**Table S2**

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| --- | --- |
|   | **Mg Rast identification** |
|  | **Unprotected** | **Protected** |
| **Subsystems** | **Hierarchy 3** | **# sequences** | **Contribution (%)** | **Hierarchy 3** | **# sequences** |
| **Carbohydrates** | Serine-glyoxylate cycle | 1171 | 11.80 | Serine-glyoxylate cycle | 1661 | 10.46 |
| (87, 89) | Pyruvate metabolism II | 701 | 7.07 | Pyruvate metabolism II | 919 | 5.79 |
|   | TCA Cycle | 480 | 4.84 | Maltose and Maltodextrin Utilization | 795 | 5.01 |
|   | Butanol Biosynthesis | 471 | 4.75 | Butanol Biosynthesis | 771 | 4.86 |
|   | Maltose and Maltodextrin Utilization | 459 | 4.63 | Entner-Doudoroff Pathway | 769 | 4.84 |
|   | Entner-Doudoroff Pathway | 435 | 4.39 | TCA Cycle | 613 | 3.86 |
|   | Dehydrogenase complexes | 403 | 4.06 | Dehydrogenase complexes | 581 | 3.66 |
|   | Pyruvate metabolism I:  | 375 | 3.78 | Sucrose Metabolism | 542 | 3.41 |
|   | Acetyl-CoA fermentation to Butyrate | 346 | 3.49 | Pyruvate metabolism  | 492 | 3.10 |
|   | Sucrose Metabolism | 327 | 3.30 | D-gluconate and ketogluconates metabolism | 456 | 2.87 |
| **Nitrogen** | Ammonia assimilation | 215 | 36.50 | Ammonia assimilation | 327 | 34.49 |
| (9,8) | Allantoin degradation | 188 | 31.92 | Nitrate and nitrite ammonification | 249 | 26.27 |
|  | Nitrate and nitrite ammonification | 103 | 17.49 | Allantoin degradation | 231 | 24.37 |
|  | Nitric oxide synthase | 58 | 9.85 | Nitric oxide synthase | 77 | 8.12 |
|  | Denitrification | 11 | 1.87 | Denitrification | 28 | 2.95 |
|  | Cyanate hydrolysis | 6 | 1.02 | Cyanate hydrolysis | 27 | 2.85 |
|  | Nitrosative stress | 5 | 0.85 | Nitrogen fixation | 7 | 0.74 |
|  | Nitrogen fixation | 2 | 0.34 | Nitrosative stress | 2 | 0.21 |
|   | De Novo Pyrimidine Synthesis | 1 | 0.17 |   |   |   |
| **Phosphorous** | Phosphate metabolism | 1200 | 91.39 | Phosphate metabolism | 1879 | 92.61 |
| (6, 8) | Phosphate transporter and control of PHO regulon | 40 | 3.05 | Alkylphosphonate utilization | 46 | 2.27 |
|   | Alkylphosphonate utilization | 33 | 2.51 | Phosphate transporter and control of PHO regulon | 33 | 1.63 |
|   | P uptake (cyanobacteria) | 14 | 1.07 | P uptake (cyanobacteria) | 32 | 1.58 |
|   | Phosphoenolpyruvate phosphomutase | 13 | 0.99 | Phosphonate metabolism | 24 | 1.18 |
|   | Phosphonate metabolism | 13 | 0.99 | Phosphoenolpyruvate phosphomutase | 13 | 0.64 |
|   |   |   |   | Lipid A modifications | 1 | 0.05 |
|   |   |   |   | NAD and NADP cofactor biosynthesis global | 1 | 0.05 |
| **Virulence** | Ton and Tol transport systems | 1241 | 0.99 | Ton and Tol transport systems | 2791 | 32.31 |
| (73, 70) | Acriflavin resistance cluster | 400 | 30.03 | Cobalt-zinc-cadmium resistance | 924 | 10.70 |
|  | Cobalt-zinc-cadmium resistance | 379 | 9.68 | Acriflavin resistance cluster | 762 | 8.82 |
|  | Resistance to fluoroquinolones | 343 | 9.17 | Multidrug Resistance Efflux Pumps | 722 | 8.36 |
|  | Multidrug Resistance Efflux Pumps | 290 | 8.30 | Resistance to fluoroquinolones | 477 | 5.52 |
|  | Transport of Iron | 205 | 7.02 | Transport of Iron | 380 | 4.40 |
|  | Beta-lactamase | 188 | 4.96 | Beta-lactamase | 346 | 4.01 |
|  | Type IV pilus | 161 | 4.55 | Type IV pilus | 320 | 3.70 |
|  | Staphylococcal pathogenicity islands SaPI | 97 | 3.90 | Staphylococcal pathogenicity islands SaPI | 173 | 2.00 |
|   | Pyoverdine biosynthesis new | 87 | 2.35 | Mannose-sensitive hemagglutinin type 4 pilus | 146 | 1.69 |
| **Stress response** | Oxidative stress | 317 | 2.11 | Copper homeostasis | 596 | 18.70 |
| (29, 30) | Copper homeostasis | 274 | 19.18 | Oxidative stress | 590 | 18.51 |
|   | Glutathione Redox Metabolism | 182 | 16.58 | Glutathione Redox Metabolism | 418 | 13.12 |
|   | Heat shock dnaK gene cluster extended | 158 | 11.01 | Heat shock dnaK gene cluster extended | 292 | 9.16 |
|   | Hfl operon | 127 | 9.56 | Periplasmic Stress Response | 202 | 6.34 |
|   | Periplasmic Stress Response | 118 | 7.68 | Acid resistance mechanisms | 180 | 5.65 |
|   | Flavohaemoglobin | 76 | 7.14 | Flavohaemoglobin | 137 | 4.30 |
|   | Acid resistance mechanisms | 64 | 4.60 | Hfl operon | 137 | 4.30 |
|   | SigmaB stress responce regulation | 44 | 3.87 | SigmaB stress responce regulation | 104 | 3.26 |
|   | Dimethylarginine metabolism | 37 | 2.66 | Carbon Starvation | 97 | 3.04 |
| **Photosynthesis** | Photosystem II | 117 | 40.77 | Photosystem II | 480 | 42.40 |
| (6, 6) | Proteorhodopsin | 72 | 25.09 | Phycobilisome | 296 | 26.15 |
|  | Photosystem I | 56 | 19.51 | Photosystem I | 259 | 22.88 |
|  | Phycobilisome | 29 | 10.10 | Proteorhodopsin | 78 | 6.89 |
|  | Photosystem II-type photosynthetic reaction center | 11 | 3.83 | Photosystem II-type photosynthetic reaction center | 18 | 1.59 |
|   | Bacterial light-harvesting proteins | 2 | 0.70 | Bacterial light-harvesting proteins | 1 | 0.09 |