

# Genome-Wide Study of the Defective Sucrose Fermenter Strain of *Vibrio cholerae* from the Latin American Cholera Epidemic

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## Table S4

### Predicted Functions of the Hypothetical Proteins of the IEC224 *Vibrio cholerae* Strain

|                                                  |           |
|--------------------------------------------------|-----------|
| <b>Amino Acids and Derivatives</b>               | <b>83</b> |
| <b>Alanine, serine, and glycine</b>              | <b>6</b>  |
| Glycine and Serine Utilization                   | 4         |
| D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) | 1         |
| D-serine/D-alanine/glycine transporter           | 1         |
| Glycerate kinase (EC 2.7.1.31)                   | 1         |

|                                                                                                                 |           |
|-----------------------------------------------------------------------------------------------------------------|-----------|
| Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2)                        | 1         |
| Glycine cleavage system                                                                                         | 1         |
| Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2)                        | 1         |
| Serine Biosynthesis                                                                                             | 1         |
| D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)                                                                | 1         |
| <b>Arginine; urea cycle, polyamines</b>                                                                         | <b>10</b> |
| Arginine and Ornithine Degradation                                                                              | 2         |
| Ornithine cyclodeaminase (EC 4.3.1.12)                                                                          | 1         |
| Succinylglutamic semialdehyde dehydrogenase (EC 1.2.1.71)                                                       | 1         |
| Arginine Biosynthesis extended                                                                                  | 2         |
| Acetylornithine deacetylase (EC 3.5.1.16)                                                                       | 1         |
| N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18)                                                      | 1         |
| Polyamine Metabolism                                                                                            | 2         |
| Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)                                   | 1         |
| Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1)                                   | 1         |
| Putrescine utilization pathways                                                                                 | 1         |
| Glycine/D-amino acid oxidase (deaminating) in putrescine utilization cluster                                    | 1         |
| Urea decomposition                                                                                              | 2         |
| Urea carboxylase-related ABC transporter, permease protein                                                      | 1         |
| Urease accessory protein UreE                                                                                   | 1         |
| Urease subunits                                                                                                 | 1         |
| Urease accessory protein UreE                                                                                   | 1         |
| <b>Aromatic amino acids and derivatives</b>                                                                     | <b>7</b>  |
| Chorismate Synthesis                                                                                            | 2         |
| 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)                                                       | 1         |
| Shikimate kinase I (EC 2.7.1.71)                                                                                | 1         |
| Chorismate: Intermediate for synthesis of PAPA antibiotics, PABA, anthranilate, 3-hydroxyanthranilate and more. | 1         |
| Anthranilate synthase, aminase component (EC 4.1.3.27)                                                          | 1         |

|                                                                                                                   |           |
|-------------------------------------------------------------------------------------------------------------------|-----------|
| Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate)                                  | 2         |
| 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19)                                                         | 1         |
| Shikimate kinase I (EC 2.7.1.71)                                                                                  | 1         |
| Tryptophan synthesis                                                                                              | 2         |
| Anthranilate synthase, aminase component (EC 4.1.3.27)                                                            | 1         |
| Tryptophan synthase alpha chain (EC 4.2.1.20)                                                                     | 1         |
| <b>Branched-chain amino acids</b>                                                                                 | <b>19</b> |
| Branched chain amino acid degradation regulons                                                                    | 3         |
| Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | 1         |
| Electron transfer flavoprotein, alpha subunit                                                                     | 1         |
| Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)                                             | 1         |
| Branched-Chain Amino Acid Biosynthesis                                                                            | 3         |
| Acetolactate synthase large subunit (EC 2.2.1.6)                                                                  | 1         |
| Dihydroxy-acid dehydratase (EC 4.2.1.9)                                                                           | 1         |
| Threonine dehydratase (EC 4.3.1.19)                                                                               | 1         |
| HMG-CoA                                                                                                           | 2         |
| Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | 1         |
| Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34)                                                                 | 1         |
| Isoleucine degradation                                                                                            | 4         |
| Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)                                                        | 1         |
| Butyrate kinase (EC 2.7.2.7)                                                                                      | 1         |
| Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | 1         |
| Enoyl-CoA hydratase (EC 4.2.1.17)                                                                                 | 1         |
| Ketoisovalerate oxidoreductase                                                                                    | 1         |
| Acetyl-coenzyme A synthetase (EC 6.2.1.1)                                                                         | 1         |
| Leucine Biosynthesis                                                                                              | 1         |
| 2-isopropylmalate synthase (EC 2.3.3.13)                                                                          | 1         |
| Leucine Degradation and HMG-CoA Metabolism                                                                        | 2         |

|                                                                                                                   |           |
|-------------------------------------------------------------------------------------------------------------------|-----------|
| Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | 1         |
| Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34)                                                                 | 1         |
| Valine degradation                                                                                                | 3         |
| Butyrate kinase (EC 2.7.2.7)                                                                                      | 1         |
| Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | 1         |
| Enoyl-CoA hydratase (EC 4.2.1.17)                                                                                 | 1         |
| <b>Glutamine, glutamate, aspartate, asparagine; ammonia assimilation</b>                                          | <b>11</b> |
| Glutamate and Aspartate uptake in Bacteria                                                                        | 1         |
| Glutamate Aspartate transport system permease protein GltK (TC 3.A.1.3.4)                                         | 1         |
| Glutamate dehydrogenases                                                                                          | 1         |
| NAD-specific glutamate dehydrogenase (EC 1.4.1.2)                                                                 | 1         |
| Glutamine synthetases                                                                                             | 1         |
| Glutamine synthetase type I (EC 6.3.1.2)                                                                          | 1         |
| Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis                                                       | 7         |
| Aspartate aminotransferase (EC 2.6.1.1)                                                                           | 1         |
| Aspartate racemase (EC 5.1.1.13)                                                                                  | 1         |
| Ferredoxin-dependent glutamate synthase (EC 1.4.7.1)                                                              | 1         |
| Glutamate synthase [NADPH] large chain (EC 1.4.1.13)                                                              | 1         |
| Glutamate synthase [NADPH] small chain (EC 1.4.1.13)                                                              | 1         |
| Glutamine synthetase type I (EC 6.3.1.2)                                                                          | 1         |
| NAD-specific glutamate dehydrogenase (EC 1.4.1.2)                                                                 | 1         |
| Poly-gamma-glutamate biosynthesis                                                                                 | 1         |
| Gamma-glutamyltranspeptidase (EC 2.3.2.2)                                                                         | 1         |
| <b>Histidine Metabolism</b>                                                                                       | <b>4</b>  |
| Histidine Biosynthesis                                                                                            | 3         |
| ATP phosphoribosyltransferase catalytic subunit (EC 2.4.2.17)                                                     | 1         |
| Histidinol dehydrogenase (EC 1.1.1.23)                                                                            | 1         |
| Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-)                                                | 1         |

|                                                              |           |
|--------------------------------------------------------------|-----------|
| Histidine Degradation                                        | 1         |
| Histidine ammonia-lyase (EC 4.3.1.3)                         | 1         |
| <b>Lysine, threonine, methionine, and cysteine</b>           | <b>23</b> |
| Cysteine Biosynthesis                                        | 1         |
| Serine acetyltransferase (EC 2.3.1.30)                       | 1         |
| Lysine Biosynthesis DAP Pathway                              | 2         |
| N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)       | 1         |
| N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18)   | 1         |
| Lysine degradation                                           | 2         |
| 5-aminopentanamidase (EC 3.5.1.30)                           | 1         |
| Lysine 2,3-aminomutase (EC 5.4.3.2)                          | 1         |
| Lysine fermentation                                          | 3         |
| Butyrate-acetoacetate CoA-transferase subunit B (EC 2.8.3.9) | 1         |
| Electron transfer flavoprotein, alpha subunit                | 1         |
| Lysine 2,3-aminomutase (EC 5.4.3.2)                          | 1         |
| Methionine Biosynthesis                                      | 7         |
| 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)       | 1         |
| Adenosylhomocysteinase (EC 3.3.1.1)                          | 1         |
| Cystathionine beta-lyase (EC 4.4.1.8)                        | 1         |
| Homoserine O-acetyltransferase (EC 2.3.1.31)                 | 1         |
| Methionine ABC transporter ATP-binding protein               | 1         |
| S-adenosylmethionine synthetase (EC 2.5.1.6)                 | 1         |
| Serine acetyltransferase (EC 2.3.1.30)                       | 1         |
| Methionine Degradation                                       | 4         |
| Adenosylhomocysteinase (EC 3.3.1.1)                          | 1         |
| Methionine ABC transporter ATP-binding protein               | 1         |
| Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)              | 1         |
| S-adenosylmethionine synthetase (EC 2.5.1.6)                 | 1         |

|                                                                 |            |
|-----------------------------------------------------------------|------------|
| Methionine Salvage                                              | 1          |
| 5-methylthioribose kinase (EC 2.7.1.100)                        | 1          |
| Threonine and Homoserine Biosynthesis                           | 2          |
| Aspartate aminotransferase (EC 2.6.1.1)                         | 1          |
| Threonine synthase (EC 4.2.3.1)                                 | 1          |
| Threonine degradation                                           | 1          |
| Threonine dehydratase (EC 4.3.1.19)                             | 1          |
| <b>Proline and 4-hydroxyproline</b>                             | <b>3</b>   |
| A Hypothetical Protein Related to Proline Metabolism            | 1          |
| Pyrroline-5-carboxylate reductase (EC 1.5.1.2)                  | 1          |
| Proline Synthesis                                               | 1          |
| Pyrroline-5-carboxylate reductase (EC 1.5.1.2)                  | 1          |
| Proline, 4-hydroxyproline uptake and utilization                | 1          |
| 4-hydroxyproline epimerase (EC 5.1.1.8)                         | 1          |
| <b>Carbohydrates</b>                                            | <b>150</b> |
| <b>Aminosugars</b>                                              | <b>5</b>   |
| Chitin and N-acetylglucosamine utilization                      | 4          |
| Beta-hexosaminidase (EC 3.2.1.52)                               | 1          |
| Chitinase (EC 3.2.1.14)                                         | 1          |
| N-Acetyl-D-glucosamine ABC transport system, permease protein 1 | 1          |
| N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)       | 1          |
| N-Acetyl-Galactosamine and Galactosamine Utilization            | 1          |
| Beta-hexosaminidase (EC 3.2.1.52)                               | 1          |
| <b>Carbon storage regulator</b>                                 | <b>2</b>   |
| Flagellar hook-associated protein FlgK                          | 1          |
| Flagellar hook-associated protein FlgK                          | 1          |
| Flagellar hook-associated protein FlgL                          | 1          |
| Flagellar hook-associated protein FlgL                          | 1          |

|                                                                                                                   |           |
|-------------------------------------------------------------------------------------------------------------------|-----------|
| <b>Central carbohydrate metabolism</b>                                                                            | <b>40</b> |
| Dehydrogenase complexes                                                                                           | 1         |
| Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | 1         |
| Dihydroxyacetone kinases                                                                                          | 1         |
| Dihydroxyacetone kinase, ATP-dependent (EC 2.7.1.29)                                                              | 1         |
| Entner-Doudoroff Pathway                                                                                          | 6         |
| 6-phosphogluconolactonase (EC 3.1.1.31)                                                                           | 1         |
| Aldehyde dehydrogenase (EC 1.2.1.3)                                                                               | 1         |
| NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)                                              | 1         |
| Phosphoglycerate mutase (EC 5.4.2.1)                                                                              | 1         |
| Polyphosphate glucokinase (EC 2.7.1.63)                                                                           | 1         |
| Pyruvate kinase (EC 2.7.1.40)                                                                                     | 1         |
| Ethylmalonyl-CoA pathway of C2 assimilation                                                                       | 1         |
| Methylsuccinyl-CoA dehydrogenase, predicted by (Erb et al, 2007)                                                  | 1         |
| Ethylmalonyl-CoA pathway of C2 assimilation, GJO                                                                  | 2         |
| Malate synthase (EC 2.3.3.9)                                                                                      | 1         |
| Methylsuccinyl-CoA dehydrogenase, predicted by (Erb et al, 2007)                                                  | 1         |
| Glycolate, glyoxylate interconversions                                                                            | 2         |
| Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD                                                              | 1         |
| Phosphoglycolate phosphatase (EC 3.1.3.18)                                                                        | 1         |
| Glycolysis and Gluconeogenesis                                                                                    | 5         |
| NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)                                              | 1         |
| Phosphoglycerate mutase (EC 5.4.2.1)                                                                              | 1         |
| Polyphosphate glucokinase (EC 2.7.1.63)                                                                           | 1         |
| Pyruvate kinase (EC 2.7.1.40)                                                                                     | 1         |
| Pyruvate,phosphate dikinase (EC 2.7.9.1)                                                                          | 1         |
| Glycolysis and Gluconeogenesis, including Archaeal enzymes                                                        | 3         |
| Phosphoglycerate mutase (EC 5.4.2.1)                                                                              | 1         |

|                                                                 |   |
|-----------------------------------------------------------------|---|
| Pyruvate kinase (EC 2.7.1.40)                                   | 1 |
| Pyruvate,phosphate dikinase (EC 2.7.9.1)                        | 1 |
| Glyoxylate bypass                                               | 2 |
| Citrate synthase (si) (EC 2.3.3.1)                              | 1 |
| Malate synthase (EC 2.3.3.9)                                    | 1 |
| Methylglyoxal Metabolism                                        | 2 |
| Aldehyde dehydrogenase (EC 1.2.1.3)                             | 1 |
| Lactoylglutathione lyase (EC 4.4.1.5)                           | 1 |
| Pentose phosphate pathway                                       | 5 |
| 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) | 1 |
| 6-phosphogluconolactonase (EC 3.1.1.31)                         | 1 |
| Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)                 | 1 |
| Transaldolase (EC 2.2.1.2)                                      | 1 |
| Transketolase (EC 2.2.1.1)                                      | 1 |
| Pyruvate Alanine Serine Interconversions                        | 2 |
| Alanine dehydrogenase (EC 1.4.1.1)                              | 1 |
| D-serine/D-alanine/glycine transporter                          | 1 |
| Pyruvate metabolism I: anaplerotic reactions, PEP               | 3 |
| Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)              | 1 |
| Pyruvate kinase (EC 2.7.1.40)                                   | 1 |
| Pyruvate,phosphate dikinase (EC 2.7.9.1)                        | 1 |
| Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate  | 3 |
| Acetyl-coenzyme A synthetase (EC 6.2.1.1)                       | 1 |
| Aldehyde dehydrogenase (EC 1.2.1.3)                             | 1 |
| Pyruvate oxidase [ubiquinone, cytochrome] (EC 1.2.2.2)          | 1 |
| Pyruvate:ferredoxin oxidoreductase                              | 1 |
| Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)                 | 1 |
| TCA Cycle                                                       | 1 |

|                                                                                           |           |
|-------------------------------------------------------------------------------------------|-----------|
| Citrate synthase (si) (EC 2.3.3.1)                                                        | 1         |
| <b>CO2 fixation</b>                                                                       | <b>9</b>  |
| Calvin-Benson cycle                                                                       | 3         |
| NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)                      | 1         |
| Phosphoribulokinase (EC 2.7.1.19)                                                         | 1         |
| Transketolase (EC 2.2.1.1)                                                                | 1         |
| Photorespiration (oxidative C2 cycle)                                                     | 6         |
| Catalase (EC 1.11.1.6)                                                                    | 1         |
| Glycerate kinase (EC 2.7.1.31)                                                            | 1         |
| Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2)  | 1         |
| Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD                                      | 1         |
| Malate synthase (EC 2.3.3.9)                                                              | 1         |
| Phosphoglycolate phosphatase (EC 3.1.3.18)                                                | 1         |
| <b>Di- and oligosaccharides</b>                                                           | <b>19</b> |
| Beta-Glucoside Metabolism                                                                 | 2         |
| 6-phospho-beta-glucosidase (EC 3.2.1.86)                                                  | 1         |
| Beta-glucosidase (EC 3.2.1.21)                                                            | 1         |
| Fructooligosaccharides(FOS) and Raffinose Utilization                                     | 3         |
| Alpha-galactosidase (EC 3.2.1.22)                                                         | 1         |
| Beta-glucosidase (EC 3.2.1.21)                                                            | 1         |
| Sucrose-6-phosphate hydrolase (EC 3.2.1.26)                                               | 1         |
| Lactose and Galactose Uptake and Utilization                                              | 5         |
| Alpha-galactosidase (EC 3.2.1.22)                                                         | 1         |
| Beta-galactosidase (EC 3.2.1.23)                                                          | 1         |
| Galactokinase (EC 2.7.1.6)                                                                | 1         |
| Galactose/methyl galactoside ABC transport system, ATP-binding protein MglA (EC 3.6.3.17) | 1         |
| UDP-glucose 4-epimerase (EC 5.1.3.2)                                                      | 1         |
| Lactose utilization                                                                       | 1         |

|                                                                       |           |
|-----------------------------------------------------------------------|-----------|
| Beta-galactosidase (EC 3.2.1.23)                                      | 1         |
| Maltose and Maltodextrin Utilization                                  | 3         |
| 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)               | 1         |
| Alpha-amylase (EC 3.2.1.1)                                            | 1         |
| Maltose/maltodextrin ABC transporter, permease protein MalG           | 1         |
| Melibiose Utilization                                                 | 1         |
| Alpha-galactosidase (EC 3.2.1.22)                                     | 1         |
| Sucrose utilization                                                   | 1         |
| Sucrose-6-phosphate hydrolase (EC 3.2.1.26)                           | 1         |
| Trehalose Biosynthesis                                                | 3         |
| Alpha-amylase (EC 3.2.1.1)                                            | 1         |
| Glycogen debranching enzyme (EC 3.2.1.-)                              | 1         |
| Trehalose-6-phosphate phosphatase (EC 3.1.3.12)                       | 1         |
| <b>Fermentation</b>                                                   | <b>15</b> |
| Acetoin, butanediol metabolism                                        | 3         |
| Acetolactate synthase large subunit (EC 2.2.1.6)                      | 1         |
| Acetolactate synthase, catabolic (EC 2.2.1.6)                         | 1         |
| Transcriptional activator of acetoin dehydrogenase operon AcoR        | 1         |
| Acetone Butanol Ethanol Synthesis                                     | 2         |
| Alcohol dehydrogenase (EC 1.1.1.1)                                    | 1         |
| Electron transfer flavoprotein, alpha subunit                         | 1         |
| Acetyl-CoA fermentation to Butyrate                                   | 5         |
| Butyrate kinase (EC 2.7.2.7)                                          | 1         |
| Butyrate-acetoacetate CoA-transferase subunit B (EC 2.8.3.9)          | 1         |
| Electron transfer flavoprotein, alpha subunit                         | 1         |
| Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1) | 1         |
| Enoyl-CoA hydratase (EC 4.2.1.17)                                     | 1         |
| Butanol Biosynthesis                                                  | 2         |

|                                                               |          |
|---------------------------------------------------------------|----------|
| Enoyl-CoA hydratase (EC 4.2.1.17)                             | 1        |
| Pyruvate formate-lyase (EC 2.3.1.54)                          | 1        |
| Fermentations: Mixed acid                                     | 3        |
| Alcohol dehydrogenase (EC 1.1.1.1)                            | 1        |
| Pyruvate formate-lyase (EC 2.3.1.54)                          | 1        |
| Sugar/maltose fermentation stimulation protein homolog        | 1        |
| <b>Lacto-N-Biose I and Galacto-N-Biose Metabolic Pathway</b>  | <b>1</b> |
| UDP-glucose 4-epimerase (EC 5.1.3.2)                          | 1        |
| UDP-glucose 4-epimerase (EC 5.1.3.2)                          | 1        |
| <b>Monosaccharides</b>                                        | <b>9</b> |
| Deoxyribose and Deoxynucleoside Catabolism                    | 1        |
| Putative deoxyribonuclease YjjV                               | 1        |
| D-galactarate, D-glucarate and D-glycerate catabolism         | 2        |
| Glucarate dehydratase (EC 4.2.1.40)                           | 1        |
| Glycerate kinase (EC 2.7.1.31)                                | 1        |
| D-Galacturonate and D-Glucuronate Utilization                 | 1        |
| D-mannonate oxidoreductase (EC 1.1.1.57)                      | 1        |
| Fructose utilization                                          | 3        |
| Phosphotransferase system, phosphocarrier protein HPr         | 1        |
| Transaldolase (EC 2.2.1.2)                                    | 1        |
| Transcriptional repressor of the fructose operon, DeoR family | 1        |
| Unknown pentose utilization                                   | 1        |
| Transketolase (EC 2.2.1.1)                                    | 1        |
| Xylose utilization                                            | 1        |
| Xylulose kinase (EC 2.7.1.17)                                 | 1        |
| <b>One-carbon Metabolism</b>                                  | <b>5</b> |
| One-carbon metabolism by tetrahydropterines                   | 1        |
| 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)        | 1        |

|                                                                     |           |
|---------------------------------------------------------------------|-----------|
| Serine-glyoxylate cycle                                             | 4         |
| 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)              | 1         |
| Citrate synthase (si) (EC 2.3.3.1)                                  | 1         |
| Glycerate kinase (EC 2.7.1.31)                                      | 1         |
| Methylmalonyl-CoA mutase (EC 5.4.99.2)                              | 1         |
| <b>Organic acids</b>                                                | <b>8</b>  |
| Alpha-acetolactate operon                                           | 1         |
| Acetolactate synthase, catabolic (EC 2.2.1.6)                       | 1         |
| Glycerate metabolism                                                | 2         |
| Glycerate kinase (EC 2.7.1.31)                                      | 1         |
| Pyruvate kinase (EC 2.7.1.40)                                       | 1         |
| Lactate utilization                                                 | 1         |
| Predicted D-lactate dehydrogenase, Fe-S protein, FAD/FMN-containing | 1         |
| Methylcitrate cycle                                                 | 1         |
| Methylisocitrate lyase (EC 4.1.3.30)                                | 1         |
| Propionate-CoA to Succinate Module                                  | 1         |
| Methylisocitrate lyase (EC 4.1.3.30)                                | 1         |
| Propionyl-CoA to Succinyl-CoA Module                                | 1         |
| Methylmalonyl-CoA mutase (EC 5.4.99.2)                              | 1         |
| Tricarballoylate Utilization                                        | 1         |
| TcuB: works with TcuA to oxidize tricarballoylate to cis-aconitate  | 1         |
| <b>Polysaccharides</b>                                              | <b>4</b>  |
| Glycogen metabolism                                                 | 4         |
| 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)             | 1         |
| Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)               | 1         |
| Glycogen debranching enzyme (EC 3.2.1.-)                            | 1         |
| Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21)       | 1         |
| <b>Sugar alcohols</b>                                               | <b>12</b> |

|                                                                                                       |           |
|-------------------------------------------------------------------------------------------------------|-----------|
| Di-Inositol-Phosphate biosynthesis                                                                    | 1         |
| Inositol-1-monophosphatase (EC 3.1.3.25)                                                              | 1         |
| Glycerol and Glycerol-3-phosphate Uptake and Utilization                                              | 5         |
| Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                                               | 1         |
| Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3) | 1         |
| Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)                            | 1         |
| Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                                                       | 1         |
| Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)                                            | 1         |
| Glycerol fermentation to 1,3-propanediol                                                              | 1         |
| Cob(I)alamin adenosyltransferase PduO (EC 2.5.1.17)                                                   | 1         |
| Inositol catabolism                                                                                   | 1         |
| Myo-inositol 2-dehydrogenase (EC 1.1.1.18)                                                            | 1         |
| Inositol utilization                                                                                  | 2         |
| Inositol-1-monophosphatase (EC 3.1.3.25)                                                              | 1         |
| Myo-inositol 2-dehydrogenase (EC 1.1.1.18)                                                            | 1         |
| Propanediol utilization                                                                               | 1         |
| Cob(I)alamin adenosyltransferase PduO (EC 2.5.1.17)                                                   | 1         |
| Ribitol, Xylitol, Arabitol, Mannitol and Sorbitol utilization                                         | 1         |
| Xylulose kinase (EC 2.7.1.17)                                                                         | 1         |
| <b>Sugar utilization in Thermotogales</b>                                                             | <b>19</b> |
| 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)                                       | 1         |
| 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)                                       | 1         |
| Alpha-galactosidase (EC 3.2.1.22)                                                                     | 1         |
| Alpha-galactosidase (EC 3.2.1.22)                                                                     | 1         |
| Beta-galactosidase (EC 3.2.1.23)                                                                      | 1         |
| Beta-galactosidase (EC 3.2.1.23)                                                                      | 1         |
| Beta-glucosidase (EC 3.2.1.21)                                                                        | 1         |
| Beta-glucosidase (EC 3.2.1.21)                                                                        | 1         |

|                                                                                                       |   |
|-------------------------------------------------------------------------------------------------------|---|
| Beta-hexosaminidase (EC 3.2.1.52)                                                                     | 1 |
| Beta-hexosaminidase (EC 3.2.1.52)                                                                     | 1 |
| D-mannonate oxidoreductase (EC 1.1.1.57)                                                              | 1 |
| D-mannonate oxidoreductase (EC 1.1.1.57)                                                              | 1 |
| Galactokinase (EC 2.7.1.6)                                                                            | 1 |
| Galactokinase (EC 2.7.1.6)                                                                            | 1 |
| Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3) | 1 |
| Glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-binding protein (TC 3.A.1.1.3) | 1 |
| Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)                            | 1 |
| Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)                            | 1 |
| Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                                                       | 1 |
| Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                                                       | 1 |
| N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)                                             | 1 |
| N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)                                             | 1 |
| NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)                                  | 1 |
| NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)                                  | 1 |
| Phosphoglycerate mutase (EC 5.4.2.1)                                                                  | 1 |
| Phosphoglycerate mutase (EC 5.4.2.1)                                                                  | 1 |
| Phosphotransferase system, phosphocarrier protein HPr                                                 | 1 |
| Phosphotransferase system, phosphocarrier protein HPr                                                 | 1 |
| Pyruvate kinase (EC 2.7.1.40)                                                                         | 1 |
| Pyruvate kinase (EC 2.7.1.40)                                                                         | 1 |
| Transaldolase (EC 2.2.1.2)                                                                            | 1 |
| Transaldolase (EC 2.2.1.2)                                                                            | 1 |
| Transketolase (EC 2.2.1.1)                                                                            | 1 |
| Transketolase (EC 2.2.1.1)                                                                            | 1 |
| UDP-glucose 4-epimerase (EC 5.1.3.2)                                                                  | 1 |
| UDP-glucose 4-epimerase (EC 5.1.3.2)                                                                  | 1 |

|                                                                      |           |
|----------------------------------------------------------------------|-----------|
| Xylulose kinase (EC 2.7.1.17)                                        | 1         |
| Xylulose kinase (EC 2.7.1.17)                                        | 1         |
| <b>Unknown carbohydrate utilization ( cluster Ydj )</b>              | <b>1</b>  |
| Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12)            | 1         |
| Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12)            | 1         |
| <b>VC0266</b>                                                        | <b>1</b>  |
| Hypothetical protein VC0266 (sugar utilization related?)             | 1         |
| Hypothetical protein VC0266 (sugar utilization related?)             | 1         |
| <b>Cell Division and Cell Cycle</b>                                  | <b>12</b> |
| <b>Bacterial Cytoskeleton</b>                                        | <b>7</b>  |
| Cell division protein FtsA                                           | 1         |
| Cell division protein FtsA                                           | 1         |
| Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) | 1         |
| Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) | 1         |
| Cell division protein FtsK                                           | 1         |
| Cell division protein FtsK                                           | 1         |
| Cell division protein FtsW                                           | 1         |
| Cell division protein FtsW                                           | 1         |
| Rod shape-determining protein MreB                                   | 1         |
| Rod shape-determining protein MreB                                   | 1         |
| Rod shape-determining protein MreD                                   | 1         |
| Rod shape-determining protein MreD                                   | 1         |
| Septum formation protein Maf                                         | 1         |
| Septum formation protein Maf                                         | 1         |
| <b>Macromolecular synthesis operon</b>                               | <b>2</b>  |
| Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)                | 1         |
| Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)                | 1         |
| Transamidase GatB domain protein                                     | 1         |

|                                                                             |           |
|-----------------------------------------------------------------------------|-----------|
| Transamidase GatB domain protein                                            | 1         |
| <b>Two cell division clusters relating to chromosome partitioning</b>       | <b>2</b>  |
| Chromosome partition protein smc                                            | 1         |
| Chromosome partition protein smc                                            | 1         |
| Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)               | 1         |
| Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)               | 1         |
| <b>YgjD and YeaZ</b>                                                        | <b>1</b>  |
| Inactive homolog of metal-dependent proteases, putative molecular chaperone | 1         |
| Inactive homolog of metal-dependent proteases, putative molecular chaperone | 1         |
| <b>Cell Wall and Capsule</b>                                                | <b>65</b> |
| <b>Capsular and extracellular polysacchrides</b>                            | <b>27</b> |
| Alginate metabolism                                                         | 1         |
| Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)                  | 1         |
| Capsular heptose biosynthesis                                               | 1         |
| GDP-L-fucose synthetase (EC 1.1.1.271)                                      | 1         |
| Capsular Polysaccharides Biosynthesis and Assembly                          | 3         |
| Capsular polysaccharide export system protein KpsC                          | 1         |
| Oligosaccharide repeat unit polymerase Wzy                                  | 1         |
| Tyrosine-protein kinase Wzc (EC 2.7.10.2)                                   | 1         |
| CMP-N-acetylneuraminate Biosynthesis                                        | 2         |
| N-Acetylneuraminate cytidylyltransferase (EC 2.7.7.43)                      | 1         |
| UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)                           | 1         |
| Colanic acid biosynthesis                                                   | 2         |
| GDP-L-fucose synthetase (EC 1.1.1.271)                                      | 1         |
| Tyrosine-protein kinase Wzc (EC 2.7.10.2)                                   | 1         |
| Exopolysaccharide Biosynthesis                                              | 2         |
| Capsular polysaccharide synthesis enzyme CpsD, exopolysaccharide synthesis  | 1         |
| Glycosyl transferase, group 2 family protein                                | 1         |

|                                                                                |           |
|--------------------------------------------------------------------------------|-----------|
| Legionaminic Acid Biosynthesis                                                 | 1         |
| UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)                              | 1         |
| Rhamnose containing glycans                                                    | 2         |
| Capsular polysaccharide export system protein KpsC                             | 1         |
| UDP-glucose 4-epimerase (EC 5.1.3.2)                                           | 1         |
| Sialic Acid Metabolism                                                         | 3         |
| N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)                      | 1         |
| N-Acetylneuraminate cytidyltransferase (EC 2.7.7.43)                           | 1         |
| UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)                              | 1         |
| Vibrio Polysaccharide (VPS) Biosynthesis                                       | 10        |
| Capsular polysaccharide synthesis enzyme CpsD, exopolysaccharide synthesis     | 1         |
| Hypothetical protein RbmB                                                      | 1         |
| Hypothetical protein RbmF                                                      | 1         |
| Hypothetical protein VpsF                                                      | 1         |
| Hypothetical protein VpsJ                                                      | 1         |
| Hypothetical protein VpsP                                                      | 1         |
| Hypothetical protein VpsQ                                                      | 1         |
| N-acetylmannosaminyltransferase (EC 2.4.1.187)                                 | 1         |
| Serine acetyltransferase (EC 2.3.1.30)                                         | 1         |
| UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)                              | 1         |
| <b>Cell wall of Mycobacteria</b>                                               | <b>3</b>  |
| linker unit-arabinogalactan synthesis                                          | 1         |
| UDP-glucose 4-epimerase (EC 5.1.3.2)                                           | 1         |
| mycolic acid synthesis                                                         | 2         |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)                      | 1         |
| Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)                    | 1         |
| <b>Gram-Negative cell wall components</b>                                      | <b>16</b> |
| Inner membrane protein YhjD and conserved cluster involved in LPS biosynthesis | 1         |

|                                                                                                               |          |
|---------------------------------------------------------------------------------------------------------------|----------|
| Uncharacterized protein YhjG                                                                                  | 1        |
| KDO2-Lipid A biosynthesis                                                                                     | 7        |
| 3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38)                                                   | 1        |
| Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129)                         | 1        |
| Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-)                                                     | 1        |
| Lipid A export ATP-binding/permease protein MsbA (EC 3.6.3.25)                                                | 1        |
| Lipid-A-disaccharide synthase (EC 2.4.1.182)                                                                  | 1        |
| Oligosaccharide repeat unit polymerase Wzy                                                                    | 1        |
| Predicted hydrolase of the metallo-beta-lactamase superfamily, clustered with KDO2-Lipid A biosynthesis genes | 1        |
| Lipid A modifications                                                                                         | 1        |
| Phosphoethanolamine transferase EptA specific for the 1 phosphate group of core-lipid A                       | 1        |
| Lipopolysaccharide assembly                                                                                   | 2        |
| Lipoprotein releasing system ATP-binding protein LolD                                                         | 1        |
| Lipoprotein releasing system transmembrane protein LolE                                                       | 1        |
| Lipopolysaccharide-related cluster in Alphaproteobacteria                                                     | 2        |
| Lipid A export ATP-binding/permease protein MsbA (EC 3.6.3.25)                                                | 1        |
| TldE/PmbA protein, part of proposed TldE/TldD proteolytic complex (PMID 12029038)                             | 1        |
| Lipoprotein sorting system                                                                                    | 2        |
| Lipoprotein releasing system ATP-binding protein LolD                                                         | 1        |
| Lipoprotein releasing system transmembrane protein LolE                                                       | 1        |
| LOS core oligosaccharide biosynthesis                                                                         | 1        |
| Lipopolysaccharide core biosynthesis protein RfaY                                                             | 1        |
| <b>Gram-Positive cell wall components</b>                                                                     | <b>2</b> |
| Teichoic and lipoteichoic acids biosynthesis                                                                  | 2        |
| N-acetylmannosaminyltransferase (EC 2.4.1.187)                                                                | 1        |
| Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)                              | 1        |
| <b>Murein Hydrolases</b>                                                                                      | <b>3</b> |
| D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)                                                             | 1        |

|                                                                         |          |
|-------------------------------------------------------------------------|----------|
| D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)                       | 1        |
| Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)   | 1        |
| Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)   | 1        |
| N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)                        | 1        |
| N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)                        | 1        |
| <b>Peptidoglycan Biosynthesis</b>                                       | <b>8</b> |
| Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)    | 1        |
| Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)    | 1        |
| D-alanine--D-alanine ligase (EC 6.3.2.4)                                | 1        |
| D-alanine--D-alanine ligase (EC 6.3.2.4)                                | 1        |
| D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)                       | 1        |
| D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)                       | 1        |
| Glutamine synthetase type I (EC 6.3.1.2)                                | 1        |
| Glutamine synthetase type I (EC 6.3.1.2)                                | 1        |
| Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)   | 1        |
| Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)   | 1        |
| Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.) | 1        |
| Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.) | 1        |
| Penicillin-binding protein 2 (PBP-2)                                    | 1        |
| Penicillin-binding protein 2 (PBP-2)                                    | 1        |
| Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)         | 1        |
| Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)         | 1        |
| <b>Peptidoglycan biosynthesis--gjo</b>                                  | <b>1</b> |
| D-alanine--D-alanine ligase (EC 6.3.2.4)                                | 1        |
| D-alanine--D-alanine ligase (EC 6.3.2.4)                                | 1        |
| <b>Recycling of Peptidoglycan Amino Acids</b>                           | <b>1</b> |
| N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)                        | 1        |
| N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)                        | 1        |

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| <b>UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis</b>          | <b>1</b>  |
| N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)                   | 1         |
| N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)                   | 1         |
| <b>YjeE</b>                                                                 | <b>3</b>  |
| ATPase YjeE, predicted to have essential role in cell wall biosynthesis     | 1         |
| ATPase YjeE, predicted to have essential role in cell wall biosynthesis     | 1         |
| COG3178: Predicted phosphotransferase related to Ser/Thr protein kinases    | 1         |
| COG3178: Predicted phosphotransferase related to Ser/Thr protein kinases    | 1         |
| Inactive homolog of metal-dependent proteases, putative molecular chaperone | 1         |
| Inactive homolog of metal-dependent proteases, putative molecular chaperone | 1         |
| <b>Cofactors, Vitamins, Prosthetic Groups, Pigments</b>                     | <b>65</b> |
| <b>Biotin</b>                                                               | <b>2</b>  |
| Biotin biosynthesis                                                         | 2         |
| Biotin synthase (EC 2.8.1.6)                                                | 1         |
| Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                              | 1         |
| <b>Coenzyme A</b>                                                           | <b>1</b>  |
| Coenzyme A Biosynthesis                                                     | 1         |
| Pantothenate:Na <sup>+</sup> symporter (TC 2.A.21.1.1)                      | 1         |
| <b>Folate and pterines</b>                                                  | <b>26</b> |
| 5-FCL-like protein                                                          | 3         |
| 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)                      | 1         |
| Alcohol dehydrogenase (EC 1.1.1.1)                                          | 1         |
| Dihydrofolate reductase (EC 1.5.1.3)                                        | 1         |
| Folate Biosynthesis                                                         | 4         |
| Dihydrofolate reductase (EC 1.5.1.3)                                        | 1         |
| Dihydropteroate synthase (EC 2.5.1.15)                                      | 1         |
| Nucleoside triphosphate pyrophosphohydrolase MazG                           | 1         |
| Transaldolase (EC 2.2.1.2)                                                  | 1         |

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| Molybdenum cofactor biosynthesis                                  | 4        |
| Molybdenum cofactor biosynthesis protein MoaB                     | 1        |
| Molybdenum transport system permease protein ModB (TC 3.A.1.8.1)  | 1        |
| Molybdopterin biosynthesis enzyme                                 | 1        |
| Molybdopterin biosynthesis protein MoeA                           | 1        |
| Pterin metabolism 3                                               | 1        |
| Dihydropteroate synthase (EC 2.5.1.15)                            | 1        |
| YgfZ                                                              | 12       |
| 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)            | 1        |
| Adenosylcobinamide-phosphate synthase                             | 1        |
| Biotin synthase (EC 2.8.1.6)                                      | 1        |
| Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22) | 1        |
| Dihydroorotase (EC 3.5.2.3)                                       | 1        |
| Dihydropteroate synthase (EC 2.5.1.15)                            | 1        |
| Glutamate synthase [NADPH] small chain (EC 1.4.1.13)              | 1        |
| Orotate phosphoribosyltransferase (EC 2.4.2.10)                   | 1        |
| Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)         | 1        |
| Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)                   | 1        |
| Thiazole biosynthesis protein ThiH                                | 1        |
| YgfY COG2938                                                      | 1        |
| YgfZ-Iron                                                         | 2        |
| Cytochrome c heme lyase subunit CcmF                              | 1        |
| Dihydroorotase (EC 3.5.2.3)                                       | 1        |
| <b>Lipoic acid</b>                                                | <b>1</b> |
| Lipoic acid metabolism                                            | 1        |
| Lipoate-protein ligase A                                          | 1        |
| <b>Molybdopterin cytosine dinucleotide</b>                        | <b>1</b> |
| Molybdopterin biosynthesis enzyme                                 | 1        |

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| Molybdopterin biosynthesis enzyme                                       | 1         |
| <b>NAD and NADP</b>                                                     | <b>1</b>  |
| NAD and NADP cofactor biosynthesis global                               | 1         |
| ADP-ribose pyrophosphatase (EC 3.6.1.13)                                | 1         |
| <b>Pyridoxine</b>                                                       | <b>3</b>  |
| Pyridoxin (Vitamin B6) Biosynthesis                                     | 3         |
| 1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)                    | 1         |
| D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)                        | 1         |
| NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)    | 1         |
| <b>Quinone cofactors</b>                                                | <b>2</b>  |
| Menaquinone and Phylloquinone Biosynthesis                              | 1         |
| Naphthoate synthase (EC 4.1.3.36)                                       | 1         |
| Ubiquinone Biosynthesis                                                 | 1         |
| 3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64)                | 1         |
| <b>Tetrapyrroles</b>                                                    | <b>28</b> |
| Chlorophyll Biosynthesis                                                | 1         |
| Light-independent protochlorophyllide reductase subunit N (EC 1.18.-.-) | 1         |
| Cobalamin synthesis                                                     | 4         |
| Adenosylcobinamide-phosphate synthase                                   | 1         |
| Cobalt-precorrin-6 synthase, anaerobic                                  | 1         |
| Cobyric acid synthase                                                   | 1         |
| Cobyric acid A,C-diamide synthase                                       | 1         |
| Coenzyme B12 biosynthesis                                               | 6         |
| Adenosylcobinamide-phosphate synthase                                   | 1         |
| Cob(I)alamin adenosyltransferase PduO (EC 2.5.1.17)                     | 1         |
| Cobalt-precorrin-6 synthase, anaerobic                                  | 1         |
| Cobyric acid synthase                                                   | 1         |
| Cobyric acid A,C-diamide synthase                                       | 1         |

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|-------------------------------------------------------------------|-----------|
| Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)             | 1         |
| CPO analysis                                                      | 6         |
| Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22) | 1         |
| Fe-S protein, homolog of lactate dehydrogenase SO1521             | 1         |
| Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)            | 1         |
| Hypothetical protein, ydbT homolog                                | 1         |
| Porphobilinogen synthase (EC 4.2.1.24)                            | 1         |
| Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)             | 1         |
| Experimental tye                                                  | 7         |
| Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22) | 1         |
| Cytochrome c-type biogenesis protein CcdA (DsbD analog)           | 1         |
| Cytochrome c-type biogenesis protein CcsA/ResC                    | 1         |
| Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)            | 1         |
| Hypothetical protein, ydbT homolog                                | 1         |
| Porphobilinogen synthase (EC 4.2.1.24)                            | 1         |
| Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)             | 1         |
| Heme and Siroheme Biosynthesis                                    | 4         |
| Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22) | 1         |
| Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)            | 1         |
| Porphobilinogen synthase (EC 4.2.1.24)                            | 1         |
| Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)             | 1         |
| <b>DNA Metabolism</b>                                             | <b>48</b> |
| <b>CRISPs</b>                                                     | <b>2</b>  |
| CRISPRs                                                           | 2         |
| CRISPR-associated protein Cas1                                    | 1         |
| CRISPR-associated protein Cas2                                    | 1         |
| <b>DNA repair</b>                                                 | <b>22</b> |
| 2-phosphoglycolate salvage                                        | 1         |

|                                                            |   |
|------------------------------------------------------------|---|
| Phosphoglycolate phosphatase (EC 3.1.3.18)                 | 1 |
| DNA Repair Base Excision                                   | 5 |
| DNA polymerase I (EC 2.7.7.7)                              | 1 |
| DNA-3-methyladenine glycosylase (EC 3.2.2.20)              | 1 |
| Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)          | 1 |
| Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-) | 1 |
| Uracil-DNA glycosylase, family 1                           | 1 |
| DNA repair, bacterial                                      | 5 |
| A/G-specific adenine glycosylase (EC 3.2.2.-)              | 1 |
| DNA polymerase IV (EC 2.7.7.7)                             | 1 |
| Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)       | 1 |
| Exonuclease SbcC                                           | 1 |
| Exonuclease SbcD                                           | 1 |
| DNA repair, bacterial MutL-MutS system                     | 1 |
| DNA mismatch repair protein MutL                           | 1 |
| DNA repair, bacterial photolyase                           | 1 |
| Deoxyribodipyrimidine photolyase (EC 4.1.99.3)             | 1 |
| DNA repair, bacterial RecBCD pathway                       | 2 |
| ATP-dependent DNA helicase SCO5183                         | 1 |
| Exodeoxyribonuclease V beta chain (EC 3.1.11.5)            | 1 |
| DNA repair, bacterial RecFOR pathway                       | 4 |
| ATP-dependent DNA helicase RecQ                            | 1 |
| DNA recombination and repair protein RecO                  | 1 |
| Recombination protein RecR                                 | 1 |
| Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-) | 1 |
| DNA repair, bacterial UvrD and related helicases           | 2 |
| ATP-dependent DNA helicase UvrD/PcrA                       | 1 |
| DNA helicase IV                                            | 1 |

|                                                                   |           |
|-------------------------------------------------------------------|-----------|
| Uracil-DNA glycosylase                                            | 1         |
| Uracil-DNA glycosylase, family 1                                  | 1         |
| <b>DNA replication</b>                                            | <b>17</b> |
| DNA replication, archaeal                                         | 1         |
| Archaeal DNA polymerase I (EC 2.7.7.7)                            | 1         |
| DNA topoisomerases, Type II, ATP-dependent                        | 3         |
| DNA gyrase subunit A (EC 5.99.1.3)                                | 1         |
| DNA gyrase subunit B (EC 5.99.1.3)                                | 1         |
| Topoisomerase IV subunit A (EC 5.99.1.-)                          | 1         |
| DNA-replication                                                   | 11        |
| ATP-dependent DNA helicase RecQ                                   | 1         |
| DNA polymerase I (EC 2.7.7.7)                                     | 1         |
| DNA polymerase III alpha subunit (EC 2.7.7.7)                     | 1         |
| DNA polymerase III beta subunit (EC 2.7.7.7)                      | 1         |
| DNA polymerase III subunits gamma and tau (EC 2.7.7.7)            | 1         |
| Exodeoxyribonuclease V beta chain (EC 3.1.11.5)                   | 1         |
| Helicase PriA essential for oriC/DnaA-independent DNA replication | 1         |
| Recombination protein RecR                                        | 1         |
| Replicative DNA helicase (EC 3.6.1.-)                             | 1         |
| Single-stranded-DNA-specific exonuclease RecJ (EC 3.1.-.-)        | 1         |
| Transcription-repair coupling factor                              | 1         |
| Plasmid replication                                               | 2         |
| Plasmid replication protein RepA                                  | 1         |
| Plasmid replication protein RepB                                  | 1         |
| <b>DNA uptake, competence</b>                                     | <b>4</b>  |
| DNA processing cluster                                            | 3         |
| DNA polymerase III subunits gamma and tau (EC 2.7.7.7)            | 1         |
| FIG000557: hypothetical protein co-occurring with RecR            | 1         |

|                                                                             |           |
|-----------------------------------------------------------------------------|-----------|
| Recombination protein RecR                                                  | 1         |
| Gram Positive Competence                                                    | 1         |
| Competence protein CoiA                                                     | 1         |
| <b>Restriction-Modification System</b>                                      | <b>1</b>  |
| Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | 1         |
| Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | 1         |
| <b>Type I Restriction-Modification</b>                                      | <b>1</b>  |
| Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | 1         |
| Type I restriction-modification system, specificity subunit S (EC 3.1.21.3) | 1         |
| <b>YcfH</b>                                                                 | <b>1</b>  |
| Putative deoxyribonuclease YjjV                                             | 1         |
| Putative deoxyribonuclease YjjV                                             | 1         |
| <b>Dormancy and Sporulation</b>                                             | <b>3</b>  |
| <b>Persister Cells</b>                                                      | <b>1</b>  |
| HipA protein                                                                | 1         |
| HipA protein                                                                | 1         |
| <b>Sporulation Cluster</b>                                                  | <b>2</b>  |
| Nucleoside triphosphate pyrophosphohydrolase MazG                           | 1         |
| Nucleoside triphosphate pyrophosphohydrolase MazG                           | 1         |
| Transcription-repair coupling factor                                        | 1         |
| Transcription-repair coupling factor                                        | 1         |
| <b>Fatty Acids, Lipids, and Isoprenoids</b>                                 | <b>30</b> |
| <b>Fatty acids</b>                                                          | <b>7</b>  |
| Fatty Acid Biosynthesis FASII                                               | 3         |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)                   | 1         |
| Enoyl-[acyl-carrier-protein] reductase [NADPH] (EC 1.3.1.10)                | 1         |
| Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)                 | 1         |
| Fatty acid degradation regulons                                             | 2         |

|                                                                  |           |
|------------------------------------------------------------------|-----------|
| Enoyl-CoA hydratase (EC 4.2.1.17)                                | 1         |
| Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                   | 1         |
| Polyunsaturated Fatty Acids synthesis                            | 1         |
| omega-3 polyunsaturated fatty acid synthase subunit, PfaA        | 1         |
| Unsaturated Fatty Acid Metabolism                                | 1         |
| Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                   | 1         |
| <b>Isoprenoids</b>                                               | <b>13</b> |
| Archaeal lipids                                                  | 1         |
| Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34)                | 1         |
| Isoprenoid Biosynthesis                                          | 5         |
| 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)   | 1         |
| 1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)             | 1         |
| 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) | 1         |
| Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34)                | 1         |
| Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)              | 1         |
| Mevalonate Branch of Isoprenoid Biosynthesis                     | 1         |
| Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34)                | 1         |
| Nonmevalonate Branch of Isoprenoid Biosynthesis                  | 3         |
| 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)   | 1         |
| 1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)             | 1         |
| 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) | 1         |
| Polyprenyl Diphosphate Biosynthesis                              | 1         |
| Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31)              | 1         |
| polyprenyl synthesis                                             | 2         |
| 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)   | 1         |
| 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) | 1         |
| <b>Phospholipids</b>                                             | <b>8</b>  |
| Glycerolipid and Glycerophospholipid Metabolism in Bacteria      | 8         |

|                                                                       |           |
|-----------------------------------------------------------------------|-----------|
| 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)          | 1         |
| Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)               | 1         |
| Alcohol dehydrogenase (EC 1.1.1.1)                                    | 1         |
| Aldehyde dehydrogenase (EC 1.2.1.3)                                   | 1         |
| Glycerate kinase (EC 2.7.1.31)                                        | 1         |
| Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                       | 1         |
| Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)            | 1         |
| Phosphatidate cytidylyltransferase (EC 2.7.7.41)                      | 1         |
| <b>Polyhydroxybutyrate metabolism</b>                                 | <b>2</b>  |
| Butyrate-acetoacetate CoA-transferase subunit B (EC 2.8.3.9)          | 1         |
| Butyrate-acetoacetate CoA-transferase subunit B (EC 2.8.3.9)          | 1         |
| Enoyl-CoA hydratase (EC 4.2.1.17)                                     | 1         |
| Enoyl-CoA hydratase (EC 4.2.1.17)                                     | 1         |
| <b>Iron acquisition and metabolism</b>                                | <b>16</b> |
| <b>Campylobacter Iron Metabolism</b>                                  | <b>2</b>  |
| Ferric siderophore transport system, periplasmic binding protein TonB | 1         |
| Ferric siderophore transport system, periplasmic binding protein TonB | 1         |
| Ferrous iron transport protein B                                      | 1         |
| Ferrous iron transport protein B                                      | 1         |
| <b>Heme, hemin uptake and utilization systems in GramPositives</b>    | <b>1</b>  |
| Hypothetical protein DUF454                                           | 1         |
| Hypothetical protein DUF454                                           | 1         |
| <b>Hemin transport system</b>                                         | <b>4</b>  |
| ABC-type hemin transport system, ATPase component                     | 1         |
| ABC-type hemin transport system, ATPase component                     | 1         |
| Ferric siderophore transport system, periplasmic binding protein TonB | 1         |
| Ferric siderophore transport system, periplasmic binding protein TonB | 1         |
| Outer membrane receptor proteins, mostly Fe transport                 | 1         |

|                                                                                               |           |
|-----------------------------------------------------------------------------------------------|-----------|
| Outer membrane receptor proteins, mostly Fe transport                                         | 1         |
| TonB-dependent hemin , ferrichrome receptor                                                   | 1         |
| TonB-dependent hemin , ferrichrome receptor                                                   | 1         |
| <b>Iron acquisition in Vibrio</b>                                                             | <b>4</b>  |
| Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB                   | 1         |
| Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB                   | 1         |
| Ferrous iron transport protein B                                                              | 1         |
| Ferrous iron transport protein B                                                              | 1         |
| Hypothetical protein colocalized with Enterobactin receptor VctA                              | 1         |
| Hypothetical protein colocalized with Enterobactin receptor VctA                              | 1         |
| TonB-dependent receptor                                                                       | 1         |
| TonB-dependent receptor                                                                       | 1         |
| <b>Siderophores</b>                                                                           | <b>4</b>  |
| Siderophore Aerobactin                                                                        | 1         |
| Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB                   | 1         |
| Siderophore assembly kit                                                                      | 3         |
| ABC-type hemin transport system, ATPase component                                             | 1         |
| Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB                   | 1         |
| TonB-dependent hemin , ferrichrome receptor                                                   | 1         |
| <b>Transport of Iron</b>                                                                      | <b>1</b>  |
| Ferrous iron transport protein B                                                              | 1         |
| Ferrous iron transport protein B                                                              | 1         |
| <b>Membrane Transport</b>                                                                     | <b>33</b> |
| <b>ABC transporters</b>                                                                       | <b>7</b>  |
| ABC transporter branched-chain amino acid (TC 3.A.1.4.1)                                      | 2         |
| Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1)          | 1         |
| High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1) | 1         |
| ABC transporter dipeptide (TC 3.A.1.5.2)                                                      | 2         |

|                                                                                            |          |
|--------------------------------------------------------------------------------------------|----------|
| Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)                            | 1        |
| Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)  | 1        |
| ABC transporter oligopeptide (TC 3.A.1.5.1)                                                | 3        |
| Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1) | 1        |
| Oligopeptide transport ATP-binding protein OppD (TC 3.A.1.5.1)                             | 1        |
| Oligopeptide transport system permease protein OppC (TC 3.A.1.5.1)                         | 1        |
| <b>Choline Transport</b>                                                                   | <b>1</b> |
| Sodium-Choline Symporter                                                                   | 1        |
| Sodium-Choline Symporter                                                                   | 1        |
| <b>ECF class transporters</b>                                                              | <b>1</b> |
| ATPase component STY3232 of energizing module of queuosine-regulated ECF transporter       | 1        |
| ATPase component STY3232 of energizing module of queuosine-regulated ECF transporter       | 1        |
| <b>Folate transporters</b>                                                                 | <b>1</b> |
| Dihydrofolate synthase (EC 6.3.2.12) / Folylpolyglutamate synthase (EC 6.3.2.17)           | 1        |
| Dihydrofolate synthase (EC 6.3.2.12) / Folylpolyglutamate synthase (EC 6.3.2.17)           | 1        |
| <b>Protein and nucleoprotein secretion system, Type IV</b>                                 | <b>2</b> |
| Type IV pilus                                                                              | 2        |
| Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)                   | 1        |
| Type IV fimbrial assembly, ATPase PilB                                                     | 1        |
| <b>Protein secretion system, Type II</b>                                                   | <b>4</b> |
| CBSS-562.2.peg.633                                                                         | 2        |
| FIG002842: hypothetical protein                                                            | 1        |
| Type IV fimbrial assembly, ATPase PilB                                                     | 1        |
| General Secretion Pathway                                                                  | 1        |
| General secretion pathway protein F                                                        | 1        |
| Widespread colonization island                                                             | 1        |
| Type II/IV secretion system ATPase TadZ/CpaE, associated with Flp pilus assembly           | 1        |
| <b>Protein secretion system, Type III</b>                                                  | <b>1</b> |

|                                                                          |          |
|--------------------------------------------------------------------------|----------|
| Type III secretion system                                                | 1        |
| Type III secretion cytoplasmic protein (YscL)                            | 1        |
| <b>Protein secretion system, Type VI</b>                                 | <b>3</b> |
| Type VI secretion systems                                                | 3        |
| ClpB protein                                                             | 1        |
| Uncharacterized protein ImpF                                             | 1        |
| VgrG protein                                                             | 1        |
| <b>Protein translocation across cytoplasmic membrane</b>                 | <b>2</b> |
| HtrA and Sec secretion                                                   | 2        |
| Protein export cytoplasm protein SecA ATPase RNA helicase (TC 3.A.5.1.1) | 1        |
| Protein-export membrane protein SecF (TC 3.A.5.1.1)                      | 1        |
| <b>Sugar Phosphotransferase Systems, PTS</b>                             | <b>1</b> |
| Sucrose-specific PTS                                                     | 1        |
| Sucrose-6-phosphate hydrolase (EC 3.2.1.26)                              | 1        |
| <b>Ton and Tol transport systems</b>                                     | <b>7</b> |
| Colicin I receptor precursor                                             | 1        |
| Colicin I receptor precursor                                             | 1        |
| Ferric siderophore transport system, periplasmic binding protein TonB    | 1        |
| Ferric siderophore transport system, periplasmic binding protein TonB    | 1        |
| MotA/TolQ/ExbB proton channel family protein                             | 1        |
| MotA/TolQ/ExbB proton channel family protein                             | 1        |
| Outer membrane lipoprotein omp16 precursor                               | 1        |
| Outer membrane lipoprotein omp16 precursor                               | 1        |
| TonB-dependent hemin , ferrichrome receptor                              | 1        |
| TonB-dependent hemin , ferrichrome receptor                              | 1        |
| TonB-dependent receptor                                                  | 1        |
| TonB-dependent receptor                                                  | 1        |
| Type I secretion outer membrane protein, TolC precursor                  | 1        |

|                                                                  |           |
|------------------------------------------------------------------|-----------|
| Type I secretion outer membrane protein, TolC precursor          | 1         |
| <b>Transport of Manganese</b>                                    | <b>1</b>  |
| Manganese ABC transporter, inner membrane permease protein SitC  | 1         |
| Manganese ABC transporter, inner membrane permease protein SitC  | 1         |
| <b>Transport of Molybdenum</b>                                   | <b>1</b>  |
| Molybdenum transport system permease protein ModB (TC 3.A.1.8.1) | 1         |
| Molybdenum transport system permease protein ModB (TC 3.A.1.8.1) | 1         |
| <b>Transport of Zinc</b>                                         | <b>1</b>  |
| Zinc ABC transporter, ATP-binding protein ZnuC                   | 1         |
| Zinc ABC transporter, ATP-binding protein ZnuC                   | 1         |
| <b>Metabolism of Aromatic Compounds</b>                          | <b>11</b> |
| <b>Benzoate transport and degradation cluster</b>                | <b>2</b>  |
| Benzoate transport, inner-membrane translocator precursor        | 1         |
| Benzoate transport, inner-membrane translocator precursor        | 1         |
| Shikimate kinase I (EC 2.7.1.71)                                 | 1         |
| Shikimate kinase I (EC 2.7.1.71)                                 | 1         |
| <b>Metabolism of central aromatic intermediates</b>              | <b>4</b>  |
| Catechol branch of beta-ketoadipate pathway                      | 1         |
| Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)            | 1         |
| Homogentisate pathway of aromatic compound degradation           | 1         |
| Transcriptional regulator, IclR family                           | 1         |
| Protocatechuate branch of beta-ketoadipate pathway               | 1         |
| Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)            | 1         |
| Salicylate and gentisate catabolism                              | 1         |
| Salicylate hydroxylase (EC 1.14.13.1)                            | 1         |
| <b>Peripheral pathways for catabolism of aromatic compounds</b>  | <b>4</b>  |
| Chloroaromatic degradation pathway                               | 1         |
| Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24)            | 1         |

|                                                                                               |           |
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| n-Phenylalkanoic acid degradation                                                             | 2         |
| Enoyl-CoA hydratase (EC 4.2.1.17)                                                             | 1         |
| Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                                                | 1         |
| Salicylate ester degradation                                                                  | 1         |
| Salicylate hydroxylase (EC 1.14.13.1)                                                         | 1         |
| <b>Phenylacetyl-CoA catabolic pathway (core)</b>                                              | <b>1</b>  |
| Phenylacetic acid degradation protein PaaN2, ring-opening aldehyde dehydrogenase (EC 1.2.1.3) | 1         |
| Phenylacetic acid degradation protein PaaN2, ring-opening aldehyde dehydrogenase (EC 1.2.1.3) | 1         |
| <b>Miscellaneous</b>                                                                          | <b>17</b> |
| <b>Broadly distributed proteins not in subsystems</b>                                         | <b>2</b>  |
| YbbL ABC transporter ATP-binding protein                                                      | 1         |
| YbbL ABC transporter ATP-binding protein                                                      | 1         |
| YciL protein                                                                                  | 1         |
| YciL protein                                                                                  | 1         |
| <b>Carbonate Biomineralization</b>                                                            | <b>4</b>  |
| Electron transfer flavoprotein, alpha subunit                                                 | 1         |
| Electron transfer flavoprotein, alpha subunit                                                 | 1         |
| Enoyl-CoA hydratase (EC 4.2.1.17)                                                             | 1         |
| Enoyl-CoA hydratase (EC 4.2.1.17)                                                             | 1         |
| Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                                                | 1         |
| Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                                                | 1         |
| Transcriptional regulator, TetR family                                                        | 1         |
| Transcriptional regulator, TetR family                                                        | 1         |
| <b>Plant-Prokaryote DOE project</b>                                                           | <b>8</b>  |
| At2g33980 At1g28960                                                                           | 2         |
| FIG017823: ATPase, MoxR family                                                                | 1         |
| tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25)                                       | 1         |
| COG2363                                                                                       | 2         |

|                                                                                           |           |
|-------------------------------------------------------------------------------------------|-----------|
| Hydroxymethylpyrimidine ABC transporter, substrate-binding component                      | 1         |
| Thiazole biosynthesis protein ThiG                                                        | 1         |
| Conserved gene cluster possibly involved in RNA metabolism                                | 1         |
| Serine acetyltransferase (EC 2.3.1.30)                                                    | 1         |
| lojap                                                                                     | 3         |
| Adenylate cyclase (EC 4.6.1.1)                                                            | 1         |
| Orotate phosphoribosyltransferase (EC 2.4.2.10)                                           | 1         |
| Phosphatidate cytidyltransferase (EC 2.7.7.41)                                            | 1         |
| <b>ZZ gjo need homes</b>                                                                  | <b>3</b>  |
| Lipid A export ATP-binding/permease protein MsbA                                          | 1         |
| Lipid A export ATP-binding/permease protein MsbA                                          | 1         |
| Na <sup>+</sup> /H <sup>+</sup> antiporter NhaB                                           | 1         |
| Na <sup>+</sup> /H <sup>+</sup> antiporter NhaB                                           | 1         |
| Sodium/glutamate symport protein                                                          | 1         |
| Sodium/glutamate symport protein                                                          | 1         |
| <b>Motility and Chemotaxis</b>                                                            | <b>23</b> |
| <b>Bacterial Chemotaxis</b>                                                               | <b>2</b>  |
| Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2) | 1         |
| Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2) | 1         |
| Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)                      | 1         |
| Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)                      | 1         |
| <b>Flagellar motility in Prokaryota</b>                                                   | <b>15</b> |
| Archaeal Flagellum                                                                        | 1         |
| Flagella-related protein Flal                                                             | 1         |
| Flagellar motility                                                                        | 5         |
| Flagellar biosynthesis protein FlhA                                                       | 1         |
| Flagellar biosynthesis protein FlhF                                                       | 1         |
| Flagellar motor rotation protein MotA                                                     | 1         |

|                                                                      |           |
|----------------------------------------------------------------------|-----------|
| Flagellar motor rotation protein MotB                                | 1         |
| Predicted signal transduction protein                                | 1         |
| Flagellum                                                            | 8         |
| Flagellar biosynthesis protein FlhA                                  | 1         |
| Flagellar biosynthesis protein FlhF                                  | 1         |
| Flagellar hook-associated protein FlgK                               | 1         |
| Flagellar hook-associated protein FlgL                               | 1         |
| Flagellar hook-length control protein FliK                           | 1         |
| Flagellar motor rotation protein MotA                                | 1         |
| Flagellar motor rotation protein MotB                                | 1         |
| Flagellar sensor histidine kinase FleS                               | 1         |
| Flagellum in Campylobacter                                           | 1         |
| Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129) | 1         |
| <b>Social motility and nonflagellar swimming in bacteria</b>         | <b>6</b>  |
| Bacterial motility:Gliding                                           | 6         |
| Cell division protein FtsX                                           | 1         |
| GldJ                                                                 | 1         |
| twitching motility protein PilH                                      | 1         |
| Type IV fimbrial assembly, ATPase PilB                               | 1         |
| type IV pili signal transduction protein Pill                        | 1         |
| type IV pilus biogenesis protein PilJ                                | 1         |
| <b>Nitrogen Metabolism</b>                                           | <b>17</b> |
| <b>Allantoin Utilization</b>                                         | <b>1</b>  |
| Glycerate kinase (EC 2.7.1.31)                                       | 1         |
| Glycerate kinase (EC 2.7.1.31)                                       | 1         |
| <b>Ammonia assimilation</b>                                          | <b>5</b>  |
| Ferredoxin-dependent glutamate synthase (EC 1.4.7.1)                 | 1         |
| Ferredoxin-dependent glutamate synthase (EC 1.4.7.1)                 | 1         |

|                                                                          |          |
|--------------------------------------------------------------------------|----------|
| Glutamate synthase [NADPH] large chain (EC 1.4.1.13)                     | 1        |
| Glutamate synthase [NADPH] large chain (EC 1.4.1.13)                     | 1        |
| Glutamate synthase [NADPH] small chain (EC 1.4.1.13)                     | 1        |
| Glutamate synthase [NADPH] small chain (EC 1.4.1.13)                     | 1        |
| Glutamine synthetase type I (EC 6.3.1.2)                                 | 1        |
| Glutamine synthetase type I (EC 6.3.1.2)                                 | 1        |
| Nitrogen regulation protein NR(II) (EC 2.7.3.-)                          | 1        |
| Nitrogen regulation protein NR(II) (EC 2.7.3.-)                          | 1        |
| <b>Denitrification</b>                                                   | <b>3</b> |
| Nitric oxide -responding transcriptional regulator Dnr (Crp/Fnr family)  | 1        |
| Nitric oxide -responding transcriptional regulator Dnr (Crp/Fnr family)  | 1        |
| Nitric oxide -responding transcriptional regulator NnrR (Crp/Fnr family) | 1        |
| Nitric oxide -responding transcriptional regulator NnrR (Crp/Fnr family) | 1        |
| NnrS protein involved in response to NO                                  | 1        |
| NnrS protein involved in response to NO                                  | 1        |
| <b>Dissimilatory nitrite reductase</b>                                   | <b>1</b> |
| Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)                    | 1        |
| Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)                    | 1        |
| <b>Nitrate and nitrite ammonification</b>                                | <b>4</b> |
| Assimilatory nitrate reductase large subunit (EC:1.7.99.4)               | 1        |
| Assimilatory nitrate reductase large subunit (EC:1.7.99.4)               | 1        |
| Nitrate ABC transporter, nitrate-binding protein                         | 1        |
| Nitrate ABC transporter, nitrate-binding protein                         | 1        |
| Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)                   | 1        |
| Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)                   | 1        |
| Response regulator NasT                                                  | 1        |
| Response regulator NasT                                                  | 1        |
| <b>Nitric oxide synthase</b>                                             | <b>1</b> |

|                                                                   |           |
|-------------------------------------------------------------------|-----------|
| putative cytochrome P450 hydroxylase                              | 1         |
| putative cytochrome P450 hydroxylase                              | 1         |
| <b>Nitrogen fixation</b>                                          | <b>1</b>  |
| AnfO protein, required for Mo- and V-independent nitrogenase      | 1         |
| AnfO protein, required for Mo- and V-independent nitrogenase      | 1         |
| <b>Nitrosative stress</b>                                         | <b>1</b>  |
| NnrS protein involved in response to NO                           | 1         |
| NnrS protein involved in response to NO                           | 1         |
| <b>Nucleosides and Nucleotides</b>                                | <b>16</b> |
| <b>Purines</b>                                                    | <b>6</b>  |
| De Novo Purine Biosynthesis                                       | 2         |
| Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)         | 1         |
| Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)                   | 1         |
| Purine conversions                                                | 2         |
| Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)             | 1         |
| Polyphosphate kinase (EC 2.7.4.1)                                 | 1         |
| Purine Utilization                                                | 2         |
| Cytosine/purine/uracil/thiamine/allantoin permease family protein | 1         |
| Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)  | 1         |
| <b>Pyrimidines</b>                                                | <b>7</b>  |
| De Novo Pyrimidine Synthesis                                      | 3         |
| Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)             | 1         |
| Dihydroorotase (EC 3.5.2.3)                                       | 1         |
| Orotate phosphoribosyltransferase (EC 2.4.2.10)                   | 1         |
| Novel non-oxidative pathway of Uracil catabolism                  | 1         |
| Uridine kinase (EC 2.7.1.48)                                      | 1         |
| pyrimidine conversions                                            | 3         |
| CTP synthase (EC 6.3.4.2)                                         | 1         |

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|--------------------------------------------------------------------------------------|-----------|
| Thioredoxin reductase (EC 1.8.1.9)                                                   | 1         |
| Uridine kinase (EC 2.7.1.48)                                                         | 1         |
| <b>Ribonucleotide reduction</b>                                                      | <b>3</b>  |
| Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1)          | 1         |
| Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1)          | 1         |
| Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)       | 1         |
| Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)       | 1         |
| Ribonucleotide reductase transcriptional regulator NrdR                              | 1         |
| Ribonucleotide reductase transcriptional regulator NrdR                              | 1         |
| <b>Phages, Prophages, Transposable elements, Plasmids</b>                            | <b>12</b> |
| <b>Pathogenicity islands</b>                                                         | <b>1</b>  |
| Staphylococcal pathogenicity islands SaPI                                            | 1         |
| Heat shock protein 60 family chaperone GroEL                                         | 1         |
| <b>Phage family-specific subsystems</b>                                              | <b>5</b>  |
| Phage cyanophage                                                                     | 3         |
| Phage protein                                                                        | 1         |
| Phage tail fiber protein                                                             | 1         |
| Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | 1         |
| T7-like cyanophage core proteins                                                     | 2         |
| Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1)          | 1         |
| Transaldolase (EC 2.2.1.2)                                                           | 1         |
| <b>Phages, Prophages</b>                                                             | <b>4</b>  |
| IbrA and IbrB: co-activators of prophage gene expression                             | 1         |
| Co-activator of prophage gene expression IbrA                                        | 1         |
| Phage tail fiber proteins                                                            | 1         |
| Phage tail fiber protein                                                             | 1         |
| Phage tail proteins                                                                  | 1         |
| Phage tail protein                                                                   | 1         |

|                                                                                      |           |
|--------------------------------------------------------------------------------------|-----------|
| Phage tail proteins 2                                                                | 1         |
| Phage tape measure                                                                   | 1         |
| <b>Plasmid related functions</b>                                                     | <b>1</b>  |
| Plasmid-encoded T-DNA transfer                                                       | 1         |
| Inner membrane protein of type IV secretion of T-DNA complex, VirB6                  | 1         |
| <b>Transposable elements</b>                                                         | <b>1</b>  |
| CBSS-203122.12.peg.188                                                               | 1         |
| Plasmid replication protein RepA                                                     | 1         |
| <b>Phosphorus Metabolism</b>                                                         | <b>16</b> |
| <b>High affinity phosphate transporter and control of PHO regulon</b>                | <b>4</b>  |
| Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | 1         |
| Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | 1         |
| Phosphate regulon transcriptional regulatory protein PhoB (SphR)                     | 1         |
| Phosphate regulon transcriptional regulatory protein PhoB (SphR)                     | 1         |
| Phosphate transport system permease protein PstA (TC 3.A.1.7.1)                      | 1         |
| Phosphate transport system permease protein PstA (TC 3.A.1.7.1)                      | 1         |
| Polyphosphate kinase (EC 2.7.4.1)                                                    | 1         |
| Polyphosphate kinase (EC 2.7.4.1)                                                    | 1         |
| <b>P uptake (cyanobacteria)</b>                                                      | <b>2</b>  |
| Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | 1         |
| Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | 1         |
| Phosphate transport system permease protein PstA (TC 3.A.1.7.1)                      | 1         |
| Phosphate transport system permease protein PstA (TC 3.A.1.7.1)                      | 1         |
| <b>Phosphate metabolism</b>                                                          | <b>10</b> |
| 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)                         | 1         |
| 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)                         | 1         |
| Low-affinity inorganic phosphate transporter                                         | 1         |
| Low-affinity inorganic phosphate transporter                                         | 1         |

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| Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)                           | 1        |
| Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)                           | 1        |
| Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | 1        |
| Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | 1        |
| Phosphate regulon transcriptional regulatory protein PhoB (SphR)                     | 1        |
| Phosphate regulon transcriptional regulatory protein PhoB (SphR)                     | 1        |
| Phosphate transport system permease protein PstA (TC 3.A.1.7.1)                      | 1        |
| Phosphate transport system permease protein PstA (TC 3.A.1.7.1)                      | 1        |
| Polyphosphate kinase (EC 2.7.4.1)                                                    | 1        |
| Polyphosphate kinase (EC 2.7.4.1)                                                    | 1        |
| Probable low-affinity inorganic phosphate transporter                                | 1        |
| Probable low-affinity inorganic phosphate transporter                                | 1        |
| Pyrophosphate-energized proton pump (EC 3.6.1.1)                                     | 1        |
| Pyrophosphate-energized proton pump (EC 3.6.1.1)                                     | 1        |
| Sodium-dependent phosphate transporter                                               | 1        |
| Sodium-dependent phosphate transporter                                               | 1        |
| <b>Photosynthesis</b>                                                                | <b>1</b> |
| <b>Light-harvesting complexes</b>                                                    | <b>1</b> |
| Phycobilisome                                                                        | 1        |
| Phycoerythrocyanin beta chain                                                        | 1        |
| <b>Potassium metabolism</b>                                                          | <b>5</b> |
| <b>Glutathione-regulated potassium-efflux system and associated functions</b>        | <b>1</b> |
| Trk system potassium uptake protein TrkA                                             | 1        |
| Trk system potassium uptake protein TrkA                                             | 1        |
| <b>Potassium homeostasis</b>                                                         | <b>4</b> |
| Potassium uptake protein TrkH                                                        | 1        |
| Potassium uptake protein TrkH                                                        | 1        |
| Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1)                   | 1        |

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| Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1)                  | 1         |
| putative Glutathione-regulated potassium-efflux system protein KefB                 | 1         |
| putative Glutathione-regulated potassium-efflux system protein KefB                 | 1         |
| Trk system potassium uptake protein TrkA                                            | 1         |
| Trk system potassium uptake protein TrkA                                            | 1         |
| <b>Protein Metabolism</b>                                                           | <b>43</b> |
| <b>Protein biosynthesis</b>                                                         | <b>19</b> |
| Ribosome biogenesis bacterial                                                       | 4         |
| hypothetical protein sometimes fused to ribosomal protein S6 glutaminyl transferase | 1         |
| Inactive homolog of metal-dependent proteases, putative molecular chaperone         | 1         |
| Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)                      | 1         |
| Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)                      | 1         |
| Ribosome LSU bacterial                                                              | 2         |
| LSU ribosomal protein L23p (L23Ae)                                                  | 1         |
| LSU ribosomal protein L25p                                                          | 1         |
| Ribosome SSU bacterial                                                              | 3         |
| SSU ribosomal protein S12p (S23e)                                                   | 1         |
| SSU ribosomal protein S1p                                                           | 1         |
| SSU ribosomal protein S7p (S5e)                                                     | 1         |
| Translation termination factors bacterial                                           | 1         |
| Peptide chain release factor 3                                                      | 1         |
| tRNA aminoacylation, Arg                                                            | 1         |
| Arginyl-tRNA synthetase (EC 6.1.1.19)                                               | 1         |
| tRNA aminoacylation, Gly                                                            | 1         |
| Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)                                     | 1         |
| tRNA aminoacylation, Leu                                                            | 1         |
| Leucyl-tRNA synthetase (EC 6.1.1.4)                                                 | 1         |
| tRNA aminoacylation, Phe                                                            | 1         |

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| Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)                             | 1         |
| Universal GTPases                                                                 | 5         |
| GTPase and tRNA-U34 5-formylation enzyme TrmE                                     | 1         |
| GTP-binding protein EngA                                                          | 1         |
| GTP-binding protein HflX                                                          | 1         |
| Probable GTPase related to EngC                                                   | 1         |
| Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1)                     | 1         |
| <b>Protein degradation</b>                                                        | <b>13</b> |
| Aminopeptidases (EC 3.4.11.-)                                                     | 2         |
| Membrane alanine aminopeptidase N (EC 3.4.11.2)                                   | 1         |
| Xaa-Pro aminopeptidase (EC 3.4.11.9)                                              | 1         |
| Metalloprotease (EC 3.4.17.-)                                                     | 1         |
| D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)                                 | 1         |
| Proteasome bacterial                                                              | 2         |
| ATP-dependent protease La (EC 3.4.21.53) Type I                                   | 1         |
| ATP-dependent protease La (EC 3.4.21.53) Type II                                  | 1         |
| Protein degradation                                                               | 1         |
| Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)                        | 1         |
| Proteolysis in bacteria, ATP-dependent                                            | 5         |
| ATP-dependent Clp protease ATP-binding subunit ClpA                               | 1         |
| ATP-dependent protease La (EC 3.4.21.53)                                          | 1         |
| ATP-dependent protease La (EC 3.4.21.53) Type I                                   | 1         |
| ATP-dependent protease La (EC 3.4.21.53) Type II                                  | 1         |
| ClpB protein                                                                      | 1         |
| Putative TldE-TldD proteolytic complex                                            | 2         |
| TldE/PmbA family protein, Actinobacterial subgroup                                | 1         |
| TldE/PmbA protein, part of proposed TldE/TldD proteolytic complex (PMID 12029038) | 1         |
| <b>Protein folding</b>                                                            | <b>5</b>  |

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| GroEL GroES                                                                                                | 1         |
| Heat shock protein 60 family chaperone GroEL                                                               | 1         |
| Peptidyl-prolyl cis-trans isomerase                                                                        | 1         |
| Peptidyl-prolyl cis-trans isomerase ppiD (EC 5.2.1.8)                                                      | 1         |
| Periplasmic disulfide interchange                                                                          | 2         |
| Cytochrome c-type biogenesis protein CcdA (DsbD analog)                                                    | 1         |
| Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)                        | 1         |
| Protein chaperones                                                                                         | 1         |
| ClpB protein                                                                                               | 1         |
| <b>Protein processing and modification</b>                                                                 | <b>5</b>  |
| N-linked Glycosylation in Bacteria                                                                         | 1         |
| UDP-glucose 4-epimerase (EC 5.1.3.2)                                                                       | 1         |
| Peptide methionine sulfoxide reductase                                                                     | 1         |
| Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12)                                                  | 1         |
| Protein Acetylation and Deacetylation in Bacteria                                                          | 1         |
| Acetyl-coenzyme A synthetase (EC 6.2.1.1)                                                                  | 1         |
| Ribosomal protein S12p Asp methylthiotransferase                                                           | 1         |
| SSU ribosomal protein S12p (S23e)                                                                          | 1         |
| Signal peptidase                                                                                           | 1         |
| Signal peptidase I (EC 3.4.21.89)                                                                          | 1         |
| <b>Selenoproteins</b>                                                                                      | <b>1</b>  |
| Glycine reductase, sarcosine reductase and betaine reductase                                               | 1         |
| Thioredoxin reductase (EC 1.8.1.9)                                                                         | 1         |
| <b>Regulation and Cell signaling</b>                                                                       | <b>13</b> |
| <b>cAMP signaling in bacteria</b>                                                                          | <b>3</b>  |
| Adenylate cyclase (EC 4.6.1.1)                                                                             | 1         |
| Adenylate cyclase (EC 4.6.1.1)                                                                             | 1         |
| cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | 1         |

|                                                                                                            |          |
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| cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases | 1        |
| Predicted signal-transduction protein containing cAMP-binding and CBS domains                              | 1        |
| Predicted signal-transduction protein containing cAMP-binding and CBS domains                              | 1        |
| <b>Cell envelope-associated LytR-CpsA-Psr transcriptional attenuators</b>                                  | <b>1</b> |
| Cell envelope-associated transcriptional attenuator LytR-CpsA-Psr, subfamily F2 (as in PMID19099556)       | 1        |
| Cell envelope-associated transcriptional attenuator LytR-CpsA-Psr, subfamily F2 (as in PMID19099556)       | 1        |
| <b>Oxygen and light sensor PpaA-PpsR</b>                                                                   | <b>1</b> |
| Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-)                                            | 1        |
| Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-)                                            | 1        |
| <b>Programmed Cell Death and Toxin-antitoxin Systems</b>                                                   | <b>2</b> |
| Murein hydrolase regulation and cell death                                                                 | 1        |
| Antiholin-like protein LrgA                                                                                | 1        |
| Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) systems                                         | 1        |
| Death on curing protein, Doc toxin                                                                         | 1        |
| <b>Quorum sensing and biofilm formation</b>                                                                | <b>2</b> |
| Biofilm Adhesin Biosynthesis                                                                               | 1        |
| Biofilm PGA synthesis deacetylase PgaB (EC 3.-)                                                            | 1        |
| Quorum Sensing: Autoinducer-2 Synthesis                                                                    | 1        |
| S-adenosylmethionine synthetase (EC 2.5.1.6)                                                               | 1        |
| <b>Sex pheromones in <i>Enterococcus faecalis</i> and other Firmicutes</b>                                 | <b>1</b> |
| Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)                 | 1        |
| Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)                 | 1        |
| <b>Zinc regulated enzymes</b>                                                                              | <b>3</b> |
| Dihydroorotase (EC 3.5.2.3)                                                                                | 1        |
| Dihydroorotase (EC 3.5.2.3)                                                                                | 1        |
| N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)                                                           | 1        |
| N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)                                                           | 1        |
| Porphobilinogen synthase (EC 4.2.1.24)                                                                     | 1        |

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| Porphobilinogen synthase (EC 4.2.1.24)                                                             | 1         |
| <b>Respiration</b>                                                                                 | <b>21</b> |
| <b>ATP synthases</b>                                                                               | <b>2</b>  |
| F0F1-type ATP synthase                                                                             | 2         |
| ATP synthase A chain (EC 3.6.3.14)                                                                 | 1         |
| ATP synthase delta chain (EC 3.6.3.14)                                                             | 1         |
| <b>Biogenesis of c-type cytochromes</b>                                                            | <b>4</b>  |
| Cytochrome c heme lyase subunit CcmF                                                               | 1         |
| Cytochrome c heme lyase subunit CcmF                                                               | 1         |
| Cytochrome c-type biogenesis protein CcdA (DsbD analog)                                            | 1         |
| Cytochrome c-type biogenesis protein CcdA (DsbD analog)                                            | 1         |
| Cytochrome c-type biogenesis protein CcsA/ResC                                                     | 1         |
| Cytochrome c-type biogenesis protein CcsA/ResC                                                     | 1         |
| Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)                | 1         |
| Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)                | 1         |
| <b>Electron accepting reactions</b>                                                                | <b>5</b>  |
| Anaerobic respiratory reductases                                                                   | 2         |
| Anaerobic dehydrogenases, typically selenocysteine-containing                                      | 1         |
| Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)                              | 1         |
| Cytochrome c oxidases d@O copy                                                                     | 1         |
| Transport ATP-binding protein CydC                                                                 | 1         |
| Terminal cytochrome d ubiquinol oxidases                                                           | 1         |
| Transport ATP-binding protein CydC                                                                 | 1         |
| Terminal cytochrome oxidases                                                                       | 1         |
| Transport ATP-binding protein CydC                                                                 | 1         |
| <b>Electron donating reactions</b>                                                                 | <b>6</b>  |
| Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes | 2         |
| Electron transport complex protein RnfB                                                            | 1         |

|                                                                                   |           |
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| Na(+)-translocating NADH-quinone reductase subunit A (EC 1.6.5.-)                 | 1         |
| Respiratory Complex I                                                             | 2         |
| NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3)                               | 1         |
| NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)                               | 1         |
| Respiratory dehydrogenases 1                                                      | 2         |
| Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                           | 1         |
| Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                                   | 1         |
| <b>Formate hydrogenase</b>                                                        | <b>1</b>  |
| formate dehydrogenase formation protein FdhE                                      | 1         |
| formate dehydrogenase formation protein FdhE                                      | 1         |
| <b>Sodium Ion-Coupled Energetics</b>                                              | <b>1</b>  |
| Na <sup>+</sup> translocating decarboxylases and related biotin-dependent enzymes | 1         |
| Oxaloacetate decarboxylase beta chain (EC 4.1.1.3)                                | 1         |
| <b>Soluble cytochromes and functionally related electron carriers</b>             | <b>2</b>  |
| Cytochrome c551/c552                                                              | 1         |
| Cytochrome c551/c552                                                              | 1         |
| soluble [2Fe-2S] ferredoxin                                                       | 1         |
| soluble [2Fe-2S] ferredoxin                                                       | 1         |
| <b>RNA Metabolism</b>                                                             | <b>45</b> |
| <b>RNA processing and modification</b>                                            | <b>40</b> |
| 16S rRNA modification within P site of ribosome                                   | 2         |
| Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)              | 1         |
| Penicillin-binding protein 2 (PBP-2)                                              | 1         |
| ATP-dependent RNA helicases, bacterial                                            | 1         |
| ATP-dependent RNA helicase Bcep18194_A5658                                        | 1         |
| mcm5s2U biosynthesis in tRNA                                                      | 1         |
| histone acetyltransferase, ELP3 family                                            | 1         |
| mnm5U34 biosynthesis bacteria                                                     | 2         |

|                                                                     |   |
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| GTPase and tRNA-U34 5-formylation enzyme TrmE                       | 1 |
| tRNA 5-methylaminomethyl-2-thiouridine synthase Tusa                | 1 |
| Polyadenylation bacterial                                           | 2 |
| Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)              | 1 |
| tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25)             | 1 |
| Queuosine-Archaeosine Biosynthesis                                  | 4 |
| glutamyl-Q-tRNA synthetase                                          | 1 |
| Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)                    | 1 |
| Permease of the drug/metabolite transporter (DMT) superfamily       | 1 |
| S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-) | 1 |
| Ribonuclease H                                                      | 1 |
| hypothetical protein ssl1918                                        | 1 |
| RNA processing and degradation, bacterial                           | 3 |
| 3'-to-5' exoribonuclease RNase R                                    | 1 |
| Exoribonuclease II (EC 3.1.13.1)                                    | 1 |
| Ribonuclease E inhibitor RraA                                       | 1 |
| RNA pseudouridine syntheses                                         | 3 |
| Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)      | 1 |
| Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)      | 1 |
| tRNA pseudouridine synthase A (EC 4.2.1.70)                         | 1 |
| rRNA modification Bacteria                                          | 2 |
| Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)      | 1 |
| Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70)      | 1 |
| tRNA modification Archaea                                           | 1 |
| tRNA pseudouridine synthase A (EC 4.2.1.70)                         | 1 |
| tRNA modification Bacteria                                          | 7 |
| glutamyl-Q-tRNA synthetase                                          | 1 |
| GTPase and tRNA-U34 5-formylation enzyme TrmE                       | 1 |

|                                                                             |          |
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| Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)              | 1        |
| S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-)         | 1        |
| tRNA 5-methylaminomethyl-2-thiouridine synthase Tusa                        | 1        |
| tRNA pseudouridine synthase A (EC 4.2.1.70)                                 | 1        |
| tRNA(Ile)-lysidine synthetase                                               | 1        |
| tRNA modification yeast cytoplasmic                                         | 3        |
| histone acetyltransferase, ELP3 family                                      | 1        |
| tRNA N2,N2-dimethyl(Guanine26-N2)-methyltransferase (EC 2.1.1.32)           | 1        |
| tRNA pseudouridine synthase A (EC 4.2.1.70)                                 | 1        |
| tRNA modification yeast mitochondrial                                       | 3        |
| GTPase and tRNA-U34 5-formylation enzyme TrmE                               | 1        |
| tRNA N2,N2-dimethyl(Guanine26-N2)-methyltransferase (EC 2.1.1.32)           | 1        |
| tRNA pseudouridine synthase A (EC 4.2.1.70)                                 | 1        |
| tRNA nucleotidyltransferase                                                 | 1        |
| tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25)                     | 1        |
| tRNA processing                                                             | 2        |
| tRNA pseudouridine synthase A (EC 4.2.1.70)                                 | 1        |
| tRNA(Ile)-lysidine synthetase                                               | 1        |
| Wyeosine-MimG Biosynthesis                                                  | 1        |
| Thioredoxin reductase (EC 1.8.1.9)                                          | 1        |
| YrdC-YciO                                                                   | 1        |
| Inactive homolog of metal-dependent proteases, putative molecular chaperone | 1        |
| <b>Transcription</b>                                                        | <b>5</b> |
| RNA polymerase bacterial                                                    | 2        |
| DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)                       | 1        |
| DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)                      | 1        |
| Transcription factors bacterial                                             | 2        |
| Transcription elongation factor GreB                                        | 1        |

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| Transcription-repair coupling factor                                               | 1         |
| Transcription initiation, bacterial sigma factors                                  | 1         |
| RNA polymerase sigma factor RpoH-related protein                                   | 1         |
| <b>Secondary Metabolism</b>                                                        | <b>3</b>  |
| <b>Bacterial cytostatics, differentiation factors and antibiotics</b>              | <b>1</b>  |
| Paerucumarin Biosynthesis                                                          | 1         |
| PvcA protein, related to known isonitrile synthases                                | 1         |
| <b>Biologically active compounds in metazoan cell defence and differentiation</b>  | <b>1</b>  |
| Steroid sulfates                                                                   | 1         |
| Arylsulfatase (EC 3.1.6.1)                                                         | 1         |
| <b>Plant Hormones</b>                                                              | <b>1</b>  |
| Auxin biosynthesis                                                                 | 1         |
| Tryptophan synthase alpha chain (EC 4.2.1.20)                                      | 1         |
| <b>Stress Response</b>                                                             | <b>22</b> |
| <b>Bacterial hemoglobins</b>                                                       | <b>1</b>  |
| diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) | 1         |
| diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) | 1         |
| <b>Detoxification</b>                                                              | <b>4</b>  |
| Housecleaning nucleoside triphosphate pyrophosphatases                             | 1         |
| 5'-nucleotidase YjjG (EC 3.1.3.5)                                                  | 1         |
| Nucleoside triphosphate pyrophosphohydrolase MazG                                  | 1         |
| Nucleoside triphosphate pyrophosphohydrolase MazG                                  | 1         |
| Nudix proteins (nucleoside triphosphate hydrolases)                                | 2         |
| Adenosine (5')-pentaphospho-(5'')-adenosine pyrophosphohydrolase (EC 3.6.1.-)      | 1         |
| ADP-ribose pyrophosphatase (EC 3.6.1.13)                                           | 1         |
| <b>Hfl operon</b>                                                                  | <b>1</b>  |
| GTP-binding protein HflX                                                           | 1         |
| GTP-binding protein HflX                                                           | 1         |

|                                                                      |           |
|----------------------------------------------------------------------|-----------|
| <b>Osmotic stress</b>                                                | <b>3</b>  |
| Choline and Betaine Uptake and Betaine Biosynthesis                  | 1         |
| High-affinity choline uptake protein BetT                            | 1         |
| Synthesis of osmoregulated periplasmic glucans                       | 2         |
| Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)                         | 1         |
| Glucans biosynthesis protein G precursor                             | 1         |
| <b>Oxidative stress</b>                                              | <b>11</b> |
| Glutathione: Biosynthesis and gamma-glutamyl cycle                   | 1         |
| Gamma-glutamyltranspeptidase (EC 2.3.2.2)                            | 1         |
| Glutathione: Non-redox reactions                                     | 1         |
| Lactoylglutathione lyase (EC 4.4.1.5)                                | 1         |
| Oxidative stress                                                     | 6         |
| Catalase (EC 1.11.1.6)                                               | 1         |
| NnrS protein involved in response to NO                              | 1         |
| Organic hydroperoxide resistance transcriptional regulator           | 1         |
| Paraquat-inducible protein B                                         | 1         |
| Peroxide stress regulator PerR, FUR family                           | 1         |
| Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-)      | 1         |
| Protection from Reactive Oxygen Species                              | 2         |
| Catalase (EC 1.11.1.6)                                               | 1         |
| Cytochrome c551 peroxidase (EC 1.11.1.5)                             | 1         |
| Redox-dependent regulation of nucleus processes                      | 1         |
| NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) | 1         |
| <b>SigmaB stress response regulation</b>                             | <b>1</b>  |
| Serine phosphatase RsbU, regulator of sigma subunit                  | 1         |
| Serine phosphatase RsbU, regulator of sigma subunit                  | 1         |
| <b>Universal stress protein family</b>                               | <b>1</b>  |
| Universal stress protein E                                           | 1         |

|                                                         |           |
|---------------------------------------------------------|-----------|
| Universal stress protein E                              | 1         |
| <b>Sulfur Metabolism</b>                                | <b>12</b> |
| <b>Galactosylceramide and Sulfatide metabolism</b>      | <b>3</b>  |
| Alpha-galactosidase (EC 3.2.1.22)                       | 1         |
| Alpha-galactosidase (EC 3.2.1.22)                       | 1         |
| Arylsulfatase (EC 3.1.6.1)                              | 1         |
| Arylsulfatase (EC 3.1.6.1)                              | 1         |
| Beta-galactosidase (EC 3.2.1.23)                        | 1         |
| Beta-galactosidase (EC 3.2.1.23)                        | 1         |
| <b>Inorganic sulfur assimilation</b>                    | <b>1</b>  |
| Inorganic Sulfur Assimilation                           | 1         |
| 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7)        | 1         |
| <b>Organic sulfur assimilation</b>                      | <b>6</b>  |
| Alkanesulfonate assimilation                            | 2         |
| Alkanesulfonates transport system permease protein      | 1         |
| Arylsulfatase (EC 3.1.6.1)                              | 1         |
| Alkanesulfonates Utilization                            | 1         |
| Alkanesulfonates transport system permease protein      | 1         |
| L-Cystine Uptake and Metabolism                         | 1         |
| Cystathionine beta-lyase (EC 4.4.1.8)                   | 1         |
| Taurine Utilization                                     | 1         |
| Taurine transport system permease protein TauC          | 1         |
| Utilization of glutathione as a sulphur source          | 1         |
| Gamma-glutamyltranspeptidase (EC 2.3.2.2)               | 1         |
| <b>Sulfur oxidation</b>                                 | <b>1</b>  |
| Cytochrome c-type biogenesis protein CcdA (DsbD analog) | 1         |
| Cytochrome c-type biogenesis protein CcdA (DsbD analog) | 1         |
| <b>Thioredoxin-disulfide reductase</b>                  | <b>1</b>  |

|                                                                                      |           |
|--------------------------------------------------------------------------------------|-----------|
| Thioredoxin reductase (EC 1.8.1.9)                                                   | 1         |
| Thioredoxin reductase (EC 1.8.1.9)                                                   | 1         |
| <b>Virulence, Disease and Defense</b>                                                | <b>34</b> |
| <b>Bacterial cyanide production and tolerance mechanisms</b>                         | <b>1</b>  |
| formate dehydrogenase formation protein FdhE                                         | 1         |
| formate dehydrogenase formation protein FdhE                                         | 1         |
| <b>Bacteriocins, ribosomally synthesized antibacterial peptides</b>                  | <b>1</b>  |
| Colicin V and Bacteriocin Production Cluster                                         | 1         |
| tRNA pseudouridine synthase A (EC 4.2.1.70)                                          | 1         |
| <b>C jejuni colonization of chick caeca</b>                                          | <b>5</b>  |
| Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | 1         |
| Branched-chain amino acid ABC transporter, amino acid-binding protein (TC 3.A.1.4.1) | 1         |
| Flagellar hook-associated protein FlgK                                               | 1         |
| Flagellar hook-associated protein FlgK                                               | 1         |
| Flagellar motor rotation protein MotA                                                | 1         |
| Flagellar motor rotation protein MotA                                                | 1         |
| Flagellar motor rotation protein MotB                                                | 1         |
| Flagellar motor rotation protein MotB                                                | 1         |
| Predicted signal transduction protein                                                | 1         |
| Predicted signal transduction protein                                                | 1         |
| <b>Fimbriae of the Chaperone/Usher Assembly Pathway</b>                              | <b>1</b>  |
| &#963;-Fimbriae                                                                      | 1         |
| Sigma-fimbriae usher protein                                                         | 1         |
| <b>Invasion and intracellular resistance</b>                                         | <b>1</b>  |
| Listeria surface proteins: Internalin-like proteins                                  | 1         |
| internalin, putative                                                                 | 1         |
| <b>Resistance to antibiotics and toxic compounds</b>                                 | <b>21</b> |
| Aminoglycoside adenylyltransferases                                                  | 1         |

|                                                                                                |   |
|------------------------------------------------------------------------------------------------|---|
| Spectinomycin 9-O-adenylyltransferase                                                          | 1 |
| Arsenic resistance                                                                             | 1 |
| Arsenic efflux pump protein                                                                    | 1 |
| Cobalt-zinc-cadmium resistance                                                                 | 4 |
| Cobalt-zinc-cadmium resistance protein CzcD                                                    | 1 |
| Heavy metal RND efflux outer membrane protein, CzcC family                                     | 1 |
| Probable Co/Zn/Cd efflux system membrane fusion protein                                        | 1 |
| Transcriptional regulator, MerR family                                                         | 1 |
| Copper homeostasis                                                                             | 2 |
| Cytochrome c heme lyase subunit CcmF                                                           | 1 |
| Multicopper oxidase                                                                            | 1 |
| Copper homeostasis: copper tolerance                                                           | 1 |
| Membrane protein, suppressor for copper-sensitivity ScsB                                       | 1 |
| Methicillin resistance in Staphylococci                                                        | 1 |
| Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-)               | 1 |
| Multidrug efflux pump in Campylobacter jejuni (CmeABC operon)                                  | 2 |
| RND efflux system, inner membrane transporter CmeB                                             | 1 |
| RND efflux system, outer membrane lipoprotein CmeC                                             | 1 |
| Multidrug Resistance Efflux Pumps                                                              | 4 |
| Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps | 1 |
| RND efflux system, inner membrane transporter CmeB                                             | 1 |
| RND efflux system, outer membrane lipoprotein CmeC                                             | 1 |
| Type I secretion outer membrane protein, TolC precursor                                        | 1 |
| Multidrug Resistance, Tripartite Systems Found in Gram Negative Bacteria                       | 1 |
| Outer membrane component of tripartite multidrug resistance system                             | 1 |
| Resistance to fluoroquinolones                                                                 | 3 |
| DNA gyrase subunit A (EC 5.99.1.3)                                                             | 1 |
| DNA gyrase subunit B (EC 5.99.1.3)                                                             | 1 |

|                                                                          |            |
|--------------------------------------------------------------------------|------------|
| Topoisomerase IV subunit A (EC 5.99.1.-)                                 | 1          |
| Zinc resistance                                                          | 1          |
| Sensor protein of zinc sigma-54-dependent two-component system           | 1          |
| <b>Streptococcus agalactiae virulome</b>                                 | <b>1</b>   |
| UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)                        | 1          |
| UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)                        | 1          |
| <b>Type III, Type IV, Type VI, ESAT secretion systems</b>                | <b>3</b>   |
| Type 4 secretion and conjugative transfer                                | 3          |
| Conjugative transfer protein TrbB                                        | 1          |
| Conjugative transfer protein TrbI                                        | 1          |
| IncF plasmid conjugative transfer DNA-nicking and unwinding protein Tral | 1          |
| <b>Total</b>                                                             | <b>816</b> |