism of central aromatic intermediates / Salicylate_and_gentisate_catabolism / salicylate esterase

MGA_22079 Cell Wall and Capsule / / UDP-N-acetylmuramate_from_Fructose-6-phosphate_Biosynthesis / UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)

MGA_6843 Metabolism of Aromatic Compounds / Metabolism of central aromatic intermediates / Catechol_branch_of_beta-ketoadipate_pathway / mandelate racemase/muconate lactonizing enzyme family protein

MGA_71081 NA / NA / NA / NA MGA_22243 NA / NA / NA / NA MGA 22259 Respiration / Electron accepting reactions / Terminal cytochrome d ubiquinol oxidases / putative Cytochrome bd2, subunit II MGA_22433 Membrane Transport / / Ton_and_Tol_transport_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins MGA_22242 NA / NA / NA / NA MGA_22820 NA / NA / NA / NA MGA_19770 Amino Acids and Derivatives / Branched-chain amino acids / Isoleucine_degradation / Predicted transcriptional regulator of leucine degradation pathway, MerR family MGA 22371 Carbohydrates / Monosaccharides / D-galactonate catabolism / D-galactonate regulator, IcIR family MGA_22327 Membrane Transport / / Ton_and_Tol_transport_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins MGA_19773 Carbohydrates / Fermentation / Acetyl-CoA_fermentation_to_Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-) MGA_53514 Stress Response / Periplasmic Stress / Periplasmic_Stress_Response / Sigma factor RpoE negative regulatory protein RseB precursor MGA_28529 Regulation and Cell signaling / / Orphan_regulatory_proteins / Two-component system response regulator QseB MGA_22684 DNA Metabolism / DNA repair / DNA_repair,_bacterial_UmuCD_system / Error-prone repair protein UmuD MGA⁻7432 NA / NA / NA / NA MGA 7502 Fatty Acids, Lipids, and Isoprenoids / Fatty acids / Phospholipid_and_Fatty_acid_biosynthesis_related_cluster / Putative histidine ammonia-lyase protein MGA_29624 NA / NA / NA / NA MGA 20077 Carbohydrates / Central carbohydrate metabolism / Dehydrogenase complexes / Enoyl-CoA hydratase [branched-chain amino acid degradation] (EC 4.2.1.17) MGA⁻28512 NA / ŃA / NA / NA MGA_49664 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper_homeostasis / Transcriptional activator protein CopR MGA_7503 NA / NA / NA / NA MGA_20186 NA / NA / NA / NA

MGA_28439 Amino Acids and Derivatives / Branched-chain amino acids / Valine_degradation / Predicted transcriptional regulator of leucine degradation pathway, MerR family

MGA_22258 Respiration / Electron accepting reactions / Terminal_cytochrome_d_ubiquinol_oxidases / putative Cytochrome bd2, subunit II MGA_29745 Cofactors, Vitamins, Prosthetic Groups, Pigments / Folate and pterines / Pterin_metabolism_3 / Dihydropteroate synthase (EC 2.5.1.15)

MGA 91571 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper homeostasis / Transcriptional activator protein CopR

MGA_49665 DNA Metabolism / DNA repair / DNA_repair,_bacterial / G:T/U mismatch-specific uracil/thymine DNA-glycosylase

MGA 93448 Carbohydrates / Fermentation / Fermentations: Mixed acid / D-lactate dehydrogenase (EC 1.1.1.28) MGA_31886 Protein Metabolism / Protein folding / GroEL_GroES / Heat shock protein 60 family co-chaperone GroES

MGA 35293 Stress Response / Heat shock / Heat shock dnaK gene cluster extended / tmRNA-binding protein SmpB

MGA_28405 Cofactors, Vitamins, Prosthetic Groups, Pigments / Folate and pterines / 5-FCL-like_protein / Thiaminase II (EC 3.5.99.2)
MGA_22775 Motility and Chemotaxis / / Bacterial_Chemotaxis / Signal transduction histidine kinase CheA (EC 2.7.3.-)
MGA_19873 NA / NA / NA / NA
MGA_50119 NA / NA / NA / NA
MGA_7336 NA / NA / NA / NA
MGA_42137 NA / NA / NA / NA
MGA_42137 NA / NA / NA / NA

MGA_22578 Respiration / / Soluble_cytochromes_and_functionally_related_electron_carriers / soluble [2Fe-2S] ferredoxin
MGA_22719 Regulation and Cell signaling / / Orphan_regulatory_proteins / Two-component system response regulator QseB
MGA_6875 Metabolism of Aromatic Compounds / / Phenylacetyl-CoA_catabolic_pathway_(core) / Putative membrane proteins / Two-components / Page | MGA 49682 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper homeostasis / Transcriptional activator protein CopR MGA_7624 Cell Wall and Capsule / Gram-Negative cell wall components / Lipoprotein_sorting_system / Outer membrane lipoprotein LolB precursor MGA_38653 Membrane Transport / / Ton_and_Tol_transport_systems / tolB protein precursor, periplasmic protein involved in the tonb-independent uptake of group A colicins MGA_19986 Membrane Transport / Protein and nucleoprotein secretion system, Type IV / pVir_Plasmid_of_Campylobacter / Type IV secretion/competence protein (VirB9) MGA_50108 Cofactors, Vitamins, Prosthetic Groups, Pigments / Tetrapyrroles / Heme_and_Siroheme_Biosynthesis / Uroporphyrinogen-III synthase, divergent, Francisella type (EC 4.2.1.75) MGA_53604 NA / NA / NA / NA MGA_7135 Stress Response / / Bacterial_hemoglobins / diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) MGA_7486 NA / NA / NA / NA MGA_66851 Protein Metabolism / Protein processing and modification / Peptide_methionine_sulfoxide_reductase / Cytochrome c-type biogenesis protein CcdA homolog, associated with MetSO reductase MGA_22458 Membrane Transport / Protein secretion system, Type II / Widespread_colonization_island / Von Willebrand factor type A domain protein, associated with Flp pilus assembly MGA_22437 Membrane Transport / Protein secretion system, Type II / Widespread_colonization_island / Von Willebrand factor type A domain protein, associated with Flp pilus assembly MGA_19983 Cofactors, Vitamins, Prosthetic Groups, Pigments / Tetrapyrroles / Coenzyme_B12_biosynthesis / Vitamin B12 ABC transporter, permease component BtuC MGA_29581 Phages, Prophages, Transposable elements / Bacteriophage integration/excision/lysogeny / Phage_integration_and_excision / Phage inihibitor of recBCD nuclease MGA_42991 NA / NA / NA / NA MGA_49627 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper_homeostasis / Transcriptional activator protein CopR_MGA_53305 Clustering-based subsystems / / CBSS-224911.1.peg.435 / Peptidase M23B precursor

Oxidative stress / Oxidative_stress / transcriptional regulator, Fur family

MGA_42277 DNA Metabolism / DNA repair / DNA_repair,_bacterial / G:T/U mismatch-specific uracil/thymine DNA-glycosylase

MGA_29679 Regulation and Cell signaling / / cAMP_signaling_in_bacteria / transcriptional activator AtxA, (pXO1-119)

MGA 53365 Nitrogen Metabolism / / Ammonia assimilation / ammonium/methylammonium permease

MGA_7189 Stress Response / / Phage_shock_protein_(psp)_operon / Phage shock protein E

MGA 38616 Stress Response / / Bacterial hemoglobins / diguanylate cyclase/phosphodiesterase (GGDÉF & EAL domains) with PAS/PAC sensor(s)

MGA_22080 Cell Wall and Capsule / Capsular and extracellular polysacchrides / Sialic_Acid_Metabolism / UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)

MGA_7412 Amino Acids and Derivatives / Arginine; urea cycle, polyamines / Putrescine_utilization_pathways / Uncharacterized protein in putrescine utilization cluster

MGA_53346 NA / NA / NA / NA MGA 19921 / / / NOT FOUND MGA_49999 NA / NA / NA / NA MGA 29486 Virulence, Disease and Defense / Resistance to antibiotics and toxic compounds / Copper homeostasis / Transcriptional activator protein CopR MGA⁻49624 NA / NA / NA / NA MGA_22692 NA / NA / NA / NA MGA_29489 NA / NA / NA / NA MGA 20146 / / NOT FOUND MGA_42173 NA / NA / NA / NA MGA 7497 NA / NA / NA / NA MGA 38380 NA / NA / NA / NA MGA_22542 NA / NA / NA / NA MGA_6842 Regulation and Cell signaling / / DNA-binding_regulatory_proteins,_strays / Xanthosine operon regulatory protein XapR, LysR family MGA_49633 NA / NA / NA / NA MGA_7615 / / NOT FOUND MGA 22747 Nucleosides and Nucleotides / Pyrimidines / pyrimidine conversions / Uridine phosphorylase (EC 2.4.2.3) MGA 7403 Amino Acids and Derivatives / Arginine; urea cycle, polyamines / Putrescine utilization pathways / Uncharacterized protein in putrescine utilization cluster MGA_42199 Cell Wall and Capsule / / Peptidoglycan_Biosynthesis / UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.10) MGA²9637 / / NOT FÖUND MGA 42830 NA / NA / NA / NA MGA_66850 NA / NA / NA / NA MGA 95530 Carbohydrates / Fermentation / Acetyl-CoA fermentation to Butyrate / Probable electron transfer flavoprotein-quinone oxidoreductase FixC (EC 1.5.5.-) MGA_7435 Carbohydrates / Aminosugars / Chitin_and_N-acetylglucosamine_utilization / Predicted chitobiose ABC transport system, permease protein 2

MGA 42930 / / NOT FOUND MGA 28438 Regulation and Cell signaling / Programmed Cell Death and Toxin-antitoxin Systems / Toxin-antitoxin systems (other than ReIBE and MazEF) / Antitoxin YgiT MGA 94859 Protein Metabolism / Protein biosynthesis / Translation elongation factors bacterial / Translation elongation factor LepA MGA 29750 Metabolism of Aromatic Compounds / Peripheral pathways for catabolism of aromatic compounds / Phenylpropanoid_compound_degradation / vannilate transporter VanK MGA 28437 Regulation and Cell signaling / Programmed Cell Death and Toxin-antitoxin Systems / Toxin-antitoxin systems (other than RelBE and MazEF) / Antitoxin YgiT MGA_22825 NA / NA / NA / NA MGA_28490 NA / NA / NA / NA MGA 42207 Protein Metabolism / Protein degradation / Protein degradation / Thimet oligopeptidase (EC 3.4.24.15) MGA 7144 Respiration / Electron donating reactions / Respiratory_dehydrogenases_1 / quinoprotein alcohol dehydrogenase MGA_38394 / / NOT FOUND MGA 7319 Membrane Transport / Protein secretion system, Type II / Widespread colonization island / Von Willebrand factor type A domain protein, associated with Flp pilus assembly MGA 20196 NA / NA / NA / NA MGA_71082 NA / NA / NA / NA MGA⁻53639 / / / NOT FOUND