

| Gene        | Hours post induction ( $\log_2(\text{induced} / \text{un-induced})$ ) |       |       |       |       |       |       | Gene Function   |
|-------------|---|-------|-------|-------|-------|-------|-------|---|
|             | 0.5   | 1     | 1.5   | 2     | 3     | 3.5   | 4     |   |
| <i>amiC</i> | -0.23   | -0.09 | 0.68  | 0.68  | 1.28  | 1.62  | 1.52  | putative amidase [b2817]  |
| <i>bolA</i> | -0.24   | -1.12 | -1.09 | -1.32 | -1.46 | -1.81 | -2.41 | possible regulator of murein genes [b0435]  |
| <i>cedA</i> | 0.32  | -0.53 | 1.28  | 0.88  | 0.93  | 0.84  | 1.42  | "orf, hypothetical protein [b1731]"   |
| <i>crcB</i> | -0.14   | -0.69 | -0.50 | -0.83 | -0.64 | 0.03  | -0.49 | "orf, hypothetical protein [b0624]"   |
| <i>dacA</i> | -0.60   | -0.11 | -0.15 | -0.24 | 0.13  | 1.34  | 1.27  | "D-alanyl-D-alanine carboxypeptidase, fraction A; penicillin-binding protein 5 [b0632]"   |
| <i>dacC</i> | -0.30   | -0.37 | -0.28 | -0.18 | -1.02 | -1.40 | -0.93 | D-alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6 [b0839]   |
| <i>damX</i> | 0.12  | -0.12 | -0.27 | -0.37 | -0.79 | -0.63 | -0.73 | putative membrane protein; interferes with cell division [b3388]  |
| <i>ddlB</i> | -0.02   | -0.11 | -0.38 | -0.07 | -0.01 | -0.29 | -0.12 | "D-alanine-D-alanine ligase B, affects cell division [b0092]"   |
| <i>dnaC</i> | 0.05  | -0.36 | -0.44 | -0.46 | -0.48 | -0.37 | -0.31 | chromosome replication; initiation and chain elongation [b4361]   |
| <i>dnaK</i> | -0.70   | 0.19  | 1.81  | 2.44  | 1.09  | 0.07  | -0.26 | chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins [b0014]  |
| <i>envC</i> | -0.30   | -0.81 | 0.27  | 0.30  | 0.27  | 0.62  | 0.84  | putative membrane protein [b3613]   |
| <i>fic</i>  | 0.03  | 0.29  | -0.90 | -0.72 | -0.59 | -1.87 | -1.76 | "induced in stationary phase, recognized by rpoS, affects cell division [b3361]"  |
| <i>ftsA</i> | -0.40   | -0.26 | -0.28 | -0.27 | -0.94 | 0.07  | -0.28 | "ATP-binding cell division protein, septation process, complexes with FtsZ, associated with junctions of inner and outer membranes [b0094]" |
| <i>ftsB</i> | 0.05  | -0.14 | 0.20  | -0.06 | 0.35  | -0.50 | -0.14 | "orf, hypothetical protein [b2748]"   |
| <i>ftsE</i> | -0.04   | -0.69 | 0.30  | 0.53  | 0.34  | 0.15  | 0.30  | ATP-binding component of a membrane-associated complex involved in cell division [b3463]  |
| <i>ftsI</i> | -0.09   | -0.73 | 0.08  | -0.28 | -0.44 | -0.59 | -0.90 | septum formation; penicillin-binding protein 3; peptidoglycan synthetase [b0084]  |
| <i>ftsK</i> | -0.06   | -0.04 | -0.40 | -0.16 | -0.48 | -0.19 | 0.15  | cell division protein [b0890]   |
| <i>ftsL</i> | 0.05  | -0.27 | -0.15 | 0.12  | 0.00  | 0.24  | -0.78 | cell division protein; ingrowth of wall at septum [b0083]   |
| <i>ftsN</i> | -0.60   | -0.17 | 0.76  | 0.45  | 0.13  | 0.25  | -0.42 | essential cell division protein [b3933]   |
| <i>ftsP</i> | 0.14  | -0.23 | -0.46 | -0.12 | -0.34 | -0.24 | 0.07  | suppressor of ftsI [b3017]  |
| <i>ftsQ</i> | -0.41   | -0.25 | -0.15 | 0.57  | 0.15  | 0.07  | -0.16 | cell division protein; ingrowth of wall at septum [b0093]   |
| <i>ftsW</i> | 0.39  | -0.68 | -0.70 | -0.28 | -0.23 | -0.36 | -0.20 | cell division; membrane protein involved in shape determination [b0089]   |
| <i>ftsX</i> | -0.26   | -0.15 | 0.17  | 0.18  | -0.15 | -0.25 | -0.62 | cell division membrane protein [b3462]  |
| <i>ftsY</i> | -0.22   | 0.08  | 0.32  | 0.74  | -0.17 | 0.92  | 0.39  | cell division membrane protein [b3464]  |
| <i>ftsZ</i> | 0.16  | 0.11  | -0.42 | -0.11 | -0.54 | -0.24 | 0.06  | cell division; forms circumferential ring; tubulin-like GTP-binding protein and GTPase [b0095]  |
| <i>groL</i> | -0.37   | -0.03 | 0.82  | 0.99  | 0.87  | -0.44 | -0.05 | "GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein [b4143]"  |
| <i>groS</i> | -0.80   | -0.58 | 0.97  | 1.24  | 0.99  | 0.02  | 0.35  | "GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, suppressing its ATPase activity [b4142]"  |
| <i>grpE</i> | -1.10   | -1.17 | 0.22  | 0.90  | 0.51  | 0.07  | 0.44  | phage lambda replication; host DNA synthesis; heat shock protein; protein repair [b2614]  |
| <i>hflB</i> | -0.38   | 0.21  | -0.12 | 0.21  | -0.19 | 0.26  | 0.11  | "degrades sigma32, integral membrane peptidase, cell division protein [b3178]"  |

|             |       |       |       |       |       |       |       |   |
|-------------|-------|-------|-------|-------|-------|-------|-------|---|
| <i>hslU</i> | -0.06 | 0.24  | 0.28  | 1.24  | 0.41  | -0.30 | -0.25 | "heat shock protein hslVU, ATPase subunit, homologous to chaperones [b3931]"  |
| <i>hslV</i> | -0.17 | 0.19  | -0.05 | 1.06  | 0.77  | 0.07  | 0.39  | "heat shock protein hslVU, proteasome-related peptidase subunit [b3932]"  |
| <i>lon</i>  | -0.05 | 0.10  | 0.97  | 1.66  | 1.57  | 0.50  | 0.73  | "DNA-binding, ATP-dependent protease La; heat shock K-protein [b0439]"  |
| <i>minC</i> | -0.42 | -0.39 | -0.15 | 0.29  | -0.16 | 1.05  | 0.43  | "cell division inhibitor, inhibits ftsZ ring formation [b1176]"   |
| <i>minD</i> | -0.92 | -0.17 | -0.46 | -0.53 | -0.89 | 0.28  | -0.59 | "cell division inhibitor, a membrane ATPase, activates minC [b1175]"<br>"cell division topological specificity factor, reverses MinC inhibition of ftsZ ring formation [b1174]" |
| <i>minE</i> | 0.38  | 0.11  | -0.40 | -0.54 | -0.46 | 1.13  | 0.95  | formation [b1174]"  |
| <i>mltA</i> | -0.15 | -0.54 | 0.58  | 0.73  | 0.15  | 0.69  | 0.45  | membrane-bound lytic murein transglycosylase A [b2813]  |
| <i>mltB</i> | 0.07  | -0.37 | 0.07  | 0.22  | -0.06 | -0.07 | -0.59 | membrane-bound lytic murein transglycosylase B [b2701]  |
| <i>mrcA</i> | 0.14  | -0.19 | 0.05  | -0.16 | -0.06 | 0.43  | 0.26  | peptidoglycan synthetase; penicillin-binding protein 1A [b3396]   |
| <i>mrcB</i> | 1.03  | 0.52  | 0.86  | 0.36  | 1.06  | 0.53  | 0.46  | peptidoglycan synthetase; penicillin-binding protein 1B [b0149]<br>"cell elongation, e phase; peptidoglycan synthetase; penicillin-binding protein 2 [b0635]"                   |
| <i>mrda</i> | 0.03  | -0.53 | 0.16  | 0.11  | -0.26 | 0.62  | 0.14  | rod shape-determining membrane protein; sensitivity to radiation and drugs [b0634]  |
| <i>mrdb</i> | -0.05 | -0.01 | -0.17 | -0.63 | -0.09 | 0.61  | 0.81  | "regulator of ftsI, penicillin binding protein 3, septation function [b3251]"   |
| <i>mreB</i> | -0.19 | -0.06 | 0.31  | 0.36  | -0.19 | 0.97  | 0.69  | kinesin-like cell division protein involved in chromosome partitioning [b0924]  |
| <i>mukB</i> | 0.09  | -0.24 | -0.08 | 0.07  | -0.07 | -0.21 | -0.17 | "orf, hypothetical protein [b0923]"   |
| <i>mukE</i> | 0.08  | 0.25  | 0.03  | 0.45  | 0.68  | 0.37  | 0.24  | mukF protein [Z1269]  |
| <i>mukF</i> | 0.03  | 0.22  | 0.14  | 0.67  | 0.15  | 0.47  | 0.29  | D-alanine:D-alanine-adding enzyme [b0086]   |
| <i>murF</i> | 0.27  | -0.16 | -0.64 | -0.54 | -0.62 | -0.50 | -0.24 | putative control proteins [b3163]   |
| <i>nlpI</i> | -0.28 | -0.62 | 0.03  | -0.35 | -0.28 | 0.36  | -0.23 | putative GTP-binding factor [b3183]   |
| <i>obgE</i> | 0.15  | 0.24  | 0.61  | 0.69  | 0.69  | 0.05  | 0.05  | penicillin-binding protein 7 [b2134]  |
| <i>pbpG</i> | -0.25 | -0.38 | 0.05  | -0.42 | -0.48 | -0.51 | -1.17 | oligopeptidase A [Z4898]  |
| <i>prfC</i> | 0.19  | -0.19 | -0.09 | 0.22  | -0.21 | -0.52 | -0.32 | bundles of cytoplasmic filaments [b3247]  |
| <i>rng</i>  | -0.02 | -0.18 | -0.03 | -0.20 | -0.47 | -0.51 | -0.65 | cell division protein [b3179]   |
| <i>rrmJ</i> | -0.60 | -0.06 | -0.07 | 0.18  | 0.01  | 0.23  | 0.66  | Regulatory protein sdiA [c_2330]  |
| <i>sdiA</i> | 0.34  | 0.87  | 0.81  | 0.78  | 1.24  | 1.49  | 1.25  | putative transcriptional regulator [b3641]  |
| <i>slmA</i> | -0.23 | -0.37 | 0.38  | 0.25  | -0.68 | 0.52  | 0.13  | soluble lytic murein transglycosylase [b4392]   |
| <i>slt</i>  | -0.02 | -0.16 | -0.55 | -0.50 | -0.73 | -0.99 | -1.09 | putative protease; htrA suppressor protein [b3129]  |
| <i>sohA</i> | -0.67 | -1.03 | -0.41 | -0.19 | -0.48 | -0.02 | -0.46 | suppressor of lon; inhibits cell division and ftsZ ring formation [b0958]   |
| <i>sula</i> | 0.16  | 0.10  | -0.11 | -0.03 | 0.70  | -1.14 | -1.27 | trigger factor; a molecular chaperone involved in cell division [b0436]   |
| <i>tig</i>  | 0.12  | -0.02 | 1.19  | 2.41  | 1.39  | 1.28  | 1.72  | outer membrane channel; specific tolerance to colicin E1; segregation of daughter chromosomes [b3035]   |
| <i>tolC</i> | -0.28 | 0.39  | 0.39  | -0.04 | -0.60 | -0.36 | -0.14 | "site-specific recombinase, acts on cer sequence of [Z5328]"  |
| <i>xerC</i> | -0.14 | -0.16 | -0.90 | -0.65 | -0.01 | 0.22  | 0.21  | "orf, hypothetical protein [b3534]"   |
| <i>yhjQ</i> | 0.39  | 0.16  | 0.33  | 0.37  | 0.49  | 0.60  | 0.52  | Probable GTP-binding protein engB [c_4812]  |
| <i>yihA</i> | -0.73 | 0.09  | 0.06  | -0.19 | 0.18  | 0.99  | 0.60  | predicted protein [b4520]   |
| <i>ymgF</i> | 0.12  | -0.39 | 0.43  | 0.39  | 1.42  | 0.91  | 2.11  |   |

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|-------------|-------|-------|-------|-------|-------|-------|-------|---|
| <i>zapA</i> | -0.08 | -0.53 | -0.95 | -0.60 | -0.19 | -1.11 | -1.75 | "orf, hypothetical protein [b2910]"                 |
| <i>zipA</i> | -0.79 | -0.40 | -0.84 | -0.87 | -0.98 | -0.48 | -0.79 | cell division protein involved in FtsZ ring [b2412] |

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