

| Gene        | Hours post induction ( $\log_2(\text{induced} / \text{un-induced})$ ) |       |       |       |       |       |       | Gene Function                                                                                                             |
|-------------|-----------------------------------------------------------------------|-------|-------|-------|-------|-------|-------|---------------------------------------------------------------------------------------------------------------------------|
|             | 0.5                                                                   | 1     | 1.5   | 2     | 3     | 3.5   | 4     |                                                                                                                           |
| <i>aer</i>  | -0.02                                                                 | -0.38 | -0.26 | -0.41 | -0.19 | 0.34  | -0.04 | "aerotaxis sensor receptor, flavoprotein [b3072]"                                                                         |
| <i>chaC</i> | -0.09                                                                 | -0.10 | -0.18 | -0.48 | -0.58 | -0.54 | -0.87 | cation transport regulator [b1218]<br>sensory transducer kinase between chemo- signal receptors and CheB and CheY [b1888] |
| <i>cheA</i> | -0.10                                                                 | -0.08 | 0.11  | -0.40 | 0.04  | 0.62  | 0.30  | response regulator for chemotaxis [b1883]                                                                                 |
| <i>cheB</i> | -0.06                                                                 | -0.24 | -0.01 | -0.14 | 0.22  | 0.25  | 0.36  | response regulator for chemotaxis; protein glutamate methyltransferase [b1884]                                            |
| <i>cheR</i> | -0.02                                                                 | -0.13 | -0.02 | -0.12 | 0.22  | 0.19  | 0.54  | positive regulator of CheA protein activity [b1887]                                                                       |
| <i>cheW</i> | -0.20                                                                 | -0.06 | -0.20 | 0.06  | -0.12 | -0.23 | -0.13 | chemotaxis regulator transmits chemoreceptor signals to flagellar motor components [b1882]                                |
| <i>cheY</i> | -0.16                                                                 | -0.41 | -0.31 | -0.38 | -0.29 | 0.81  | 0.76  | Chemotaxis protein cheZ [c_2296]                                                                                          |
| <i>cheZ</i> | -0.30                                                                 | -0.02 | -0.08 | -0.23 | 0.72  | 0.66  | 0.55  | "carbon storage regulator; controls glycogen synthesis, gluconeogenesis, cell size and surface properties [b2696]"        |
| <i>csrA</i> | -1.61                                                                 | -1.10 | -1.14 | -1.26 | -1.75 | -1.27 | -2.05 | reoxidizes DsbA protein following formation of disulfide bond in P-ring of flagella. [b1185]                              |
| <i>dsbB</i> | -0.88                                                                 | -1.47 | 0.12  | 0.82  | 0.14  | 0.40  | 0.24  | flagellar biosynthesis; assembly of basal-body periplasmic P ring [b1072]                                                 |
| <i>flgA</i> | -0.08                                                                 | 0.20  | 0.07  | -0.11 | -0.05 | 0.11  | 0.00  | "flagellar biosynthesis, cell-proximal portion of basal-body rod [b1073]"                                                 |
| <i>flgB</i> | -0.05                                                                 | 0.04  | 0.07  | -0.22 | 0.09  | 0.34  | -0.08 | "flagellar biosynthesis, cell-proximal portion of basal-body rod [b1074]"                                                 |
| <i>flgC</i> | 0.01                                                                  | 0.04  | 0.07  | -0.31 | 0.02  | 0.56  | 0.19  | "flagellar biosynthesis, initiation of hook assembly [b1075]"                                                             |
| <i>flgD</i> | -0.07                                                                 | -0.01 | 0.03  | -0.55 | 0.10  | 0.48  | 0.23  | "flagellar biosynthesis, hook protein [b1076]"                                                                            |
| <i>flgE</i> | -0.11                                                                 | -0.16 | -0.14 | -0.33 | 0.13  | 0.23  | 0.28  | "flagellar biosynthesis, cell-proximal portion of basal-body rod [b1077]"                                                 |
| <i>flgF</i> | -0.04                                                                 | 0.35  | 0.14  | -0.15 | -0.40 | -0.08 | -0.21 | "flagellar biosynthesis, cell-distal portion of basal-body rod [b1078]"                                                   |
| <i>flgG</i> | 0.14                                                                  | 0.20  | 0.12  | -0.20 | 0.13  | -0.23 | 0.24  | "flagellar biosynthesis, basal-body outer-membrane L [b1079]"                                                             |
| <i>flgH</i> | -0.02                                                                 | -0.09 | -0.03 | -0.25 | -0.12 | 0.60  | 0.30  | homolog of Salmonella P-ring of flagella basal body [b1080]                                                               |
| <i>flgI</i> | -0.09                                                                 | 0.18  | -0.15 | -0.47 | -0.12 | 0.55  | 0.45  | flagellar biosynthesis [b1081]                                                                                            |
| <i>flgJ</i> | 0.00                                                                  | 0.06  | 0.03  | -0.27 | -0.05 | 0.49  | 0.25  | "flagellar biosynthesis, hook-filament junction protein 1 [b1082]"                                                        |
| <i>flgK</i> | -0.12                                                                 | -0.39 | 0.04  | -0.17 | 0.00  | -0.10 | -0.21 | flagellar biosynthesis; hook-filament junction protein [b1083]                                                            |
| <i>flgL</i> | -0.18                                                                 | -0.26 | -0.04 | -0.14 | -0.16 | 0.01  | 0.23  | anti-FlhA [b1071]                                                                                                         |
| <i>flgM</i> | -0.85                                                                 | -0.11 | -0.59 | -0.59 | -0.66 | -0.65 | -0.84 | protein of flagellar biosynthesis [b1070]                                                                                 |
| <i>flgN</i> | -0.33                                                                 | -0.23 | -0.87 | -0.80 | -0.89 | -0.89 | -1.35 | flagellar biosynthesis; possible export of flagellar proteins [b1879]                                                     |
| <i>flhA</i> | 0.04                                                                  | 0.00  | 0.13  | -0.05 | -0.05 | 0.37  | 0.04  | regulator of flagellar biosynthesis acting on class 2 operons; transcription initiation factor [b1891]                    |
| <i>flhC</i> | -0.43                                                                 | -0.19 | 2.11  | 2.29  | 1.20  | 2.74  | 1.84  | "regulator of flagellar biosynthesis, acting on class 2 operons; transcriptional initiation factor [b1892]"               |
| <i>flhD</i> | -0.46                                                                 | -0.49 | 1.91  | 2.13  | 1.12  | 3.80  | 3.22  | flagellar biosynthesis; alternative sigma factor 28; regulation of flagellar operons [b1922]                              |
| <i>fliA</i> | 0.00                                                                  | 0.05  | 0.22  | 0.01  | 0.03  | 0.39  | 0.18  |                                                                                                                           |

|             |       |       |       |       |       |       |       |                                                                                                                                                                                 |
|-------------|-------|-------|-------|-------|-------|-------|-------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>fliC</i> | 0.03  | 0.00  | -0.10 | 0.08  | 0.28  | 0.12  | 0.12  | Flagellin [c_2338]                                                                                                                                                              |
| <i>fliD</i> | 0.03  | 0.43  | 0.09  | -0.24 | -0.10 | 0.36  | 0.05  | flagellar biosynthesis; filament capping protein; enables filament assembly [b1924]                                                                                             |
| <i>fliE</i> | -0.04 | 0.38  | 0.07  | -0.17 | 0.43  | 0.35  | 0.46  | "flagellar biosynthesis; basal-body component, possibly at [b1937]"                                                                                                             |
| <i>fliF</i> | 0.11  | 0.03  | -0.06 | -0.08 | 0.30  | 0.12  | 0.23  | flagellar biosynthesis; basal-body MS [b1938]<br>"flagellar biosynthesis, component of motor switching and energizing, enabling rotation and determining its direction [b1939]" |
| <i>fliG</i> | 0.00  | 0.29  | -0.10 | -0.15 | 0.10  | 0.46  | 0.06  | rotation and determining its direction [b1939]"                                                                                                                                 |
| <i>fliH</i> | 0.05  | 0.27  | -0.05 | -0.28 | 0.06  | 0.22  | 0.09  | flagellar biosynthesis; export of flagellar proteins? [b1940]                                                                                                                   |
| <i>fliJ</i> | 0.00  | 0.00  | -0.07 | -0.16 | -0.06 | 0.46  | 0.51  | flagellar fliJ protein [b1942]                                                                                                                                                  |
| <i>fliK</i> | 0.14  | 0.01  | 0.02  | -0.13 | -0.07 | 0.18  | 0.23  | flagellar hook-length control protein [b1943]                                                                                                                                   |
| <i>fliL</i> | -0.18 | 0.05  | 0.02  | -0.26 | 0.05  | 0.44  | 0.44  | flagellar biosynthesis [b1944]<br>"flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction [b1945]"                   |
| <i>fliM</i> | 0.00  | 0.54  | 0.07  | -0.28 | 0.13  | 0.30  | 0.32  | "flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction [b1946]"                                                     |
| <i>fliN</i> | -0.11 | -0.22 | -0.13 | -0.20 | 0.31  | 0.36  | 0.31  | and determining its direction [b1946]"                                                                                                                                          |
| <i>fliO</i> | -0.12 | -0.25 | 0.00  | -0.34 | 0.16  | 0.60  | 0.61  | flagellar biosynthesis [Z3037]                                                                                                                                                  |
| <i>fliP</i> | -0.01 | -0.13 | 0.03  | -0.19 | 0.28  | 0.56  | 0.51  | Flagellar biosynthetic protein fliP precursor [c_2365]                                                                                                                          |
| <i>fliS</i> | -0.09 | -0.05 | 0.02  | -0.16 | 0.06  | 0.46  | 0.44  | Flagellar protein fliS [c_2340]                                                                                                                                                 |
| <i>fliT</i> | 1.37  | 1.07  | 0.33  | 0.39  | 0.13  | -0.17 | 0.09  | flagellar biosynthesis; repressor of class 3a and 3b operons [b1926]<br>periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis [b4034]         |
| <i>malE</i> | -0.33 | 0.12  | -2.27 | -3.35 | -2.58 | -3.04 | -1.15 | chemotaxis [b4034]                                                                                                                                                              |
| <i>motA</i> | -0.01 | -0.17 | 0.65  | 0.92  | 0.56  | 1.03  | 1.03  | proton conductor component of motor; no effect on switching [b1890]                                                                                                             |
| <i>motB</i> | 0.06  | -0.09 | 0.24  | 0.30  | 0.51  | 0.41  | 0.47  | "enables flagellar motor rotation, linking torque machinery to cell wall [b1889]"                                                                                               |
| <i>mqsR</i> | 0.14  | -0.61 | 0.54  | 0.39  | 0.16  | 0.42  | 0.66  | "orf, hypothetical protein [b3022]"                                                                                                                                             |
| <i>nikA</i> | -0.02 | -0.13 | -0.02 | -0.01 | -0.05 | 0.26  | 0.17  | periplasmic binding protein for nickel [b3476]                                                                                                                                  |
| <i>tap</i>  | -0.02 | 0.01  | 0.11  | -0.34 | 0.03  | 0.44  | 0.16  | "methyl-accepting chemotaxis protein IV, peptide sensor receptor [b1885]"                                                                                                       |
| <i>tar</i>  | -0.02 | 0.13  | -0.05 | -0.39 | 0.31  | 0.06  | 0.04  | "methyl-accepting chemotaxis protein II, aspartate sensor receptor [b1886]"                                                                                                     |
| <i>trg</i>  | 0.14  | 0.05  | -0.07 | -0.04 | -0.36 | 0.13  | -0.10 | "methyl-accepting chemotaxis protein III, ribose sensor receptor [b1421]"                                                                                                       |
| <i>tsr</i>  | -0.05 | -0.02 | -0.04 | -0.02 | -0.07 | 0.27  | 0.02  | Methyl-accepting chemotaxis protein I [c_5430]                                                                                                                                  |
| <i>ycgR</i> | -0.10 | -0.06 | -0.16 | -0.28 | 0.13  | 0.48  | 0.28  | "orf, hypothetical protein [b1194]"                                                                                                                                             |
| <i>yehP</i> | 0.00  | 0.20  | -0.04 | 0.02  | -0.21 | 0.24  | -0.05 | "orf, hypothetical protein [b2121]"                                                                                                                                             |
| <i>yeiA</i> | -0.23 | -0.28 | -1.36 | -0.99 | -1.87 | -2.10 | -2.18 | putative oxidoreductase [b2147]                                                                                                                                                 |
| <i>yhjH</i> | 0.02  | -0.51 | 0.02  | -0.10 | 0.32  | 0.37  | 0.47  | "orf, hypothetical protein [b3525]"                                                                                                                                             |