

TABLE S2. *P. alcaliphila* 34 statistically significant ( $p < 0.05$ ) genes exhibiting  $\log_2FC \geq 1.0$  or  $\log_2FC \leq -1.0$  at least at one time points during Cr(VI) stress exposure

| peg ID                      | Subsystem                                                   | Role                                                                                     | Mean (K <sub>2</sub> CrO <sub>4</sub> /control) <sup>a</sup> at time <i>t</i> (min) <sup>b</sup> |         |         |         |          |
|-----------------------------|-------------------------------------------------------------|------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------|---------|---------|---------|----------|
|                             |                                                             |                                                                                          | Cr5min                                                                                           | Cr30min | Cr60min | Cr90min | Cr120min |
| Amino Acids and Derivatives |                                                             |                                                                                          |                                                                                                  |         |         |         |          |
| 23630.peg.444               | Alanine biosynthesis                                        | Iron-sulfur cluster regulator IscR                                                       |                                                                                                  | 0.6     |         | 1.1     |          |
| 23630.peg.439               | Alanine biosynthesis                                        | Chaperone protein HscA                                                                   |                                                                                                  |         |         | 1.0     |          |
| 23630.peg.2352              | Alanine biosynthesis                                        | Alanine racemase (EC 5.1.1.1)                                                            | -0.7                                                                                             |         |         | -1.1    |          |
| 23630.peg.1075              | Arginine and Ornithine Degradation                          | Agmatinase (EC 3.5.3.11)                                                                 | -0.9                                                                                             | -1.2    | 1.0     |         |          |
| 23630.peg.1669              | Arginine and Ornithine Degradation                          | Ornithine cyclodeaminase (EC 4.3.1.12)                                                   | -1.4                                                                                             | -1.5    |         |         |          |
| 23630.peg.3649              | Arginine Biosynthesis extended                              | Predicted arginine uptake transporter                                                    |                                                                                                  |         |         |         | -1.4     |
| 23630.peg.4721              | Aromatic amino acid interconversions with aryl acids        | Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits                        |                                                                                                  |         | 1.0     |         | 0.7      |
| 23630.peg.4722              | Branched-Chain Amino Acid Biosynthesis                      | Leucine dehydrogenase (EC 1.4.1.9)                                                       | 1.1                                                                                              |         |         |         |          |
| 23630.peg.4374              | Cyanophycin Metabolism                                      | Secreted cyanophycinase CphE (EC 3.4.15.6)                                               |                                                                                                  | -1.3    |         |         |          |
| 23630.peg.1370              | Cysteine Biosynthesis                                       | Sulfate and thiosulfate binding protein CysP                                             | 1.8                                                                                              | 1.7     |         | 1.6     | 1.6      |
| 23630.peg.3551              | Cysteine Biosynthesis                                       | Cys regulon transcriptional activator CysB                                               | 0.9                                                                                              | 1.1     | 0.7     |         | 1.4      |
| 23630.peg.2992              | Cysteine Biosynthesis                                       | Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)                             | 1.1                                                                                              | 1.1     |         | 0.9     | 0.7      |
| 23630.peg.2635              | Cysteine Biosynthesis                                       | Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)                                       | 1.4                                                                                              |         |         |         | 0.6      |
| 23630.peg.1697              | Cysteine Biosynthesis                                       | Sulfate permease                                                                         | -1.5                                                                                             | -1.0    | 1.0     |         | -1.1     |
| 23630.peg.1373              | Cysteine Biosynthesis                                       | Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)                    |                                                                                                  |         |         | 1.1     |          |
| 23630.peg.1372              | Cysteine Biosynthesis                                       | Sulfate transport system permease protein CysW                                           |                                                                                                  |         | -0.5    | 1.0     |          |
| 23630.peg.1753              | Glutamate and Aspartate uptake in Bacteria                  | Sodium/glutamate symport protein                                                         | 0.8                                                                                              | 1.0     | 1.6     | 1.4     | 0.6      |
| 23630.peg.1134              | Glutamate and Aspartate uptake in Bacteria                  | Glutamate Aspartate transport system permease protein GltK (TC 3.A.1.3.4)                |                                                                                                  | 0.5     |         |         | -1.2     |
| 23630.peg.1133              | Glutamate and Aspartate uptake in Bacteria                  | Glutamate Aspartate transport system permease protein GltJ (TC 3.A.1.3.4)                |                                                                                                  | -1.2    |         |         |          |
| 23630.peg.3683              | Glutamate dehydrogenases                                    | NADP-specific glutamate dehydrogenase (EC 1.4.1.4)                                       | 1.0                                                                                              |         |         |         | 0.7      |
| 23630.peg.2213              | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] small chain (EC 1.4.1.13)                                     | -1.0                                                                                             |         | -0.6    |         | -1.0     |
| 23630.peg.1752              | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate ammonia-lyase (EC 4.3.1.1)                                                     |                                                                                                  |         |         | 1.8     |          |
| 23630.peg.4738              | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | glutamine synthetase family protein                                                      |                                                                                                  | -0.7    | -0.7    | -1.1    |          |
| 23630.peg.754               | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)  |                                                                                                  |         |         | -1.2    |          |
| 23630.peg.2023              | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | glutamine synthetase family protein                                                      | 1.0                                                                                              |         |         |         |          |
| 23630.peg.1566              | Glycine and Serine Utilization                              | L-serine dehydratase (EC 4.3.1.17)                                                       |                                                                                                  |         | 1.0     |         | 0.5      |
| 23630.peg.4141              | Glycine and Serine Utilization                              | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2) |                                                                                                  |         |         | -1.9    |          |
| 23630.peg.2630              | Histidine Biosynthesis                                      | Histidinol-phosphate aminotransferase (EC 2.6.1.9)                                       | -1.2                                                                                             |         |         | -1.4    |          |
| 23630.peg.1088              | Histidine Degradation                                       | Conserved hypothetical protein (perhaps related to histidine degradation)                | -1.6                                                                                             |         |         |         | 0.6      |
| 23630.peg.1087              | Histidine Degradation                                       | Imidazolonepropionase (EC 3.5.2.7)                                                       |                                                                                                  | -1.3    |         |         |          |
| 23630.peg.2880              | HMG CoA Synthesis                                           | Methylglutaconyl-CoA hydratase (EC 4.2.1.18)                                             |                                                                                                  | 1.5     |         | 1.0     |          |
| 23630.peg.2878              | HMG CoA Synthesis                                           | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)                                             |                                                                                                  | 1.0     | -0.5    | 0.9     |          |
| 23630.peg.2884              | HMG CoA Synthesis                                           | Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family     |                                                                                                  | 0.6     | 1.2     |         |          |
| 23630.peg.424               | Leucine Biosynthesis                                        | 2-isopropylmalate synthase (EC 2.3.3.13)                                                 |                                                                                                  | 1.0     |         |         |          |
| 23630.peg.4332              | Leucine Degradation and HMG-CoA Metabolism                  | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)                    |                                                                                                  |         |         | 1.2     |          |
| 23630.peg.4333              | Leucine Degradation and HMG-CoA Metabolism                  | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5)                    |                                                                                                  | 0.7     |         | 1.0     |          |
| 23630.peg.2879              | Leucine Degradation and HMG-CoA Metabolism                  | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)                    |                                                                                                  | 1.0     |         | 0.3     |          |
| 23630.peg.1352              | Lysine degradation                                          | Outer membrane porin, OprD family                                                        |                                                                                                  | 1.1     |         |         | 1.0      |
| 23630.peg.1034              | Lysine degradation                                          | Outer membrane porin, OprD family                                                        | -1.7                                                                                             |         |         |         | -1.5     |

|                      |                                                             |                                                                                                                         |      |      |      |      |      |
|----------------------|-------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.1022       | Lysine degradation                                          | Outer membrane porin, OprD family                                                                                       | -2.3 | -1.6 | -1.1 |      | -1.7 |
| 23630.peg.2828       | Methionine Biosynthesis                                     | Methionine ABC transporter substrate-binding protein                                                                    | 2.0  | 1.7  | 1.1  | 1.5  | 2.0  |
| 23630.peg.1528       | Methionine Biosynthesis                                     | Methionine ABC transporter permease protein                                                                             | 1.0  | 1.1  | 0.6  |      | 1.3  |
| 23630.peg.1527       | Methionine Biosynthesis                                     | Methionine ABC transporter ATP-binding protein                                                                          | 0.8  | 1.2  |      | 1.5  | 1.0  |
| 23630.peg.2842       | Methionine Biosynthesis                                     | Methionine ABC transporter permease protein                                                                             | 1.1  | 0.7  |      |      |      |
| 23630.peg.2027       | Polyamine Metabolism                                        | Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)                                              | 1.1  |      |      |      | 0.7  |
| 23630.peg.1076       | Polyamine Metabolism                                        | Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)                                              | -1.0 |      | 1.1  |      |      |
| 23630.peg.2549       | Polyamine Metabolism                                        | Ornithine decarboxylase (EC 4.1.1.17) / Arginine decarboxylase (EC 4.1.1.19)                                            |      |      | 1.0  |      |      |
| 23630.peg.1215       | Polyamine Metabolism                                        | Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)                                           | 1.0  |      |      |      |      |
| 23630.peg.798        | Proline Synthesis                                           | Gamma-glutamyl phosphate reductase (EC 1.2.1.41)                                                                        | 1.0  | 0.9  |      |      | 0.7  |
| 23630.peg.1596       | Proline, 4-hydroxyproline uptake and utilization            | L-Proline/Glycine betaine transporter ProP                                                                              | -1.2 | -1.4 |      | -0.5 | -1.1 |
| 23630.peg.1905       | Putrescine utilization pathways                             | 5-aminovalerate aminotransferase (EC 2.6.1.48) / Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.6.1.19) |      |      | -1.0 |      |      |
| 23630.peg.1754       | Threonine and Homoserine Biosynthesis                       | Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)                                 | -1.0 |      | -1.5 |      |      |
| 23630.peg.755        | Threonine degradation                                       | Threonine dehydratase (EC 4.3.1.19)                                                                                     | 0.7  |      | 1.1  |      | 0.9  |
| 23630.peg.859        | Urea carboxylase and Allophanate hydrolase cluster          | Biotin carboxylase (EC 6.3.4.14)                                                                                        | 1.4  |      | -0.6 |      |      |
| 23630.peg.3071       | Urea carboxylase and Allophanate hydrolase cluster          | Biotin carboxylase (EC 6.3.4.14)                                                                                        | -1.5 |      | -0.8 |      |      |
| 23630.peg.4126       | Urea carboxylase and Allophanate hydrolase cluster          | Urea carboxylase (EC 6.3.4.6)                                                                                           |      | -1.6 |      |      |      |
| 23630.peg.2429       | Urea decomposition                                          | Urea carboxylase (EC 6.3.4.6)                                                                                           | -1.3 | -2.1 |      |      | -0.3 |
| 23630.peg.2541       | Urea decomposition                                          | Urea ABC transporter, ATPase protein UrtD                                                                               | -1.5 | -1.3 |      |      | -0.7 |
| 23630.peg.4125       | Urea decomposition                                          | Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10)                                                           |      | -1.7 |      |      | -1.0 |
| 23630.peg.2539       | Urea decomposition                                          | Urea ABC transporter, permease protein UrtB                                                                             | -2.3 | -2.8 |      |      | -1.0 |
| 23630.peg.4119       | Urea decomposition                                          | Urea carboxylase-related ABC transporter, ATPase protein                                                                | -1.0 |      |      |      | -1.3 |
| 23630.peg.2426       | Urea decomposition                                          | Urea ABC transporter, permease protein UrtB                                                                             | -1.1 | -1.2 |      |      | -1.5 |
| 23630.peg.4117       | Urea decomposition                                          | Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein                                         | -1.4 |      | 0.9  |      |      |
| 23630.peg.2540       | Urea decomposition                                          | Urea ABC transporter, permease protein UrtC                                                                             | -1.1 |      |      |      |      |
| 23630.peg.2377       | Urease subunits                                             | Urease accessory protein UreG                                                                                           | 1.0  |      | 1.5  |      | 0.8  |
| 23630.peg.2413       | Urease subunits                                             | Urease accessory protein UreD                                                                                           |      |      | 1.1  |      |      |
| 23630.peg.2378       | Urease subunits                                             | Urease accessory protein UreF                                                                                           |      | -1.6 |      |      |      |
| 23630.peg.2412       | Urease subunits                                             | Urease gamma subunit (EC 3.5.1.5)                                                                                       | 1.0  |      |      |      |      |
| <b>Carbohydrates</b> |                                                             |                                                                                                                         |      |      |      |      |      |
| 23630.peg.2153       | Acetyl-CoA fermentation to Butyrate                         | Electron transfer flavoprotein, alpha subunit                                                                           |      | -1.3 |      | -1.2 | -0.8 |
| 23630.peg.4280       | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | D-galactarate permease                                                                                                  | -1.4 | -0.6 |      |      | -1.0 |
| 23630.peg.4819       | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)                                                                       |      |      | -1.3 | -0.8 | -1.1 |
| 23630.peg.4281       | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | Glucarate dehydratase (EC 4.2.1.40)                                                                                     |      | -0.7 | -1.0 |      |      |
| 23630.peg.1694       | D-gluconate and ketogluconates metabolism                   | Methylglyoxal reductase, acetol producing (EC 1.1.1.-) / 2,5-diketeto-D-gluconic acid reductase B (EC 1.1.1.274)        |      |      |      | 1.0  |      |
| 23630.peg.4818       | Entner-Doudoroff Pathway                                    | D-glycerate 2-kinase (EC 2.7.1.-)                                                                                       | 2.0  | 0.5  | 0.4  | 0.7  |      |
| 23630.peg.287        | Entner-Doudoroff Pathway                                    | Gluconolactonase (EC 3.1.1.17)                                                                                          |      |      | -0.7 | -1.0 |      |
| 23630.peg.126        | Entner-Doudoroff Pathway                                    | 4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)              | -1.0 |      |      |      |      |
| 23630.peg.4201       | Fermentations: Lactate                                      | Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9); Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)                   |      |      |      | -1.3 |      |
| 23630.peg.2532       | Fructose utilization                                        | 1-phosphofructokinase (EC 2.7.1.56)                                                                                     |      |      | -0.8 | -1.0 |      |

|                |                                                                |                                                                               |      |      |      |      |      |
|----------------|----------------------------------------------------------------|-------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.4820 | Glycerate metabolism                                           | Hydroxypyruvate isomerase (EC 5.3.1.22)                                       |      |      | -1.6 | -1.8 | -0.8 |
| 23630.peg.4821 | Glycerate metabolism                                           | Glyoxylate carboligase (EC 4.1.1.47)                                          |      |      | -0.7 | -1.3 |      |
| 23630.peg.2897 | Glycerol and Glycerol-3-phosphate Uptake and Utilization       | Glycerol-3-phosphate ABC transporter, permease protein UgpA (TC 3.A.1.1.3)    | 1.8  |      | -0.5 |      | 0.8  |
| 23630.peg.2893 | Glycerol and Glycerol-3-phosphate Uptake and Utilization       | Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3) | 1.5  | -0.6 |      |      | 0.5  |
| 23630.peg.1237 | Glycerol and Glycerol-3-phosphate Uptake and Utilization       | Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)                     |      |      | 1.2  | 1.1  | 0.3  |
| 23630.peg.2895 | Glycerol and Glycerol-3-phosphate Uptake and Utilization       | Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)    | 1.2  | -0.7 |      |      | 0.2  |
| 23630.peg.3082 | Glycogen metabolism                                            | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)                       | -1.4 |      |      | -0.6 |      |
| 23630.peg.1828 | Glycolate, glyoxylate interconversions                         | Hypothetical protein GlcG in glycolate utilization operon                     | 2.2  | 1.8  |      | 0.0  | 1.2  |
| 23630.peg.1831 | Glycolate, glyoxylate interconversions                         | Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD                          | 0.8  |      |      | -1.5 |      |
| 23630.peg.1829 | Glycolate, glyoxylate interconversions                         | Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF              |      |      | -0.9 | -2.0 |      |
| 23630.peg.1830 | Glycolate, glyoxylate interconversions                         | Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE              | 0.8  |      | -0.6 | -2.0 |      |
| 23630.peg.4817 | Glycolysis and Gluconeogenesis                                 | Pyruvate kinase (EC 2.7.1.40)                                                 | 2.2  |      | 0.8  | 0.5  | 1.2  |
| 23630.peg.1827 | Glyoxylate bypass                                              | Malate synthase G (EC 2.3.3.9)                                                | 3.2  | 2.1  | 0.9  |      | 2.3  |
| 23630.peg.2957 | Glyoxylate bypass                                              | Citrate synthase (si) (EC 2.3.3.1)                                            | 1.2  | 1.2  | 1.1  | 0.9  | 0.9  |
| 23630.peg.1109 | Glyoxylate bypass                                              | Malate synthase G (EC 2.3.3.9)                                                | 1.2  | 1.0  |      |      | 0.8  |
| 23630.peg.1826 | Lactate utilization                                            | L-lactate permease                                                            | 3.0  | 1.9  | 0.7  | 0.6  | 2.5  |
| 23630.peg.2154 | Lactate utilization                                            | Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF   | -2.0 | -0.9 |      |      | -0.8 |
| 23630.peg.624  | Lactate utilization                                            | D-Lactate dehydrogenase (EC 1.1.2.5)                                          | -1.6 |      | -0.5 |      |      |
| 23630.peg.1851 | Malonate decarboxylase                                         | Malonate decarboxylase alpha subunit                                          | 1.0  | 1.5  |      | 0.9  | 1.0  |
| 23630.peg.1855 | Malonate decarboxylase                                         | Malonate decarboxylase gamma subunit                                          | 2.0  | 0.6  |      | 1.0  | 0.7  |
| 23630.peg.1852 | Malonate decarboxylase                                         | Triphosphoribosyl-dephospho-CoA synthetase (EC 2.7.8.25)                      | 2.2  |      | -0.6 |      | 0.6  |
| 23630.peg.1857 | Malonate decarboxylase                                         | Malonyl CoA acyl carrier protein transacylase (EC 2.3.1.39)                   |      |      |      |      | -1.3 |
| 23630.peg.1856 | Malonate decarboxylase                                         | Phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.-)                         | 1.0  |      |      | -0.6 |      |
| 23630.peg.1854 | Malonate decarboxylase                                         | Malonate decarboxylase beta subunit                                           | 1.2  | -0.6 |      |      |      |
| 23630.peg.3081 | Maltose and Maltodextrin Utilization                           | Malto-oligosyltrehalose synthase (EC 5.4.99.15)                               | -1.4 | -1.3 | 1.0  | -1.0 |      |
| 23630.peg.128  | Pentose phosphate pathway                                      | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)                             | 1.1  | 0.9  | 0.8  |      | 0.7  |
| 23630.peg.3822 | Pentose phosphate pathway                                      | Transketolase, N-terminal section (EC 2.2.1.1)                                | 1.1  | 0.9  |      |      | -0.8 |
| 23630.peg.4416 | Pentose phosphate pathway                                      | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)                               | 0.9  |      | 1.0  |      |      |
| 23630.peg.71   | Peripheral Glucose Catabolism Pathways                         | Glucose ABC transporter, ATP-binding subunit (EC 3.6.3.-)                     | 1.0  |      | 1.0  | 0.3  | 0.9  |
| 23630.peg.72   | Peripheral Glucose Catabolism Pathways                         | Glucose ABC transport system, inner membrane component 2                      | 0.4  | -0.8 |      |      | -1.1 |
| 23630.peg.74   | Peripheral Glucose Catabolism Pathways                         | Glucose ABC transport system, periplasmic sugar-binding protein               |      |      | -0.9 | -1.2 |      |
| 23630.peg.1920 | Pyruvate Alanine Serine Interconversions                       | D-amino acid dehydrogenase small subunit (EC 1.4.99.1)                        | 0.4  |      | 2.0  | -0.8 | 2.1  |
| 23630.peg.1507 | Pyruvate metabolism I: anaplerotic reactions, PEP              | Pyruvate carboxyl transferase subunit A (EC 6.4.1.1)                          | 1.7  | 1.0  | 1.7  |      | 1.4  |
| 23630.peg.631  | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Phosphate acetyltransferase (EC 2.3.1.8)                                      |      | 0.7  | 1.2  |      | 0.9  |
| 23630.peg.1115 | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetate permease ActP (cation/acetate symporter)                              | 0.8  |      | -0.8 | -1.2 |      |
| 23630.peg.630  | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetate kinase (EC 2.7.2.1)                                                   |      | -1.0 |      |      |      |
| 23630.peg.1880 | Serine-glyoxylate cycle                                        | Malate dehydrogenase (EC 1.1.1.37)                                            | 1.9  |      |      |      | 1.1  |
| 23630.peg.63   | TCA Cycle                                                      | Malate:quinone oxidoreductase (EC 1.1.99.16)                                  |      | -1.1 | 0.6  |      | -0.7 |
| 23630.peg.4369 | TCA Cycle                                                      | Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4)   | 1.1  |      |      |      |      |
| 23630.peg.3083 | Trehalose Biosynthesis                                         | Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141)                       |      | -0.6 | 1.6  |      | -0.8 |

|                                                         |                                                             |                                                                                                           |      |      |      |      |      |
|---------------------------------------------------------|-------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.3067                                          | Trehalose Biosynthesis                                      | Trehalose synthase (EC 5.4.99.16)                                                                         | -1.0 | -1.8 | -0.7 |      | -1.2 |
| <b>Cell Division and Cell Cycle</b>                     |                                                             |                                                                                                           |      |      |      |      |      |
| 23630.peg.4253                                          | Bacterial Cytoskeleton                                      | Septum site-determining protein MinC                                                                      | 1.3  | 1.0  | 1.0  | 1.1  | 1.0  |
| 23630.peg.2600                                          | Bacterial Cytoskeleton                                      | Rod shape-determining protein MreB                                                                        | 1.1  |      | 0.9  | 1.2  |      |
| 23630.peg.999                                           | Macromolecular synthesis operon                             | SSU ribosomal protein S21p                                                                                | 1.1  |      | 1.2  | 1.4  |      |
| 23630.peg.4590                                          | MukBEF Chromosome Condensation                              | Chromosome partition protein MukB                                                                         | -0.9 | -1.0 |      | -1.3 | -0.8 |
| 23630.peg.4591                                          | MukBEF Chromosome Condensation                              | Chromosome partition protein MukE                                                                         | -0.8 | -1.1 | -0.6 | -1.0 | -0.8 |
| 23630.peg.4592                                          | MukBEF Chromosome Condensation                              | Chromosome partition protein MukF                                                                         |      | -1.0 |      |      |      |
| <b>Cell Wall and Capsule</b>                            |                                                             |                                                                                                           |      |      |      |      |      |
| 23630.peg.4443                                          | Alginate metabolism                                         | Outer membrane protein AlgE                                                                               | 0.8  | 1.2  |      |      | 1.1  |
| 23630.peg.4703                                          | Alginate metabolism                                         | Outer membrane protein AlgE                                                                               | -1.4 | -1.1 |      |      | -0.8 |
| 23630.peg.4012                                          | Alginate metabolism                                         | RNA polymerase sigma-H factor AlgT                                                                        | -0.8 | -1.0 |      |      | -1.2 |
| 23630.peg.4708                                          | Alginate metabolism                                         | GDP-mannose 6-dehydrogenase (EC 1.1.1.132)                                                                |      |      |      | 1.3  |      |
| 23630.peg.4439                                          | Alginate metabolism                                         | GDP-mannose 6-dehydrogenase (EC 1.1.1.132)                                                                |      |      |      | 1.1  |      |
| 23630.peg.4699                                          | Alginate metabolism                                         | Alginate biosynthesis protein AlgX                                                                        |      | 0.8  | 0.7  | 1.0  |      |
| 23630.peg.4702                                          | Alginate metabolism                                         | Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)                                                | -1.1 | -1.1 |      | -0.8 |      |
| 23630.peg.4442                                          | Alginate metabolism                                         | Alginate biosynthesis protein AlgK precursor                                                              |      |      |      | -1.1 |      |
| 23630.peg.4700                                          | Alginate metabolism                                         | Alginate o-acetyltransferase AlgF                                                                         |      | -1.0 |      |      |      |
| 23630.peg.4446                                          | Alginate metabolism                                         | Alginate lyase precursor (EC 4.2.2.3)                                                                     | -1.0 |      |      |      |      |
| 23630.peg.4705                                          | Alginate metabolism                                         | Alginate biosynthesis protein Alg44                                                                       | -1.2 |      |      |      |      |
| 23630.peg.4444                                          | Alginate metabolism                                         | Poly (beta-D-mannuronate) C5 epimerase precursor (EC 5.1.3.-)                                             | -1.2 |      |      |      |      |
| 23630.peg.2287                                          | Core Oligosaccharide Glycosylation in Pseudomonas           | Glycosyl transferase in large core OS assembly cluster                                                    | -0.9 | -0.7 | -0.9 |      | -1.1 |
| 23630.peg.2918                                          | Murein Hydrolases                                           | Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-)                                     | 0.9  |      | 1.2  |      |      |
| 23630.peg.1598                                          | Recycling of Peptidoglycan Amino Acids                      | AmpG permease                                                                                             |      | -1.4 |      |      |      |
| 23630.peg.286                                           | Rhamnose containing glycans                                 | UDP-glucose 4-epimerase (EC 5.1.3.2)                                                                      |      |      | -1.2 |      | -1.1 |
| 23630.peg.1874                                          | Sialic Acid Metabolism                                      | TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter           | 0.7  |      | 1.2  |      | 0.7  |
| 23630.peg.2386                                          | Sialic Acid Metabolism                                      | TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter           |      | -1.2 | -0.9 |      |      |
| 23630.peg.2627                                          | UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)                                            |      | 0.8  |      | 1.0  |      |
| <b>Cofactors, Vitamins, Prosthetic Groups, Pigments</b> |                                                             |                                                                                                           |      |      |      |      |      |
| 23630.peg.2392                                          | 5-FCL-like protein                                          | Alcohol dehydrogenase (EC 1.1.1.1)                                                                        | 1.2  |      |      |      | 0.8  |
| 23630.peg.770                                           | 5-FCL-like protein                                          | Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)                                                          |      | 1.1  |      |      | 0.7  |
| 23630.peg.299                                           | 5-FCL-like protein                                          | Formyltetrahydrofolate deformylase (EC 3.5.1.10)                                                          | 1.3  | 0.6  | 0.8  |      | 0.6  |
| 23630.peg.2435                                          | 5-FCL-like protein                                          | IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) |      |      |      | 1.1  |      |
| 23630.peg.1741                                          | 5-FCL-like protein                                          | Alcohol dehydrogenase (EC 1.1.1.1)                                                                        |      |      |      | -1.2 |      |
| 23630.peg.972                                           | 5-FCL-like protein                                          | Alcohol dehydrogenase (EC 1.1.1.1)                                                                        | -1.1 |      | -0.5 |      |      |
| 23630.peg.253                                           | Biotin biosynthesis                                         | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                                                            |      | 0.7  | 2.2  |      | 1.4  |
| 23630.peg.816                                           | Biotin biosynthesis                                         | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)                         | 1.4  | 0.6  |      | 1.0  | 0.6  |
| 23630.peg.4727                                          | Biotin biosynthesis                                         | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                                                            | -1.0 | -1.4 | -0.8 |      |      |
| 23630.peg.1097                                          | Biotin biosynthesis                                         | Biotin synthesis protein BioH                                                                             | -1.7 | -1.2 |      |      |      |
| 23630.peg.1098                                          | Biotin synthesis cluster                                    | 8-amino-7-oxononanoate synthase (EC 2.3.1.47)                                                             |      | 0.8  |      | 1.0  | 0.6  |
| 23630.peg.3359                                          | Biotin synthesis cluster                                    | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)                                                            |      |      | -1.0 |      |      |
| 23630.peg.3704                                          | Cobalamin synthesis                                         | Cob(I)alamin adenosyltransferase (EC 2.5.1.17)                                                            | -1.2 |      |      |      |      |

|                       |                                           |                                                                                                         |      |      |      |  |      |      |
|-----------------------|-------------------------------------------|---------------------------------------------------------------------------------------------------------|------|------|------|--|------|------|
| 23630.peg.706         | Coenzyme B12 biosynthesis                 | Optional hypothetical component of the B12 transporter BtuN                                             |      | 1.1  |      |  |      | -0.7 |
| 23630.peg.1609        | Coenzyme B12 biosynthesis                 | ChlD component of cobalt chelatase involved in B12 biosynthesis                                         |      |      |      |  | 1.2  |      |
| 23630.peg.1588        | Coenzyme B12 biosynthesis                 | Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)                                                           |      | 0.7  |      |  | 1.0  |      |
| 23630.peg.3695        | Coenzyme B12 biosynthesis                 | Cobalamin synthase                                                                                      |      | -1.2 |      |  |      |      |
| 23630.peg.3702        | Coenzyme B12 biosynthesis                 | Cobalamin biosynthesis protein BluB @ 5,6-dimethylbenzimidazole synthase, flavin destructase family     | -1.0 |      |      |  |      |      |
| 23630.peg.2762        | Coenzyme PQQ synthesis                    | Coenzyme PQQ synthesis protein B                                                                        |      |      |      |  | -1.2 |      |
| 23630.peg.4955        | Coenzyme PQQ synthesis                    | Coenzyme PQQ synthesis protein B                                                                        |      |      |      |  | -1.2 |      |
| 23630.peg.3435        | Heme and Siroheme Biosynthesis            | Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22)                                       |      |      | 0.6  |  | -1.0 |      |
| 23630.peg.1366        | Molybdenum cofactor biosynthesis          | Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1)                                            |      | 0.4  | 0.7  |  | 1.0  | 0.8  |
| 23630.peg.1365        | Molybdenum cofactor biosynthesis          | Molybdenum transport system permease protein ModB (TC 3.A.1.8.1)                                        |      | 0.9  | 1.1  |  |      |      |
| 23630.peg.1364        | Molybdenum cofactor biosynthesis          | Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1)                  |      | 0.9  | 1.1  |  |      |      |
| 23630.peg.4072        | NAD and NADP cofactor biosynthesis global | Nicotinamidase (EC 3.5.1.19)                                                                            |      |      |      |  | -2.5 | 0.9  |
| 23630.peg.4073        | NAD and NADP cofactor biosynthesis global | Nicotinate phosphoribosyltransferase (EC 2.4.2.11)                                                      | -1.0 |      |      |  | -1.2 |      |
| 23630.peg.3742        | Pterin carbinolamine dehydratase          | Fumarylacetoacetase (EC 3.7.1.2)                                                                        |      | 1.2  |      |  | 1.0  | 0.7  |
| 23630.peg.3744        | Pterin carbinolamine dehydratase          | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)                                                     |      | 1.1  |      |  | 0.7  |      |
| 23630.peg.3741        | Pterin carbinolamine dehydratase          | Maleylacetoacetate isomerase (EC 5.2.1.2) @ Glutathione S-transferase, zeta (EC 2.5.1.18)               | -0.7 | 1.1  |      |  | 0.5  |      |
| 23630.peg.651         | Pyridoxin (Vitamin B6) Biosynthesis       | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)                                                        | 1.0  | 0.9  | 0.8  |  | 0.9  | 0.7  |
| 23630.peg.4177        | Pyridoxin (Vitamin B6) Biosynthesis       | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)                                    | 1.2  |      |      |  |      |      |
| 23630.peg.4160        | Thiamin biosynthesis                      | Thiamin ABC transporter, transmembrane component                                                        | -0.7 | -1.0 | -0.7 |  | -0.8 | -0.7 |
| 23630.peg.1151        | Thiamin biosynthesis                      | tRNA S(4)U 4-thiouridine synthase (former ThiI) / Rhodanese-like domain required for thiamine synthesis | 1.0  |      | 0.6  |  |      |      |
| 23630.peg.1431        | Ubiquinone Biosynthesis - gjo             | Chorismate--pyruvate lyase (EC 4.1.3.40)                                                                |      |      | 0.6  |  | 1.1  |      |
| <b>DNA Metabolism</b> |                                           |                                                                                                         |      |      |      |  |      |      |
| 23630.peg.3595        | 2-phosphoglycolate salvage                | Similar to phosphoglycolate phosphatase, clustered with ubiquinone biosynthesis                         |      | 0.7  |      |  | 1.3  | 0.6  |
| 23630.peg.1656        | DNA Repair Base Excision                  | SAM-dependent O-methyltransferase                                                                       |      |      |      |  |      |      |
| 23630.peg.799         | DNA Repair Base Excision                  | DNA-3-methyladenine glycosylase (EC 3.2.2.20)                                                           | 1.4  | 1.6  | 0.8  |  | 1.4  | 1.2  |
| 23630.peg.3892        | DNA repair, bacterial                     | DNA-3-methyladenine glycosylase II (EC 3.2.2.21)                                                        | 1.0  |      | 0.9  |  |      |      |
| 23630.peg.3219        | DNA repair, bacterial                     | SOS-response repressor and protease LexA (EC 3.4.21.88)                                                 | 1.4  | 1.3  |      |  |      | 1.2  |
| 23630.peg.420         | DNA repair, bacterial                     | DNA repair protein RadC                                                                                 |      |      | 1.4  |  | -1.9 |      |
| 23630.peg.2707        | DNA repair, bacterial                     | Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)                                                    |      | 1.0  |      |  |      |      |
| 23630.peg.1123        | DNA repair, bacterial DinG and relatives  | DNA repair protein RadC                                                                                 | -1.2 |      |      |  |      |      |
| 23630.peg.4398        | DNA repair, bacterial photolyase          | DinG family ATP-dependent helicase CPE1197                                                              |      | -0.7 | -1.1 |  |      |      |
| 23630.peg.4570        | DNA repair, bacterial RecFOR pathway      | Deoxyribodipyrimidine photolyase (EC 4.1.99.3)                                                          |      | 0.6  |      |  |      | 1.1  |
| 23630.peg.4843        | DNA structural proteins, bacterial        | RecA protein                                                                                            | 1.0  | 0.7  |      |  | 0.9  |      |
| 23630.peg.3474        | DNA structural proteins, bacterial        | Chromosome partition protein smc                                                                        | -1.1 |      | -0.8 |  |      | -0.8 |
| 23630.peg.1112        | DNA-replication                           | DNA-binding protein HU-beta                                                                             |      |      | 0.7  |  | 1.1  |      |
| 23630.peg.2803        | DNA-replication                           | DNA polymerase III epsilon subunit (EC 2.7.7.7)                                                         |      |      | -1.1 |  | -0.9 | -0.7 |
| 23630.peg.1419        | DNA-replication                           | Exodeoxyribonuclease V beta chain (EC 3.1.11.5)                                                         | -1.0 |      |      |  | -0.9 | -0.8 |
| 23630.peg.3103        | DNA-replication                           | ATP-dependent DNA helicase RecG (EC 3.6.1.-)                                                            |      |      |      |  |      | -1.0 |
| 23630.peg.2782        | Restriction-Modification System           | DNA polymerase III alpha subunit (EC 2.7.7.7)                                                           | -1.2 | -0.8 |      |  |      |      |
| 23630.peg.4935        | Restriction-Modification System           | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)                             |      |      |      |  |      | -1.0 |
| 23630.peg.2781        | Restriction-Modification System           | Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)                             |      |      |      |  |      | -1.0 |
|                       |                                           | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)                   | -1.1 | -0.9 |      |  |      | -1.5 |

|                                             |                                                             |                                                                                        |      |      |      |      |      |
|---------------------------------------------|-------------------------------------------------------------|----------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.4936                              | Restriction-Modification System                             | Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)  | -1.1 | -0.9 |      |      | -1.5 |
| 23630.peg.2716                              | Type I Restriction-Modification                             | Type I restriction-modification system, specificity subunit S (EC 3.1.1.21.3)          | -1.4 | -0.7 |      |      | -1.3 |
| <b>Dormancy and Sporulation</b>             |                                                             |                                                                                        |      |      |      |      |      |
| 23630.peg.4419                              | Sporulation-associated proteins with broader functions      | Peptidyl-tRNA hydrolase (EC 3.1.1.29)                                                  |      |      |      | 1.1  |      |
| <b>Fatty Acids, Lipids, and Isoprenoids</b> |                                                             |                                                                                        |      |      |      |      |      |
| 23630.peg.3820                              | Fatty Acid Biosynthesis FASII                               | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)                              | 1.2  | 1.0  |      |      | 0.9  |
| 23630.peg.338                               | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                                        | 0.9  | -1.2 |      | -0.8 | 0.8  |
| 23630.peg.3076                              | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Cardiolipin synthetase (EC 2.7.8.-)                                                    |      | -1.0 | -0.6 |      | -0.4 |
| 23630.peg.3911                              | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)                                | -1.7 |      | -0.6 | -0.8 | -1.0 |
| 23630.peg.2391                              | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Aldehyde dehydrogenase (EC 1.2.1.3)                                                    | 0.9  |      |      | -1.0 |      |
| 23630.peg.2761                              | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Aldehyde dehydrogenase (EC 1.2.1.3)                                                    |      |      | -0.8 | -1.1 |      |
| 23630.peg.4956                              | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Aldehyde dehydrogenase (EC 1.2.1.3)                                                    |      |      | -0.8 | -1.1 |      |
| 23630.peg.3910                              | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Glycerol kinase (EC 2.7.1.30)                                                          | -1.5 |      | -0.9 |      |      |
| 23630.peg.29                                | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Phosphatidate cytidyltransferase (EC 2.7.7.41)                                         |      | 1.0  |      |      |      |
| 23630.peg.2725                              | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Aldehyde dehydrogenase (EC 1.2.1.3)                                                    | -0.7 | -1.1 |      |      |      |
| 23630.peg.2793                              | Glycerolipid and Glycerophospholipid Metabolism in Bacteria | Aldehyde dehydrogenase (EC 1.2.1.3)                                                    | -1.2 |      |      |      |      |
| 23630.peg.4415                              | Nonmevalonate Branch of Isoprenoid Biosynthesis             | 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)                       | 1.2  |      | 1.0  |      |      |
| 23630.peg.28                                | Nonmevalonate Branch of Isoprenoid Biosynthesis             | 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)                         | -1.2 |      |      |      |      |
| 23630.peg.3616                              | Phospholipid and Fatty acid biosynthesis related cluster    | FIG027190: Putative transmembrane protein                                              | 1.3  |      |      |      | 0.8  |
| 23630.peg.2237                              | Phospholipid and Fatty acid biosynthesis related cluster    | 3-hydroxydecanoyl-[ACP] dehydratase (EC 4.2.1.60)                                      | -1.1 | -0.8 | -0.5 |      | -0.9 |
| 23630.peg.2254                              | Phospholipid and Fatty acid biosynthesis related cluster    | 3-oxoacyl-[ACP] synthase                                                               |      | 0.6  | 1.1  |      |      |
| 23630.peg.2244                              | Phospholipid and Fatty acid biosynthesis related cluster    | FIG027190: Putative transmembrane protein                                              | -1.0 |      |      |      |      |
| 23630.peg.2248                              | Phospholipid and Fatty acid biosynthesis related cluster    | FIG143263: Glycosyl transferase                                                        | -1.0 |      |      |      |      |
| 23630.peg.2185                              | Polyhydroxybutyrate metabolism                              | polyhydroxyalkanoate granule-associated protein PhaI                                   | -1.1 |      |      |      | -0.8 |
| 23630.peg.1073                              | Polyhydroxybutyrate metabolism                              | D-beta-hydroxybutyrate permease                                                        | -2.2 | -0.6 | -1.6 | -1.2 | -2.5 |
| <b>Iron acquisition and metabolism</b>      |                                                             |                                                                                        |      |      |      |      |      |
| 23630.peg.1583                              | ABC transporter [iron.B12.siderophore.hemin]                | Outer membrane (iron.B12.siderophore.hemin) receptor                                   | -1.3 | -1.8 |      |      | -1.2 |
| 23630.peg.1580                              | ABC transporter [iron.B12.siderophore.hemin]                | ABC transporter (iron.B12.siderophore.hemin) , periplasmic substrate-binding component | -2.2 | -2.8 |      | -2.2 | -2.2 |
| 23630.peg.4736                              | Heme, hemin uptake and utilization systems in GramNegatives | Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)                         | 2.2  | 1.6  | 1.1  |      | 1.5  |
| 23630.peg.766                               | Heme, hemin uptake and utilization systems in GramNegatives | Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)                         | -1.8 |      | 0.7  |      | -0.9 |
| 23630.peg.1530                              | Heme, hemin uptake and utilization systems in GramPositives | FIG039061: hypothetical protein related to heme utilization                            | 1.6  | 0.7  | 0.9  |      | 0.9  |
| 23630.peg.566                               | Hemin transport system                                      | Periplasmic hemin-binding protein                                                      | -1.0 | -0.7 | 1.0  | -1.5 | -1.9 |
| 23630.peg.888                               | Hemin transport system                                      | Ferric siderophore transport system, periplasmic binding protein TonB                  |      |      |      | 1.1  |      |
| 23630.peg.2008                              | Iron acquisition in Streptococcus                           | Ferric iron ABC transporter, iron-binding protein                                      | 1.3  | 1.7  | 0.6  |      | 1.2  |
| 23630.peg.4647                              | Siderophore Pyoverdine                                      | FIG137594: Putative iron-regulated membrane protein                                    | 0.9  | 1.4  | 1.1  | 1.3  | 1.2  |
| 23630.peg.4642                              | Siderophore Pyoverdine                                      | ABC transporter in pyoverdin gene cluster, ATP-binding component                       |      |      |      | 1.1  | 1.1  |
| 23630.peg.4725                              | Siderophore Pyoverdine                                      | L-ornithine 5-monooxygenase (EC 1.13.12.-), PvdA of pyoverdin biosynthesis             | 1.1  | 0.6  |      | 1.0  | 0.7  |
| 23630.peg.4643                              | Siderophore Pyoverdine                                      | FIG014801: Cation ABC transporter, periplasmic cation-binding protein                  | -0.1 | 0.9  | 0.9  | 2.1  |      |
| 23630.peg.4645                              | Siderophore Pyoverdine                                      | FIG137877: Hypothetical protein in pyoverdin gene cluster                              |      | 0.6  |      | 1.2  |      |
| 23630.peg.4641                              | Siderophore Pyoverdine                                      | ABC transporter in pyoverdin gene cluster, permease component                          | -1.2 | -0.6 | 0.8  |      |      |
| 23630.peg.4646                              | Siderophore Pyoverdine                                      | FIG139991: Putative thiamine pyrophosphate-requiring enzyme                            | -2.6 |      | 0.8  |      |      |
| 23630.peg.4640                              | Siderophore Pyoverdine                                      | ABC transporter in pyoverdin gene cluster, periplasmic component                       | -1.1 |      |      |      |      |
| <b>Membrane Transport</b>                   |                                                             |                                                                                        |      |      |      |      |      |
| 23630.peg.1574                              | A TRAP transporter and a hypothetical                       | TRAP transporter solute receptor, unknown substrate 1                                  | 1.4  |      |      |      | 0.9  |

|                |                                                 |                                                                                                               |      |      |      |      |      |
|----------------|-------------------------------------------------|---------------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.1572 | A TRAP transporter and a hypothetical           | DUF1850 domain-containing protein                                                                             | 1.0  |      |      |      |      |
| 23630.peg.3769 | ABC transporter alkylphosphonate (TC 3.A.1.9.1) | Phosphonate ABC transporter ATP-binding protein (TC 3.A.1.9.1)                                                |      | 0.9  | 1.7  | 0.5  |      |
| 23630.peg.3767 | ABC transporter alkylphosphonate (TC 3.A.1.9.1) | Phosphonate ABC transporter permease protein phnE (TC 3.A.1.9.1)                                              | -1.2 |      |      |      |      |
| 23630.peg.3768 | ABC transporter alkylphosphonate (TC 3.A.1.9.1) | Phosphonate ABC transporter phosphate-binding periplasmic component (TC 3.A.1.9.1)                            | -1.4 |      |      |      |      |
| 23630.peg.4501 | Conjugative transfer                            | Conjugative transfer protein TrbL                                                                             | -1.5 | -1.1 | -0.4 |      | -1.5 |
| 23630.peg.4507 | Conjugative transfer                            | Conjugative transfer protein TrbB                                                                             | -2.5 |      |      |      |      |
| 23630.peg.4306 | Magnesium transport                             | Mg/Co/Ni transporter MgtE / CBS domain                                                                        |      | -0.8 |      | -1.4 |      |
| 23630.peg.4051 | Multi-subunit cation antiporter                 | Na(+) H(+) antiporter subunit A; Na(+) H(+) antiporter subunit B                                              |      |      | -0.8 | -1.0 |      |
| 23630.peg.2851 | sigma-Fimbriae                                  | Sigma-fimbriae usher protein                                                                                  | 1.0  |      | 0.9  |      |      |
| 23630.peg.2852 | sigma-Fimbriae                                  | Sigma-fimbriae chaperone protein                                                                              |      |      | -1.0 |      |      |
| 23630.peg.892  | Ton and Tol transport systems                   | TonB system biopolymer transport component; Chromosome segregation ATPase                                     | 1.2  | 0.8  |      |      | 1.0  |
| 23630.peg.1603 | Ton and Tol transport systems                   | TonB-dependent receptor                                                                                       | -1.0 |      | 1.2  |      | -0.8 |
| 23630.peg.1597 | Ton and Tol transport systems                   | Outer membrane receptor proteins, likely involved in siderophore uptake @ TonB-dependent siderophore receptor |      |      | 1.4  | -0.7 |      |
| 23630.peg.2553 | Ton and Tol transport systems                   | TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins                           |      | 1.1  |      |      |      |
| 23630.peg.3723 | Ton and Tol transport systems                   | TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins                           | -1.2 |      |      |      |      |
| 23630.peg.2631 | Transport of Nickel and Cobalt                  | Additional periplasmic component NikK of nickel ECF transporter                                               | -0.9 |      |      |      | -1.1 |
| 23630.peg.2389 | TRAP Transporter collection                     | TRAP-type C4-dicarboxylate transport system, periplasmic component                                            | 1.6  |      |      |      | 0.9  |
| 23630.peg.106  | TRAP Transporter collection                     | TRAP-type C4-dicarboxylate transport system, periplasmic component                                            | 1.1  |      |      |      | 0.9  |
| 23630.peg.290  | TRAP Transporter collection                     | TRAP-type C4-dicarboxylate transport system, large permease component                                         |      | -0.8 | -0.8 |      | -1.1 |
| 23630.peg.1848 | TRAP Transporter collection                     | TRAP-type C4-dicarboxylate transport system, periplasmic component                                            | -1.0 | -1.3 | 0.7  |      | -1.4 |
| 23630.peg.2970 | TRAP Transporter collection                     | TRAP-type C4-dicarboxylate transport system, large permease component                                         |      |      |      | -1.0 |      |
| 23630.peg.102  | TRAP Transporter collection                     | TRAP-type C4-dicarboxylate transport system, periplasmic component                                            |      |      | -1.3 | -1.2 |      |
| 23630.peg.1764 | TRAP Transporter unknown substrate 7            | TRAP dicarboxylate transporter, DctQ subunit, unknown substrate 6                                             | -0.9 | -1.2 | -0.7 |      |      |
| 23630.peg.1763 | TRAP Transporter unknown substrate 9            | TRAP transporter solute receptor, unknown substrate 6                                                         |      | -1.1 |      |      |      |
| 23630.peg.4323 | Tricarboxylate transport system                 | Tricarboxylate transport membrane protein TctA                                                                | -0.9 | 0.6  | 0.8  |      | -1.2 |
| 23630.peg.4021 | Tricarboxylate transport system                 | Tricarboxylate porin OpdH                                                                                     |      |      | -1.3 | -0.3 |      |
| 23630.peg.4324 | Tricarboxylate transport system                 | Tricarboxylate transport protein TctB                                                                         |      | -1.0 |      | -0.9 |      |
| 23630.peg.4679 | Tricarboxylate transport system                 | Tricarboxylate porin OpdH                                                                                     |      |      | 1.1  |      |      |
| 23630.peg.4983 | Tricarboxylate transport system                 | Tricarboxylate porin OpdH                                                                                     | -1.6 | -0.8 |      |      |      |
| 23630.peg.4025 | Tricarboxylate transport system                 | Ammonia monooxygenase                                                                                         |      | -1.2 |      |      |      |
| 23630.peg.1881 | Tricarboxylate transport system                 | Tricarboxylate transport membrane protein TctA                                                                | 1.1  |      |      |      |      |
| 23630.peg.2205 | Type IV pilus                                   | Type IV pilus biogenesis protein PilO                                                                         |      | -1.0 |      | -0.9 | -0.9 |
| 23630.peg.2207 | Type IV pilus                                   | Type IV pilus biogenesis protein PilQ                                                                         |      | -1.2 | -0.8 | -1.2 | -0.9 |
| 23630.peg.2204 | Type IV pilus                                   | Type IV pilus biogenesis protein PilN                                                                         |      | -0.9 | -0.6 | -0.8 | -1.0 |
| 23630.peg.4466 | Type IV pilus                                   | Two-component sensor PilS                                                                                     | 0.8  | 0.6  |      | 1.2  |      |
| 23630.peg.2873 | Type IV pilus                                   | Twitching motility protein PilT                                                                               |      |      |      | -1.0 |      |
| 23630.peg.3179 | Type VI secretion systems                       | Uncharacterized protein ImpF                                                                                  | 1.5  | 0.8  | 0.9  |      | 1.3  |
| 23630.peg.3180 | Type VI secretion systems                       | Protein ImpG/VasA                                                                                             | 1.2  |      |      |      | 0.9  |
| 23630.peg.1517 | Type VI secretion systems                       | VgrG protein                                                                                                  | 1.1  | 1.2  | 0.7  | 1.4  | 0.7  |
| 23630.peg.3176 | Type VI secretion systems                       | Uncharacterized protein ImpB                                                                                  | 1.0  |      |      | 0.9  | 0.7  |
| 23630.peg.1714 | Type VI secretion systems                       | Uncharacterized protein ImpB                                                                                  |      | 1.0  |      | 1.4  | 0.4  |
| 23630.peg.1719 | Type VI secretion systems                       | Protein ImpG/VasA                                                                                             | -1.3 | -1.2 |      |      | -1.1 |

|                                         |                                                     |                                                                                                          |      |      |      |      |      |
|-----------------------------------------|-----------------------------------------------------|----------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.1726                          | Type VI secretion systems                           | Uncharacterized protein ImpJ/VasE                                                                        |      | -0.5 |      | 1.3  |      |
| 23630.peg.1716                          | Type VI secretion systems                           | Uncharacterized protein similar to VCA0109                                                               | -1.0 | -0.9 | 0.8  | 1.1  |      |
| 23630.peg.1516                          | Type VI secretion systems                           | Secreted protein Hcp                                                                                     |      |      |      | 1.0  |      |
| 23630.peg.3182                          | Type VI secretion systems                           | ClpB protein                                                                                             | 0.6  |      |      | 1.0  |      |
| 23630.peg.1728                          | Type VI secretion systems                           | IcmF-related protein                                                                                     | -1.3 |      |      | -0.2 |      |
| 23630.peg.2546                          | Type VI secretion systems                           | ClpB protein                                                                                             |      | -1.5 |      | -1.0 |      |
| <b>Metabolism of Aromatic Compounds</b> |                                                     |                                                                                                          |      |      |      |      |      |
| 23630.peg.839                           | Benzoate degradation                                | benzoate-specific porin                                                                                  |      | 1.0  |      |      |      |
| 23630.peg.846                           | Benzoate degradation                                | Benzoate 1,2-dioxygenase, ferredoxin reductase component                                                 | 1.1  |      |      |      |      |
| 23630.peg.4339                          | Biphenyl Degradation                                | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-)                                         |      | 1.0  |      |      |      |
| 23630.peg.831                           | Catechol branch of beta-ketoadipate pathway         | 3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6); Glutaconate CoA-transferase subunit B (EC 2.8.3.12) | -1.3 | -1.0 |      | -1.3 |      |
| 23630.peg.2064                          | Gentisare degradation                               | putative 4-hydroxybenzoyl-CoA thioesterase                                                               | 1.0  |      |      |      |      |
| 23630.peg.4147                          | Protocatechuate branch of beta-ketoadipate pathway  | PhaK-like protein                                                                                        |      | -1.0 | -0.7 |      | -0.8 |
| <b>Motility and Chemotaxis</b>          |                                                     |                                                                                                          |      |      |      |      |      |
| 23630.peg.1441                          | Bacterial Chemotaxis                                | Flagellar motor switch protein FliM                                                                      | 1.0  | 0.9  | 2.4  | 0.7  | 0.7  |
| 23630.peg.1437                          | Bacterial Chemotaxis                                | Flagellar motor switch protein FliG                                                                      | -1.0 |      | -0.5 |      | -0.8 |
| 23630.peg.2444                          | Bacterial Chemotaxis                                | Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)                                     | -1.1 |      |      | 1.1  | -0.9 |
| 23630.peg.125                           | Bacterial Chemotaxis                                | Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)                                     | -2.4 |      | 0.9  | 1.2  |      |
| 23630.peg.3342                          | Bacterial Chemotaxis                                | Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)                                     |      | -1.2 |      | -0.7 |      |
| 23630.peg.1442                          | Bacterial Chemotaxis                                | Flagellar motor switch protein FliN                                                                      |      |      | 1.1  |      |      |
| 23630.peg.1836                          | Flagellar motility                                  | Flagellar basal-body rod modification protein FlgD                                                       |      | 1.1  | 0.7  | 0.7  | -0.7 |
| 23630.peg.1824                          | Flagellum                                           | Flagellin protein FlaA                                                                                   | 0.8  |      | 1.1  |      | 0.6  |
| 23630.peg.4771                          | Flagellum                                           | Flagellar assembly protein FliH                                                                          |      |      | -1.3 |      | -0.8 |
| 23630.peg.4760                          | Flagellum                                           | Flagellin protein FlaG                                                                                   |      | -1.0 | -0.6 |      | -0.8 |
| 23630.peg.1835                          | Flagellum                                           | Flagellar basal-body rod protein FlgC                                                                    |      |      |      | 0.8  | -1.0 |
| 23630.peg.1440                          | Flagellum                                           | Flagellar regulatory protein FleQ                                                                        | 0.9  |      | 1.6  | 0.7  |      |
| 23630.peg.1443                          | Flagellum                                           | Flagellar biosynthesis protein FliP                                                                      |      |      |      | -1.2 |      |
| 23630.peg.4770                          | Flagellum                                           | Flagellar motor switch protein FliG                                                                      |      |      | -0.8 | -1.4 |      |
| 23630.peg.1435                          | Flagellum                                           | Flagellum-specific ATP synthase FliI                                                                     |      |      | 1.0  |      |      |
| 23630.peg.1837                          | Flagellum                                           | Flagellar hook protein FlgE                                                                              |      | 1.2  | 0.9  |      |      |
| 23630.peg.1834                          | Flagellum in Campylobacter                          | Flagellar basal-body rod protein FlgB                                                                    |      | 0.6  |      | 0.7  | -1.0 |
| 23630.peg.4759                          | Flagellum in Campylobacter                          | Flagellin protein FlaB                                                                                   | -1.0 | -0.7 | -0.6 |      |      |
| <b>Nitrogen Metabolism</b>              |                                                     |                                                                                                          |      |      |      |      |      |
| 23630.peg.3978                          | Cyanate hydrolysis                                  | Cyanate transport protein CynX                                                                           | 1.3  | 2.8  | 1.0  | 0.9  | 1.3  |
| 23630.peg.679                           | Cyanate hydrolysis                                  | Carbonic anhydrase (EC 4.2.1.1)                                                                          | 2.2  | 1.9  | 1.1  | 0.7  | 0.8  |
| 23630.peg.2215                          | Cyanate hydrolysis                                  | Cyanate ABC transporter, substrate binding protein                                                       | -1.3 |      | 1.3  |      | -0.9 |
| 23630.peg.979                           | Nitrate and nitrite ammonification                  | Nitrate/nitrite sensor protein (EC 2.7.3.-)                                                              | -1.1 |      | -1.0 | -0.9 | -0.9 |
| 23630.peg.3017                          | Nitrate and nitrite ammonification                  | Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4)                                                   |      | -1.6 |      |      | -1.5 |
| 23630.peg.2748                          | Nitrate and nitrite ammonification                  | Nitrate/nitrite sensor protein (EC 2.7.3.-)                                                              |      |      | -0.7 | -1.2 |      |
| 23630.peg.4969                          | Nitrate and nitrite ammonification                  | Nitrate/nitrite sensor protein (EC 2.7.3.-)                                                              |      |      | -0.7 | -1.2 |      |
| 23630.peg.3018                          | Nitrate and nitrite ammonification                  | Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)                                                   | -1.3 | -1.5 |      |      |      |
| 23630.peg.1367                          | Nitrosative stress                                  | Anaerobic nitric oxide reductase transcription regulator NorR                                            | 1.7  | 1.1  |      | 1.5  | 1.8  |
| <b>Nucleosides and Nucleotides</b>      |                                                     |                                                                                                          |      |      |      |      |      |
| 23630.peg.1740                          | De Novo Purine Biosynthesis                         | Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)                                 | 1.0  | 0.8  | 0.8  |      | 0.9  |
| 23630.peg.3502                          | De Novo Pyrimidine Synthesis                        | Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)                                                       |      |      | 1.0  |      |      |
| 23630.peg.167                           | Nudix proteins (nucleoside triphosphate hydrolases) | Nudix hydrolase family protein PA3470                                                                    | 0.7  | 0.4  | 1.2  |      | 0.7  |



|                                                           |                                                                        |                                                                                      |      |      |      |       |      |
|-----------------------------------------------------------|------------------------------------------------------------------------|--------------------------------------------------------------------------------------|------|------|------|-------|------|
| 23630.peg.436                                             | Purine conversions                                                     | Nucleoside diphosphate kinase (EC 2.7.4.6)                                           | 0.7  |      | 1.0  |       |      |
| 23630.peg.4455                                            | pyrimidine conversions                                                 | Thioredoxin reductase (EC 1.8.1.9)                                                   | 0.9  | 1.0  | 0.8  | 0.9   | 1.2  |
| 23630.peg.2502                                            | pyrimidine conversions                                                 | Thymidine phosphorylase (EC 2.4.2.4)                                                 | -0.7 | -0.6 | -1.1 |       | -0.9 |
| 23630.peg.3746                                            | pyrimidine conversions                                                 | CTP synthase (EC 6.3.4.2)                                                            |      |      | -0.6 | -1.0  |      |
| 23630.peg.4526                                            | Xanthine dehydrogenase subunits                                        | Xanthine-uracil permease                                                             | -1.6 | -0.8 |      |       |      |
| 23630.peg.688                                             | Xanthine Metabolism in Bacteria                                        | Xanthine permease                                                                    | 0.9  | 1.1  | 0.6  |       | 0.7  |
| 23630.peg.1791                                            | Xanthine Metabolism in Bacteria                                        | Xanthine permease                                                                    | 1.1  | 1.0  |      | 1.2   |      |
| <b>Phages, Prophages, Transposable elements, Plasmids</b> |                                                                        |                                                                                      |      |      |      |       |      |
| 23630.peg.53                                              | Integrons                                                              | Integron integrase IntIPac                                                           |      | -1.3 | 0.6  |       |      |
| <b>Phosphorus Metabolism</b>                              |                                                                        |                                                                                      |      |      |      |       |      |
| 23630.peg.3763                                            | Alkylphosphonate utilization                                           | PhnI protein                                                                         | -1.5 |      |      |       | -0.7 |
| 23630.peg.3760                                            | Alkylphosphonate utilization                                           | Phosphonates transport ATP-binding protein PhnL                                      | -1.2 |      |      | 0.8   |      |
| 23630.peg.3766                                            | Alkylphosphonate utilization                                           | Transcriptional regulator PhnF                                                       |      | -1.0 | 0.7  |       |      |
| 23630.peg.3765                                            | Alkylphosphonate utilization                                           | PhnG protein                                                                         | -1.0 | 0.8  |      |       |      |
| 23630.peg.3759                                            | Alkylphosphonate utilization                                           | Metal-dependent hydrolase involved in phosphonate metabolism                         | -1.6 |      |      |       |      |
| 23630.peg.3764                                            | Alkylphosphonate utilization                                           | PhnH protein                                                                         | -1.7 |      |      |       |      |
| 23630.peg.3762                                            | Alkylphosphonate utilization                                           | PhnJ protein                                                                         | -1.8 |      |      |       |      |
| 23630.peg.1809                                            | High affinity phosphate transporter and control of PHO regulon         | Phosphate transport system permease protein PstA (TC 3.A.1.7.1)                      | -1.0 | 0.7  |      |       |      |
| 23630.peg.1810                                            | High affinity phosphate transporter and control of PHO regulon         | Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1)                          | -1.2 |      |      |       |      |
| 23630.peg.1453                                            | Phosphate metabolism                                                   | NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)                                   | 1.0  |      |      |       | 1.0  |
| 23630.peg.2448                                            | Phosphate metabolism                                                   | Alkaline phosphatase (EC 3.1.3.1)                                                    | -0.9 |      | -0.6 |       | -1.0 |
| 23630.peg.4239                                            | Phosphate metabolism                                                   | Pyrophosphate-specific outer membrane porin OprO                                     | -1.9 |      |      |       | -1.0 |
| 23630.peg.4237                                            | Phosphate metabolism                                                   | Inorganic pyrophosphatase (EC 3.6.1.1)                                               | -1.7 |      |      |       | -1.0 |
| 23630.peg.1428                                            | Phosphate metabolism                                                   | Phosphate regulon transcriptional regulatory protein PhoB (SphR)                     |      |      |      | 1.7   |      |
| 23630.peg.1427                                            | Phosphate metabolism                                                   | Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)                           |      |      |      | 1.4   |      |
| 23630.peg.1807                                            | Phosphate metabolism                                                   | Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) |      | 0.6  | 0.7  | 1.3   |      |
| 23630.peg.1811                                            | Phosphate metabolism                                                   | Phosphate transport system regulatory protein PhoU                                   | -1.3 |      |      |       |      |
| <b>Potassium metabolism</b>                               |                                                                        |                                                                                      |      |      |      |       |      |
| 23630.peg.3188                                            | Glutathione-regulated potassium-efflux system and associated functions | Glutathione-regulated potassium-efflux system protein KefB                           | -1.3 | -0.7 |      |       |      |
| 23630.peg.1345                                            | Potassium homeostasis                                                  | Potassium-transporting ATPase C chain (EC 3.6.3.12) (TC 3.A.3.7.1)                   | 1.1  | 1.6  | 1.0  |       | 0.9  |
| 23630.peg.1347                                            | Potassium homeostasis                                                  | Potassium-transporting ATPase A chain (EC 3.6.3.12) (TC 3.A.3.7.1)                   | -1.7 | -2.1 | -0.5 |       | -1.1 |
| <b>Protein Metabolism</b>                                 |                                                                        |                                                                                      |      |      |      |       |      |
| 23630.peg.1558                                            | G3E family of P-loop GTPases (metallocenter biosynthesis)              | Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family       | -1.1 |      |      |       | 0.7  |
| 23630.peg.159                                             | Peptidyl-prolyl cis-trans isomerase                                    | Peptidyl-prolyl cis-trans isomerase PpiC (EC 5.2.1.8)                                | 0.7  | 0.7  | 0.7  | 1.0   | 0.6  |
| 23630.peg.744                                             | Periplasmic disulfide interchange                                      | Cytochrome c-type biogenesis protein CcmG/DsbE, thiol:disulfide oxidoreductase       | -1.1 |      |      |       |      |
| 23630.peg.4272                                            | Proteasome bacterial                                                   | ATP-dependent protease La (EC 3.4.21.53) Type I                                      | 0.8  | 1.1  |      | 0.7   | 0.6  |
| 23630.peg.2729                                            | Protein degradation                                                    | Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)                               | -1.6 | -1.2 | -0.6 | -1.43 | -0.6 |
| 23630.peg.1670                                            | Protein degradation                                                    | Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)                               | -1.8 | -2.0 | 0.1  | -1.5  | -1.4 |
| 23630.peg.2193                                            | Proteolysis in bacteria, ATP-dependent                                 | ATP-dependent hsl protease ATP-binding subunit HslU                                  | 1.2  | 0.9  |      |       | 0.7  |
| 23630.peg.2194                                            | Proteolysis in bacteria, ATP-dependent                                 | ATP-dependent protease HslV (EC 3.4.25.-)                                            |      |      |      | 1.1   | 0.6  |
| 23630.peg.1640                                            | Ribosome LSU bacterial                                                 | LSU ribosomal protein L34p                                                           | 1.8  | 1.2  | 1.5  | 1.6   | 1.1  |
| 23630.peg.3854                                            | Ribosome LSU bacterial                                                 | LSU ribosomal protein L32p                                                           | 0.9  |      |      | 1.5   |      |
| 23630.peg.2350                                            | Ribosome LSU bacterial                                                 | LSU ribosomal protein L9p                                                            |      |      |      | 1.4   |      |

|                                      |                                                                                                    |                                                                                                                     |      |      |      |           |
|--------------------------------------|----------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------|------|------|------|-----------|
| 23630.peg.936                        | Ribosome LSU bacterial                                                                             | LSU ribosomal protein L10p (P0)                                                                                     |      |      |      | 1.3       |
| 23630.peg.909                        | Ribosome LSU bacterial                                                                             | LSU ribosomal protein L30p (L7e)                                                                                    |      |      |      | 1.2       |
| 23630.peg.924                        | Ribosome LSU bacterial                                                                             | LSU ribosomal protein L2p (L8e)                                                                                     |      |      |      | 1.2       |
| 23630.peg.1396                       | Ribosome LSU bacterial                                                                             | LSU ribosomal protein L28p                                                                                          | 1.1  | 1.2  |      | 1.0       |
| 23630.peg.937                        | Ribosome LSU bacterial                                                                             | LSU ribosomal protein L1p (L10Ae)                                                                                   |      |      |      | 1.0       |
| 23630.peg.2198                       | Ribosome LSU bacterial                                                                             | LSU ribosomal protein L31p @ LSU ribosomal protein L31p, zinc-dependent                                             | 1.0  | 0.9  |      | 0.9       |
| 23630.peg.2648                       | Ribosome LSU bacterial                                                                             | LSU ribosomal protein L13p (L13Ae)                                                                                  | 0.8  | 1.0  |      |           |
| 23630.peg.4227                       | tRNA aminoacylation, Pro                                                                           | Prolyl-tRNA synthetase (EC 6.1.1.15), bacterial type                                                                | 0.9  | 0.7  | 1.0  | 1.0       |
| 23630.peg.1150                       | Universal GTPases                                                                                  | GTP-binding protein TypA/BipA                                                                                       |      |      | 1.4  |           |
| <b>Regulation and Cell signaling</b> |                                                                                                    |                                                                                                                     |      |      |      |           |
| 23630.peg.3210                       | cAMP signaling in bacteria                                                                         | cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases          |      |      |      | -1.0      |
| 23630.peg.2487                       | cAMP signaling in bacteria                                                                         | 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17)                                                             | -1.3 |      |      |           |
| 23630.peg.4115                       | DNA-binding regulatory proteins, strays                                                            | LysR family transcriptional regulator PA0739                                                                        | -1.9 |      | -0.7 |           |
| 23630.peg.4331                       | DNA-binding regulatory proteins, strays                                                            | LysR family transcriptional regulator near succinyl-CoA:3-ketoacid-coenzyme A transferase                           | -0.9 |      | -1.2 |           |
| 23630.peg.1508                       | DNA-binding regulatory proteins, strays                                                            | LysR family transcriptional regulator PA5437                                                                        | -1.5 |      |      |           |
| 23630.peg.1865                       | Extracellular matrix proteins (PEL) involved in glucose-rich biofilm formation in Pseudomonas      | Extracellular Matrix protein PelA                                                                                   |      | -0.9 | -1.0 |           |
| 23630.peg.419                        | LysR-family proteins in Salmonella enterica Typhimurium                                            | LysR-family transcriptional regulator STM3020                                                                       |      | 1.0  | 0.8  |           |
| 23630.peg.135                        | Orphan regulatory proteins                                                                         | Transcriptional regulatory protein RstA                                                                             |      |      |      | -1.5      |
| 23630.peg.4693                       | Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) systems                                 | Death on curing protein, Doc toxin                                                                                  |      |      |      | -1.0      |
| 23630.peg.1559                       | Zinc regulated enzymes                                                                             | C4-type zinc finger protein, DksA/TraR family                                                                       | 0.8  |      | -0.6 | -1.1      |
| <b>Respiration</b>                   |                                                                                                    |                                                                                                                     |      |      |      |           |
| 23630.peg.4530                       | Anaerobic respiratory reductases                                                                   | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1; Vanillate O-demethylase oxidoreductase (EC 1.14.13.-) | -1.4 | -1.4 |      | -0.9 -1.8 |
| 23630.peg.4810                       | Biogenesis of c-type cytochromes                                                                   | Cytochrome c heme lyase subunit CcmL                                                                                | -1.2 |      |      |           |
| 23630.peg.1774                       | Biogenesis of cytochrome c oxidases                                                                | Cytochrome oxidase biogenesis protein Cox11-CtaG, copper delivery to Cox1                                           | 1.9  |      |      | -0.9 0.7  |
| 23630.peg.3961                       | Biogenesis of cytochrome c oxidases                                                                | Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX10-CtaB                                           | -1.2 |      |      | 1.0       |
| 23630.peg.1777                       | Biogenesis of cytochrome c oxidases                                                                | Cytochrome oxidase biogenesis protein Surf1, facilitates heme A insertion                                           | 1.3  |      |      | -1.1      |
| 23630.peg.1779                       | Biogenesis of cytochrome c oxidases                                                                | Heme A synthase, cytochrome oxidase biogenesis protein Cox15-CtaA                                                   | 1.3  |      |      |           |
| 23630.peg.2068                       | Formate hydrogenase                                                                                | Putative formate dehydrogenase oxidoreductase protein                                                               | 1.0  |      | -0.4 | 0.0 0.6   |
| 23630.peg.3879                       | Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes | Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)                                                   | -1.1 |      | -0.7 | -0.7      |
| 23630.peg.4080                       | Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes | Electron transport complex protein RnfA                                                                             |      |      | 0.8  | 1.3       |
| 23630.peg.3881                       | Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes | Na(+)-translocating NADH-quinone reductase subunit D (EC 1.6.5.-)                                                   |      |      |      | 1.0       |
| 23630.peg.3303                       | Respiratory Complex I                                                                              | NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)                                                                 | -0.7 | -1.0 | -0.7 | -1.1      |
| 23630.peg.3107                       | Respiratory dehydrogenases 2                                                                       | NADH dehydrogenase (EC 1.6.99.3)                                                                                    | 0.9  | 1.0  |      | 0.9       |
| 23630.peg.3828                       | Respiratory dehydrogenases 3                                                                       | NADH dehydrogenase (EC 1.6.99.3)                                                                                    |      | -1.0 |      | -0.8      |
| 23630.peg.1773                       | Terminal cytochrome C oxidases                                                                     | Cytochrome c oxidase polypeptide I (EC 1.9.3.1)                                                                     | 1.7  |      |      | 0.9       |
| 23630.peg.3424                       | Terminal cytochrome C oxidases                                                                     | Cytochrome c oxidase subunit CcoQ (EC 1.9.3.1)                                                                      | -1.4 |      |      | -0.7      |
| 23630.peg.1775                       | Terminal cytochrome C oxidases                                                                     | Cytochrome c oxidase polypeptide III (EC 1.9.3.1)                                                                   | 1.3  | -0.8 |      | -1.4      |
| 23630.peg.3425                       | Terminal cytochrome C oxidases                                                                     | Cytochrome c oxidase subunit CcoP (EC 1.9.3.1)                                                                      | -1.2 |      |      |           |

|                        |                                                     |                                                                                      |      |      |      |           |
|------------------------|-----------------------------------------------------|--------------------------------------------------------------------------------------|------|------|------|-----------|
| 23630.peg.2471         | Terminal cytochrome d ubiquinol oxidases            | putative Cytochrome bd2, subunit I / Cyanide insensitive terminal oxidase, subunit I |      |      |      | 1.4       |
| 23630.peg.3965         | Terminal cytochrome O ubiquinol oxidase             | Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-)                              | -1.1 |      |      | 0.8       |
| 23630.peg.3964         | Terminal cytochrome oxidases                        | Cytochrome O ubiquinol oxidase subunit I (EC 1.10.3.-)                               | -1.7 | -0.7 |      |           |
| 23630.peg.3962         | Terminal cytochrome oxidases                        | Cytochrome O ubiquinol oxidase subunit IV (EC 1.10.3.-)                              | -1.8 | -0.9 |      |           |
| 23630.peg.3963         | Terminal cytochrome oxidases                        | Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)                             | -1.2 | -0.9 |      |           |
| 23630.peg.2472         | Terminal cytochrome oxidases                        | putative Cytochrome bd2, subunit II                                                  | -1.0 |      |      |           |
| <b>RNA Metabolism</b>  |                                                     |                                                                                      |      |      |      |           |
| 23630.peg.775          | Methylthiotransferases                              | tRNA-i(6)A37 methylthiotransferase                                                   | 1.2  |      | 1.2  | 0.8       |
| 23630.peg.994          | Polyadenylation bacterial                           | tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25)                              | 1.1  |      | 0.9  | 0.7       |
| 23630.peg.4196         | Queuosine-Archaeosine Biosynthesis                  | Permease of the drug/metabolite transporter (DMT) superfamily                        | 1.3  |      | 0.7  |           |
| 23630.peg.1674         | Queuosine-Archaeosine Biosynthesis                  | Putative preQ0 transporter                                                           | 1.1  |      | 0.7  |           |
| 23630.peg.213          | Queuosine-Archaeosine Biosynthesis                  | Permease of the drug/metabolite transporter (DMT) superfamily                        | -1.0 | 0.7  |      |           |
| 23630.peg.2890         | Queuosine-Archaeosine Biosynthesis                  | Permease of the drug/metabolite transporter (DMT) superfamily                        | -1.0 |      |      |           |
| 23630.peg.3581         | Ribonucleases in Bacillus                           | Metallo-beta-lactamase family protein, RNA-specific                                  | -1.8 | -1.0 |      | -1.0      |
| 23630.peg.4202         | Ribonucleases in Bacillus                           | Metallo-beta-lactamase family protein, RNA-specific                                  |      |      |      | -1.4      |
| 23630.peg.4922         | RNA methylation                                     | 23S rRNA (guanine-N-2-) -methyltransferase rlmG (EC 2.1.1.-)                         | -1.9 |      |      | -0.9      |
| 23630.peg.751          | RNA pseudouridine syntheses                         | Ribosomal large subunit pseudouridine synthase E (EC 4.2.1.70)                       | 1.3  | 1.2  | 0.7  | 0.9       |
| 23630.peg.4463         | RNA pseudouridine syntheses                         | Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)                       | 0.8  |      | 1.0  |           |
| 23630.peg.939          | Transcription factors bacterial                     | Transcription antitermination protein NusG                                           |      | -1.2 |      |           |
| 23630.peg.2976         | Transcription factors bacterial                     | Transcription elongation factor GreB                                                 | 1.3  |      |      |           |
| 23630.peg.3919         | Transcription initiation, bacterial sigma factors   | RNA polymerase sigma factor RpoE                                                     |      |      |      | -1.2      |
| 23630.peg.2437         | tRNA modification Bacteria                          | tRNA dihydrouridine synthase B (EC 1.-.-.)                                           | 1.0  | 0.7  | 0.7  | 0.7       |
| 23630.peg.3605         | tRNA modification Bacteria                          | COG0613, Predicted metal-dependent phosphoesterases (PHP family)                     | 1.0  |      | 0.9  | 0.6       |
| 23630.peg.2335         | tRNA modification Bacteria                          | tRNA dimethylallyltransferase (EC 2.5.1.75)                                          |      | -1.1 |      | -0.8      |
| 23630.peg.4875         | tRNA modification Bacteria                          | tRNA 5-methylaminomethyl-2-thiouridine synthase TusA                                 |      |      |      | -1.1      |
| 23630.peg.4630         | tRNA modification Bacteria                          | tRNA(Cytosine32)-2-thiocytidine synthetase                                           | 0.8  |      | 1.0  |           |
| 23630.peg.113          | tRNA processing                                     | tRNA-specific adenosine-34 deaminase (EC 3.5.4.-)                                    |      |      |      | -1.1      |
| <b>Stress Response</b> |                                                     |                                                                                      |      |      |      |           |
| 23630.peg.4169         | Bacterial hemoglobins                               | diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)   | -0.6 | -1.0 |      | 1.2 -0.7  |
| 23630.peg.80           | Bacterial hemoglobins                               | diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)   | -1.0 |      |      |           |
| 23630.peg.1142         | Choline and Betaine Uptake and Betaine Biosynthesis | Sarcosine oxidase delta subunit (EC 1.5.3.1)                                         | 1.0  | 1.1  |      | 1.2       |
| 23630.peg.1141         | Choline and Betaine Uptake and Betaine Biosynthesis | Sarcosine oxidase alpha subunit (EC 1.5.3.1)                                         | 1.4  | 1.1  |      | 0.5       |
| 23630.peg.1690         | Choline and Betaine Uptake and Betaine Biosynthesis | Choline-sulfatase (EC 3.1.6.6)                                                       | -1.2 |      | -1.0 | -0.8      |
| 23630.peg.2149         | Choline and Betaine Uptake and Betaine Biosynthesis | L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1)       |      | -1.1 | -0.8 | -1.2      |
| 23630.peg.2732         | Choline and Betaine Uptake and Betaine Biosynthesis | High-affinity choline uptake protein BetT                                            | -1.7 | -1.1 |      | -1.0      |
| 23630.peg.524          | Choline and Betaine Uptake and Betaine Biosynthesis | Sarcosine oxidase beta subunit (EC 1.5.3.1)                                          |      | 1.0  |      |           |
| 23630.peg.329          | Glutaredoxins                                       | Glutaredoxin-related protein                                                         | 0.8  | 0.9  |      | 1.2       |
| 23630.peg.1271         | Glutaredoxins                                       | Glutaredoxin 3 (Grx3)                                                                | 0.8  | 0.7  | 0.8  | 1.0       |
| 23630.peg.4151         | Glutathione: Non-redox reactions                    | Glutathione S-transferase (EC 2.5.1.18)                                              | 1.2  | 2.2  |      | 0.9 1.5   |
| 23630.peg.2786         | Glutathione: Non-redox reactions                    | Glutathione S-transferase (EC 2.5.1.18)                                              | -1.0 | -1.4 |      | -1.0 -1.5 |
| 23630.peg.4931         | Glutathione: Non-redox reactions                    | Glutathione S-transferase (EC 2.5.1.18)                                              | -1.0 | -1.4 |      | -1.0 -1.5 |
| 23630.peg.3491         | Glutathione: Non-redox reactions                    | Glutathione S-transferase, unnamed subgroup (EC 2.5.1.18)                            |      |      | 0.8  | 1.0       |
| 23630.peg.4529         | Glutathione: Non-redox reactions                    | Glutathione S-transferase, unnamed subgroup (EC 2.5.1.18)                            | -2.6 | -2.6 | -0.8 | -0.8      |

|                                       |                                                              |                                                                                                            |      |      |      |      |      |
|---------------------------------------|--------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.10                          | Glutathione-dependent pathway of formaldehyde detoxification | Transcriptional regulator, LysR family, in formaldehyde detoxification operon                              | -1.2 |      |      |      |      |
| 23630.peg.2439                        | Heat shock dnaK gene cluster extended                        | Ribosomal protein L11 methyltransferase (EC 2.1.1.-)                                                       | 1.0  |      | 0.8  |      |      |
| 23630.peg.591                         | Osmoregulation                                               | Osmotically inducible protein OsmY                                                                         |      |      |      | 1.2  |      |
| 23630.peg.4061                        | Osmoregulation                                               | Outer membrane protein A precursor                                                                         |      |      |      | -1.0 |      |
| 23630.peg.1341                        | Oxidative stress                                             | Alkyl hydroperoxide reductase subunit C-like protein                                                       | 1.8  | 1.1  |      | 1.7  | 1.7  |
| 23630.peg.4145                        | Oxidative stress                                             | Redox-sensitive transcriptional activator SoxR                                                             | 0.9  | 0.9  |      |      | -1.4 |
| 23630.peg.3087                        | Oxidative stress                                             | Catalase (EC 1.11.1.6)                                                                                     | -1.3 |      |      |      | -1.7 |
| 23630.peg.385                         | Oxidative stress                                             | Organic hydroperoxide resistance protein                                                                   |      |      |      | 1.4  |      |
| 23630.peg.2017                        | Protection from Reactive Oxygen Species                      | Cytochrome c551 peroxidase (EC 1.11.1.5)                                                                   |      |      |      | -1.4 |      |
| 23630.peg.1825                        | Rubrerethrin                                                 | Rubredoxin                                                                                                 | 1.0  | 0.9  |      | 0.8  |      |
| 23630.peg.2726                        | Rubrerethrin                                                 | Rubredoxin                                                                                                 | -1.5 | -1.3 |      |      |      |
| 23630.peg.3193                        | Synthesis of osmoregulated periplasmic glucans               | Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)                                                               | -2.1 | -1.4 |      |      | -0.7 |
| 23630.peg.234                         | Universal stress protein family                              | Universal stress protein E                                                                                 |      | -0.8 |      | -1.6 |      |
| 23630.peg.2892                        | Uptake of selenate and selenite                              | Various polyols ABC transporter, ATP-binding component                                                     | 1.4  |      | -0.7 |      | 0.3  |
| 23630.peg.1496                        | Uptake of selenate and selenite                              | Various polyols ABC transporter, periplasmic substrate-binding protein                                     |      |      | -1.3 |      | -0.8 |
| <b>Sulfur Metabolism</b>              |                                                              |                                                                                                            |      |      |      |      |      |
| 23630.peg.1340                        | Alkanesulfonate assimilation                                 | FMN reductase (EC 1.5.1.29)                                                                                | 1.6  | 1.4  | 0.6  |      | 1.8  |
| 23630.peg.2835                        | Alkanesulfonate assimilation                                 | ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components                           | 1.2  | 2.0  | 0.7  | 0.9  | 1.5  |
| 23630.peg.2831                        | Alkanesulfonate assimilation                                 | Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17)                                          | 2.2  | 1.5  | 0.5  | 1.0  | 1.3  |
| 23630.peg.1355                        | Alkanesulfonate assimilation                                 | Acyl-CoA dehydrogenase; probable dibenzothiophene desulfurization enzyme                                   | 1.0  | 0.4  |      | 0.2  | 1.2  |
| 23630.peg.1351                        | Alkanesulfonate assimilation                                 | ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components                           | 1.3  | 0.8  |      | 1.8  | 1.1  |
| 23630.peg.2846                        | Alkanesulfonate assimilation                                 | Acyl-CoA dehydrogenase; probable dibenzothiophene desulfurization enzyme                                   | 1.1  | 1.2  |      |      | 0.7  |
| 23630.peg.1334                        | Alkanesulfonate assimilation                                 | Organosulfonate utilization protein SsuF                                                                   |      |      |      | 1.0  |      |
| 23630.peg.1349                        | Alkanesulfonate assimilation                                 | Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB | -1.0 |      |      |      |      |
| 23630.peg.1336                        | Alkanesulfonates Utilization                                 | Alkanesulfonates transport system permease protein                                                         |      |      |      | 1.3  |      |
| 23630.peg.66                          | Inorganic Sulfur Assimilation                                | Oxidoreductase probably involved in sulfite reduction                                                      | -1.2 | -1.3 |      | -1.2 | -1.6 |
| <b>Virulence, Disease and Defense</b> |                                                              |                                                                                                            |      |      |      |      |      |
| 23630.peg.3837                        | Arsenic resistance                                           | Arsenical resistance operon repressor                                                                      |      | -1.0 |      |      |      |
| 23630.peg.2888                        | Beta-lactamase                                               | Beta-lactamase (EC 3.5.2.6)                                                                                |      | 1.1  |      | 1.2  |      |
| 23630.peg.3320                        | Cobalt-zinc-cadmium resistance                               | Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA                             |      | -1.1 |      |      | -0.8 |
| 23630.peg.1006                        | Cobalt-zinc-cadmium resistance                               | Heavy metal RND efflux outer membrane protein, CzcC family                                                 | -1.6 |      |      | -0.9 | -1.0 |
| 23630.peg.1054                        | Cobalt-zinc-cadmium resistance                               | Heavy metal sensor histidine kinase                                                                        | -1.2 |      |      |      | -1.1 |
| 23630.peg.1053                        | Cobalt-zinc-cadmium resistance                               | Copper-sensing two-component system response regulator CusR                                                | -1.5 | -0.7 | -0.6 | -1.6 | -1.1 |
| 23630.peg.1007                        | Cobalt-zinc-cadmium resistance                               | Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family                           | -1.9 |      |      |      | -1.2 |
| 23630.peg.1008                        | Cobalt-zinc-cadmium resistance                               | Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA                             | -2.4 | -1.1 | -1.2 | -1.2 | -1.9 |
| 23630.peg.1027                        | Cobalt-zinc-cadmium resistance                               | Heavy metal RND efflux outer membrane protein, CzcC family                                                 | -2.0 | -1.6 | -0.7 |      | -2.4 |
| 23630.peg.747                         | Cobalt-zinc-cadmium resistance                               | Cobalt-zinc-cadmium resistance protein                                                                     |      |      |      | 1.7  |      |
| 23630.peg.3214                        | Cobalt-zinc-cadmium resistance                               | DNA-binding heavy metal response regulator                                                                 | -0.9 |      |      | -1.1 |      |
| 23630.peg.3318                        | Cobalt-zinc-cadmium resistance                               | Heavy metal RND efflux outer membrane protein, CzcC family                                                 | -1.5 |      |      | -1.1 |      |

|                                             |                                                                                       |                                                                                                                                   |      |      |      |      |      |
|---------------------------------------------|---------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.3477                              | Copper homeostasis                                                                    | Multicopper oxidase                                                                                                               | -1.0 |      | -0.6 |      | -0.7 |
| 23630.peg.1051                              | Copper homeostasis                                                                    | Copper tolerance protein                                                                                                          | -1.4 |      |      |      | -0.7 |
| 23630.peg.1039                              | Copper homeostasis                                                                    | Multicopper oxidase                                                                                                               | -1.3 | -0.6 |      | -0.9 | -1.0 |
| 23630.peg.1037                              | Copper homeostasis                                                                    | Copper resistance protein B                                                                                                       | -1.2 |      |      |      | -1.0 |
| 23630.peg.1038                              | Copper homeostasis                                                                    | Multicopper oxidase                                                                                                               | -1.7 |      |      |      | -1.4 |
| 23630.peg.1050                              | Copper homeostasis                                                                    | Copper tolerance protein                                                                                                          | -2.0 |      |      |      | -1.7 |
| 23630.peg.2565                              | Copper homeostasis                                                                    | Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5);<br>Copper-translocating P-type ATPase (EC 3.6.3.4) | -2.2 | 0.6  |      |      | -1.8 |
| 23630.peg.1045                              | Copper homeostasis                                                                    | Copper chaperone                                                                                                                  | -2.2 | -1.1 | -0.9 |      | -2.1 |
| 23630.peg.2567                              | Copper homeostasis                                                                    | Copper chaperone                                                                                                                  | -2.7 | -1.6 | -1.3 |      | -2.6 |
| 23630.peg.2571                              | Copper homeostasis                                                                    | Multidrug resistance transporter, Bcr/CflA family                                                                                 | 1.0  |      |      |      |      |
| 23630.peg.3478                              | Copper homeostasis                                                                    | Copper tolerance protein                                                                                                          | -1.1 |      |      |      |      |
| 23630.peg.2822                              | Copper homeostasis: copper tolerance                                                  | Magnesium and cobalt efflux protein CorC                                                                                          |      |      |      |      | -1.4 |
| 23630.peg.1705                              | Lysozyme inhibitors                                                                   | Inhibitor of vertebrate lysozyme precursor                                                                                        | -1.0 |      |      |      | -0.9 |
| 23630.peg.3115                              | MexE-MexF-OprN Multidrug Efflux System                                                | Outer membrane protein OprN                                                                                                       |      | -1.1 | 0.7  |      | -0.9 |
| 23630.peg.1930                              | Multidrug Resistance Efflux Pumps                                                     | Multidrug and toxin extrusion (MATE) family efflux pump YdhE/NorM, homolog                                                        |      | 1.0  |      |      | 0.7  |
| 23630.peg.2570                              | Multidrug Resistance Efflux Pumps                                                     | RND efflux system, inner membrane transporter CmeB                                                                                | 1.3  |      |      |      | 0.6  |
| 23630.peg.717                               | Multidrug Resistance Efflux Pumps                                                     | RND efflux system, outer membrane lipoprotein CmeC                                                                                |      | 1.0  |      |      | 0.1  |
| 23630.peg.715                               | Multidrug Resistance Efflux Pumps                                                     | Membrane fusion protein of RND family multidrug efflux pump                                                                       |      |      | 0.8  | 1.2  |      |
| 23630.peg.4710                              | Multidrug Resistance Efflux Pumps                                                     | RND multidrug efflux transporter; Acriflavin resistance protein                                                                   |      | -1.3 |      | -0.9 |      |
| 23630.peg.4877                              | Multidrug Resistance Efflux Pumps                                                     | Multidrug and toxin extrusion (MATE) family efflux pump YdhE/NorM                                                                 |      |      | 1.1  |      |      |
| 23630.peg.89                                | Multidrug Resistance Efflux Pumps                                                     | RND efflux system, inner membrane transporter CmeB                                                                                | -1.5 |      |      |      |      |
| 23630.peg.716                               | Multidrug Resistance Efflux Pumps                                                     | RND efflux system, inner membrane transporter CmeB                                                                                | -1.5 |      |      |      |      |
| 23630.peg.2775                              | Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins) | LSU ribosomal protein L20p                                                                                                        |      | -0.8 |      |      | -1.1 |
| 23630.peg.4942                              | Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins) | LSU ribosomal protein L20p                                                                                                        |      | -0.8 |      |      | -1.1 |
| 23630.peg.2774                              | Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins) | LSU ribosomal protein L35p                                                                                                        |      |      |      | 1.0  |      |
| 23630.peg.4943                              | Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins) | LSU ribosomal protein L35p                                                                                                        |      |      |      | 1.0  |      |
| 23630.peg.942                               | Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins) | Translation elongation factor Tu                                                                                                  |      |      |      | 1.4  |      |
| 23630.peg.1120                              | Tolerance to colicin E2                                                               | Inner membrane protein CreD                                                                                                       | -0.9 | -1.0 |      |      | -0.6 |
| <b>DEGs non classified in RAST Category</b> |                                                                                       |                                                                                                                                   |      |      |      |      |      |
| 23630.peg.4130                              |                                                                                       | (R)-3-hydroxydecanoyl-ACP:CoA transacylase PhaG (3-hydroxyacyl-CoA-acyl carrier protein transferase) (EC 2.4.1.-)                 | -1.3 |      | 0.8  |      |      |
| 23630.peg.3213                              |                                                                                       | (Y14336) putative extracellular protein containing predicted 35aa signal peptide                                                  | -1.1 |      |      |      |      |
| 23630.peg.4156                              |                                                                                       | 2-aminoethylphosphonate uptake and metabolism regulator                                                                           |      |      |      | 1.1  |      |
| 23630.peg.4528                              |                                                                                       | 2-Oxobutyrate oxidase, putative                                                                                                   |      | -1.3 |      |      |      |
| 23630.peg.4535                              |                                                                                       | 2-Oxobutyrate oxidase, putative                                                                                                   | -1.6 |      |      |      |      |
| 23630.peg.2048                              |                                                                                       | 33 kDa chaperonin (Heat shock protein 33) (HSP33)                                                                                 | 1.3  |      | 0.9  |      |      |
| 23630.peg.4111                              |                                                                                       | 3-hydroxyisobutyryl-CoA hydrolase (EC 3.1.2.4)                                                                                    | 1.7  |      |      |      |      |
| 23630.peg.2978                              |                                                                                       | ABC transporter ATP-binding protein YvcR                                                                                          | 1.0  | 0.7  | 0.8  |      | 0.8  |
| 23630.peg.2742                              |                                                                                       | ABC transporter permease protein                                                                                                  |      | -1.4 |      |      |      |

|                |                                                                                                                                                        |      |      |      |      |      |
|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.4975 | ABC transporter permease protein                                                                                                                       | -1.4 |      |      |      |      |
| 23630.peg.3748 | ABC transporter, ATP-binding/permease protein                                                                                                          |      | -0.6 |      | -1.2 |      |
| 23630.peg.2915 | ABC transporter, periplasmic substrate-binding protein                                                                                                 |      | 1.0  | 0.6  |      | 0.8  |
| 23630.peg.2484 | ABC transporter, permease protein                                                                                                                      | -0.6 | -1.2 |      | -0.8 |      |
| 23630.peg.695  | ABC transporter, permease protein                                                                                                                      |      | -1.2 | 0.8  |      |      |
| 23630.peg.3638 | ABC transporter, transmembrane region:ABC transporter:Peptidase C39, bacteriocin processing                                                            |      |      | -0.7 | -1.0 |      |
| 23630.peg.2228 | ABC-2                                                                                                                                                  | 1.1  |      | 0.8  |      | 0.7  |
| 23630.peg.480  | ABC-type amino acid transport/signal transduction system                                                                                               |      |      |      | -1.0 |      |
| 23630.peg.3350 | ABC-type antimicrobial peptide transport system, ATPase component                                                                                      | 1.1  |      | -0.6 |      | 0.7  |
| 23630.peg.835  | ABC-type branched-chain amino acid transport systems, ATPase component                                                                                 | 1.0  | 0.9  |      |      | 0.6  |
| 23630.peg.1995 | ABC-type multidrug transport system, permease component                                                                                                | -1.0 |      |      |      | -0.6 |
| 23630.peg.1996 | ABC-type multidrug transport system, permease component                                                                                                | -1.0 | -0.7 |      | -0.9 |      |
| 23630.peg.761  | Acyl-CoA dehydrogenase (EC 1.3.99.3)                                                                                                                   | 0.9  | 0.9  | 1.0  |      | 1.3  |
| 23630.peg.254  | Acyl-CoA long-chain enzyme transcriptional related heme family                                                                                         |      | 0.8  | 2.1  |      | 1.6  |
| 23630.peg.4621 | Aerobic C4-dicarboxylate transporter for fumarate, L-malate, D-malate, succinate                                                                       |      | -0.9 |      |      | -1.6 |
| 23630.peg.3641 | aerotaxis receptor, putative                                                                                                                           |      |      | -1.1 |      |      |
| 23630.peg.293  | Aldose 1-epimerase                                                                                                                                     | -1.4 |      |      | -0.9 |      |
| 23630.peg.4114 | Alkyl sulfatase and related hydrolases                                                                                                                 | -1.7 |      | 0.4  |      | -0.9 |
| 23630.peg.2385 | alpha/beta hydrolase fold                                                                                                                              | 1.1  |      |      |      |      |
| 23630.peg.1873 | Altronate hydrolase (EC 4.2.1.7)                                                                                                                       | 1.0  |      |      |      |      |
| 23630.peg.2417 | Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine                                                                       |      |      | -1.0 |      | -0.9 |
| 23630.peg.491  | amino acid permease-associated region                                                                                                                  | -1.2 |      |      |      | 0.8  |
| 23630.peg.642  | AraC-type DNA-binding domain-containing proteins                                                                                                       | -1.0 | -0.8 | -0.6 |      |      |
| 23630.peg.1385 | AttT protein                                                                                                                                           |      |      |      |      | -1.0 |
| 23630.peg.2371 | Azurin                                                                                                                                                 | -1.1 |      |      |      |      |
| 23630.peg.4094 | Bacterioferritin-associated ferredoxin                                                                                                                 | 2.9  | 1.9  | 0.7  | 1.3  | 1.7  |
| 23630.peg.2840 | Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase ( NADPH:quinone reductase) (EC 1.1.1.-); Similar to arginate lyase | -1.2 | -1.5 | 1.0  | -1.3 | -0.6 |
| 23630.peg.3475 | Bll2208 protein                                                                                                                                        | -1.0 | -1.0 | -0.6 |      |      |
| 23630.peg.4536 | bmp family protein                                                                                                                                     | -1.1 |      |      | -1.2 |      |
| 23630.peg.1747 | BNR/Asp-box repeat protein                                                                                                                             | 1.7  | 1.5  | 2.6  | 1.2  | 1.3  |
| 23630.peg.4558 | BNR/Asp-box repeat protein                                                                                                                             |      | -0.7 |      |      | -1.4 |
| 23630.peg.2699 | Bsl0049 protein                                                                                                                                        |      |      |      | -1.3 |      |
| 23630.peg.4349 | Ca ion P-type ATPase                                                                                                                                   |      |      | 0.5  | -1.1 |      |
| 23630.peg.539  | Carboxynorspermidine decarboxylase                                                                                                                     | 1.2  |      | 1.0  |      |      |
| 23630.peg.538  | Carboxynorspermidine dehydrogenase                                                                                                                     |      |      | 0.7  | 1.3  |      |
| 23630.peg.394  | CcsA-related protein                                                                                                                                   |      |      | 1.1  |      |      |
| 23630.peg.3893 | Cell division inhibitor-related protein                                                                                                                | 1.3  | 1.3  |      |      | 1.1  |
| 23630.peg.2719 | chemotaxis protein MotB-related protein                                                                                                                | -1.7 | -1.1 | -0.7 | -0.8 | -1.2 |
| 23630.peg.107  | Citrate lyase beta chain (EC 4.1.3.6)                                                                                                                  | 2.0  |      | 1.0  |      |      |
| 23630.peg.2845 | Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases                                | -1.6 | -1.2 |      |      |      |
| 23630.peg.223  | COG0553: Superfamily II DNA/RNA helicases, SNF2 family                                                                                                 |      |      |      | 1.0  |      |

|                |                                                                                                        |      |      |      |      |      |
|----------------|--------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.1056 | COG0582: Integrase                                                                                     | -1.0 |      |      |      |      |
| 23630.peg.4401 | COG2907: Amine oxidase, flavin-containing                                                              | 1.2  |      |      | 1.1  | 1.3  |
| 23630.peg.2518 | COG3744: Uncharacterized protein conserved in bacteria                                                 |      |      |      |      | -1.0 |
| 23630.peg.2853 | COG5430: Uncharacterized secreted protein                                                              | 1.5  |      | 0.6  |      | 1.1  |
| 23630.peg.111  | COGs COG3777                                                                                           |      |      |      | 1.1  |      |
| 23630.peg.466  | cold acclimation protein B                                                                             | -0.9 | -1.2 | -0.8 |      | -1.6 |
| 23630.peg.3566 | competence protein ComEA helix-hairpin-helix repeat protein                                            |      | -0.7 | -0.6 |      | -1.0 |
| 23630.peg.2801 | competence protein ComEA helix-hairpin-helix repeat protein                                            | -0.7 | -0.8 | -1.0 |      | -1.1 |
| 23630.peg.880  | Conserved domain protein                                                                               | 1.8  | 1.6  | 0.6  | 1.2  | 1.9  |
| 23630.peg.2288 | Conserved domain protein                                                                               | -0.8 | -1.0 |      |      | -0.7 |
| 23630.peg.1043 | Conserved domain protein                                                                               | -1.4 |      |      | -1.0 | -1.2 |
| 23630.peg.3466 | Conserved domain protein                                                                               |      |      | 0.8  | 1.8  |      |
| 23630.peg.1805 | Conserved domain protein                                                                               |      |      |      | 1.4  |      |
| 23630.peg.4260 | conserved hypothetical protein                                                                         | -1.6 |      |      |      |      |
| 23630.peg.4554 | Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)                                            | -1.0 |      |      |      |      |
| 23630.peg.41   | Cysteine desulfurase CsdA-CsdE, sulfur acceptor protein CsdE                                           | -1.0 | -0.7 | -0.6 |      |      |
| 23630.peg.701  | Cytochrome b                                                                                           | 1.1  | 1.3  | 2.6  | 0.7  | 2.0  |
| 23630.peg.3731 | Cytochrome B561                                                                                        |      | -1.0 |      | -1.5 |      |
| 23630.peg.1973 | Cytochrome c family protein                                                                            |      | -0.7 |      | 1.1  | -0.7 |
| 23630.peg.1036 | Cytochrome c family protein                                                                            | -1.0 |      | -0.5 |      | -1.2 |
| 23630.peg.1979 | DedA family protein                                                                                    | 0.9  | 1.0  | 0.8  | 0.9  | 0.9  |
| 23630.peg.4300 | deoxyribodipyrimidine photolyase-related protein                                                       | -1.3 |      |      |      |      |
| 23630.peg.1645 | diguanylate cyclase                                                                                    | -0.9 | -1.0 | -0.5 |      |      |
| 23630.peg.140  | diguanylate cyclase                                                                                    | -1.1 |      |      |      |      |
| 23630.peg.2167 | diguanylate cyclase with PAS/PAC sensor                                                                |      | 0.5  | 0.7  |      | -1.3 |
| 23630.peg.225  | diguanylate cyclase/phosphodiesterase                                                                  | -0.8 | -1.3 | -0.6 | -1.2 | -0.9 |
| 23630.peg.987  | dimethyladenosine transferase( EC:2.1.1.48 )                                                           | 1.1  | 0.9  | 1.4  | 1.2  | 1.0  |
| 23630.peg.3102 | DNA polymerase-like protein PA0670                                                                     |      | -1.0 |      |      | -0.8 |
| 23630.peg.3013 | DNA-directed RNA polymerase specialized sigma subunit, sigma24-like                                    |      | -0.7 |      |      | -1.0 |
| 23630.peg.3619 | Dolichol-phosphate mannosyltransferase (EC 2.4.1.83) in lipid-linked oligosaccharide synthesis cluster | -1.6 |      |      | 1.1  |      |
| 23630.peg.4136 | Endonuclease I precursor (EC 3.1.21.1)                                                                 |      | 0.6  | 0.7  |      | -1.6 |
| 23630.peg.1789 | Endonuclease/exonuclease/phosphatase family protein                                                    |      |      |      | 1.0  |      |
| 23630.peg.3077 | Endonuclease/Exonuclease/phosphatase family protein                                                    | -2.1 |      |      | -1.1 |      |
| 23630.peg.1921 | Endoribonuclease L-PSP                                                                                 |      |      | 1.8  |      | 0.9  |
| 23630.peg.2865 | Endoribonuclease L-PSP                                                                                 |      |      |      | -1.3 |      |
| 23630.peg.4110 | Enoyl-CoA hydratase [valine degradation] (EC 4.2.1.17)                                                 | 1.6  | 0.8  | 0.8  |      |      |
| 23630.peg.860  | Epoxide hydrolase (EC 3.3.2.9)                                                                         | -0.9 | -1.0 | 0.7  | -1.4 |      |
| 23630.peg.3506 | Ethanolamine ammonia-lyase heavy chain (EC 4.3.1.7)                                                    |      |      | 1.1  |      |      |
| 23630.peg.2728 | Ethanolamine utilization protein eutQ                                                                  | -1.1 |      |      | -1.3 |      |
| 23630.peg.4729 | Ferrichrome-iron receptor                                                                              | -0.6 | -1.0 | -1.0 |      | -1.6 |
| 23630.peg.416  | Ferrichrome-iron receptor                                                                              | -1.0 | -1.2 | 0.6  |      | -1.9 |
| 23630.peg.411  | Ferrichrome-iron receptor                                                                              |      |      |      | 1.0  |      |
| 23630.peg.2632 | Ferrichrome-iron receptor                                                                              |      | -0.7 | 1.2  | 1.0  |      |
| 23630.peg.2354 | Fe-S OXIDOREDUCTASE (1.8.-.-)                                                                          | 1.7  | 0.7  |      | 1.3  |      |
| 23630.peg.169  | FHA domain containing protein                                                                          |      |      |      | -1.0 |      |
| 23630.peg.3339 | FIG001454: Transglutaminase-like enzymes, putative cysteine proteases                                  | -1.3 |      |      | -0.7 |      |

|                |                                                      |      |      |      |      |      |
|----------------|------------------------------------------------------|------|------|------|------|------|
| 23630.peg.4337 | FIG002188: hypothetical protein                      |      |      |      | 1.1  |      |
| 23630.peg.3483 | FIG002283: Isochorismatase family protein            | 1.1  | 0.9  | 0.9  |      | 0.7  |
| 23630.peg.85   | FIG002577: Putative lipoprotein precursor            |      |      |      |      | 1.0  |
| 23630.peg.4399 | FIG002994: Putative transcriptional regulator        | 1.3  |      |      |      | 1.2  |
| 23630.peg.2349 | FIG003573: hypothetical protein                      |      |      |      | 1.0  |      |
| 23630.peg.3286 | FIG00456413: hypothetical protein                    | -1.1 | -0.9 |      |      |      |
| 23630.peg.2161 | FIG004891: hypothetical protein in carnitine cluster | -1.1 |      | -0.5 |      |      |
| 23630.peg.3915 | FIG005107: hypothetical protein                      | -2.0 | -1.8 |      | -0.8 | -1.1 |
| 23630.peg.2474 | FIG006045: Sigma factor, ECF subfamily               |      | 1.8  |      |      |      |
| 23630.peg.814  | FIG00784312: hypothetical protein                    | 1.9  |      |      | 1.2  |      |
| 23630.peg.2266 | FIG00784450: hypothetical protein                    | -1.2 | -1.5 |      |      | -1.4 |
| 23630.peg.2807 | FIG00857858: hypothetical protein                    | 1.0  | 0.9  |      |      |      |
| 23630.peg.4651 | FIG00953208: hypothetical protein                    |      |      |      | -1.0 |      |
| 23630.peg.2745 | FIG00953323: hypothetical protein                    |      |      |      | -1.1 | -0.6 |
| 23630.peg.4972 | FIG00953323: hypothetical protein                    |      |      |      | -1.1 | -0.6 |
| 23630.peg.3737 | FIG00953335: hypothetical protein                    | 1.8  |      |      |      | 0.7  |
| 23630.peg.1368 | FIG00953394: hypothetical protein                    | 2.0  | 1.5  |      | 0.4  | 1.5  |
| 23630.peg.1316 | FIG00953395: hypothetical protein                    |      |      | 1.4  | 0.6  | 0.9  |
| 23630.peg.1938 | FIG00953808: hypothetical protein                    |      | -1.1 | -0.9 | 1.0  | -1.2 |
| 23630.peg.3752 | FIG00954136: hypothetical protein                    | 0.9  | 0.8  | 1.0  |      | 0.8  |
| 23630.peg.1456 | FIG00954150: hypothetical protein                    |      |      | 1.7  |      | 0.6  |
| 23630.peg.3869 | FIG00954461: hypothetical protein                    |      |      | 0.6  | 1.0  |      |
| 23630.peg.3990 | FIG00954516: hypothetical protein                    | -1.0 | -1.3 | -0.6 | -1.0 | -1.8 |
| 23630.peg.404  | FIG00955190: hypothetical protein                    |      |      |      | 1.4  |      |
| 23630.peg.1040 | FIG00955197: hypothetical protein                    | -1.8 |      |      | -0.9 | -1.3 |
| 23630.peg.3223 | FIG00955278: hypothetical protein                    |      | -1.0 |      |      | -1.4 |
| 23630.peg.774  | FIG00955339: hypothetical protein                    | 1.4  |      | 1.0  |      |      |
| 23630.peg.1648 | FIG00955422: hypothetical protein                    |      |      |      |      | -1.0 |
| 23630.peg.4005 | FIG00955424: hypothetical protein                    | -1.2 | -1.6 | -0.7 |      | -1.1 |
| 23630.peg.2164 | FIG00955680: hypothetical protein                    | 1.7  |      |      | 1.0  |      |
| 23630.peg.3640 | FIG00955751: hypothetical protein                    | 1.0  |      |      |      |      |
| 23630.peg.1425 | FIG00955818: hypothetical protein                    | -1.1 |      |      |      |      |
| 23630.peg.662  | FIG00955938: hypothetical protein                    | -1.0 |      |      | 1.0  | -0.7 |
| 23630.peg.1369 | FIG00956018: hypothetical protein                    | 2.1  | 1.3  |      | 0.9  | 1.6  |
| 23630.peg.3259 | FIG00956188: hypothetical protein                    |      |      |      | 1.0  |      |
| 23630.peg.943  | FIG00956751: hypothetical protein                    |      |      |      | -1.0 |      |
| 23630.peg.323  | FIG00957314: hypothetical protein                    |      |      | 1.1  | 1.7  |      |
| 23630.peg.4200 | FIG00957354: hypothetical protein                    |      |      |      | -1.5 |      |
| 23630.peg.785  | FIG00957593: hypothetical protein                    |      |      | 1.2  | -1.1 | 0.7  |
| 23630.peg.1033 | FIG00958355: hypothetical protein                    | -2.6 |      | -0.3 |      | -1.9 |
| 23630.peg.2986 | FIG00958794: hypothetical protein                    | -1.1 | -1.0 | -0.7 |      | -0.7 |
| 23630.peg.3189 | FIG00959020: hypothetical protein                    | -0.9 | -0.6 | -0.9 |      | -1.6 |
| 23630.peg.153  | FIG00959330: hypothetical protein                    |      | -1.3 |      |      | -0.9 |
| 23630.peg.4238 | FIG00960458: hypothetical protein                    | -1.2 |      |      |      |      |
| 23630.peg.168  | FIG00964654: hypothetical protein                    | -1.1 |      | 0.7  | -1.1 |      |
| 23630.peg.4510 | FIG01066055: hypothetical protein                    | -1.1 | -0.8 |      |      |      |
| 23630.peg.256  | FIG01200150: hypothetical protein                    |      |      | 1.1  |      | 0.9  |



|                |                                                     |      |      |      |      |      |
|----------------|-----------------------------------------------------|------|------|------|------|------|
| 23630.peg.1272 | FIG136845: Rhodanese-related sulfurtransferase      | 1.1  |      | 1.1  | 1.2  |      |
| 23630.peg.4187 | FMN-dependent NADH-azoreductase                     |      | 0.6  | 0.6  | 1.0  |      |
| 23630.peg.97   | FOG: EAL domain protein                             |      |      |      | -1.3 |      |
| 23630.peg.318  | GCN5-related N-acetyltransferase                    | 1.1  |      |      |      |      |
| 23630.peg.2015 | GENE II AND X PROTEINS                              |      | -1.1 |      |      |      |
| 23630.peg.1091 | GGDEF domain protein                                | 1.1  |      |      |      |      |
| 23630.peg.3646 | glutamine ABC transporter ATP-binding component     |      | -1.3 | 1.1  | -0.5 |      |
| 23630.peg.4459 | Glycosyltransferase                                 | -1.2 |      |      | 1.1  |      |
| 23630.peg.3373 | Helicase subunit of the DNA excision repair complex |      |      |      | 1.4  |      |
| 23630.peg.3057 | HemK family modification methylase PA2179           | -1.0 |      |      |      |      |
| 23630.peg.1230 | Hemolysin activation/secretion protein              | -1.0 | -0.9 |      | -1.0 | -0.9 |
| 23630.peg.3664 | Hemolysin-type calcium-binding region               |      | 0.7  | 0.6  | -1.5 |      |
| 23630.peg.2283 | Heptose kinase WapQ, eukaryotic type                | -0.8 | -0.7 | -0.7 |      | -1.2 |
| 23630.peg.1997 | HlyD family secretion protein                       |      | -1.2 |      | -1.0 |      |
| 23630.peg.4716 | hydrolase, alpha/beta fold family                   |      |      |      | -1.5 |      |
| 23630.peg.3070 | Hydrolases of the alpha/beta superfamily            | -1.1 |      |      | -0.7 |      |
| 23630.peg.4031 | hypothetical membrane protein                       | -1.2 |      |      | -0.9 |      |
| 23630.peg.1748 | hypothetical protein                                | 2.2  | 2.1  | 3.5  | 1.0  | 2.6  |
| 23630.peg.767  | hypothetical protein                                | 2.8  | 2.8  | 1.0  | 2.4  | 2.0  |
| 23630.peg.1746 | hypothetical protein                                | 1.2  | 1.3  | 1.8  |      | 1.5  |
| 23630.peg.702  | hypothetical protein                                |      | 1.2  | 2.1  |      | 1.5  |
| 23630.peg.760  | hypothetical protein                                | 0.7  | 1.0  | 0.9  |      | 1.2  |
| 23630.peg.4924 | hypothetical protein                                |      |      | 0.7  |      | 1.1  |
| 23630.peg.3922 | hypothetical protein                                | 0.9  |      |      | 1.0  | 1.0  |
| 23630.peg.3029 | hypothetical protein                                | 1.5  | 1.3  |      |      | 1.0  |
| 23630.peg.2067 | hypothetical protein                                | 0.8  | 0.7  | 1.0  | 1.0  | 0.9  |
| 23630.peg.3024 | hypothetical protein                                | 0.7  |      | 1.0  | 0.9  | 0.8  |
| 23630.peg.3232 | hypothetical protein                                |      | 1.0  |      |      | 0.8  |
| 23630.peg.3023 | hypothetical protein                                | 0.9  |      | 1.0  |      | 0.8  |
| 23630.peg.2394 | hypothetical protein                                | 1.3  |      |      | 0.7  | 0.7  |
| 23630.peg.176  | hypothetical protein                                | 0.8  |      | 1.0  |      | 0.7  |
| 23630.peg.149  | hypothetical protein                                | 1.0  | 0.6  | 0.8  |      | 0.7  |
| 23630.peg.1108 | hypothetical protein                                | -1.0 |      |      |      | -0.7 |
| 23630.peg.3198 | hypothetical protein                                |      |      | -0.7 | -1.0 | -0.7 |
| 23630.peg.3900 | hypothetical protein                                | -1.0 |      |      |      | -0.7 |
| 23630.peg.4550 | hypothetical protein                                | -0.9 | -1.0 | -0.7 | -0.9 | -0.7 |
| 23630.peg.4377 | hypothetical protein                                | -1.1 |      | -0.2 | -0.7 | -0.7 |
| 23630.peg.2701 | hypothetical protein                                |      |      | -1.3 |      | -0.8 |
| 23630.peg.1707 | hypothetical protein                                | -1.1 | -1.1 |      |      | -0.8 |
| 23630.peg.493  | hypothetical protein                                | -1.0 | -0.8 | -0.7 |      | -0.8 |
| 23630.peg.2693 | hypothetical protein                                |      | -1.0 | -0.8 | -0.8 | -0.8 |
| 23630.peg.3931 | hypothetical protein                                |      | -1.6 |      |      | -0.9 |
| 23630.peg.2901 | hypothetical protein                                | -1.0 | -1.0 | -0.8 | -1.1 | -0.9 |
| 23630.peg.1028 | hypothetical protein                                | -1.9 |      |      | -0.7 | -0.9 |
| 23630.peg.1607 | hypothetical protein                                | -0.9 | -1.2 | -0.7 |      | -0.9 |
| 23630.peg.4981 | hypothetical protein                                | -1.1 | -1.5 | -0.7 | -1.0 | -0.9 |
| 23630.peg.3384 | hypothetical protein                                |      |      |      | -1.0 | -0.9 |

|                |                      |      |      |      |      |      |
|----------------|----------------------|------|------|------|------|------|
| 23630.peg.2900 | hypothetical protein |      | -1.1 |      |      | -0.9 |
| 23630.peg.3576 | hypothetical protein | -1.1 | -1.3 | -1.2 | -1.4 | -1.0 |
| 23630.peg.312  | hypothetical protein | -1.1 | -1.3 |      |      | -1.0 |
| 23630.peg.3222 | hypothetical protein | -1.8 |      | -0.3 | -2.0 | -1.0 |
| 23630.peg.3036 | hypothetical protein |      |      |      |      | -1.0 |
| 23630.peg.2821 | hypothetical protein | -1.8 | -1.0 | -0.5 | -1.6 | -1.0 |
| 23630.peg.1052 | hypothetical protein | -1.6 |      |      |      | -1.1 |
| 23630.peg.2903 | hypothetical protein | -0.7 | -1.2 | -1.4 | -1.1 | -1.1 |
| 23630.peg.319  | hypothetical protein |      |      |      |      | -1.2 |
| 23630.peg.2148 | hypothetical protein | -1.0 | -0.8 |      |      | -1.3 |
| 23630.peg.3019 | hypothetical protein | -3.0 | -2.6 |      | -2.3 | -1.3 |
| 23630.peg.4421 | hypothetical protein | -1.1 |      |      | -0.8 | -1.4 |
| 23630.peg.3022 | hypothetical protein |      | -1.0 | 0.6  |      | -1.4 |
| 23630.peg.190  | hypothetical protein | -0.8 | -1.1 | -0.8 | -1.4 | -1.4 |
| 23630.peg.2759 | hypothetical protein |      |      |      |      | -1.6 |
| 23630.peg.4958 | hypothetical protein |      |      |      |      | -1.6 |
| 23630.peg.1044 | hypothetical protein | -2.0 | -0.6 | -0.7 |      | -1.7 |
| 23630.peg.3981 | hypothetical protein | -1.5 | -1.6 |      | -0.7 | -1.7 |
| 23630.peg.4131 | hypothetical protein | -1.3 | -1.8 | -0.9 | -0.7 | -1.7 |
| 23630.peg.3580 | hypothetical protein | -1.0 | -1.2 |      |      | -1.7 |
| 23630.peg.1118 | hypothetical protein | -1.1 |      | -0.4 |      | -1.9 |
| 23630.peg.410  | hypothetical protein | -1.6 | -1.7 |      | -1.0 | -2.1 |
| 23630.peg.1599 | hypothetical protein |      |      |      | 1.4  |      |
| 23630.peg.4709 | hypothetical protein |      |      |      | 1.3  |      |
| 23630.peg.3389 | hypothetical protein |      |      |      | 1.3  |      |
| 23630.peg.1847 | hypothetical protein |      |      | 0.7  | 1.3  |      |
| 23630.peg.1743 | hypothetical protein | 0.8  |      |      | 1.3  |      |
| 23630.peg.664  | hypothetical protein |      |      |      | 1.2  |      |
| 23630.peg.3407 | hypothetical protein |      |      |      | 1.2  |      |
| 23630.peg.720  | hypothetical protein |      | 0.7  |      | 1.2  |      |
| 23630.peg.2338 | hypothetical protein |      |      |      | 1.2  |      |
| 23630.peg.1974 | hypothetical protein |      |      | 0.9  | 1.2  |      |
| 23630.peg.2009 | hypothetical protein |      | 1.5  |      | 1.1  |      |
| 23630.peg.772  | hypothetical protein |      | 0.6  |      | 1.1  |      |
| 23630.peg.381  | hypothetical protein |      |      | 0.8  | 1.1  |      |
| 23630.peg.2434 | hypothetical protein | 1.0  |      |      | 1.1  |      |
| 23630.peg.2220 | hypothetical protein |      |      |      | 1.1  |      |
| 23630.peg.2945 | hypothetical protein |      |      |      | 1.0  |      |
| 23630.peg.1121 | hypothetical protein |      | 0.6  |      | 1.0  |      |
| 23630.peg.145  | hypothetical protein |      | 0.6  |      | 1.0  |      |
| 23630.peg.2383 | hypothetical protein |      | 0.6  |      | 1.0  |      |
| 23630.peg.2190 | hypothetical protein |      |      |      | 1.0  |      |
| 23630.peg.800  | hypothetical protein | 1.2  |      |      | 0.9  |      |
| 23630.peg.3367 | hypothetical protein | 0.8  | 2.0  | 0.6  | 0.5  |      |
| 23630.peg.3808 | hypothetical protein | -1.0 |      |      | -0.6 |      |
| 23630.peg.1299 | hypothetical protein | -1.0 | -1.7 |      | -0.8 |      |
| 23630.peg.2492 | hypothetical protein |      | -1.0 |      | -0.9 |      |

|                |                      |      |      |      |      |
|----------------|----------------------|------|------|------|------|
| 23630.peg.1298 | hypothetical protein | -1.5 |      |      | -1.0 |
| 23630.peg.2837 | hypothetical protein |      |      |      | -1.0 |
| 23630.peg.412  | hypothetical protein | -1.3 |      |      | -1.0 |
| 23630.peg.3099 | hypothetical protein |      |      |      | -1.1 |
| 23630.peg.1301 | hypothetical protein | -0.9 |      |      | -1.1 |
| 23630.peg.3031 | hypothetical protein | -0.9 | -0.7 | 0.8  | -1.2 |
| 23630.peg.2838 | hypothetical protein | -1.1 |      | -0.5 | -1.2 |
| 23630.peg.4432 | hypothetical protein |      |      |      | -1.2 |
| 23630.peg.160  | hypothetical protein |      |      | 0.9  | -1.4 |
| 23630.peg.2882 | hypothetical protein | -0.6 |      | -0.6 | -1.5 |
| 23630.peg.4582 | hypothetical protein |      |      |      | -1.5 |
| 23630.peg.4523 | hypothetical protein | -1.1 | -0.8 |      | -1.7 |
| 23630.peg.4438 | hypothetical protein | -2.0 | -1.5 |      | -2.3 |
| 23630.peg.2507 | hypothetical protein | -0.7 |      | 1.5  |      |
| 23630.peg.1388 | hypothetical protein |      |      | 1.3  |      |
| 23630.peg.756  | hypothetical protein |      |      | 1.0  |      |
| 23630.peg.2225 | hypothetical protein |      |      | 1.0  |      |
| 23630.peg.678  | hypothetical protein | 0.9  | 0.6  | 1.0  |      |
| 23630.peg.3868 | hypothetical protein | 1.0  |      | 0.7  |      |
| 23630.peg.4597 | hypothetical protein | -1.1 | -0.6 | 0.7  |      |
| 23630.peg.4713 | hypothetical protein | -1.4 | -1.0 | -0.5 |      |
| 23630.peg.4285 | hypothetical protein | -1.0 | -0.7 | -0.6 |      |
| 23630.peg.3839 | hypothetical protein | -1.2 |      | -0.6 |      |
| 23630.peg.3301 | hypothetical protein | -1.0 | -1.2 | -0.6 |      |
| 23630.peg.1569 | hypothetical protein | -1.0 |      | -0.8 |      |
| 23630.peg.1338 | hypothetical protein | -0.4 | -1.2 | -0.8 |      |
| 23630.peg.2643 | hypothetical protein |      | 0.3  | -1.0 |      |
| 23630.peg.3705 | hypothetical protein | 1.4  | 0.7  |      |      |
| 23630.peg.3155 | hypothetical protein | -1.0 | -0.2 |      |      |
| 23630.peg.2795 | hypothetical protein | -1.3 | -0.9 |      |      |
| 23630.peg.3685 | hypothetical protein |      | -1.0 |      |      |
| 23630.peg.1300 | hypothetical protein | -0.8 | -1.0 |      |      |
| 23630.peg.3033 | hypothetical protein | -1.4 | -1.2 |      |      |
| 23630.peg.4357 | hypothetical protein |      | -1.4 |      |      |
| 23630.peg.221  | hypothetical protein |      | -1.4 |      |      |
| 23630.peg.3956 | hypothetical protein | -1.5 | -1.4 |      |      |
| 23630.peg.2402 | hypothetical protein | 1.0  |      |      |      |
| 23630.peg.2868 | hypothetical protein | -1.0 |      |      |      |
| 23630.peg.3065 | hypothetical protein | -1.0 |      |      |      |
| 23630.peg.697  | hypothetical protein | -1.0 |      |      |      |
| 23630.peg.1188 | hypothetical protein | -1.0 |      |      |      |
| 23630.peg.4133 | hypothetical protein | -1.0 |      |      |      |
| 23630.peg.3462 | hypothetical protein | -1.1 |      |      |      |
| 23630.peg.2703 | hypothetical protein | -1.2 |      |      |      |
| 23630.peg.4904 | hypothetical protein | -1.2 |      |      |      |
| 23630.peg.58   | hypothetical protein | -1.3 |      |      |      |
| 23630.peg.2734 | hypothetical protein | -1.4 |      |      |      |

|                |                                                                                                         |      |      |      |      |      |
|----------------|---------------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.3043 | hypothetical protein                                                                                    | -1.4 |      |      |      |      |
| 23630.peg.2141 | hypothetical protein                                                                                    | -1.5 |      |      |      |      |
| 23630.peg.4672 | hypothetical protein PA3071                                                                             |      |      |      | -1.0 |      |
| 23630.peg.2045 | hypothetical protein sometimes fused to ribosomal protein S6 glutaminyl transferase                     |      |      |      | 1.0  |      |
| 23630.peg.348  | Inactive homolog of metal-dependent proteases, putative molecular chaperone                             | 1.1  | 0.6  | 0.9  |      | 0.8  |
| 23630.peg.1971 | Integral membrane protein TerC                                                                          |      |      | -1.0 |      | -0.8 |
| 23630.peg.3688 | integral membrane sensor hybrid histidine kinase                                                        |      |      | -0.8 |      | -1.1 |
| 23630.peg.3471 | Integrase                                                                                               | -1.9 | -1.5 | -0.5 | -0.7 | -1.1 |
| 23630.peg.316  | Iron-regulated protein A precursor                                                                      | 2.0  | 1.6  |      | 1.5  | 1.0  |
| 23630.peg.3689 | Lipase chaperone (Lipase foldase) (Lipase helper protein) (Lipase activator protein) (Lipase modulator) | -1.3 |      |      |      |      |
| 23630.peg.663  | lipoprotein, putative                                                                                   | 1.2  | 1.0  | 1.1  | 1.0  | 1.0  |
| 23630.peg.3832 | lipoprotein, putative                                                                                   | 1.2  | 0.8  | 0.9  |      |      |
| 23630.peg.879  | lipoprotein, putative                                                                                   | 1.0  |      |      |      |      |
| 23630.peg.4358 | Lysine efflux permease                                                                                  |      |      |      |      | -1.0 |
| 23630.peg.2982 | Major outer membrane lipoprotein I                                                                      |      |      | 0.6  | 1.1  |      |
| 23630.peg.4707 | mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase( EC:2.7.7.22 )                    |      | 0.7  |      | 2.0  |      |
| 23630.peg.3623 | membrane protein, putative                                                                              |      | 1.0  |      |      | 0.7  |
| 23630.peg.4719 | membrane protein, putative                                                                              |      | 0.7  | 1.3  |      |      |
| 23630.peg.1376 | membrane protein, putative                                                                              | 1.0  |      |      |      |      |
| 23630.peg.3335 | Methyl-accepting chemotaxis protein                                                                     |      | -1.2 |      | -1.6 |      |
| 23630.peg.2102 | Methyl-accepting chemotaxis protein                                                                     | -2.2 | -1.5 | -1.5 | -1.8 |      |
| 23630.peg.2814 | Methyl-accepting chemotaxis protein                                                                     |      | -0.8 | -1.1 |      |      |
| 23630.peg.2459 | Methyl-accepting chemotaxis protein                                                                     |      |      | -1.5 |      |      |
| 23630.peg.656  | Methyl-accepting chemotaxis protein                                                                     | 1.0  |      |      |      |      |
| 23630.peg.1358 | MFS general substrate transporter                                                                       |      |      | 0.8  |      | 1.5  |
| 23630.peg.3942 | MFS transporter                                                                                         | 1.0  | 0.6  |      | 0.8  | 1.0  |
| 23630.peg.826  | Mobile element protein                                                                                  |      |      | 0.8  | 1.0  |      |
| 23630.peg.4982 | Mobile element protein                                                                                  | -1.6 | -1.5 |      | -2.9 |      |
| 23630.peg.3562 | Multidrug resistance protein A                                                                          |      |      |      | 1.7  |      |
| 23630.peg.4032 | NAD(FAD)-utilizing dehydrogenase, sl10175 homolog                                                       | 1.3  |      |      |      |      |
| 23630.peg.4144 | NADPH-dependent FMN reductase                                                                           | 2.6  | 1.1  | 1.3  |      | 1.9  |
| 23630.peg.2794 | N-ethylmaleimide reductase (EC 1.-.-.)                                                                  | -1.1 |      |      |      |      |
| 23630.peg.1673 | NLP/P60 family protein                                                                                  | 1.0  |      | 0.8  |      |      |
| 23630.peg.4527 | Nucleoside-binding outer membrane protein                                                               | -1.9 | -1.0 |      | -1.4 | -1.5 |
| 23630.peg.4385 | Nucleoside-binding outer membrane protein                                                               |      |      |      | -1.1 |      |
| 23630.peg.3207 | OmpA/MotB domain protein                                                                                | -1.4 | -1.0 |      |      |      |
| 23630.peg.1255 | Outer membrane protein                                                                                  | 0.9  | 1.0  |      |      | 0.8  |
| 23630.peg.2735 | Outer membrane protein (porin)                                                                          | -1.4 | -1.0 | -0.9 | -1.0 |      |
| 23630.peg.4616 | outer membrane protein H1                                                                               | -1.0 | -1.1 | -0.7 | 0.4  | -0.8 |
| 23630.peg.2744 | outer membrane protein, putative                                                                        | 1.0  | -0.5 | -0.6 | -0.7 | -0.7 |
| 23630.peg.4973 | outer membrane protein, putative                                                                        | 1.0  | -0.5 | -0.6 | -0.7 | -0.7 |
| 23630.peg.261  | Oxidoreductase, short chain dehydrogenase/reductase family                                              | 1.0  | 0.9  |      |      | 1.0  |
| 23630.peg.255  | Oxidoreductase, short-chain dehydrogenase/reductase family                                              |      |      | 1.8  |      | 1.4  |

|                |                                                                                                  |      |      |      |      |      |
|----------------|--------------------------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.4400 | Oxidoreductase, short-chain dehydrogenase/reductase family (EC 1.1.1.-)                          | 1.5  |      |      |      | 1.1  |
| 23630.peg.3609 | P pilus assembly/Cpx signaling pathway, periplasmic inhibitor/zinc-resistance associated protein |      | 1.0  |      |      |      |
| 23630.peg.2933 | Peptidase, U7 family                                                                             |      |      |      | -1.1 |      |
| 23630.peg.4731 | periplasmic binding protein                                                                      | -1.8 | -0.8 |      |      |      |
| 23630.peg.4391 | Permeases of the major facilitator superfamily                                                   | 1.7  |      |      |      |      |
| 23630.peg.2902 | Phage late control D                                                                             | -0.8 | -1.1 |      |      |      |
| 23630.peg.3470 | phage single-stranded DNA-binding protein, putative                                              | -1.1 | 0.5  |      | -0.9 |      |
| 23630.peg.3328 | Phosphate-binding protein                                                                        |      |      |      | 1.0  |      |
| 23630.peg.2515 | Pilin glycosylation enzyme                                                                       | -0.9 | -1.0 |      |      | -1.2 |
| 23630.peg.3909 | Pirin-like protein CC_1473                                                                       |      |      |      | 1.3  | 0.8  |
| 23630.peg.746  | Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)                         |      | 0.6  | 0.8  | 1.2  |      |
| 23630.peg.1734 | Polysaccharide deacetylase                                                                       |      | -0.8 |      | -1.0 |      |
| 23630.peg.3996 | POSSIBLE MEMBRANE PROTEIN                                                                        | 1.1  | 0.6  |      |      | 0.9  |
| 23630.peg.883  | Predicted zinc-binding protein                                                                   | -1.5 |      |      |      |      |
| 23630.peg.4856 | Probable 3-phenylpropionic acid transporter                                                      |      | 1.0  |      |      | 0.5  |
| 23630.peg.110  | Probable acyl-CoA dehydrogenase (EC 1.3.99.3)                                                    | 1.2  | 0.6  |      |      | 0.7  |
| 23630.peg.3032 | Probable bacteriophage integrase                                                                 | -1.8 | -0.6 |      | -0.8 |      |
| 23630.peg.189  | probable helicase                                                                                | -1.3 | -0.8 |      | -0.6 | -0.8 |
| 23630.peg.3558 | Probable hydrolase                                                                               | -1.3 |      |      |      |      |
| 23630.peg.2101 | probable membrane protein NMA1176                                                                | -1.4 |      | 0.6  |      | -1.8 |
| 23630.peg.694  | probable permease of ABC transporter                                                             |      | -1.3 | 1.4  |      |      |
| 23630.peg.4891 | Probable RND efflux membrane fusion protein                                                      |      | 1.0  |      |      |      |
| 23630.peg.196  | Probable short chain dehydrogenase                                                               | -1.0 | -1.7 | -0.6 |      |      |
| 23630.peg.199  | probable short-chain dehydrogenase                                                               |      | -1.0 |      |      | -0.6 |
| 23630.peg.3519 | Probable short-chain dehydrogenase                                                               | 1.1  |      |      |      |      |
| 23630.peg.4336 | probable transcriptional regulator                                                               |      |      | -1.5 |      |      |
| 23630.peg.1536 | probable transcriptional regulator                                                               | 1.0  |      |      |      |      |
| 23630.peg.2896 | Probable transmembrane protein                                                                   | 1.5  |      | -0.6 |      | 0.3  |
| 23630.peg.2014 | Probable transmembrane protein                                                                   | -1.3 | -0.8 |      | -0.8 |      |
| 23630.peg.1778 | Probable transmembrane protein                                                                   | 1.4  |      |      |      |      |
| 23630.peg.3503 | Probable two-component response regulator                                                        | -1.4 |      | 1.0  |      |      |
| 23630.peg.1912 | protein of unknown function DUF1127                                                              | -1.3 | -0.7 |      | -2.0 |      |
| 23630.peg.3129 | protein of unknown function DUF1272                                                              |      |      | 0.7  | 1.0  |      |
| 23630.peg.1357 | protein of unknown function DUF395, YeeE/YedE                                                    |      | -1.0 |      | -0.7 |      |
| 23630.peg.1766 | protein of unknown function DUF81                                                                |      | -1.1 |      |      |      |
| 23630.peg.146  | protein of unknown function DUF861, cupin_3                                                      |      | -2.0 |      | -0.7 |      |
| 23630.peg.1729 | Protein serine/threonine phosphatase PrpC, regulation of stationary phase                        |      | -1.1 |      |      |      |
| 23630.peg.1256 | Protein ygiW precursor                                                                           | 1.3  | 1.1  | 0.6  |      | 0.7  |
| 23630.peg.1561 | Protein YidD                                                                                     | 0.1  |      | 1.0  | 2.0  | -0.6 |
| 23630.peg.1638 | Protein YidD                                                                                     | 0.9  |      | 0.8  | 1.1  |      |
| 23630.peg.1799 | Protein-glutamate methylesterase (EC 3.1.1.61)                                                   | 0.9  | 0.6  |      | 1.0  |      |
| 23630.peg.3577 | Pseudaminic acid cytidyltransferase (EC 2.7.7.43)                                                | -1.1 | -1.1 | -0.7 |      | -1.3 |
| 23630.peg.3945 | putative 2-pyrone-4,6-dicarboxylic acid hydrolase                                                |      | -0.6 |      |      | -1.0 |
| 23630.peg.4258 | putative ABC transporter                                                                         |      | -0.9 |      | -0.8 | -1.2 |
| 23630.peg.1319 | Putative activity regulator of membrane protease YbbK                                            |      |      | -1.0 |      |      |
| 23630.peg.2264 | putative acyl-CoA dehydrogenase                                                                  |      | 1.0  |      |      | 0.7  |

|                |                                                                                                      |      |      |      |      |
|----------------|------------------------------------------------------------------------------------------------------|------|------|------|------|
| 23630.peg.1985 | Putative amino acid ABC transporter, permease protein                                                | 0.7  |      | 1.0  |      |
| 23630.peg.4375 | putative amino acid binding protein                                                                  | 1.4  | 1.4  | 1.2  |      |
| 23630.peg.3645 | putative bacterial extracellular solute-binding protein, family 3                                    | 0.7  | 1.3  |      | 0.7  |
| 23630.peg.4197 | Putative cytoplasmic protein                                                                         |      |      |      | 1.4  |
| 23630.peg.3178 | Putative cytoplasmic protein USSDB7A                                                                 | 1.3  | 0.7  |      | 1.0  |
| 23630.peg.2875 | Putative diguanylate cyclase (GGDEF domain)                                                          |      |      | -1.0 |      |
| 23630.peg.461  | putative DNA-binding protein                                                                         | -1.5 | -1.4 | -0.6 |      |
| 23630.peg.2783 | putative exonuclease                                                                                 | -1.3 |      |      | -0.8 |
| 23630.peg.4934 | putative exonuclease                                                                                 | -1.3 |      |      | -0.8 |
| 23630.peg.4346 | Putative hemolysin                                                                                   | -0.9 |      | 1.1  |      |
| 23630.peg.273  | putative membrane protein                                                                            |      |      | 1.3  | 0.6  |
| 23630.peg.3300 | Putative phosphatase                                                                                 | -1.7 |      | -0.7 | -0.7 |
| 23630.peg.4030 | putative polyketide synthase                                                                         | 1.0  |      | 0.9  |      |
| 23630.peg.2800 | putative short-chain dehydrogenase                                                                   |      |      |      | -1.3 |
| 23630.peg.2126 | Putative stomatin/prohibitin-family membrane protease subunit aq_911                                 | 1.1  |      | -1.1 | 0.7  |
| 23630.peg.3138 | Putrescine ABC transporter, periplasmic putrescine-binding protein                                   |      |      | -0.7 | -1.0 |
| 23630.peg.1158 | Radical SAM domain protein                                                                           | 1.5  | 0.7  |      | 0.7  |
| 23630.peg.3416 | Rhodanese domain protein                                                                             |      |      | -1.0 |      |
| 23630.peg.2741 | Rhodanese-related sulfurtransferase                                                                  | 1.3  |      |      |      |
| 23630.peg.4976 | Rhodanese-related sulfurtransferase                                                                  | 1.3  |      |      |      |
| 23630.peg.11   | ribosomal subunit interface protein, putative                                                        | -1.0 |      |      | -0.7 |
| 23630.peg.3494 | RNA polymerase sigma-70 factor, ECF subfamily                                                        | 2.7  | 2.0  | 0.7  | 1.7  |
| 23630.peg.1360 | SAM-dependent methyltransferases                                                                     | 0.8  | 0.6  |      | 0.7  |
| 23630.peg.3370 | SAM-dependent methyltransferases                                                                     | 0.8  | 1.6  | 0.6  | 1.5  |
| 23630.peg.1803 | Sensory box histidine kinase                                                                         |      |      |      | 1.1  |
| 23630.peg.2738 | Sensory box histidine kinase/response regulator                                                      | -1.3 | -1.2 | -1.3 | -1.2 |
| 23630.peg.4979 | Sensory box histidine kinase/response regulator                                                      | -1.3 | -1.2 | -1.3 | -1.2 |
| 23630.peg.633  | Sensory box/GGDEF family protein                                                                     |      |      | -0.7 | -1.0 |
| 23630.peg.1002 | Sensory box/GGDEF family protein                                                                     |      |      |      | -1.1 |
| 23630.peg.1649 | Ser/Thr and Tyr protein phosphatase (dual specificity)                                               | -2.2 |      |      |      |
| 23630.peg.3620 | Ser/Thr protein phosphatase family protein, UDP-2,3-diacylglucosamine hydrolase (EC 3.6.1.-) homolog | -0.6 |      | 1.5  |      |
| 23630.peg.2285 | Serine/threonine protein kinase                                                                      |      | -1.0 | -0.5 | -1.1 |
| 23630.peg.1730 | Serine/threonine protein kinase (EC 2.7.11.1)                                                        |      | -1.5 |      |      |
| 23630.peg.3948 | short-chain dehydrogenase/reductase                                                                  | -1.6 | -1.8 | 1.0  |      |
| 23630.peg.2891 | sigma-54 dependent transcriptional regulator                                                         | 1.2  |      |      |      |
| 23630.peg.3504 | Signal transduction histidine kinase                                                                 | -0.9 |      |      | 1.0  |
| 23630.peg.4296 | Signal transduction histidine kinase                                                                 |      |      | 0.6  | -1.1 |
| 23630.peg.2733 | Similar to pyrroloquinoline quinone biosynthesis protein F                                           |      |      | -0.8 | -1.0 |
| 23630.peg.130  | Sodium-dependent transporter                                                                         | 1.4  |      |      |      |
| 23630.peg.619  | Sodium-dependent transporter family protein                                                          | 0.9  |      |      | 1.0  |
| 23630.peg.3740 | Sodium-dependent transporter family protein                                                          | 0.7  | 1.1  |      |      |
| 23630.peg.4135 | sodium-solute symporter, putative                                                                    | 1.2  |      |      |      |
| 23630.peg.3923 | Spermidine/putrescine-binding periplasmic protein                                                    | -1.0 | -1.2 |      |      |
| 23630.peg.1470 | SrfB                                                                                                 | -1.0 |      | -0.5 | -0.8 |
| 23630.peg.593  | SSU ribosomal protein S15p (S13e)                                                                    |      |      |      | 1.0  |
| 23630.peg.3584 | SSU ribosomal protein S1p                                                                            |      |      |      | 1.0  |

|                |                                                                               |      |      |      |      |      |
|----------------|-------------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.4481 | SSU ribosomal protein S20p                                                    | 1.0  |      | 0.9  | 1.0  |      |
| 23630.peg.34   | SSU ribosomal protein S2p (SAe)                                               | 1.0  |      | 0.8  |      |      |
| 23630.peg.1978 | Sterol desaturase                                                             |      |      |      | -1.5 |      |
| 23630.peg.2088 | still frameshift probable component of chemotactic signal transduction system |      |      | -0.6 |      | -1.0 |
| 23630.peg.970  | Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)                    |      | 1.1  |      |      |      |
| 23630.peg.693  | Sugar ABC transporter, ATP-binding protein                                    |      | -0.9 | 0.5  | -1.0 |      |
| 23630.peg.1907 | Sugar efflux permease, MFS-like                                               |      | -1.1 |      |      |      |
| 23630.peg.1887 | SUGAR TRANSPORTER                                                             | 1.3  | 0.7  |      | 1.1  |      |
| 23630.peg.569  | Sugar/maltose fermentation stimulation protein homolog                        |      |      | 1.0  |      | -1.3 |
| 23630.peg.4560 | sulfatase                                                                     | -1.5 | -1.9 |      | -1.0 | -1.2 |
| 23630.peg.2199 | Thermonuclease family protein                                                 |      |      |      | -1.0 |      |
| 23630.peg.252  | Thermostable hemolysin delta-VPH                                              | 2.3  | 2.4  | 4.0  | 1.6  | 3.0  |
| 23630.peg.3951 | ThiJ/PfpI family protein                                                      |      |      | 0.8  |      | -1.0 |
| 23630.peg.2163 | thioesterase-like protein                                                     |      | -0.7 |      |      | -1.2 |
| 23630.peg.1751 | Transcriptional regulator                                                     |      |      | 0.8  | 1.3  |      |
| 23630.peg.1600 | transcriptional regulator, AraC family                                        | 1.0  | 1.3  |      | 0.9  | 0.8  |
| 23630.peg.4862 | Transcriptional regulator, AraC family                                        | -1.5 |      |      |      | -0.8 |
| 23630.peg.500  | Transcriptional regulator, AraC family                                        | -1.2 |      | 0.7  |      | -0.8 |
| 23630.peg.582  | Transcriptional regulator, AraC family                                        | -1.4 | -2.5 | -1.0 | -1.3 | -1.4 |
| 23630.peg.2468 | Transcriptional regulator, AraC family                                        | 0.8  |      |      | 1.1  |      |
| 23630.peg.245  | Transcriptional regulator, AraC family                                        | -1.2 |      |      | -1.2 |      |
| 23630.peg.1266 | Transcriptional regulator, AraC family                                        | -1.5 |      |      |      |      |
| 23630.peg.517  | transcriptional regulator, AraC-family                                        | 1.1  |      |      |      |      |
| 23630.peg.516  | transcriptional regulator, AraC-family                                        | -1.5 |      |      |      |      |
| 23630.peg.2108 | Transcriptional regulator, ArsR family / Methyltransferase fusion             | -0.7 | -1.1 |      | 0.0  |      |
| 23630.peg.2214 | transcriptional regulator, Fis family                                         | -1.5 |      |      |      | -1.6 |
| 23630.peg.2740 | Transcriptional regulator, LuxR family                                        | 1.1  |      |      |      |      |
| 23630.peg.4977 | Transcriptional regulator, LuxR family                                        | 1.1  |      |      |      |      |
| 23630.peg.4045 | Transcriptional regulator, LysR family                                        |      |      | -1.0 |      | -0.8 |
| 23630.peg.197  | Transcriptional regulator, LysR family                                        | -1.9 | -1.7 |      |      | -1.0 |
| 23630.peg.4291 | Transcriptional regulator, LysR family                                        | -2.6 | -1.2 | 0.8  | -1.8 | -1.1 |
| 23630.peg.3747 | Transcriptional regulator, LysR family                                        | -0.7 |      |      |      | -1.1 |
| 23630.peg.4534 | Transcriptional regulator, LysR family                                        | -1.0 | -1.6 | -0.5 | -1.1 |      |
| 23630.peg.2798 | Transcriptional regulator, LysR family                                        | -1.5 |      |      |      |      |
| 23630.peg.3976 | Transcriptional regulator, MarR family                                        | 1.3  | 2.5  | 0.9  | 0.8  | 1.3  |
| 23630.peg.4824 | Transcriptional regulator, TetR family                                        | 1.1  |      | 1.2  | 1.0  | 0.9  |
| 23630.peg.1906 | Transcriptional regulator, TetR family                                        |      |      | -1.2 | -1.0 | -0.8 |
| 23630.peg.2789 | Transcriptional regulator, TetR family                                        |      | -0.7 |      | -1.1 |      |
| 23630.peg.4928 | Transcriptional regulator, TetR family                                        |      | -0.7 |      | -1.1 |      |
| 23630.peg.1199 | Transcriptional regulator, TetR family                                        |      | 1.1  | 0.9  |      |      |
| 23630.peg.3559 | Transcriptional regulator, TetR family                                        | -1.2 | -0.8 |      |      |      |
| 23630.peg.1900 | Transcription-repair coupling factor (superfamily II helicase)                |      | -1.9 | -0.5 | -0.7 | -1.1 |
| 23630.peg.4888 | Transglutaminase-like enzymes, putative cysteine proteases                    | -1.0 |      |      |      | -0.9 |
| 23630.peg.3333 | Transglycosylase, Slt family                                                  |      |      | -0.6 | -1.1 | -1.0 |
| 23630.peg.3495 | Transmembrane sensor                                                          | 1.6  | 1.2  |      | 0.8  | 1.1  |
| 23630.peg.768  | Transport protein                                                             | -1.0 |      | 0.7  |      |      |

|                |                                                                             |      |      |      |      |      |
|----------------|-----------------------------------------------------------------------------|------|------|------|------|------|
| 23630.peg.3977 | TRANSPORTER, DME FAMILY                                                     | 2.4  | 4.7  | 2.5  | 1.6  | 2.5  |
| 23630.peg.3498 | Transporter, LysE family                                                    |      | 0.6  | 1.2  |      | 0.9  |
| 23630.peg.3212 | Transthyretin family protein                                                | -1.0 |      |      |      |      |
| 23630.peg.1015 | TraX family protein                                                         | -1.3 | -0.7 |      |      |      |
| 23630.peg.2260 | TrkA domain protein                                                         | 1.2  |      | 0.7  |      | 0.7  |
| 23630.peg.2796 | Twin-arginine translocation pathway signal                                  | -1.3 | -1.4 |      |      |      |
| 23630.peg.4509 | Type IV secretion system protein VirD4                                      | -1.3 | -1.2 |      |      | -0.6 |
| 23630.peg.2698 | Type IV secretory pathway, protease TraF                                    | -1.9 | -1.6 |      | -3.0 | -1.1 |
| 23630.peg.3047 | UDP-glucose dehydrogenase (EC 1.1.1.22)                                     | -1.0 | -1.7 | 0.6  | 1.4  |      |
| 23630.peg.1042 | Uncharacterized protein conserved in bacteria, NMA0228-like                 | -1.5 |      | -0.9 | -1.1 | -1.3 |
| 23630.peg.2038 | Uncharacterized protein, possibly involved in aromatic compounds catabolism |      |      |      | 1.1  |      |
| 23630.peg.2257 | Universal stress protein family                                             |      | -0.7 |      | -1.2 |      |
| 23630.peg.2538 | Urea ABC transporter, urea binding protein                                  |      |      | 1.1  |      |      |
| 23630.peg.3053 | UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)                   | 1.0  | 1.0  | 0.7  | 1.1  | 0.6  |
| 23630.peg.3527 | von Willebrand factor, type A                                               |      |      | -0.6 | -1.1 |      |
| 23630.peg.1524 | Zinc ABC transporter, inner membrane permease protein ZnuB                  | 1.1  | 1.7  | 0.8  | 2.0  | 0.8  |

<sup>a</sup> Relative gene expression is presented as the mean ratio of the fluorescence intensity of K<sub>2</sub>CrO<sub>4</sub>-exposed cells to control

<sup>b</sup> Time in minutes at which cells were harvested for RNA isolation following addition of 1 mM K<sub>2</sub>CrO<sub>4</sub> to the experimental culture.