| Gene name | Blattner # | Initial plaque | Validation plaque | Gene description |
|---|---|---|---|---|
| *acrE* | b3613 | il | s | protease with a role in cell division |
| *atpA* | b3734 | il | s | F1 sector of membrane-bound ATP synthase, alpha subunit |
| *bglG* | b3723 | s | s | transcriptional antiterminator of the bgl operon |
| *cmk* | b0910 | s | s | cytidylate kinase |
| *crr* | b2417 | s | s | glucose-specific enzyme IIA component of PTS |
| *cyaA* | b3806 | il | 0 | adenylate cyclase |
| *dnaJ* | b0015 | 0 | 0 | chaperone Hsp40, co-chaperone with DnaK, DNA-binding |
| *fruR* | b0080 | s | s | DNA-binding transcriptional dual regulator |
| *fucA* | b2800 | s | s | L-fuculose-1-phosphate aldolase |
| *glnD* | b0167 | il | s | uridylyltransferase |
| *gmhA* | b0222 | 0 | s | D-sedoheptulose 7-phosphate isomerase |
| *gmhB* | b0200 | 0 | s | D,D-heptose 1,7-bisphosphate phosphatase |
| *hflC* | b4175 | s | s | modulator for HflB protease specific for phage lambda cII repressor |
| *hflD* | b1132 | 0 | s | predicted lysogenization regulator |
| *hflK* | b4174 | s | s | modulator for HflB protease specific for phage lambda cII repressor |
| *hldD* | b3619 | 0 | s | ADP-L-glycero-D-mannoheptose-6-epimerase, NAD(P)-binding domain |
| *hldE* | b3052 | il | s | fused heptose 7-phosphate kinase and heptose 1-phosphate adenyltransferase |
| *ihfA* | b1712 | s | s | integration host factor (IHF), DNA-binding protein, alpha subunit |
| *ihfB* | b0912 | 0 | s | integration host factor (IHF), DNA-binding protein, beta subunit |
| *iscS* | b2530 | il | s | cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent |
| *lamB* | b4036 | 0 | 0 | maltose outer membrane porin (maltoporin) |
| *malI* | b1620 | 0 | 0 | DNA-binding transcriptional repressor |
| *malT* | b3418 | 0 | 0 | DNA-binding transcriptional activator, maltotriose-ATP-binding |
| *manZ* | b1819 | 0 | 0 | mannose-specific enzyme IID component of PTS |
| *mnmA* | b1133 | 0 | s | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase |
| *nlpI* | b3163 | s | s | conserved protein |
| *nusB* | b0416 | 0 | 0 | transcription antitermination protein |
| *pabA* | b3360 | il | s | aminodeoxychorismate synthase, subunit II |
| *pdxA* | b0052 | s | s | 4-hydroxy-L-threonine phosphate dehydrogenase, NAD-dependent |
| *pdxH* | b1638 | il | 0 | pyridoxine 5'-phosphate oxidase |
| *pepA* | b4260 | s | s | aminopeptidase A, a cyteinylglycinase |
| *pgi* | b4025 | 0 | s | glucosephosphate isomerase |
| *pgm* | b0688 | 0 | s | phosphoglucomutase |
| *phoU* | b3724 | s | s | DNA-binding transcriptional regulator |
| *rfaC* | b3621 | 0 | 0 | ADP-heptose:LPS heptosyl transferase I |
| *rfaF* | b3620 | s | 0 | ADP-heptose:LPS heptosyltransferase II |
| *rfaH* | b3842 | s | s | DNA-binding transcriptional antiterminator |
| *rfaP* | b3630 | 0 | s | kinase that phosphorylates core heptose of lipopolysaccharide |
| *rimP* | b3170 | 0 | s | conserved protein |
| *rlmE* | b3179 | s | s | 23S rRNA methyltransferase |
| *rpoZ* | b3649 | 0 | s | RNA polymerase, omega subunit |
| *rstA* | b1608 | s | s | DNA-bindng response regulator in two-component regulatory system with RstB |
| *rutE* | b1008 | s | s | predicted nitroreductase |
| *speB* | b2937 | 0 | s | agmatinase |
| *spr* | b2175 | 0 | 0 | predicted peptidase, outer membrane lipoprotein |
| *srmB* | b2576 | 0 | s | ATP-dependent RNA helicase |
| *talB* | b0008 | s | s | transaldolase B |
| *tatB* | b3838 | s | s | TatABCE protein translocation system subunit |
| *tesA* | b0494 | s | s | multifunctional acyl-CoA thioesterase I and protease I and lysophospholipase L1 |
| *thyA* | b2827 | il | 0 | thymidylate synthetase |
| *tpx* | b1324 | 0 | s | lipid hydroperoxide peroxidase |
| *tusA* | b3470 | 0 | s | mediator of IscS desulfur transfer, 2-thiolation step of mnm(5)-s(2)U34-tRNA synthesis |
| *tusE* | b0969 | 0 | s | tRNA 2-thiouridine synthesizing protein, sulfur mediator, TusE |
| *ybeD* | b0631 | 0 | s | conserved protein |
| *yecR* | b1904 | 0 | s | predicted protein |
| *yfiM* | b2586 | s | s | predicted protein |
| *yneJ* | b1526 | 0 | 0 | predicted DNA-binding transcriptional regulator |