**Supplemental Table S1: Comparison of the deleted genes in the genome-reduced strains**

**Legend**

1 Locus tag according to the reference genome sequence of B. subtilis 168 (NC_000964)

Genes highlighted in blue have been deleted from the respective strains

Genes highlighted in green have been inserted into the indicated strain, they are present in all following strains

Regions highlighted in red could not be deleted as a unit

Regions highlighted in orange were not deleted in the genome-reduced strains since their deletion resulted in severe growth defects

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| dnaA | BSU00010 | replication initiation protein | | | | |
| dnaN | BSU00020 | DNA polymerase III (beta subunit), beta clamp | | | | |
| yaaA | BSU00030 | unknown | | | | |
| recF | BSU00040 | repair, recombination | | | | |
| remB | BSU00050 | involved in the activation of biofilm matrix biosynthetic operons | | | | |
| gyrB | BSU00060 | DNA-Gyrase (subunit B) | | | | |
| gyrA | BSU00070 | DNA-Gyrase (subunit A) | | | | |
| rrnO-16S- trnO-Ala- trnO-Ile- rrnO-23S- rrnO-5S | | | | | | |
| yaaC | BSU00080 | unknown | | | | |
| guaB | BSU00090 | IMP dehydrogenase | | | | |
| dacA | BSU00100 | penicillin-binding protein 5*, D-alanyl-D-alanine carboxypeptidase | | | | |
| pdxS | BSU00110 | pyridoxal-5'-phosphate synthase (synthase domain) | | | | |
| pdxT | BSU00120 | pyridoxal-5'-phosphate synthase (glutaminase domain) | | | | |
| serS | BSU00130 | seryl-tRNA-synthetase | | | | |
| trnSL-Ser1 | | | | | | |
| dck | BSU00140 | deoxyadenosin/deoxycytidine kinase | | | | |
| dgk | BSU00150 | deoxyguanosine kinase | | | | |
| yaaH | BSU00160 | general stress protein, survival of ethanol stress, SafA-dependent spore coat | | | | |
| yaaI | BSU00170 | general stress protein, similar to isochorismatase | | | | |
| yaaJ | BSU00180 | tRNA specific adenosine deaminase | | | | |
| scr | BSU_misc_RNA_2 | 4.5 S RNA | | | | |
| dnaX | BSU00190 | DNA polymerase III (gamma and tau subunits) | | | | |
| yaaK | BSU00200 | unknown | | | | |
| recR | BSU00210 | repair, recombination | | | | |
| yaaL | BSU00220 | unknown | | | | |
| bofA | BSU00230 | inhibition of the pro-sigma-K processing machinery | | | | |
| rrnA-16S- trnA-Ile- trnA-Ala- rrnA-23S- rrnA-5S | | | | | | |
| gin | BSU00240 | forespore-specific protein, inhibitor of SigG and of SigE | | | | |
| xpaC | BSU00250 | hydrolysis of 5-bromo-4-chloroindolyl phosphate | | | | |
| yaaN | BSU00260 | unknown | | | | |
| yaaO | BSU00270 | similar to arginine decarboxylase | | | | |
| tmk | BSU00280 | thymidylate kinase | | | | |
| yaaQ | BSU00290 | unknown | | | | |
| yaaR | BSU00300 | unknown | | | | |
| holB | BSU00310 | DNA polymerase III (delta subunit) | | | | |
| yaaT | BSU00320 | control of the phosphorelay | | | | |
| yabA | BSU00330 | inhibitor of DnaA oligomerization | | | | |
| yabB | BSU00340 | unknown | | | | |
| yazA | BSU00350 | unknown | | | | |
| yabC | BSU00360 | similar to 16S rRNA methyltransferase | | | | |
| abrB | BSU00370 | transcriptional regulator of transition state genes | | | | |
| metS | BSU00380 | methionyl-tRNA synthetase | | | | |
| yabD | BSU00390 | unknown | | | | |
| yabE | BSU00400 | similar to cell wall binding protein | | | | |
| rnmV | BSU00410 | RNase M5 | | | | |
| ksgA | BSU00420 | rRNA adenine dimethyltransferase | | | | |
| yabG | BSU00430 | protease | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| veg | BSU00440 | unknown | | | | |
| sspF | BSU00450 | small acid-soluble spore protein (minor) | | | | |
| ispE | BSU00460 | 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase | | | | |
| purR | BSU00470 | transcription repressor of the pur operon | | | | |
| yabJ | BSU00480 | required for activity of PurR | | | | |
| spoVG | BSU00490 | negative effector of asymetric septation at the onset of sporulation | | | | |
| gcaD | BSU00500 | UDP-N-acetylglucosamine pyrophosphorylase | | | | |
| prs | BSU00510 | phosphoribosylpyrophosphate synthetase, universally conserved protein | | | | |
| ctc | BSU00520 | general stress protein, similar to ribosomal protein L25 | | | | |
| spoVC | BSU00530 | general stress protein, putative peptidyl-tRNA hydrolase | | | | |
| fin | BSU00540 | suppressor of recU mutations | | | | |
| mfd | BSU00550 | transcription-repair coupling factor | | | | |
| spoVT | BSU00560 | transcription activator and repressor of SigG-dependent genes | | | | |
| yabM | BSU00570 | may function in a previously observed alternate pathway for peptidoglycan | | | | |
| yabN | BSU00580 | unknown | | | | |
| yabO | BSU00590 | similar to heat shock protein Hsp15 | | | | |
| yabP | BSU00600 | required for sporulation at a late stage | | | | |
| yabQ | BSU00610 | required for sporulation at a late stage | | | | |
| divIC | BSU00620 | cell-division initiation protein (septum formation), component of septosome (with DivIB) | | | | |
| yabR | BSU00630 | similar to polyribonucleotide nucleotidyltransferase | | | | |
| trnSL-Met1- trnSL-Glu1 | | | | | | |
| spoIIE | BSU00640 | protein serine phosphatase, septum-associated PP2C, dephosphorylation of SpoIIAA | | | | |
| yabS | BSU00650 | unknown | | | | |
| yabT | BSU00660 | Ser/Thr kinase, controls DNA integrity during spore development | | | | |
| tilS | BSU00670 | tRNAIle-lysidine synthetase | | | | |
| hprT | BSU00680 | hypoxanthine phosphoribosyltransferase | | | | |
| ftsH | BSU00690 | ATP-dependent metalloprotease | | | | |
| coaX | BSU00700 | hypothetical protein | | | | |
| yacC | BSU00710 | similar to chaperonin (HSP33 Homolog), putative disulfide bond chaperone | | | | |
| yacD | BSU00720 | similar to secretion protein PrsA | | | | |
| cysK | BSU00730 | trigger enzyme: cysteine synthetase A and control of CymR activity | | | | |
| pabB | BSU00740 | para-aminobenzoate synthase (subunit A) | | | | |
| pabA | BSU00750 | para-aminobenzoate synthase (subunit B)/ anthranilate synthase (subunit II) | | | | |
| pabC | BSU00760 | aminodeoxychorismate lyase | | | | |
| sul | BSU00770 | dihydropteroate synthase | | | | |
| folB | BSU00780 | dihydroneopterin aldolase | | | | |
| folK | BSU00790 | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase | | | | |
| yazB | BSU00800 | unknown | | | | |
| yacF | BSU00810 | putative tRNA-dihydrouridine synthase B | | | | |
| lysS | BSU00820 | lysyl-tRNA synthetase | | | | |
| rrnJ-16S- rrnJ-23S- rrnJ-5S- trnJ-Ala- trnJ-Arg- trnJ-Gly- trnJ-Leu1- trnJ-Leu2- trnJ-Lys- trnJ-Pro- trnJ-Thr- trnJ-Val- rrnW- | | | | | | |
| ctsR | BSU00830 | transcription repressor of class III heat shock genes (clpC operon, clpE, clpP) | | | | |
| mcsA | BSU00840 | modulator of CtsR-dependent repression, McsA activates kinase activity of McsB | | | | |
| mcsB | BSU00850 | protein arginine kinase, phosphorylates CtsR, modulator of CtsR-dependent repression | | | | |
| clpC | BSU00860 | ATP-dependent Clp protease, ATPase subunit | | | | |
| radA | BSU00870 | negative effector of DisA activity | | | | |
| disA | BSU00880 | DNA integrity scanning protein | | | | |
| yacL | BSU00890 | general stress protein, survival of salt and ethanol stresses | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ispD | BSU00900 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, third step in the MEP pathway of isoprenoid biosynthesis | | | | |
| ispF | BSU00910 | 2-C-methyl-D-erythrol-2,4-cyclodiphosphate synthase, 5th step in the MEP pathway of isoprenoid biosynthesis | | | | |
| gltX | BSU00920 | glutamyl-tRNA synthetase, universally conserved protein | | | | |
| cysE | BSU00930 | serine O-acetyltransferase | | | | |
| cysS | BSU00940 | cysteine-tRNA synthetase | | | | |
| mrnC | BSU00950 | RNase Mini-III | | | | |
| yacO | BSU00960 | putative 23S rRNA methyltransferase | | | | |
| yacP | BSU00970 | unknown | | | | |
| sigH | BSU00980 | RNA polymerase sigma factor SigH | | | | |
| rpmGB | BSU00990 | ribosomal protein L33 | | | | |
| secE | BSU01000 | preprotein translocase subunit | | | | |
| nusG | BSU01010 | transcription antitermination factor | | | | |
| rplK | BSU01020 | ribosomal protein L11 | | | | |
| rplA | BSU01030 | ribosomal protein L1 | | | | |
| rplJ | BSU01040 | ribosomal protein L10 | | | | |
| rplL | BSU01050 | ribosomal protein L12 | | | | |
| ybxB | BSU01060 | unknown | | | | |
| rpoB | BSU01070 | RNA polymerase beta subunit | | | | |
| rpoC | BSU01080 | RNA polymerase beta' subunit | | | | |
| ybxF | BSU01090 | similar to ribosomal protein L7 family, associated with the ribosome during exponential growth | | | | |
| rpsL | BSU01100 | ribosomal protein S12 | | | | |
| rpsG | BSU01110 | ribosomal protein S7 | | | | |
| fusA | BSU01120 | elongation factor G | | | | |
| tufA | BSU01130 | elongation factor Tu | | | | |
| ybaC | BSU01140 | similar to proline iminopeptidase | | | | |
| rpsJ | BSU01150 | ribosomal protein S10 | | | | |
| rplC | BSU01160 | ribosomal protein L3 | | | | |
| rplD | BSU01170 | ribosomal protein L4 | | | | |
| rplW | BSU01180 | ribosomal protein L23 | | | | |
| rplB | BSU01190 | ribosomal protein L2 | | | | |
| rpsS | BSU01200 | ribosomal protein S19 | | | | |
| rplV | BSU01210 | ribosomal protein L22 | | | | |
| rpsC | BSU01220 | ribosomal protein S3 | | | | |
| rplP | BSU01230 | ribosomal protein L16 | | | | |
| rpmC | BSU01240 | ribosomal protein L29 | | | | |
| rpsQ | BSU01250 | ribosomal protein S17 | | | | |
| rplN | BSU01260 | ribosomal protein L14 | | | | |
| rplX | BSU01270 | ribosomal protein L24 | | | | |
| rplE | BSU01280 | ribosomal protein L5 | | | | |
| rpsN | BSU01290 | ribosomal protein S14 | | | | |
| rpsH | BSU01300 | ribosomal protein S8 | | | | |
| rplF | BSU01310 | ribosomal protein L6 | | | | |
| rplR | BSU01320 | ribosomal protein L18 | | | | |
| rpsE | BSU01330 | ribosomal protein S5 | | | | |
| rpmD | BSU01340 | ribosomal protein L30 | | | | |
| rplO | BSU01350 | ribosomal protein L15 | | | | |
| secY | BSU01360 | preprotein translocase subunit, universally conserved protein | | | | |
| adk | BSU01370 | adenylate kinase | | | | |
| map | BSU01380 | methionine aminopeptidase | | | | |
| ybzG | BSU01389 | unknown | | | | |
| infA | BSU01390 | translation initiation factor IF-1 | | | | |
| rpmJ | BSU01400 | ribosomal protein L36 | | | | |
| rpsM | BSU01410 | ribosomal protein S13 | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| rpsK | BSU01420 | ribosomal protein S11 | | | | |
| rpoA | BSU01430 | RNA polymerase alpha subunit | | | | |
| rplQ | BSU01440 | ribosomal protein L17 | | | | |
| ybxA | BSU01450 | ATP-binding A1 component of ECF transporters | | | | |
| ybaE | BSU01460 | ATP-binding A2 component of ECF transporters | | | | |
| ybaF | BSU01470 | trans-membrane T component of ECF transporters | | | | |
| truA | BSU01480 | pseudouridylate synthase I, universally conserved protein | | | | |
| rplM | BSU01490 | ribosomal protein L13 | | | | |
| rpsI | BSU01500 | ribosomal protein S9 | | | | |
| ybaJ | BSU01510 | unknown | | | | |
| ybaK | BSU01520 | unknown | | | | |
| cwlD | BSU01530 | N-acetylmuramoyl-L-alanine amidase | | | | |
| salA | BSU01540 | negative regulator of scoC expression | | | | |
| gerD | BSU01550 | required for fast repsonse to the presence of germinants | | | | |
| kbaA | BSU01560 | activation of the KinB-dependent pathway to sporulation | | | | |
| pdaB | BSU01570 | polysaccharide deacetylase | | | | |
| rrnI-16S- rrnI-23S- trnI-Ala- trnI-Arg- trnI-Asn- trnI-Gly- trnI-Pro- trnI-Thr rrnH-16S- rrnH-23S- rrnH-5S- rrnG-16S- rrnG- | | | | | | |
| ybaR | BSU01580 | unknown | | | | |
| ybaS | BSU01590 | similar to Na+-dependent transporter | | | | |
| ybbA | BSU01600 | putative bacillibactin esterase | | | | |
| feuC | BSU01610 | ABC transporter for the siderophores Fe-enterobactin and Fe-bacillibactin (integral membrane protein) | | | | |
| feuB | BSU01620 | ABC transporter for the siderophores Fe-enterobactin and Fe-bacillibactin (integral membrane protein) | | | | |
| feuA | BSU01630 | ABC transporter for the siderophores Fe-enterobactin and Fe-bacillibactin (binding protein), with YusV as ATPase | | | | |
| btr | BSU01640 | transcription activator (AraC family DNA-binding domain fused to FeuA-like substrate-binding domain) | | | | |
| ybbC | BSU01650 | unknown | | | | |
| nagZ | BSU01660 | N-acetylglucosaminidase | | | | |
| amiE | BSU01670 | N-acetylmuramyl-L-alanine amidase | | | | |
| murP | BSU01680 | N-acetyl muramic acid-specific phosphotransferase system, EIIBC component of the PTS | | | | |
| murR | BSU01690 | probably transcriptional regulator of genes required for the utilization of N-acetylmuramic acid, homolog to E. coli MurR | | | | |
| murQ | BSU01700 | similar to E. coli MurQ (etherase, cleaves lactate from N-acetylmuramic acid) | | | | |
| ybbJ | BSU01710 | unknown | | | | |
| ybbK | BSU01720 | unknown | | | | |
| trnSL-Gln2- trnSL-Glu2 - trnSL-Thr1- trnSL-Tyr1 - trnSL-Val1 | | | | | | |
| sigW | BSU01730 | RNA polymerase ECF-type sigma factor SigW | | | | |
| rsiW | BSU01740 | anti-SigW | | | | |
| cdaA | BSU01750 | diadenylate cyclase, synthesis of c-di-AMP in vegetative cells | | | | |
| cdaR | BSU01760 | effector protein controlling CdaA diadenylate cyclase activity | | | | |
| glmM | BSU01770 | phosphoglucosamine mutase, required for cell wall synthesis | | | | |
| glmS | BSU01780 | glutamine-fructose-6-phosphate transaminase | | | | |
| alkA | BSU01800 | DNA-3-methyladenine glycosylase | 🟦 | 🟦 | 🟦 | 🟦 |
| adaA | BSU01810 | trigger enzyme: methylphosphotriester-DNA alkyltransferase/ transcriptional activator of the adaA-adaB operon | 🟦 | 🟦 | 🟦 | 🟦 |
| adaB | BSU01820 | O6-methylguanine-DNA methyltransferase | 🟦 | 🟦 | 🟦 | 🟦 |
| ndhF | BSU01830 | NADH dehydrogenase (subunit 5) | 🟦 | 🟦 | 🟦 | 🟦 |
| ybcC | BSU01845 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| ybcF | BSU01860 | similar to carbonic anhydrase | 🟦 | 🟦 | 🟦 | 🟦 |
| ybcH | BSU01870 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| ybcI | BSU01880 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| ybzH | BSU01889 | putative transcriptional regulator (ArsR family) | 🟦 | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number [1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ybcL | BSU01890 | similar to chloramphenicol resistance protein | 🟦 | 🟦 | 🟦 | 🟦 |
| ybcM | BSU01900 | similar to glucosamine-fructose-6-phosphate aminotransferase | 🟦 | 🟦 | 🟦 | 🟦 |
| skfA | BSU01910 | spore killing factor | 🟦 | 🟦 | 🟦 | 🟦 |
| skfB | BSU01920 | thioether bond forming radical SAM enzyme, catalyzes the first step in the maturation of spore killing factor | 🟦 | 🟦 | 🟦 | 🟦 |
| skfC | BSU01935 | may be involved in spore killing | 🟦 | 🟦 | 🟦 | 🟦 |
| skfE | BSU01950 | ABC transporter (binding protein), export of the spore killing factor | 🟦 | 🟦 | 🟦 | 🟦 |
| skfF | BSU01960 | ABC transporter (permease), export of the spore killing factor | 🟦 | 🟦 | 🟦 | 🟦 |
| skfG | BSU01970 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| skfH | BSU01980 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| ybdG | BSU01990 | unknown |  | 🟦 | 🟦 | 🟦 |
| ybdJ | BSU02000 | two-component response regulator |  | 🟦 | 🟦 | 🟦 |
| ybdK | BSU02010 | two-component sensor kinase |  | 🟦 | 🟦 | 🟦 |
| ybzI | BSU02019 | unknown |  | 🟦 | 🟦 | 🟦 |
| prkD | BSU02030 | protein kinase D |  | 🟦 | 🟦 | 🟦 |
| ybdN | BSU02040 | unknown |  | 🟦 | 🟦 | 🟦 |
| ybdO | BSU02050 | unknown |  | 🟦 | 🟦 | 🟦 |
| ybxG | BSU02060 | similar to amino acid permease |  | 🟦 | 🟦 | 🟦 |
| csgA | BSU02070 | required for the ability of the germinating spore to resume vegetative growth |  | 🟦 | 🟦 | 🟦 |
| ybxH | BSU02080 | unknown |  | 🟦 | 🟦 | 🟦 |
| ybxI | BSU02090 | beta-lactamase |  | 🟦 | 🟦 | 🟦 |
| cypC | BSU02100 | fatty acid beta-hydroxylating cytochrome P450, hydroxylates myristic acid to beta-hydroxymyristic |  | 🟦 | 🟦 | 🟦 |
| ybyB | BSU02110 | general stress protein, survival of ethanol stress |  | 🟦 | 🟦 | 🟦 |
| ybeC | BSU02120 | similar to amino acid transporter |  | 🟦 | 🟦 | 🟦 |
| glpQ | BSU02130 | glycerolphosphate diester phosphodiesterase |  |  |  |  |
| glpT | BSU02140 | glycerol-3-phosphate permease |  |  |  |  |
| ybeF | BSU02150 | unknown |  |  |  |  |
| ybfA | BSU02160 | unknown |  |  |  |  |
| ybfB | BSU02170 | unknown |  |  |  |  |
| ybfE | BSU02180 | unknown |  |  |  |  |
| ybfF | BSU02190 | unknown |  |  |  |  |
| ybfG | BSU02200 | carboxylesterase NP, 1,2-O-isopropylideneglycerol caprylate esterase |  |  |  |  |
| ybfH | BSU02210 | unknown |  |  |  |  |
| ybfI | BSU02220 | similar to transcription regulator (AraC family) |  |  |  |  |
| purT | BSU02230 | phosphoribosylglycinamide formyltransferase 2 |  |  |  |  |
| mpr | BSU02240 | extracellular metalloprotease |  | 🟦 | 🟦 | 🟦 |
| ybfJ | BSU02250 | unknown |  | 🟦 | 🟦 | 🟦 |
| ybfK | BSU02260 | similar to carboxylesterase |  |  |  |  |
| pssA | BSU02270 | phosphatidylserine synthase |  |  |  |  |
| ybfM | BSU02280 | similar to alkaline phosphatase |  |  |  |  |
| psd | BSU02290 | phosphatidylserine decarboxylase |  |  |  |  |
| ybfN | BSU02300 | unknown |  |  |  |  |
| ybfO | BSU02310 | similar to erythromycin esterase |  |  |  |  |
| ybfP | BSU02320 | similar to transcription regulator (AraC family) |  |  |  |  |
| ybfQ | BSU02330 | unknown |  |  |  |  |
| gltP | BSU02340 | similar to H+/glutamate symporter |  |  |  |  |
| gamP | BSU02350 | glucosamine-specific phosphotransferase system, EIICBA of the PTS |  |  |  |  |
| gamA | BSU02360 | glucosamine-6-phosphate deaminase |  |  |  |  |
| ybgA | BSU02370 | transcriptional repressor (GntR family) of the *gamA-gamP* operon |  |  |  |  |
| ybgB | BSU02380 | putative immunity protein |  |  |  |  |
| ybgE | BSU02390 | branched-chain amino acid aminotransferase |  |  |  |  |
| ybgF | BSU02400 | similar to histidine permease |  |  |  |  |
| ybgG | BSU02410 | similar to E. coli S-methylmethionine:homocysteine methyltransferase MmuM |  |  |  |  |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| glnT | BSU02420 | glutamine transporter (proton symport) | | | | |
| glsA | BSU02430 | glutaminase, low affinity for glutamine | | | | |
| glnK | BSU02440 | two-component sensor kinase, regulation of the glsA-glnT operon | | | | |
| glnL | BSU02450 | two-component response regulator, regulation of the glsA-glnT operon | | | | |
| ycbC | BSU02460 | 5-dehydro-4-deoxyglucarate dehydratase | | 🟦 | 🟦 | 🟦 |
| ycbD | BSU02470 | NADP(+)-dependent alpha-ketoglutaric semialdehyde dehydrogenase | | 🟦 | 🟦 | 🟦 |
| ycbE | BSU02480 | galactarate/glucarate transporter in (proton symport) | | 🟦 | 🟦 | 🟦 |
| ycbF | BSU02490 | glucarate dehydratase | | 🟦 | 🟦 | 🟦 |
| ycbG | BSU02500 | transcription regulator of the glucarate/galactarate utilization operon | | 🟦 | 🟦 | 🟦 |
| ycbH | BSU02510 | galactarate dehydratase | | 🟦 | 🟦 | 🟦 |
| ycbJ | BSU02520 | similar to macrolide 2'-phosphotransferase | | 🟦 | 🟦 | 🟦 |
| rtpA | BSU02530 | anti-TRAP | | | | |
| ycbK | BSU02540 | similar to efflux system | | | | |
| ycbL | BSU02550 | two-component response regulator | | | | |
| ycbM | BSU02560 | two-component sensor kinase | | | | |
| ycbN | BSU02570 | similar to ABC transporter (ATP-binding protein) | | | | |
| ycbO | BSU02580 | unknown | | | | |
| ycbP | BSU02590 | general stress protein | | | | |
| cwlJ | BSU02600 | spore coat protein, cell wall hydrolase | | | | |
| ycbR | BSU02610 | similar to toxic cation resistance protein | | | | |
| yczK | BSU02619 | unknown | | | | |
| phoD | BSU02620 | phosphodiesterase/alkaline phosphatase | | | | |
| tatAD | BSU02630 | component of the TatAdCd twin-arginine translocase | | | | |
| tatCD | BSU02640 | component of the TatAdCd twin-arginine translocase | | | | |
| pcp | BSU02650 | pyrrolidone-carboxylate peptidase | | | | |
| ycbU | BSU02660 | cysteine desulfurase | | | | |
| lmrB | BSU02670 | lincomycin-resistance protein (multidrug resistance pump) | | | | |
| lmrA | BSU02680 | transcriptional regulator, control of yxaG-yxaH and lmrA-lmrB | | | | |
| ansZ | BSU02690 | asparaginase | | | | |
| lip | BSU02700 | extracellular lipase | | | | |
| yczC | BSU02710 | unknown | | | | |
| yccF | BSU02720 | unknown | | | | |
| natK | BSU02730 | two-component sensor kinase, regulation of the natA-natB operon | | | | |
| natR | BSU02740 | two-component response regulator, regulation of the natA-natB operon | | | | |
| natA | BSU02750 | Na+ ABC transporter (export) (ATP-binding protein) | | | | |
| natB | BSU02760 | Na+ ABC transporter (export) (ATP-binding protein) | | | | |
| yccK | BSU02770 | similar to ion channel | | | | |
| ycdA | BSU02780 | lipoprotein, required for swarming motility | | | | |
| ycdB | BSU02790 | unknown | | | | |
| ycdC | BSU02800 | unknown | | | | |
| cwlK | BSU02810 | peptidoglycan hydrolytic L,D-endopeptidase | | | | |
| rapJ | BSU02820 | response regulator aspartate phosphatase | | | | |
| ycdF | BSU02830 | general stress protein, similar to glucose 1-dehydrogenase, survival of ethanol stress and low temperatures | | | | |
| ycdG | BSU02840 | general stress protein, similar to oligo-1,6-glucosidase | | | | |
| znuA | BSU02850 | ABC transporter for zinc (binding protein) | | | | |
| znuC | BSU02860 | ABC transporter for zinc (ATP-binding protein) | | | | |
| znuB | BSU02870 | ABC transporter for zinc (permease) | | | | |
| yceB | BSU02880 | similar to monooxygenase | | | | 🟦 |
| yceC | BSU02890 | similar to tellurium resistance protein | | | | 🟦 |
| yceD | BSU02900 | general stress protein, similar to tellurium resistance protein | | | | 🟦 |
| yceE | BSU02910 | general stress protein, similar to tellurium resistance protein | | | | 🟦 |
| yceF | BSU02920 | general stress protein, similar to tellurium resistance protein | | | | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yceG | BSU02930 | general stress protein, survival of ethanol stress | | | | 🟦 |
| yceH | BSU02940 | similar to toxic anion resistance protein | | | | 🟦 |
| niaP | BSU02950 | nicotinate transporter | | | | 🟦 |
| yceJ | BSU02960 | similar to multidrug-efflux transporter | | | | 🟦 |
| yceK | BSU02970 | similar to transcriptional regulator (ArsR family) | | | | 🟦 |
| opuAA | BSU02980 | glycine betaine ABC transporter (ATP-binding protein) | | | | 🟦 |
| opuAB | BSU02990 | glycine betaine ABC transporter (permease) | | | | 🟦 |
| opuAC | BSU03000 | glycine betaine ABC transporter (binding protein) | | | | 🟦 |
| amhX | BSU03010 | amidohydrolase | | | | 🟦 |
| ycgA | BSU03020 | unknown | | | | 🟦 |
| ycgB | BSU03030 | unknown | | | | 🟦 |
| amyE | BSU03040 | alpha-amylase | | | | 🟦 |
| ldh | BSU03050 | L-lactate dehydrogenase | | | | 🟦 |
| lctP | BSU03060 | lactate permease, excretion | | | | 🟦 |
| mdr | BSU03070 | multidrug-efflux transporter (puromycin, nerfloxacin, tosufloxacin) | | | | 🟦 |
| ycgE | BSU03080 | similar to transcription regulator | | | | 🟦 |
| ycgF | BSU03090 | unknown | | | | 🟦 |
| ycgG | BSU03100 | unknown | | | | 🟦 |
| ycgH | BSU03110 | similar to amino acid transporter | | | | |
| ycgI | BSU03120 | unknown | | | | |
| nadE | BSU03130 | NH3-dependent NAD+ synthetase | | | | |
| tmrB | BSU03140 | tunicamycin resistance protein, ATP-binding membrane protein | | | | |
| aroK | BSU03150 | shikimate kinase | | | | |
| ycgJ | BSU03160 | similar to predicted S-adenosylmethionine-dependent methyltransferase | | | | |
| ycgK | BSU03170 | similar to transcriptional regulator (LysR family) | | | | |
| cah | BSU03180 | cephalosporin C deacetylase | | | | |
| ycgL | BSU03190 | unknown | | | | |
| putB | BSU03200 | proline oxidase (L-proline, NAD) | | | | |
| putC | BSU03210 | 1-pyrroline-5-carboxylate dehydrogenase | | | | |
| putP | BSU03220 | high affinity proline permease | | | | |
| putR | BSU03230 | transcriptional activator of the proline utilization operon *putB-putC-putP* | | | | |
| ycgQ | BSU03240 | unknown | | | | |
| ycgR | BSU03250 | unknown | | | | |
| ycgS | BSU03260 | similar to aromatic hydrocarbon catabolism | | | | |
| ycgT | BSU03270 | similar to ferredoxin-NAD(P)+ oxidoreductase | | | | |
| nasF | BSU03280 | uroporphyrinogen methyltransferase | | | | |
| nasE | BSU03290 | assimilatory nitrite reductase (subunit) | | | | |
| nasD | BSU03300 | assimilatory nitrite reductase (subunit) | | | | |
| nasC | BSU03310 | nitrate reductase (catalytic subunit) | | | | |
| nasB | BSU03320 | nitrate reductase (electron transfer subunit) | | | | |
| nasA | BSU03330 | nitrate transporter | | | | |
| folE2 | BSU03340 | GTP cyclohydrolase IB, replaces FolE under conditions of zinc starvation | | | | |
| yciB | BSU03350 | zinc transporter | | | | |
| yczL | BSU03359 | unknown | | | | |
| yciC | BSU03360 | putative metallochaperone | | | | |
| yckA | BSU03370 | similar to amino acid ABC transporter (permease) | | | | |
| yckB | BSU03380 | similar to amino acid ABC transporter (binding protein) | | | | |
| yckC | BSU03390 | unknown | | | | |
| yckD | BSU03400 | unknown | | | | |
| yckE | BSU03410 | aryl-β-glucosidase | | | | |
| nin | BSU03420 | inhibitor of the DNA degrading activity of NucA | | | | |
| nucA | BSU03430 | membrane-associated nuclease, catalyzes DNA cleavage during transformation | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| tlpC | BSU03440 | methyl-accepting chemotaxis protein | | | | |
| hxlB | BSU03450 | 6-phospho-3-hexuloisomerase | | | | |
| hxlA | BSU03460 | 3-hexulose-6-phosphate synthase | | | | |
| hxlR | BSU03470 | transcription activator of the hxlA-hxlB operon | | | | |
| srfAA | BSU03480 | surfactin synthetase / competence | | | | |
| srfAB | BSU03490 | surfactin synthetase / competence | | | | |
| comS | BSU03500 | antiadaptor protein, assembly link between regulatory components of the competence signal transduction pathway | | | | |
| srfAC | BSU03510 | surfactin synthetase / competence | | | | 🟦 |
| srfAD | BSU03520 | surfactin synthetase / competence | | | | 🟦 |
| ycxA | BSU03530 | unknown | | | | 🟦 |
| ycxB | BSU03540 | unknown | | | | 🟦 |
| ycxC | BSU03550 | unknown | | | | 🟦 |
| ycxD | BSU03560 | similar to transcriptional regulator (GntR family) | | | | 🟦 |
| sfp/1 | BSU03569 | 4'-phosphopantetheinyl transferase (surfactin synthetase-activating enzyme), inactive pseudogene in strain 168 | | | | 🟦 |
| sfp/2 | BSU03570 | 4'-phosphopantetheinyl transferase (surfactin synthetase-activating enzyme), inactive pseudogene in strain 168 | | | | 🟦 |
| yczE | BSU03580 | unknown | | | | |
| tcyC | BSU03590 | cystine ABC transporter, ATP-binding protein | | | | |
| tcyB | BSU03600 | cystine ABC transporter (permease), membrane protein | | | | |
| tcyA | BSU03610 | cystine ABC transporter (binding protein) | | | | |
| bsdA | BSU03620 | transcriptional activator of the bsdB-bsdC-bsdD operon | | | | |
| bsdB | BSU03630 | phenolic acid decarboxylase | | | | |
| bsdC | BSU03640 | phenolic acid decarboxylase | | | | |
| bsdD | BSU03651 | phenolic acid decarboxylase, reversible nonoxidative vanillate/4-hydroxybenzoate decarboxylase subunit | | | | |
| yclD | BSU03652 | putative FMN-binding subunit of phenolic acid decarboxylase | | | | |
| yclE | BSU03660 | similar to prolyl aminopeptidase | | | | |
| yclF | BSU03670 | peptide transporter | | | | |
| yclG | BSU03680 | unknown | | 🟦 | 🟦 | 🟦 |
| gerKD | BSU03690 | negative effector (D protein) of the GerKA-GerKB-GerKC germinant receptor | | 🟦 | 🟦 | 🟦 |
| gerKA | BSU03700 | nutrient receptor | | 🟦 | 🟦 | 🟦 |
| gerKC | BSU03710 | Nutrient receptor | | 🟦 | 🟦 | 🟦 |
| gerKB | BSU03720 | Nutrient receptor | | 🟦 | 🟦 | 🟦 |
| yclH | BSU03730 | similar to ABC transporter (ATP-binding protein) | | 🟦 | 🟦 | 🟦 |
| yclI | BSU03740 | similar to ABC transporter (membrane protein) | | 🟦 | 🟦 | 🟦 |
| yclJ | BSU03750 | two-component response regulator, active under anaerobic conditions | | 🟦 | 🟦 | 🟦 |
| yclK | BSU03760 | two-component sensor kinase | | 🟦 | 🟦 | 🟦 |
| rapC | BSU03770 | response regulator aspartate phosphatase, controls ComA activity | | 🟦 | 🟦 | 🟦 |
| phrC | BSU03780 | response regulator aspartate phosphatase (RapC) regulator / competence and sporulation stimulating factor (CSF) | | 🟦 | 🟦 | 🟦 |
| yczM | BSU03788 | putative toxin | | 🟦 | 🟦 | 🟦 |
| yczN | BSU03789 | putative toxin | | 🟦 | 🟦 | 🟦 |
| yclM | BSU03790 | aspartokinase III | | 🟦 | 🟦 | 🟦 |
| yclN | BSU03800 | petrobactin (3.4-catecholate siderophore) ABC transporter (permease) | | 🟦 | 🟦 | 🟦 |
| yclO | BSU03810 | petrobactin (3.4-catecholate siderophore) ABC transporter (permease) | | 🟦 | 🟦 | 🟦 |
| yclP | BSU03820 | petrobactin (3.4-catecholate siderophore) ABC transporter (ATP-binding protein) | | 🟦 | 🟦 | 🟦 |
| yclQ | BSU03830 | petrobactin (3.4-catecholate siderophore) ABC transporter (binding protein), major component of the secretome | | 🟦 | 🟦 | 🟦 |
| ycnB | BSU03840 | similar to multidrug resistance protein | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number [1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ycnC | BSU03850 | similar to transcriptional regulator (TetR/AcrR family) | | 🟦 | 🟦 | 🟦 |
| ycnD | BSU03860 | NADPH-FMN oxidoreductase, delivers reduced FMN to enzymes that require the reduced cofactor for activity | | 🟦 | 🟦 | 🟦 |
| ycnE | BSU03870 | unknown | | 🟦 | 🟦 | 🟦 |
| yczG | BSU03880 | similar to transcriptional regulator (ArsR family) | | 🟦 | 🟦 | 🟦 |
| gabR | BSU03890 | transcription activator of gabT-gabD, repressor of gabR | | | | |
| gabT | BSU03900 | gamma-aminobutyrate transaminase, general stress protein | | | | |
| gabD | BSU03910 | succinate-semialdehyde dehydrogenase (NADP), general stress protein | | | | |
| glcU | BSU03920 | probable glucose uptake protein | | | | |
| gdh | BSU03930 | glucose 1-dehydrogenase (NAD) | | | | |
| ycnI | BSU03940 | unknown | | | | |
| ycnJ | BSU03950 | copper transporter | | | | |
| ycnK | BSU03960 | transcription repressor of the ycnJ gene | | | | |
| ycnL | BSU03970 | unknown | | | | |
| mtlA | BSU03981 | trigger enzyme: mannitol-specific phosphotransferase system, EIICB of the PTS | | | | |
| mtlF | BSU03982 | phosphotransferase system (PTS) mannitol-specific enzyme IIA component | | | | |
| mtlD | BSU03990 | mannitol-1-phosphate 5-dehydrogenase | | | | |
| ycsA | BSU04000 | malic enzyme | | | | |
| sipU | BSU04010 | signal peptidase I | | | | |
| yczH | BSU04020 | unknown | | | | |
| ycsD | BSU04030 | β-hydroxyacyl-(acyl carrier protein) dehydratase | | | | |
| yczO | BSU04039 | unknown | | | | |
| ycsE | BSU04040 | unknown | | | | |
| ycsF | BSU04050 | similar to lactam utilization protein | | | | |
| ycsG | BSU04060 | similar to branched chain amino acids transporter | | | | |
| ycsI | BSU04070 | unknown | | | | |
| kipI | BSU04080 | inhibitor of KinA | | | | |
| kipA | BSU04090 | antagonist of KipI | | | | |
| kipR | BSU04100 | transcriptional regulator of the kip operon | | | | |
| lipC | BSU04110 | spore coat protein, phospholipase implicated in spore germination | | | | |
| yczI | BSU04120 | unknown | | | | |
| yczJ | BSU04130 | unknown | | | | |
| pbpC | BSU04140 | penicillin-binding protein 3 | | | | |
| ycsN | BSU04150 | similar to aryl-alcohol dehydrogenase | | | | |
| mtlR | BSU04160 | transcriptional activator of the mtlA-mtlD operon | | | | |
| ydaB | BSU04170 | unknown | | | | |
| ydaC | BSU04180 | unknown | | | | |
| ydaD | BSU04190 | general stress protein, similar to alcohol dehydrogenase | | | | |
| ydaE | BSU04200 | lyxose isomerase, general stress protein, survival of ethanol stress and low temperatures | | | | |
| ydaF | BSU04210 | similar to acetyltransferase | | | | |
| ydaG | BSU04220 | general stress protein | | | | |
| bsrC | | small RNA | | | | |
| amj | BSU04230 | Lipid II flippase | | | | |
| ydzA | BSU04240 | unknown | | | | |
| lrpC | BSU04250 | transcription regulator | | | | |
| topB | BSU04260 | DNA topoisomerase III | | | | |
| ydaJ | BSU04270 | general stress protein of unknown function | | | | |
| ydaK | BSU04280 | general stress protein, may act as c-di-GMP receptor | | | | |
| ydaL | BSU04290 | general stress protein of unknown function | | | | |
| ydaM | BSU04300 | general stress protein, similar to cellulose synthase | | | | |
| ydaN | BSU04310 | general stress protein of unknown function | | | | |
| ydaO | BSU04320 | unknown | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| mutT | BSU04330 | antimutator protein | | | | |
| ydaP | BSU04340 | general stress protein, required for survival of ethanol stress, putative pyruvate oxidase | | | | |
| ydzK | BSU04359 | unknown | | | | |
| mntH | BSU04360 | manganese transporter (proton symport) | | | | |
| ydaS | BSU04370 | general stress protein | | | | 🟦 |
| ydaT | BSU04380 | general stress protein, survival of ethanol stress and low temperatures | | | | 🟦 |
| ydbA | BSU04390 | similar to ABC transporter (binding protein) | | | | 🟦 |
| gsiB | BSU04400 | general stress protein, prevents enzyme inactivation upon freeze-thaw treatments | | | | 🟦 |
| ydbB | BSU04410 | unknown | | | | 🟦 |
| ydbC | BSU04420 | unknown | | | | 🟦 |
| ydbD | BSU04430 | general stress protein, similar to manganese-containing catalase | | | | 🟦 |
| dctB | BSU04440 | C4-dicarboxylate binding protein | | | | 🟦 |
| dctS | BSU04450 | two-component sensor kinase, regulation of the dctS-dctR-dctP operon | | | | 🟦 |
| dctR | BSU04460 | two-component response regulator, regulation of the dctS-dctR-dctP operon | | | | 🟦 |
| dctP | BSU04470 | fumarate/succinate transport in/out via proton symport, L-malate transport in via proton symport | | | | 🟦 |
| ydbI | BSU04480 | unknown | | | | 🟦 |
| ydbJ | BSU04490 | similar to ABC transporter (ATP-binding protein) | | | | 🟦 |
| ydbK | BSU04500 | similar to ABC transporter (membrane protein) | | | | 🟦 |
| ydbL | BSU04510 | unknown | | | | 🟦 |
| ydbM | BSU04520 | acyl-CoA dehydrogenase | | | | 🟦 |
| fbpB | BSU04530 | Fur-regulated basic protein, acts as RNA chaperone for fsrA, response to iron limitation | | | | 🟦 |
| fbpA | | Fur-regulated basic protein, acts as RNA chaperone for fsrA, response to iron limitation | | | | 🟦 |
| ydbO | BSU04540 | similar to cation efflux system | | | | 🟦 |
| ydbP | BSU04550 | similar to thioredoxin | | | | |
| ddl | BSU04560 | D-alanine-D-alanine ligase | | | | |
| murF | BSU04570 | UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine synthetase | | | | |
| cshA | BSU04580 | DEAD-box RNA helicase | | | | |
| ydbS | BSU04590 | resistence against antimicrobial compounds from B. amyloliquefaciens | | | | |
| ydbT | BSU04600 | resistence against antimicrobial compounds from B. amyloliquefaciens | | | | |
| ydcA | BSU04610 | unknown | | | | |
| acpS | BSU04620 | acyl-carrier protein synthase, 4'-phosphopantetheine transferases | | | | |
| ydcC | BSU04630 | unknown | | | | |
| alr | BSU04640 | alanine racemase | | | | |
| ndoAI | BSU04650 | antitoxin, inhibits EndoA | | | | |
| ndoA | BSU04660 | RNase EndoA, MazF family toxin, cleaves cellular mRNAs at specific, but frequently occuring sites | | | | |
| rsbR | BSU04670 | activator of RsbT kinase activity, part of the stressosome | | | | |
| rsbS | BSU04680 | anti-RsbT, part of the stressosome | | | | |
| rsbT | BSU04690 | PP2C activator, protein serine kinase, phosphorylates RsbS, part of the stressosome | | | | |
| rsbU | BSU04700 | protein serine phosphatase, environmental PP2C, dephosphorylates RsbV | | | | |
| rsbV | BSU04710 | anti-anti-SigB, antagonist of RsbW | | | | |
| rsbW | BSU04720 | Anti-SigB, protein serine kinase, phosphorylates RsbV | | | | |
| sigB | BSU04730 | RNA polymerase sigma factor SigB | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| rsbX | BSU04740 | protein serine phosphatase, feedback PP2C, dephosphorylates RsbS | | | | |
| ydcF | BSU04750 | unknown | | | | |
| ydcG | BSU04760 | unknown | | | | |
| ydcH | BSU04770 | unknown | | | | |
| ydcI | BSU04780 | unknown | | | | |
| cmpA | | cortex morphogenetic protein A | | | | |
| ydcK | BSU04790 | unknown | | | | |
| trnS-Asn- trnS-Gln- trnS-Glu- trnS-Leu1- trnS-Leu2- trnS-Lys- trnS-Ser | | | | | | |
| int | BSU04800 | integrase | 🟦 | 🟦 | 🟦 | 🟦 |
| immA | BSU04810 | protease, degrades ImmR at a specific site | 🟦 | 🟦 | 🟦 | 🟦 |
| immR | BSU04820 | transcriptional repressor, controls expression of genes of the mobile genetic element ICEBs1 | 🟦 | 🟦 | 🟦 | 🟦 |
| xis | BSU04830 | excisionase | 🟦 | 🟦 | 🟦 | 🟦 |
| ydzL | BSU04839 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| ydcO | BSU04840 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| helP | BSU04850 | helicase processivity factor | 🟦 | 🟦 | 🟦 | 🟦 |
| ydcQ | BSU04860 | similar to transposon protein | 🟦 | 🟦 | 🟦 | 🟦 |
| nicK | BSU04870 | DNA relaxase, similar to transposon protein | 🟦 | 🟦 | 🟦 | 🟦 |
| ydcS | BSU04880 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| ydcT | BSU04890 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yddA | BSU04900 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yddB | BSU04910 | similar to transposon protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yddC | BSU04920 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yddD | BSU04930 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| conE | BSU04940 | conjugation protein of the integrative and conjugative element ICEBs1 | 🟦 | 🟦 | 🟦 | 🟦 |
| yddF | BSU04950 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yddG | BSU04960 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| cwlT | BSU04970 | cell wall hydrolase, C-terminal domain hydrolyzes bond between D-Glu and m-DAP | 🟦 | 🟦 | 🟦 | 🟦 |
| yddI | BSU04980 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yddJ | BSU04990 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yddK | BSU05000 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| rapI | BSU05010 | response regulator aspartate phosphatase, antagonist of ImmR | 🟦 | 🟦 | 🟦 | 🟦 |
| phrI | BSU05020 | response regulator aspartate phosphatase (RapI) regulator | 🟦 | 🟦 | 🟦 | 🟦 |
| yddM | BSU05030 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yddN | BSU05040 | similar to alkanal monooxygenase | | | | |
| lrpA | BSU05050 | transcriptional regulator involved in repression of glyA transcription and KinB-dependent sporulation | | | | |
| lrpB | BSU05060 | transcriptional regulator involved in repression of glyA transcription and KinB-dependent sporulation | | | | |
| yddQ | BSU05070 | unknown | | | | |
| yddR | BSU05080 | unknown | | | | |
| yddS | BSU05090 | similar to metabolite transport protein | | | | |
| ydzM | BSU05099 | unknown | | | | |
| yddT | BSU05100 | unknown | | | | |
| ydzN | BSU05109 | unknown | | | | |
| ydeA | BSU05110 | glyoxalase III-like enzyme | | | | |
| cspC | BSU05120 | cold shock protein | | | | |
| ydeB | BSU05130 | similar to transcriptional regulator | | | | |
| ydzE | BSU05140 | unknown | | | | |
| ydeC | BSU05150 | similar to transcriptional regulator (AraC family) | | | | |
| ydeD | BSU05160 | unknown | | | | |
| ydeE | BSU05170 | similar to transcriptional regulator (AraC family) | | | | |
| ydeF | BSU05180 | similar to transcriptional regulator (GntR family) | | | | |
| ydeG | BSU05190 | similar to metabolite transport protein | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ydeH | BSU05200 | unknown | | | | |
| ydeI | BSU05210 | unknown | | | | |
| ydeJ | BSU05220 | unknown | | | | |
| ydeK | BSU05230 | unknown | | | | |
| ydeL | BSU05240 | similar to transcriptional regulator (GntR family) | | | | |
| ydeM | BSU05250 | unknown | | | | |
| ydeN | BSU05260 | unknown | | | | |
| ydzF | BSU05270 | similar to cinnamoyl ester hydrolase | | | | |
| ydeO | BSU05280 | unknown | | | | |
| ydeP | BSU05290 | MarR/DUF24-family transcription regulator | | | | |
| ydeQ | BSU05300 | similar to NAD(P)H oxidoreductase | | | | |
| ydeR | BSU05310 | similar to antibiotic resistance protein | | | | |
| ydeS | BSU05320 | similar to transcriptional regulator (TetR family) | | | | |
| ydzO | BSU05329 | unknown | | | | |
| aseR | BSU05330 | transcriptional repressor of aseA and aseR | | | | |
| aseA | BSU05340 | As(III) efflux pump | | | | |
| ydzS/1 | BSU05343 | part of the ydzS pseudogene | | | | |
| ydzS/2 | BSU05344 | part of the ydzS pseudogene | | | | |
| ydfB | BSU05350 | similar to antibiotic resistance protein | | | | |
| ydfC | BSU05360 | unknown | | | | |
| ydfD | BSU05370 | similar to transcriptional regulator (GntR family) | | | | |
| ydfE | BSU05380 | unknown | | | | |
| ydfF | BSU05390 | unknown | | | | |
| ydfG | BSU05400 | unknown | | | | |
| ydzP | BSU05408 | unknown | | | | |
| ydzQ | BSU05409 | unknown | | | | |
| ydfH | BSU05410 | two-component sensor kinase, control of ydfJ expression | | | | |
| ydfI | BSU05420 | two-component response regulator, control of ydfJ expression | | | | |
| ydfJ | BSU05430 | similar to antibiotic transport-associated protein | | | | |
| nap | BSU05440 | carboxylesterase NA | | | | |
| ydfK | BSU05450 | unknown | | | | |
| ydfL | BSU05460 | similar to multidrug-efflux transporter regulator | | | | |
| ydfM | BSU05470 | similar to cation efflux system | | | | |
| mhqN | BSU05480 | similar to NAD(P)H nitroreductase | | | | |
| mhqO | BSU05490 | hydroquinone-specific dioxygenase, confers resistence to methyl-hydroxyquinone | | | | |
| mhqP | BSU05500 | may be involved in protection against methyl-hydroquinone | | | | |
| ydfQ | BSU05510 | similar to thioredoxin | | | | |
| ydzH | BSU05520 | unknown | | | | |
| ydzR | BSU05529 | unknown | | | | |
| ydfR | BSU05530 | unknown | | | | |
| ydfS | BSU05540 | unknown | | | | |
| cotP | BSU05550 | inner spore coat protein | | | | |
| ydgA | BSU05560 | unknown | | | | |
| ydgB | BSU05570 | unknown | | | | |
| ydgC | BSU05580 | unknown | | | | |
| ydgD | BSU05590 | unknown | | | | |
| ydgE | BSU05600 | unknown | | | | |
| vmlR | BSU05610 | ABC transporter (ATP-binding protein), efflux of antibiotics (virginiamycin M, lincomycin) | | | | |
| ydgF | BSU05620 | similar to amino acid ABC transporter (permease) | | | | |
| dinB | BSU05630 | nuclease inhibitor | | | | |
| ydgG | BSU05640 | similar to transcriptional regulator (MarR family) | | 🟦 | 🟦 | 🟦 |
| ydgH | BSU05650 | similar to transporter | | 🟦 | 🟦 | 🟦 |
| ydgI | BSU05660 | similar to NADH dehydrogenase | | 🟦 | 🟦 | 🟦 |
| ydgJ | BSU05670 | similar to transcriptional regulator (MarR family) | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ydgK | BSU05680 | similar to bicyclomycin resistance protein | | ■ | ■ | ■ |
| ydhB | BSU05690 | unknown | | ■ | ■ | ■ |
| ydhC | BSU05700 | similar to transcriptional regulator (GntR family) | | ■ | ■ | ■ |
| ydhD | BSU05710 | probable peptidoglycan hydrolase | | ■ | ■ | ■ |
| ydhE | BSU05720 | similar to macrolide glycosyltransferase | | ■ | ■ | ■ |
| ydhF | BSU05730 | unknown | | ■ | ■ | ■ |
| phoB | BSU05740 | alkaline phosphatase A | | ■ | ■ | ■ |
| fra | BSU05750 | frataxin-like protein, required for the biosynthesis of iron-sulfur clusters | | ■ | ■ | ■ |
| ydhH | BSU05760 | unknown | | ■ | ■ | ■ |
| ydhI | BSU05770 | unknown | | ■ | ■ | ■ |
| ydhJ | BSU05780 | unknown | | ■ | ■ | ■ |
| ydhK | BSU05790 | general stress protein, survival of ethanol stress | | ■ | ■ | ■ |
| pbuE | BSU05800 | putative hypoxanthine exporter | | ■ | ■ | ■ |
| gmuB | BSU05810 | glucomannan-specific phosphotransferase system, EIIB component of the PTS | | ■ | ■ | ■ |
| gmuA | BSU05820 | glucomannan-specific phosphotransferase system, EIIA component of the PTS | | ■ | ■ | ■ |
| gmuC | BSU05830 | glucomannan-specific phosphotransferase system, EIIC component of the PTS | | ■ | ■ | ■ |
| gmuD | BSU05840 | phospho-beta-mannosidase | | ■ | ■ | ■ |
| gmuR | BSU05850 | transcriptional repressor of the gmu operon | | ■ | ■ | ■ |
| gmuE | BSU05860 | mannose kinase | | ■ | ■ | ■ |
| gmuF | BSU05870 | mannose-6-P-isomerase | | ■ | ■ | ■ |
| gmuG | BSU05880 | beta-1,4-mannanase | | ■ | ■ | ■ |
| ydhU/1 | BSU05890 | similar to Mn catalase, inactive pseudogene in strain 168 | | ■ partial | ■ partial | ■ partial |
| ydhU/2 | BSU05899 | similar to Mn catalase, inactive pseudogene in strain 168 | | | | |
| trnE-Arg- trnE-Gly- rrnE-16S- rrnE-23S- rrnE-5S- trnE-Asp- trnE-Met | | | | | | |
| thiL | BSU05900 | thiamine-monophosphate kinase | | | | |
| tsaE | BSU05910 | P-loop ATPase | | | | |
| tsaB | BSU05920 | required for threonyl carbamoyl adenosine (t6A) modification of tRNAs that pair with ANN codons in mRNA | | | | |
| ydiD | BSU05930 | similar to to ribosomal-protein-alanine N-acetyltransferase | | | | |
| tsaD | BSU05940 | required for threonyl carbamoyl adenosine (t6A) modification of tRNAs that pair with ANN codons in mRNA | | | | |
| ydiF | BSU05950 | similar to ABC transporter (ATP-binding protein) | | | | |
| ydiG | BSU05960 | similar to molybdopterin precursor biosynthesis | | | | |
| rex | BSU05970 | transcriptional repressor of anaerobically expressed genes involved in anaerobic respiration and fermentation | | | | |
| tatAY | BSU05980 | component of the TatAyCy twin-arginine translocase | | | | |
| tatCY | BSU05990 | component of the TatAYCY twin-arginine translocase | | | | |
| ydiK | BSU06000 | unknown | | | | |
| ydiL | BSU06010 | unknown | | | | |
| groES | BSU06020 | chaperonin, universally conserved protein | | | | |
| groEL | BSU06030 | chaperonin and co-repressor for HrcA | | | | |
| ydzT/1 | BSU06033 | putative integrase (fragment); C-terminal part of YdzT | | | | |
| ydzT/2 | BSU06034 | putative integrase (fragment); internal part of YdzT | | | | |
| ydzT/3 | BSU06036 | putative integrase (fragment); internal part of YdzT | | | | |
| ydzT/4 | BSU06037 | putative integrase (fragment); internal part of YdzT | | | | |
| ydzT/5 | BSU06038 | putative integrase (fragment); N-terminal part of YdzT | | | | |
| ydiM | BSU06040 | unknown | ■ | ■ | ■ | ■ |
| ydzU | BSU06048 | unknown | ■ | ■ | ■ | ■ |
| ydzV | BSU06049 | unknown, fragment of putative phage terminase | ■ | ■ | ■ | ■ |
| ydiO | BSU06060 | similar to DNA-3-methyladenine glycosidase II | ■ | ■ | ■ | ■ |
| ydiP | BSU06070 | similar to DNA-3-methyladenine glycosidase II | ■ | ■ | ■ | ■ |
| ydzW/1 | BSU06073 | putative phosphomannomutase, C-terminal part of YdzW | ■ | ■ | ■ | ■ |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ydzW/2 | BSU06074 | putative phosphomannomutase, internal part of YdzW | ■ | ■ | ■ | ■ |
| ydzW/3 | BSU06076 | putative phosphomannomutase, internal part of YdzW | ■ | ■ | ■ | ■ |
| ydzW/4 | BSU06077 | putative phosphomannomutase, internal part of YdzW | ■ | ■ | ■ | ■ |
| ydzW/5 | BSU06078 | putative phosphomannomutase, internal part of YdzW | ■ | ■ | ■ | ■ |
| ydzW/6 | BSU06079 | putative phosphomannomutase, internal part of YdzW | ■ | ■ | ■ | ■ |
| ydzW/7 | BSU06083 | putative phosphomannomutase, N-terminal part of YdzW | ■ | ■ | ■ | ■ |
| ydiR | BSU06090 | component of the BsuM DNA restriction system | ■ | ■ | ■ | ■ |
| ydiS | BSU06100 | component of the BsuM DNA restriction system | ■ | ■ | ■ | ■ |
| ydjA | BSU06110 | component of the BsuM DNA restriction system | ■ | ■ | ■ | ■ |
| ydjB | BSU06120 | unknown | ■ | ■ | ■ | ■ |
| ydjC | BSU06130 | unknown | ■ | ■ | ■ | ■ |
| gutR | BSU06140 | transcription activator of the gutB-gutP operon | | | | |
| gutB | BSU06150 | D-sorbitol dehydrogenase | | | | |
| gutP | BSU06160 | glucitol permease | | | | |
| fruC | BSU06170 | fructokinase | | | | |
| pspA | BSU06180 | phage shock protein A homolog | | ■ | ■ | ■ |
| ydjG | BSU06190 | unknown | | ■ | ■ | ■ |
| ydjH | BSU06200 | unknown | | ■ | ■ | ■ |
| ydjI | BSU06210 | unknown | | ■ | ■ | ■ |
| ydjJ | BSU06220 | unknown | | ■ | ■ | ■ |
| iolT | BSU06230 | major transporter for inositol | | ■ | ■ | ■ |
| bdhA | BSU06240 | acetoine/ butanediol dehydrogenase | | ■ | ■ | ■ |
| ydjM | BSU06250 | member of the WalR regulon | | ■ | ■ | ■ |
| ydjN | BSU06260 | unknown | | ■ | ■ | ■ |
| ydzJ | BSU06269 | unknown | | ■ | ■ | ■ |
| ydjO | BSU06270 | unknown | | ■ | ■ | ■ |
| ydjP | BSU06280 | similar to chloroperoxydase | | ■ | ■ | ■ |
| yeaA | BSU06290 | unknown | | ■ | ■ | ■ |
| cotA | BSU06300 | laccase, bilirubin oxidase, spore coat protein (outer) | | ■ | ■ | ■ |
| gabP | BSU06310 | gamma-amino butyric acid permease | | ■ | ■ | ■ |
| ydzX | BSU06319 | unknown | | ■ | ■ | ■ |
| yeaB | BSU06320 | similar to cation efflux system | | ■ | ■ | ■ |
| yeaC | BSU06330 | similar to methanol dehydrogenase regulation | | ■ | ■ | ■ |
| yeaD | BSU06340 | unknown | | ■ | ■ | ■ |
| yebA | BSU06350 | unknown | | partial | partial | partial |
| guaA | BSU06360 | GMP synthase (glutamine-hydrolysing) | | | | |
| pbuG | BSU06370 | hypoxanthin/ guanine permease | | | | |
| yebC | BSU06380 | unknown | | | | |
| yebD | BSU06390 | unknown | | | | |
| yebE | BSU06400 | unknown | | | | |
| yebG | BSU06410 | unknown | | | | |
| purE | BSU06420 | phosphoribosylaminoimidazole carboxylase (ATP-dependent) | | | | |
| purK | BSU06430 | phosphoribosylaminoimidazole carboxylase (ATP-dependent) | | | | |
| purB | BSU06440 | adenylsuccinate lyase | | | | |
| purC | BSU06450 | phosphoribosylaminoimidazole succinocarboxamide synthase | | | | |
| purS | BSU06460 | phosphoribosylformylglycinamidine synthase | | | | |
| purQ | BSU06470 | phosphoribosylformylglycinamidine synthase | | | | |
| purL | BSU06480 | phosphoribosylformylglycinamidine synthase | | | | |
| purF | BSU06490 | glutamine phosphoribosyldiphosphate amidotransferase | | | | |
| purM | BSU06500 | phosphoribosylaminoimidazole synthetase | | | | |
| purN | BSU06510 | phosphoribosylglycinamide formyltransferase, irreversible | | | | |
| purH | BSU06520 | phosphoribosylaminoimidazole carboxamide formyltransferase | | | | |
| purD | BSU06530 | phosphoribosylglycinamide synthetase | | | | |
| yezC | BSU06540 | similar to transcriptional regulator (Lrp family) | | | | |
| yecA | BSU06550 | similar to amino acid permease | | | | |
| yezF | BSU06559 | unknown | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yerA | BSU06560 | similar to adenine desaminase | | | | |
| yerB | BSU06570 | PcrA interaction protein | | | | |
| yerC | BSU06580 | unknown | | | | |
| yerD | BSU06590 | general stress protein, similar to glutamate synthase (ferredoxin) | | | | |
| pcrB | BSU06600 | unknown | | | | |
| pcrA | BSU06610 | ATP-dependent DNA helicase, facilitates unwinding of ICEBs1 DNA for horizontal transfer | | | | |
| ligA | BSU06620 | DNA ligase (NAD-dependent) | | | | |
| yerH | BSU06630 | unknown | | | | |
| yerI | BSU06640 | unknown | | | | |
| sapB | BSU06650 | a specific mutant activates alkaline phosphatase during sporulation independently of SigF and SigE | | | | |
| opuE | BSU06660 | proline transporter | | | | |
| gatC | BSU06670 | production of glutamyl-tRNA(Gln) | | | | |
| gatA | BSU06680 | production of glutamyl-tRNA(Gln) | | | | |
| gatB | BSU06690 | production of glutamyl-tRNA(Gln) | | | | |
| yerO | BSU06700 | similar to transcriptional regulator (TetR family) | | | | |
| swrC | BSU06710 | similar to acriflavin resistance protein | | | | |
| dgkB | BSU06720 | diacylglycerol kinase | | | | |
| rlmCD | BSU06730 | rRNA methyltransferase | | | | |
| yefB | BSU06740 | similar to site-specific recombinase | | 🟦 | 🟦 | 🟦 |
| yefC | BSU06750 | similar to resolvase | | 🟦 | 🟦 | 🟦 |
| yeeA | BSU06760 | unknown | | 🟦 | 🟦 | 🟦 |
| yeeB | BSU06770 | unknown | | 🟦 | 🟦 | 🟦 |
| yeeC | BSU06780 | unknown | | 🟦 | 🟦 | 🟦 |
| yeeD | BSU06790 | unknown | | 🟦 | 🟦 | 🟦 |
| yezA | BSU06800 | unknown | | 🟦 | 🟦 | 🟦 |
| yezG | BSU06811 | putative antitoxin | | 🟦 | 🟦 | 🟦 |
| yeeF | BSU06812 | putative toxin | | 🟦 | 🟦 | 🟦 |
| yeeG | BSU06820 | unknown | | 🟦 | 🟦 | 🟦 |
| rapH | BSU06830 | response regulator aspartate phosphatase | | 🟦 | 🟦 | 🟦 |
| phrH | BSU06839 | secreted regulator of the activity of phosphatase RapH | | 🟦 | 🟦 | 🟦 |
| yeeI | BSU06840 | unknown | | 🟦 | 🟦 | 🟦 |
| yeeK | BSU06850 | spore coat protein | | 🟦 | 🟦 | 🟦 |
| yezE | BSU06860 | similar to transcriptional regulator (TetR family) | | 🟦 | 🟦 | 🟦 |
| yesE | BSU06870 | unknown | | 🟦 | 🟦 | 🟦 |
| yesF | BSU06880 | unknown | | 🟦 | 🟦 | 🟦 |
| cotJA | BSU06890 | polypeptide composition of the spore coat | | 🟦 | 🟦 | 🟦 |
| cotJB | BSU06900 | polypeptide composition of the spore coat | | 🟦 | 🟦 | 🟦 |
| cotJC | BSU06910 | polypeptide composition of the spore coat | | 🟦 | 🟦 | 🟦 |
| yesJ | BSU06920 | unknown | | 🟦 | 🟦 | 🟦 |
| yesK | BSU06930 | unknown | | 🟦 | 🟦 | 🟦 |
| yesL | BSU06940 | unknown | | 🟦 | 🟦 | 🟦 |
| yesM | BSU06950 | two-component sensor kinase | | 🟦 | 🟦 | 🟦 |
| yesN | BSU06960 | two-component response regulator | | 🟦 | 🟦 | 🟦 |
| yesO | BSU06970 | similar to ABC transporter (sugar-binding protein) | | 🟦 | 🟦 | 🟦 |
| yesP | BSU06980 | similar to ABC transporter (membrane protein) | | 🟦 | 🟦 | 🟦 |
| yesQ | BSU06990 | similar to ABC transporter (membrane protein) | | 🟦 | 🟦 | 🟦 |
| yesR | BSU07000 | galacturonyl hydrolase, catalyses intracellular degradation of disaccharides generated by YesX | | 🟦 | 🟦 | 🟦 |
| yesS | BSU07010 | transcriptional activator (AraC family) of the rhamnogalacturonan operon | | 🟦 | 🟦 | 🟦 |
| yesT | BSU07020 | rhamnogalacturonan acetylesterase | | 🟦 | 🟦 | 🟦 |
| yesU | BSU07030 | unknown | | 🟦 | 🟦 | 🟦 |
| yesV | BSU07040 | unknown | | 🟦 | 🟦 | 🟦 |
| yesW | BSU07050 | rhamnogalacturonan lyase, generates oligosaccharides | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yesX | BSU07060 | rhamnogalacturonanlyase, degrades oligo- to disaccharides |  | 🟦 | 🟦 | 🟦 |
| yesY | BSU07070 | similar to rhamnogalacturonan acetylesterase |  | 🟦 | 🟦 | 🟦 |
| yesZ | BSU07080 | beta-galactosidase |  | 🟦 | 🟦 | 🟦 |
| yetA | BSU07090 | unknown |  | 🟦 | 🟦 | 🟦 |
| lplA | BSU07100 | lipoprotein, putative ABC transporter (solute binding protein) |  | 🟦 | 🟦 | 🟦 |
| lplB | BSU07110 | transmembrane lipoprotein, putative ABC transporter (permease) |  | 🟦 | 🟦 | 🟦 |
| lplC | BSU07120 | transmembrane lipoprotein, putative ABC transporter (membrane protein) |  | 🟦 | 🟦 | 🟦 |
| lplD | BSU07130 | α-galacturonidase |  | 🟦 | 🟦 | 🟦 |
| yetF | BSU07140 | unknown |  | 🟦 | 🟦 | 🟦 |
| hmoA | BSU07150 | heme monooxygenase |  | 🟦 | 🟦 | 🟦 |
| yetH | BSU07160 | unknown |  | 🟦 | 🟦 | 🟦 |
| yetI | BSU07170 | split paralog of RsbR with YezB |  | 🟦 | 🟦 | 🟦 |
| yezB | BSU07180 | split paralog of RsbR (with YetI) |  | 🟦 | 🟦 | 🟦 |
| yezD | BSU07190 | unknown |  | 🟦 | 🟦 | 🟦 |
| yetJ | BSU07200 | unknown |  | 🟦 | 🟦 | 🟦 |
| yetK | BSU07210 | unknown |  | 🟦 | 🟦 | 🟦 |
| yetL | BSU07220 | transcriptional repressor of yetM and yetL, induction in response to flavonoids |  | 🟦 | 🟦 | 🟦 |
| yetM | BSU07230 | FAD-dependent monooxygenase |  | 🟦 | 🟦 | 🟦 |
| yetN | BSU07240 | unknown |  | 🟦 | 🟦 | 🟦 |
| yetO | BSU07250 | similar to cytochrome P450 / NADPH-cytochrome P450 reductase |  | 🟦 partial | 🟦 partial | 🟦 partial |
| yfnI | BSU07260 | general stress protein, minor lipoteichoic acid synthetase, major secreted protein |  |  |  |  |
| yfnH | BSU07270 | similar to glucose-1-phosphate cytidylyltransferase |  |  |  |  |
| yfnG | BSU07280 | similar to CDP-glucose 4,6-dehydratase |  |  |  |  |
| yfnF | BSU07290 | unknown |  |  |  |  |
| yfnE | BSU07300 | unknown |  |  |  |  |
| yfnD | BSU07310 | unknown |  |  |  |  |
| yfnC | BSU07320 | similar to fosmidmycin resistance protein |  |  |  |  |
| yfnB | BSU07330 | unknown |  |  |  |  |
| yfnA | BSU07340 | similar to metabolite transport protein |  |  |  |  |
| yfmT | BSU07350 | similar to benzaldehyde dehydrogenase |  |  |  |  |
| yfmS | BSU07360 | soluble chemotaxis receptor |  |  |  |  |
| yfmR | BSU07370 | similar to ABC transporter (ATP-binding protein) |  |  |  |  |
| yfmQ | BSU07380 | unknown |  |  |  |  |
| yfmP | BSU07390 | transcription repressor of the yfmP-yfmO operon |  |  |  |  |
| yfmO | BSU07400 | similar to multidrug-efflux transporter |  |  |  |  |
| yfmN | BSU07410 | unknown |  |  |  |  |
| yfmM | BSU07420 | similar to ABC transporter (ATP-binding protein) |  |  |  |  |
| yfmL | BSU07430 | DEAD-box RNA helicase |  |  |  |  |
| yfmK | BSU07440 | unknown |  |  |  |  |
| yfmJ | BSU07450 | similar to predicted oxidoreductase, Zn-dependent and NAD(P)-binding |  |  |  |  |
| yfmI | BSU07460 | similar to macrolide-efflux transporter |  |  |  |  |
| yfmG | BSU07480 | unknown |  |  |  |  |
| yfmF | BSU07490 | iron/citrate ABC transporter (ATP-binding protein) |  |  |  |  |
| yfmE | BSU07500 | iron/citrate ABC transporter (permease) |  |  |  |  |
| yfmD | BSU07510 | iron/citrate ABC transporter (permease) |  |  |  |  |
| yfmC | BSU07520 | iron/ citrate ABC transporter (binding protein) |  |  |  |  |
| yfmB | BSU07530 | unknown |  |  |  |  |
| yfmA | BSU07540 | unknown |  |  |  |  |
| yflT | BSU07550 | general stress protein, survival of ethanol stress |  |  |  |  |
| pel | BSU07560 | pectate lyase C |  |  |  |  |
| yflS | BSU07570 | malate transporter |  |  |  |  |
| citS | BSU07580 | two-component sensor kinase, regulation of citrate uptake |  |  |  |  |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| citT | BSU07590 | two-component response regulator, regulation of citrate uptake | | | | |
| yflP | BSU07600 | unknown | | | | |
| citM | BSU07610 | Mg2+-citrate transporter | | | | |
| yflN | BSU07620 | unknown | | | | |
| nos | BSU07630 | nitric-oxide synthase | | | | |
| yflL | BSU07640 | unknown | | | | |
| yflK | BSU07650 | unknown | | | | |
| yflJ | BSU07660 | unknown | | | | |
| yflI | BSU07670 | unknown | | | | |
| yflH | BSU07680 | general stress protein | | | | |
| yflG | BSU07690 | methionine aminopeptidase | | | | |
| nagP | BSU07700 | N-acetylglucosamine-specific phosphotransferase system, EIICB | | | | |
| ltaS | BSU07710 | lipoteichoic acid synthase | | | | |
| yflD | BSU07720 | unknown | | | | |
| yflB | BSU07735 | unknown | | | | |
| yflA | BSU07750 | general stress protein, similar to amino acid carrier protein | | | | |
| yfkT | BSU07760 | general stress protein, part of the YfkQ-YfkR-YfkT germinant receptor of unknown specificity | | | | |
| yfkS | BSU07770 | D protein for the YfkQ-YfkR-YfkT germinant receptor of unknown specificity | | | | |
| yfkR | BSU07780 | part of the YfkQ-YfkR-YfkT germinant receptor of unknown specificity | | | | |
| yfkQ | BSU07790 | part of the YfkQ-YfkR-YfkT germinant receptor of unknown specificity | | | | |
| treP | BSU07800 | trehalose-specific phosphotransferase system, EIIBC component of the PTS | | | | |
| treA | BSU07810 | phospho-alpha-glucosidase | | | | |
| treR | BSU07820 | transcription repressor of the treP-treA-treR operon, (GntR family) | | | | |
| hypO | BSU07830 | NAD(P)H-flavin oxidoreductase, probably involved in NaOCl and diamide detoxification | | | | |
| yfkN | BSU07840 | extracellular 2',3' cyclic nucleotide phosphodiesterase, 2' (or 3') nucleotidase and 5' nucleotidase | | | | |
| yfkM | BSU07850 | glyoxalase III-like enzyme, general stress protein, survival of salt, paraquat and ethanol stresses | | | | |
| yfkL | BSU07860 | similar to multidrug resistance protein | | | | |
| yfkK | BSU07870 | unknown | | | | |
| yfkJ | BSU07880 | general stress protein, protein tyrosine phosphatase | | | | |
| yfkI | BSU07890 | general stress protein | | | | |
| yfkH | BSU07900 | general stress protein, survival of ethanol stress | | | | |
| yfkF | BSU07910 | similar to multidrug-efflux transporter | | | | |
| chaA | BSU07920 | H+/Ca2+ exchanger | | | | |
| yfkD | BSU07930 | unknown | | | | |
| yfkC | BSU07940 | mechanosensitive channel, similar to MscS | | | | |
| yfkA | BSU07955 | putative Fe-S oxidoreductase | | | | |
| yfjT | BSU07970 | unknown | | | | |
| pdaA | BSU07980 | polysaccharide deacetylase, required for germination | | | | |
| yfjR | BSU07990 | similar to 3-hydroxyisobutyrate dehydrogenase | | | | |
| yfjQ | BSU08000 | minor magnesium transporter | | | | |
| yfjP | BSU08010 | similar to DNA-3-methyladenine glycosidase II | | | | |
| yfjO | BSU08020 | similar to RNA methyltransferase | | | | |
| yfzA | BSU08029 | unknown | | | | |
| yfjN | BSU08030 | putative tRNA-dihydrouridine synthase 2 | | | | |
| yfjM | BSU08040 | unknown | | | | |
| yfjL | BSU08050 | similar to ribosomal protein L6 | | | | |
| acoA | BSU08060 | acetoin dehydrogenase E1 component (TPP-dependent alpha subunit) | | | | |
| acoB | BSU08070 | acetoin dehydrogenase E1 component (TPP-dependent beta subunit) | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| acoC | BSU08080 | acetoin dehydrogenase E2 component (dihydrolipoamide acetyltransferase) | | | | |
| acoL | BSU08090 | acetoin dehydrogenase E3 component (dihydrolipoamide dehydrogenase) | | | | |
| acoR | BSU08100 | transcriptional activator of the acoA-acoB-acoC-acoL operon | | | | |
| sspH | BSU08110 | small acid-soluble spore protein (minor) | | ■ | ■ | ■ |
| yfjF | BSU08120 | unknown | | ■ | ■ | ■ |
| yfjE | BSU08130 | unknown | | ■ | ■ | ■ |
| yfjD | BSU08140 | unknown | | ■ | ■ | ■ |
| yfjC | BSU08150 | unknown | | ■ | ■ | ■ |
| yfjB | BSU08160 | unknown | | ■ | ■ | ■ |
| yfjA | BSU08170 | unknown | | ■ | ■ | ■ |
| malA | BSU08180 | 6-phospho-alpha-glucosidase | | ■ | ■ | ■ |
| glvR | BSU08190 | transcriptional activator of the malA-glvR-malP operon | | ■ | ■ | ■ |
| malP | BSU08200 | maltose-specific phosphotransferase system, EIICB of the PTS | | ■ | ■ | ■ |
| yfiB | BSU08210 | similar to ABC transporter (ATP-binding protein) | | ■ | ■ | ■ |
| yfiC | BSU08220 | similar to ABC transporter (ATP-binding protein) | | ■ | ■ | ■ |
| catD | BSU08230 | essential for viability in the presence of catechol | | ■ | ■ | ■ |
| catE | BSU08240 | catechol 2,3-dioxygenase | | ■ | ■ | ■ |
| yfiF | BSU08250 | similar to transcriptional regulator (AraC family) | | ■ | ■ | ■ |
| yfiG | BSU08260 | D-chiro-inositol transport protein | | ■ | ■ | ■ |
| yfiH | BSU08270 | unknown | | ■ | ■ | ■ |
| yfiI | BSU08280 | unknown | | ■ | ■ | ■ |
| yfiJ | BSU08290 | two-component sensor kinase | | ■ | ■ | ■ |
| yfiK | BSU08300 | two-component response regulator | | ■ | ■ | ■ |
| yfiL | BSU08310 | similar to ABC transporter (ATP-binding protein) | | ■ | ■ | ■ |
| yfiM | BSU08320 | similar to ABC transporter (membrane protein) | | ■ | ■ | ■ |
| yfiN | BSU08330 | similar to ABC transporter (membrane protein) | | ■ | ■ | ■ |
| padR | BSU08340 | repressor of yveF-yveG-padC, induction occurs by binding of phenolic acids,stress response | | ■ | ■ | ■ |
| lipB | BSU08350 | extracellular esterase, lipase | | ■ | ■ | ■ |
| yfiQ | BSU08360 | similar to surface adhesion | | ■ | ■ | ■ |
| yfiR | BSU08370 | similar to transcriptional regulator (TetR family) | | ■ | ■ | ■ |
| yfiS | BSU08380 | similar to multidrug resistance protein | | ■ | ■ | ■ |
| yfiT | BSU08390 | bacillithiol S-transferase | | ■ | ■ | ■ |
| yfiU | BSU08400 | similar to multidrug-efflux transporter | | ■ | ■ | ■ |
| yfiV | BSU08410 | similar to transcriptional regulator (MarR family) | | ■ | ■ | ■ |
| mprF | BSU08425 | synthesis of lysylphosphatidylglycerol (L-PG) | | | | |
| yfiY | BSU08440 | ABC transporter for the siderophore schizokinen and arthrobactin (binding protein), works with ATPase YusV | | | | |
| yfiZ | BSU08450 | ABC transporter for the siderophore schizokinen and arthrobactin (permease), works with ATPase YusV | | | | |
| yfhA | BSU08460 | ABC transporter for the siderophore schizokinen and arthrobactin (permease), works with ATPase YusV | | | | |
| yfhB | BSU08470 | unknown | | | | |
| yfhC | BSU08480 | unknown | | | | |
| yfhD | BSU08490 | general stress protein, survival of ethanol stress and low temperatures | | | | |
| yfhE | BSU08500 | general stress protein, survival of salt and ethanol stresses and low temperatures | | | | |
| yfhF | BSU08510 | general stress protein, similar to cell division inhibitor | | | | |
| recX | BSU08520 | recombination protein | | | | |
| yfhH | BSU08530 | unknown | | ■ | ■ | ■ |
| yfhI | BSU08540 | similar to antibiotic resistance protein | | ■ | ■ | ■ |
| sspK | BSU08550 | small acid-soluble spore protein (minor) SASP | | ■ | ■ | ■ |
| yfhJ | BSU08560 | unknown | | ■ | ■ | ■ |

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| yfhK | BSU08570 | general stress protein, similar to cell division inhibitor | | 🟦 | 🟦 | 🟦 |
| yfhL | BSU08580 | general stress protein | | 🟦 | 🟦 | 🟦 |
| yfhM | BSU08590 | general stress protein, similar to epoxide hydrolase | | 🟦 | 🟦 | 🟦 |
| csbB | BSU08600 | putative bactoprenol glycosyltransferase, general stress protein | | 🟦 | 🟦 | 🟦 |
| yfhO | BSU08610 | unknown | | 🟦 | 🟦 | 🟦 |
| yfhP | BSU08620 | unknown | | 🟦 | 🟦 | 🟦 |
| mutY | BSU08630 | A/G-specific adenine glycosylase | | | | |
| yfhS | BSU08640 | unknown | | | | |
| fabL | BSU08650 | enoyl-acyl carrier protein reductase | | | | |
| sspE | BSU08660 | small acid-soluble spore protein (major gamma-type SASP) | | | | |
| ygaB | BSU08670 | unknown | | | | |
| ygaC | BSU08680 | unknown | | | | |
| ygaD | BSU08690 | similar to ABC transporter (ATP-binding protein) | | | | |
| ygaE | BSU08700 | unknown | | | | |
| gsaB | BSU08710 | glutamate-1-semialdehyde aminotransferase | | | | |
| ygaF | BSU08720 | similar to thioredoxin-dependent hydroperoxide peroxidase | | | | |
| perR | BSU08730 | transcriptional repressor of the peroxide regulon | | | | |
| ygzB | BSU08740 | unknown | | | | |
| ygxA | BSU08750 | unknown | | | | |
| rrnD-16S- rrnD-23S- rrnD-5S - trnD-Asn- trnD-Asp- trnD-Cys- trnD-Gln- trnD-Glu- trnD-Gly- trnD-His- trnD-Leu1- trnD-Leu2- trnD-Met- trnD-Phe- trnD-Ser- trnD-Thr- trnD-Trp- trnD-Tyr- trnD-Val | | | | | | |
| spo0M | BSU08760 | sporulation-control gene | | | | |
| ygzA | BSU08770 | unknown | | | | |
| ygzC | BSU08779 | unknown | | | | |
| ygaJ | BSU08780 | unknown | | | | |
| thiC | BSU08790 | biosynthesis of the pyrimidine moiety of thiamine | | | | |
| ygaK | BSU08800 | similar to reticuline oxidase | | | | |
| senS | BSU08810 | transcriptional regulator of extracellular enzyme genes | | | | |
| katA | BSU08820 | vegetative catalase 1 | | | | |
| ssuB | BSU08830 | aliphatic sulfonate ABC transporter (binding protein) | | | | |
| ssuA | BSU08840 | aliphatic sulfonate ABC transporter (binding lipoprotein) | | | | |
| ssuC | BSU08850 | epoxyqueuosine reductase | | | | |
| ssuD | BSU08860 | aliphatic sulfonate monooxygenase | | | | |
| ygaN | BSU08870 | unknown | | | | |
| yhzA | BSU08880 | alternative ribosomal protein S14, can replace RpsN under conditions of zinc limitation | | | | |
| ygaO | BSU08890 | unknown | | | | |
| ygzD | BSU08899 | putative HTH-type transcriptional regulator | | | | |
| trnSL-Gly1 | | | | | | |
| yhzB | BSU08900 | unknown | | | | |
| queG | BSU08910 | unknown | | | | |
| yhbB | BSU08920 | unknown | | | | |
| cspR | BSU08930 | similar to tRNA (Um34/Cm34) methyltransferase | | | | |
| yhbD | BSU08940 | unknown | | | | |
| yhbE | BSU08950 | unknown | | | | |
| yhbF | BSU08960 | unknown | | | | |
| prkA | BSU08970 | putative serine protein kinase | | | | |
| yhbH | BSU08980 | SigE-dependent sporulation gene | | | | |
| yhbI | BSU08990 | similar to transcriptional regulator (MarR family) | | | | |
| yhbJ | BSU09000 | unknown | | | | |
| yhcA | BSU09010 | similar to multidrug resistance protein | | | | |
| yhcB | BSU09020 | similar to trp repressor binding protein | | | | |
| yhcC | BSU09030 | unknown | | | | |
| yhcD | BSU09040 | unknown | | | | |
| yhcE | BSU09050 | similar to ABC transporter (membrane protein) | | | | |
| yhcF | BSU09060 | similar to transcriptional regulator (GntR family) | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yhcG | BSU09070 | similar to ABC transporter (ATP-binding protein) | | | | |
| yhcH | BSU09080 | similar to ABC transporter (ATP-binding protein) | | | | |
| yhcI | BSU09090 | similar to ABC transporter (membrane protein) | | | | |
| cspB | BSU09100 | major cold-shock protein | | | | |
| yhcJ | BSU09110 | similar to ABC transporter (binding lipoprotein) | | | | |
| dgcK | BSU09120 | diguanylate cyclase | | | | |
| tcyP | BSU09130 | cystine transporter, membrane protein | | | | |
| yhcM | BSU09140 | general stress protein | | | | |
| yhcN | BSU09150 | forespore-specific gene | | | | |
| yhcO | BSU09165 | unknown | | | | |
| yhcQ | BSU09180 | unknown | | | | |
| yhcR | BSU09190 | extracellular non-specific endonuclease, Rnase | | | | |
| yhcS | BSU09200 | sortase | | | | |
| yhcT | BSU09210 | unknown | | | | |
| yhcU | BSU09220 | unknown | | | | |
| yhcV | BSU09230 | forespore-specific sporulation protein | | | | |
| yhcW | BSU09240 | similar to phosphoglycolate phosphatase | | | | |
| yhcX | BSU09250 | unknown | | | | |
| yhzG | BSU09259 | unknown, putative pseudogene | | | | |
| yhxA | BSU09260 | similar to adenosylmethionine-8-amino-7-oxononanoate aminotransferase | | | | |
| glpP | BSU09270 | transcriptional antiterminator of the glpT-glpQ and glpF-glpK-glpD operons | | | | |
| glpF | BSU09280 | glycerol facilitator | | | | |
| glpK | BSU09290 | glycerol kinase | | | | |
| glpD | BSU09300 | glycerol-3-phosphate dehydrogenase (menaquinone 7) | | | | |
| pgcA | BSU09310 | alpha-phosphoglucomutase, required for UDP-glucose synthesis | | | | |
| yhcY | BSU09320 | two-component sensor kinase | | | | |
| yhcZ | BSU09330 | two-component response regulator | | | | |
| yhdA | BSU09340 | similar to NADPH-dependent azobenzene FMN reductase | | | | |
| yhdB | BSU09350 | unknown | | | | |
| yhdC | BSU09360 | unknown | | | | |
| lytF | BSU09370 | gamma-D-glutamate-meso-diaminopimelate muropeptidase (major autolysin) | | | | |
| nsrR | BSU09380 | nitric oxide-responsive regulator | | | | |
| ygxB | BSU09390 | general stress protein | | | | |
| spoVR | BSU09400 | involved in spore cortex synthesis | | | | |
| phoA | BSU09410 | alkaline phosphatase A | | | | |
| lytE | BSU09420 | cell wall hydrolase (major autolysin) for cell elongation and separation, D,L-endopeptidase-type autolysin | | | | |
| citR | BSU09430 | transcriptional repressor of citA | | | | |
| citA | BSU09440 | minor citrate synthase | | | | |
| yhdF | BSU09450 | similar to glucose 1-dehydrogenase | | | | |
| bcaP | BSU09460 | branched-chain amino acid transporter | | | | |
| yhdH | BSU09470 | similar to sodium-dependent transporter | | | | |
| yhdI | BSU09480 | similar to transcriptional regulator (GntR family) | | | | |
| yhdJ | BSU09490 | unknown | | | | |
| yhdK | BSU09500 | anti-SigM protein | | | | |
| yhdL | BSU09510 | anti-SigM protein | | | | |
| sigM | BSU09520 | RNA polymerase ECF-type sigma factor SigM, responsible for intrinsic resistance against beta-lactam antibiotics | | | | |
| yhdN | BSU09530 | general stress protein, broad specificity aldo-keto reductase that converts MG to acetol | | | | |
| plsC | BSU09540 | acyl-ACP:1-acylglycerolphosphate acyltransferase | | | | |
| yhdP | BSU09550 | similar to hemolysin | | | | |
| cueR | BSU09560 | transcriptional regulator of the copZ-copA operon | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yhdR | BSU09570 | similar to aspartate aminotransferase | | | | |
| yhdT | BSU09590 | similar to hemolysin | | | | |
| yhdU | BSU09600 | unknown | | | | |
| yhdV | BSU09610 | unknown | | | | |
| yhdW | BSU09620 | similar to glycerophosphodiester phosphodiesterase | | | | |
| yhdX | BSU09630 | unknown | | | | |
| yhdY | BSU09640 | mechanosensitive channel, similar to MscS | | | | |
| srtN | BSU09650 | protein deacetylase for the control of AcsA activity | | | | |
| yheN | BSU09660 | similar to endo-1,4-beta-xylanase | | | | |
| dat | BSU09670 | D-alanine aminotransferase | | | | |
| nhaC | BSU09680 | Na+/H+ antiporter | | | | |
| nhaX | BSU09690 | general stress protein | | | | |
| yheJ | BSU09700 | unknown | | | | |
| bmrC | BSU09710 | multidrug ABC transporter (ATP-binding protein) | | | | |
| bmrD | BSU09720 | multidrug ABC transporter (ATP-binding protein) | | | | |
| yheG | BSU09730 | similar to calcium-binding protein | | | | |
| yheF | BSU09740 | unknown | | | | |
| sspB | BSU09750 | small acid-soluble spore protein (major beta-type SASP) | | | | |
| yheE | BSU09760 | unknown | | | | |
| yheD | BSU09770 | spore coat protein | | | | |
| yheC | BSU09780 | unknown | | | | |
| yheB | BSU09790 | unknown | | | | |
| yheA | BSU09800 | unknown | | | | |
| yhaZ | BSU09810 | similar to DNA alkylation repair enzyme | | | | |
| yhaX | BSU09830 | SigE-dependent spore coat protein | | | | |
| hemZ | BSU09840 | coproporphyrinogen III oxidase | | | | |
| khtU | BSU09850 | K+/H+ antiporter for K+ efflux | | | | |
| khtT | BSU09860 | K+/H+ antiporter for K+ efflux | | | | |
| khtS | BSU09870 | modulator of YhaU activity | | | | |
| yhaR | BSU09880 | similar to enoyl CoA hydratase | | | | |
| yhzD | BSU09889 | unknown | | | | |
| yhaQ | BSU09890 | similar to ABC transporter (ATP-binding protein) | | | | |
| yhaP | BSU09900 | similar to ABC transporter (membrane protein) | | | | |
| yhaO | BSU09910 | unknown | | | | |
| sbcE | BSU09920 | SMC-like protein, involved in DNA double-strand break repair and competence | | | | |
| yhaM | BSU09930 | RNase, 3'-> 5' exoribonuclease | | | | |
| yhaL | BSU09940 | SigE-dependent sporulation gene | | | | |
| prsA | BSU09950 | protein secretion (post-translocation molecular chaperone) | | | | |
| sscA | BSU09958 | small sporulation protein | | | | |
| yhaJ | BSU09965 | putative bacteriocin | | | | |
| yhaI | BSU09980 | unknown | | | | |
| scoC | BSU09990 | transcriptional repressor of genes expressed in the transition phase | | | | |
| yhaH | BSU10000 | unknown | | | | |
| yhzF | BSU10009 | unknown | | | | |
| trpP | BSU10010 | S protein of tryptophan ECF transporter | | | | |
| serC | BSU10020 | 3-phosphoserine aminotransferase | | | | |
| hit | BSU10030 | Hit-like protein involved in cell-cycle regulation | | | | |
| ecsA | BSU10040 | ABC transporter (ATP-binding protein), mutation affects proteolysis by RasP (no processing of RsiW and FtsL) | | | | |
| ecsB | BSU10050 | ABC transporter ( membrane protein) | | | | |
| ecsC | BSU10060 | unknown | | | | |
| sndC | BSU10070 | sulphur compound N-deacetylase | | | | |
| yhfA | BSU10080 | unknown | | | | |
| yhgB | BSU10090 | unknown | | | | |
| hmoB | BSU10100 | heme monooxygenase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| pbpF | BSU10110 | penicillin-binding protein 2C | | | | |
| hemE | BSU10120 | uroporphyrinogen decarboxylase (uroporphyrinogen III) | | | | |
| hemH | BSU10130 | Ferrochelatase | | | | |
| hemY | BSU10140 | protoporphyrinogen IX oxidase | | | | |
| yhgD | BSU10150 | similar to transcriptional regulator (TetR family) | | | | |
| yhgE | BSU10160 | similar to phage infection protein | | | | |
| fabHB | BSU10170 | beta-ketoacyl-acyl carrier protein synthase III | | | | |
| yhfC | BSU10180 | unknown | | | | |
| yhfE | BSU10200 | similar to glucanase | | | | |
| yhfF | BSU10210 | unknown | | | | |
| gltT | BSU10220 | major H+/Na+-glutamate symport protein | | | | |
| yhfH | BSU10230 | unknown | | | | |
| yhfI | BSU10240 | unknown | | | | |
| lplJ | BSU10250 | lipoate-protein ligase | | | | |
| yhfK | BSU10260 | unknown | | | | |
| lcfB | BSU10270 | long-chain fatty-acid-CoA ligase | | | | |
| yhfM | BSU10280 | unknown | | 🟦 | 🟦 | 🟦 |
| yhfN | BSU10290 | unknown | | 🟦 | 🟦 | 🟦 |
| aprE | BSU10300 | extracellular alkaline serine protease (subtilisin E) | | 🟦 | 🟦 | 🟦 |
| yhfO | BSU10310 | predicted acyltransferase | | 🟦 | 🟦 | 🟦 |
| yhfP | BSU10320 | similar to predicted oxidoreductase, Zn-dependent and NAD(P)-binding | | 🟦 | 🟦 | 🟦 |
| yhfQ | BSU10330 | iron/ citrate ABC transporter (solute-binding protein) | | 🟦 partial | 🟦 partial | 🟦 partial |
| yhfR | BSU10340 | phosphatase involved in isopentenol (isoprenoid) biosynthesis | | | | |
| yhfS | BSU10350 | similar to acetyl-CoA C-acetyltransferase | | | | |
| yhfT | BSU10360 | similar to long-chain fatty-acid-CoA ligase | | | | |
| yhfU | BSU10370 | S protein of biotin ECF transporter | | | | |
| hemAT | BSU10380 | haem-based aerotactic transducer | | | | |
| yhfW | BSU10390 | similar to Rieske [2Fe-2S] iron-sulfur protein | | | | |
| yhxC | BSU10400 | similar to alcohol dehydrogenase | | | | |
| yhzC | BSU10410 | unknown | | | | |
| comK | BSU10420 | competence transcription factor (CTF) | | | | |
| yhxD | BSU10430 | general stress protein, similar to alcohol dehydrogenase, | | | | |
| yhjA | BSU10440 | unknown | | | | |
| yhjB | BSU10450 | similar to metabolite permease | | | | |
| yhjC | BSU10460 | unknown | | | | |
| yhjD | BSU10470 | unknown | | | | |
| yhjE | BSU10480 | unknown | | | | |
| sipV | BSU10490 | signal peptidase I | | | | |
| yhjG | BSU10500 | similar to monooxygenase | | | | |
| yhjH | BSU10510 | unknown | | | | |
| glcP | BSU10520 | probable glucose/mannose:H+ symporter | | 🟦 | 🟦 | 🟦 |
| ntdC | BSU10530 | NAD-dependent glucose-6-phosphate dehydrogenase | | 🟦 | 🟦 | 🟦 |
| ntdB | BSU10540 | kanosamine-6-phosphate phosphatase | | 🟦 | 🟦 | 🟦 |
| ntdA | BSU10550 | pyridoxal phosphate-dependent 3-oxo-glucose-6-phosphate:glutamate aminotransferase | | 🟦 | 🟦 | 🟦 |
| ntdR | BSU10560 | transcription activator of the ntdA-ntdB-ntdC operon | | 🟦 | 🟦 | 🟦 |
| yhjN | BSU10570 | unknown | | | | |
| yhjO | BSU10580 | similar to multidrug-efflux transporter | | | | |
| yhjP | BSU10590 | similar to ABC transporter (peptide binding protein) | | | | |
| yhjQ | BSU10600 | unknown | | | | |
| yhjR | BSU10610 | inner spore coat protein | | | | |
| addB | BSU10620 | ATP-dependent deoxyribonuclease (subunit B) | | | | |
| addA | BSU10630 | ATP-dependent deoxyribonuclease (subunit A) | | | | |
| sbcD | BSU10640 | exonuclease SbcD homolog | | | | |
| sbcC | BSU10650 | DNA exonuclease | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| hlpB | BSU10660 | HNH nuclease-like protein, rescues AddA-AddB-mediated recombination intermediates | | | | |
| gerPF | BSU10670 | probable spore germination protein | | 🟦 | 🟦 | 🟦 |
| gerPE | BSU10680 | probable spore germination protein | | 🟦 | 🟦 | 🟦 |
| gerPD | BSU10690 | probable spore germination protein | | 🟦 | 🟦 | 🟦 |
| gerPC | BSU10700 | probable spore germination protein | | 🟦 | 🟦 | 🟦 |
| gerPB | BSU10710 | probable spore germination protein | | 🟦 | 🟦 | 🟦 |
| gerPA | BSU10720 | probable spore germination protein | | 🟦 | 🟦 | 🟦 |
| yisI | BSU10730 | Spo0A-P phosphatase, control of the phosphorelay | | 🟦 | 🟦 | 🟦 |
| yisJ | BSU10740 | unknown | | 🟦 | 🟦 | 🟦 |
| yisK | BSU10750 | similar to 5-oxo-1,2,5-tricarboxilic-3-penten acid decarboxylase | | 🟦 | 🟦 | 🟦 |
| yisL | BSU10760 | unknown | | 🟦 | 🟦 | 🟦 |
| wprA | BSU10770 | cell wall-associated protein precursor | | 🟦 | 🟦 | 🟦 |
| yisN | BSU10780 | unknown | | | 🟦 | |
| asnO | BSU10790 | asparagine synthase (glutamine-hydrolysing) | | | 🟦 | |
| yizA | BSU10800 | unknown | | | 🟦 | |
| yisP | BSU10810 | unknown | | | 🟦 | |
| yisQ | BSU10820 | unknown | | | 🟦 | |
| yisR | BSU10830 | similar to transcriptional regulator (AraC family) | | | 🟦 | |
| degA | BSU10840 | transcriptional activator involved in the degradation of glutamine phosphoribosylpyrophosphate amidotransferase | | | 🟦 | |
| iolX | BSU10850 | scyllo-inositol 2-dehydrogenase | | | 🟦 | |
| yisT | BSU10860 | similar to nuclease inhibitor | | | 🟦 | |
| yisU | BSU10870 | similiar to arginine export protein | | | 🟦 | |
| yisV | BSU10880 | similar to transcriptional regulator (GntR family) | | | 🟦 | |
| yisX | BSU10890 | unknown | | | 🟦 | |
| yisY | BSU10900 | spore coat protein, similar to chloride peroxidase | | | 🟦 | |
| yisZ | BSU10910 | adenylylsulfate kinase | | | 🟦 | |
| yitA | BSU10920 | sulfate adenylyltransferase | | | 🟦 | |
| yitB | BSU10930 | phospho-adenylylsulfate sulfotransferase | | | 🟦 | |
| yitC | BSU10940 | mother cell-specific sporulation protein | | | 🟦 | |
| yitD | BSU10950 | unknown | | | 🟦 | |
| yitE | BSU10960 | unknown | | | 🟦 | |
| yitF | BSU10970 | similar to mandelate racemase | | | 🟦 | |
| yitG | BSU10980 | similar to multidrug resistance protein | | | 🟦 | |
| yitH | BSU10990 | unknown | | | 🟦 | |
| yitI | BSU11000 | unknown | | | 🟦 | |
| yitJ | BSU11010 | probable 5,10-methylenetetrahydrofolate reductase (NADP) | | | 🟦 | |
| yitK | BSU11020 | unknown | | | 🟦 | |
| yitL | BSU11030 | unknown | | | 🟦 | |
| yitM | BSU11040 | unknown | | 🟦 | 🟦 | 🟦 |
| yitO | BSU11055 | unknown | | 🟦 | 🟦 | 🟦 |
| yitP | BSU11070 | unknown | | 🟦 | 🟦 | 🟦 |
| yizB | BSU11079 | unknown | | 🟦 | 🟦 | 🟦 |
| yitQ | BSU11080 | unknown | | 🟦 | 🟦 | 🟦 |
| yitR | BSU11090 | unknown | | 🟦 | 🟦 | 🟦 |
| nprB | BSU11100 | extracellular neutral protease B | | 🟦 | 🟦 | 🟦 |
| yitS | BSU11110 | unknown | | | 🟦 | |
| yitT | BSU11120 | general stress protein | | | 🟦 | |
| ipi | BSU11130 | intracellular proteinase inhibitor | | | 🟦 | |
| yizC | BSU11139 | unknown | | | 🟦 | |
| yitU | BSU11140 | unknown | | | 🟦 | |
| yitV | BSU11150 | unknown | | | 🟦 | |
| yitW | BSU11160 | unknown | | | 🟦 | |
| yitY | BSU11170 | similar to oxidoreductase | | | 🟦 | |
| yitZ | BSU11180 | similar to multidrug resistance protein | | | 🟦 | |

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| argC | BSU11190 | N-acetyl-g-glutamyl-phosphate reductase | | | 🟦 | |
| argJ | BSU11200 | N-acetylglutamate synthase | | | 🟦 | |
| argB | BSU11210 | N-acetylglutamate 5-phosphotransferase | | | 🟦 | |
| argD | BSU11220 | acetylornithine transaminase | | | 🟦 | |
| carA | BSU11230 | carbamoyl-phosphate transferase-arginine (subunit A) | | | 🟦 | |
| carB | BSU11240 | carbamoyl-phosphate transferase-arginine subunit B) | | | 🟦 | |
| argF | BSU11250 | ornithine carbamoyltransferase | | | 🟦 | |
| yjzC | BSU11260 | unknown | | | 🟦 | |
| yjzD | BSU11270 | unknown | | | 🟦 | |
| yjaU | BSU11280 | unknown | | | 🟦 | |
| yjaV | BSU11290 | SigE-dependent sporulation gene, similar to UDP-glucose 4-epimerase | | | 🟦 | |
| med | BSU11300 | lipoprotein, positive regulator of *comK* , stimulates KinD-dependent phosphorylation of Spo0A | | | | |
| comZ | BSU11310 | late competence gene | | | | |
| yjzB | BSU11320 | spore coat protein | | | | |
| fabHA | BSU11330 | beta-ketoacyl-acyl carrier protein synthase III | | | | |
| fabF | BSU11340 | beta-ketoacyl-acyl carrier protein synthase II, involved in the control of membrane fluidity | | | | |
| yjaZ | BSU11350 | unknown | | | | |
| appD | BSU11360 | oligopeptide ABC transporter (ATP-binding protein) | | | | |
| appF | BSU11370 | oligopeptide ABC transporter (ATP-binding protein) | | | | |
| appA/1 | BSU11381 | oligopeptide ABC transporter, inactive pseudogene in strain 168 | | | | |
| appA/2 | BSU11382 | oligopeptide ABC transporter, inactive pseudogene in strain 168 | | | | |
| appB | BSU11390 | oligopeptide ABC transporter (permease) | | | | |
| appC | BSU11400 | oligopeptide ABC transporter (permease) | | | | |
| yjbA | BSU11410 | unknown | | | | |
| trpS | BSU11420 | tryptophanyl-tRNA synthetase | | | | |
| oppA | BSU11430 | oligopeptide ABC transporter (binding protein) | | | | |
| oppB | BSU11440 | oligopeptide ABC transporter (permease) | | | | |
| oppC | BSU11450 | oligopeptide ABC transporter (permease) | | | | |
| oppD | BSU11460 | oligopeptide ABC transporter (ATP-binding protein) | | | | |
| oppF | BSU11470 | oligopeptide ABC transporter (ATP-binding protein) | | | | |
| yjbB | BSU11480 | similar to macrolide-efflux transporter | | | | |
| yjbC | BSU11490 | general stress protein, required for survival of salt stress | | | | |
| spx | BSU11500 | Transcriptional regulator Spx, involved in regulation of many genes. | | | | |
| yjbE | BSU11510 | unknown | | | | |
| mecA | BSU11520 | buffering protein for development, dampens transitions to spore, biofilm exopolysaccharide and competence expression | | | | |
| coiA | BSU11530 | protein involved in establishment of DNA transport in competence | | | | |
| pepF | BSU11540 | oligoendopeptidase | | | | |
| yizD | BSU11549 | unknown | | | | |
| yjbH | BSU11550 | adaptor protein for ClpX-ClpP-catalyzed Spx degradation, confers resistance against nitrosating agents | | | | |
| yjbI | BSU11560 | truncated hemoglobin, NO protection | | | | |
| cwlQ | BSU11570 | cell wall hydrolase | | | | |
| yjbK | BSU11580 | unknown | | | | |
| yjbL | BSU11590 | unknown | | | | |
| sasB | BSU11600 | (p)ppGpp synthetase | | | | |
| nadF | BSU11610 | NAD kinase | | | | |
| yjbO | BSU11620 | unknown | | | | |
| prpE | BSU11630 | protein tyrosine phosphatase | | | | |
| yjbQ | BSU11640 | similar to Na+/H+ antiporter | | | | |
| tenA | BSU11650 | thiaminase II | | | | |
| tenI | BSU11660 | thiazole tautomerase | | | | |
| thiO | BSU11670 | FAD-dependent glycine oxidase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| thiS | BSU11680 | hydroxyethylthiazole phosphate biosynthesis | | | | |
| thiG | BSU11690 | hydroxyethylthiazole phosphate biosynthesis | | | | |
| thiF | BSU11700 | hydroxyethylthiazole phosphate biosynthesis | | | | |
| thiD | BSU11710 | 4-amino-5-hydroxymethyl-2-methylpyrimidine and 4-amino-5-hydroxymethyl-2-methylpyrimidine pyrophosphate kinase | | | | |
| fabI | BSU11720 | enoyl-acyl carrier protein reductase | | | | |
| cotO | BSU11730 | spore coat morphogenetic protein, controls assembly of the coat layers and coat surface topography | | 🟦 | 🟦 | 🟦 |
| cotZ | BSU11740 | spore coat protein (insoluble fraction) | | 🟦 | 🟦 | 🟦 |
| cotY | BSU11750 | spore coat protein (insoluble fraction) | | 🟦 | 🟦 | 🟦 |
| cotX | BSU11760 | spore coat protein (insoluble fraction) | | 🟦 | 🟦 | 🟦 |
| cotW | BSU11770 | spore coat protein (insoluble fraction) | | 🟦 | 🟦 | 🟦 |
| cotV | BSU11780 | spore coat protein (insoluble fraction) | | 🟦 | 🟦 | 🟦 |
| yjcA | BSU11790 | unknown | | 🟦 | 🟦 | 🟦 |
| yjzK | BSU11799 | unknown | | 🟦 | 🟦 | 🟦 |
| yjcZ | BSU11809 | unknown | | 🟦 | 🟦 | 🟦 |
| spoVIF | BSU11810 | required for spore coat assembly and resistance | | 🟦 | 🟦 | 🟦 |
| yjcD | BSU11820 | similar to ATP-dependent DNA helicase | | | | |
| yjzE | BSU11839 | general stress protein | | | | |
| yjcF | BSU11840 | unknown | | | | |
| yjcG | BSU11850 | putative 2'-5' RNA-ligase | | | | |
| yjcH | BSU11860 | unknown | | | | |
| metI | BSU11870 | O-succinylhomoserine lyase (L-cysteine, H2S, methanethiol, elimination) | | | | |
| metC | BSU11880 | cystathionine beta-lyase | | | | |
| yjcK | BSU11890 | similar to ribosomal-protein-alanine N-acetyltransferase | | | | |
| yjcL | BSU11900 | unknown | | | | |
| trnSL-Val2 | | | | | | |
| yjcM | BSU11910 | unknown | | | | |
| yjcN | BSU11920 | unknown | | | | |
| yjzF | BSU11928 | unknown | | | | |
| yjzG | BSU11929 | unknown | | | | |
| yjcO | BSU11930 | unknown | | | | |
| yjcP | BSU11940 | unknown | | | | |
| yjcQ | BSU11950 | unknown | | | | |
| yjcR | BSU11960 | unknown | | | | |
| yjcS | BSU11970 | unknown | | | | |
| yjdA | BSU11980 | similar to 3-oxoacyl-acyl-carrier protein reductase | | | | |
| yjdB | BSU11990 | unknown | | | | |
| manR | BSU12000 | transcriptional activator of the manP-manA operon | | | | |
| manP | BSU12010 | trigger enzyme: mannose-specific phosphotransferase system, EIIBCA of the PTS | | 🟦 | 🟦 | 🟦 |
| manA | BSU12020 | mannose-6-phosphate isomerase | | 🟦 | 🟦 | 🟦 |
| yjdF | BSU12030 | unknown | | 🟦 | 🟦 | 🟦 |
| yjdG | BSU12040 | unknown | | 🟦 | 🟦 | 🟦 |
| yjdH | BSU12050 | unknown | | 🟦 | 🟦 | 🟦 |
| yjdI | BSU12060 | similiar to Cys-tRNA(Pro) and Cys-tRNA(Cys) deacylase | | 🟦 | 🟦 | 🟦 |
| yjzH | BSU12069 | unknown | | 🟦 | 🟦 | 🟦 |
| yjdJ | BSU12070 | unknown | | 🟦 | 🟦 | 🟦 |
| ctaO | BSU12080 | heme O synthase (minor enzyme) | | | | |
| cotT | BSU12090 | spore coat protein (inner) | | 🟦 | 🟦 | 🟦 |
| pdaC | BSU12100 | peptidoglycan deacetylase C | | 🟦 | 🟦 | 🟦 |
| yjfA | BSU12110 | unknown | | 🟦 | 🟦 | 🟦 |
| yjfB | BSU12120 | unknown | | 🟦 | 🟦 | 🟦 |
| yjfC | BSU12130 | unknown | | 🟦 | 🟦 | 🟦 |
| yjgA | BSU12140 | unknown | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number [1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yjgB | BSU12150 | general stress protein, survival of ethanol stress |  | 🟦 | 🟦 | 🟦 |
| yjgC | BSU12160 | general stress protein, formate dehydrogenase |  | 🟦 | 🟦 | 🟦 |
| yjgD | BSU12170 | general stress protein, survival of ethanol stress |  | 🟦 | 🟦 | 🟦 |
| yjhA | BSU12180 | unknown |  | 🟦 | 🟦 | 🟦 |
| yjhB | BSU12190 | similar to mutator MutT protein |  | 🟦 | 🟦 | 🟦 |
| yjiA | BSU12200 | unknown |  | 🟦 | 🟦 | 🟦 |
| yjiB | BSU12210 | similar to monooxygenase |  | 🟦 | 🟦 | 🟦 |
| yjiC | BSU12220 | similar to macrolide glycosyltransferase |  | 🟦 | 🟦 | 🟦 |
| yjzI | BSU12229 | unknown |  | 🟦 | 🟦 | 🟦 |
| yjjA | BSU12230 | unknown |  | 🟦 | 🟦 | 🟦 |
| yjkA | BSU12240 | similar to amino acid ABC transporter (membrane protein) |  | 🟦 | 🟦 | 🟦 |
| yjkB | BSU12250 | similar to amino acid ABC transporter (ATP-binding protein) |  | 🟦 | 🟦 | 🟦 |
| yjlA | BSU12260 | similar to intracellular alkaline protease |  | 🟦 | 🟦 | 🟦 |
| yjlB | BSU12270 | unknown |  | 🟦 | 🟦 | 🟦 |
| yjlC | BSU12280 | unknown |  | 🟦 | 🟦 | 🟦 |
| ndh | BSU12290 | NADH dehydrogenase (Menaquinone 7 & no proton) |  |  |  |  |
| uxaC | BSU12300 | glucuronate isomerase (D-glucuronate, D-galacturonate) |  | 🟦 | 🟦 | 🟦 |
| yjmB | BSU12310 | similar to Na+:galactoside symporter |  | 🟦 | 🟦 | 🟦 |
| yjmC | BSU12320 | unknown, may be involved in galacturonate utilization |  | 🟦 | 🟦 | 🟦 |
| yjmD | BSU12330 | galactitol-1-phosphate dehydrogenase |  | 🟦 | 🟦 | 🟦 |
| uxuA | BSU12340 | D-mannonate hydrolyase |  | 🟦 | 🟦 | 🟦 |
| yjmF | BSU12350 | similar to D-mannonate oxidoreductase/ fructuronate reductase |  | 🟦 | 🟦 | 🟦 |
| exuT | BSU12360 | galacturonate transport in via proton symport, glucuronate transport in via proton symport |  | 🟦 | 🟦 | 🟦 |
| exuR | BSU12370 | repression of the hexuronate utilization operon (uxaC-yjmB-yjmC-yjmD-uxuA-yjmF-exuT-exuR-uxaB-uxaA) |  | 🟦 | 🟦 | 🟦 |
| uxaB | BSU12380 | tagaturonate reductase |  | 🟦 | 🟦 | 🟦 |
| uxaA | BSU12390 | altronate hydrolase |  | 🟦 | 🟦 | 🟦 |
| yjnA | BSU12400 | unknown |  | 🟦 | 🟦 | 🟦 |
| yjoA | BSU12410 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yjoB | BSU12420 | AAA family, ATPase activity , similar to cell-division protein FtsH | 🟦 | 🟦 | 🟦 | 🟦 |
| rapA | BSU12430 | response regulator aspartate phosphatase, dephosphorylates Spo0F-P, control of the phosphorelay | 🟦 | 🟦 | 🟦 | 🟦 |
| phrA | BSU12440 | response regulator aspartate phosphatase (RapA) inhibitor, control of the phosphorelay | 🟦 | 🟦 | 🟦 | 🟦 |
| yjpA | BSU12450 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| xlyB | BSU12460 | N-acetylmuramoyl-L-alanine amidase | 🟦 | 🟦 | 🟦 | 🟦 |
| yjqA | BSU12470 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yjqB | BSU12480 | phage-derived gamma polyglutamic acid hydrolase | 🟦 | 🟦 | 🟦 | 🟦 |
| yjqC | BSU12490 | similar to manganese-containing catalase | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdA | BSU12500 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xre | BSU12510 | transcriptional repressor of PBSX genes | 🟦 | 🟦 | 🟦 | 🟦 |
| yjzJ | BSU12519 | unknown PBSX prophage protein | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdB | BSU12520 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdC | BSU12530 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| ykzK | BSU12539 | unknown PBSX prophage protein | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdD | BSU12540 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xtrA | BSU12550 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xpf | BSU12560 | PBSX phage RNA polymerase sigma factor | 🟦 | 🟦 | 🟦 | 🟦 |
| xtmA | BSU12570 | PBSX terminase (small subunit) | 🟦 | 🟦 | 🟦 | 🟦 |
| xtmB | BSU12580 | PBSX terminase (large subunit) | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdE | BSU12590 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdF | BSU12600 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdG | BSU12610 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| ykzL | BSU12619 | unknown PBSX prophage protein | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdH | BSU12620 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| xkdI | BSU12630 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdJ | BSU12640 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| ykzM | BSU12649 | unknown PBSX prophage protein | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdK | BSU12650 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdM | BSU12660 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdN | BSU12671 | unknown PBSX prophage protein | 🟦 | 🟦 | 🟦 | 🟦 |
| xkzB | BSU12672 | unknown PBSX prophage protein | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdO | BSU12680 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdP | BSU12690 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdQ | BSU12700 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdR | BSU12710 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdS | BSU12720 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdT | BSU12730 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdU | BSU12740 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkzA | BSU12749 | unknown PBSX prophage protein | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdV | BSU12750 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdW | BSU12760 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xkdX | BSU12770 | PBSX prophage | 🟦 | 🟦 | 🟦 | 🟦 |
| xepA | BSU12780 | PBSX prophage lytic exoenzyme | 🟦 | 🟦 | 🟦 | 🟦 |
| xhlA | BSU12790 | involved in cell lysis upon induction of PBSX | 🟦 | 🟦 | 🟦 | 🟦 |
| xhlB | BSU12800 | putative holin | 🟦 | 🟦 | 🟦 | 🟦 |
| xlyA | BSU12810 | N-acetylmuramoyl-L-alanine amidase | 🟦 partial | 🟦 | 🟦 | 🟦 |
| spoIISB | BSU12820 | disruption blocks sporulation after septum formation |  | 🟦 | 🟦 | 🟦 |
|  |  |  |  | 🟦 | 🟦 | 🟦 |
| spoIISA | BSU12830 | lethal when synthesized during vegetative growth in the absence of SpoIISB |  | 🟦 | 🟦 | 🟦 |
| pit | BSU12840 | low-affinity inorganic phosphate transporter, proton symporter |  |  |  |  |
| ykaA | BSU12850 | unknown |  |  |  |  |
| steT | BSU12860 | serine/ threonine exchanger transporter |  |  |  |  |
| mhqA | BSU12870 | hydroquinone-specific dioxygenase, confers resistence to methyl-hydroxyquinone |  |  |  |  |
| ykcB | BSU12880 | unknown |  |  |  |  |
| ykcC | BSU12890 | similar to dolichol phosphate mannose synthase |  |  |  |  |
| htrA | BSU12900 | serine protease Do (heat-shock protein) |  |  |  |  |
| proG | BSU12910 | 1-pyrroline-5-carboxylate dehydrogenase |  |  |  |  |
| dppA | BSU12920 | D-alanyl-aminopeptidase |  |  |  |  |
| dppB | BSU12930 | dipeptide ABC transporter (permease) |  |  |  |  |
| dppC | BSU12940 | dipeptide ABC transporter (permease) |  |  |  |  |
| dppD | BSU12950 | dipeptide ABC transporter (ATP-binding protein) |  |  |  |  |
| dppE | BSU12960 | dipeptide ABC transporter (dipeptide-binding protein) |  |  |  |  |
| ykfA | BSU12970 | similar to immunity to bacteriotoxins |  |  |  |  |
| ykfB | BSU12980 | L-Ala-D/L-Glu epimerase |  |  |  |  |
| ykfC | BSU12990 | D-glutamyl-L-amino acid peptidase |  |  |  |  |
| ykfD | BSU13000 | similar to oligopeptide ABC transporter (permease) |  |  |  |  |
| ykgB | BSU13010 | 6-phosphogluconolactonase, general stress protein |  |  |  |  |
| ykgA | BSU13020 | general stress protein, survival of salt and ethanol stresses |  |  |  |  |
| ykhA | BSU13030 | similar to acyl-CoA hydrolase |  |  |  |  |
| hmp | BSU13040 | flavohemoglobin, involved in resistance to nitric oxide (NO) |  |  |  |  |
| ykzH | BSU13050 | unknown |  |  |  |  |
| ykjA | BSU13060 | unknown |  |  |  |  |
| ykkA | BSU13070 | unknown |  |  |  |  |
| ykkB | BSU13080 | similar to N-acetyltransferase |  |  |  |  |
| ykkC | BSU13090 | similar to molecular chaperone |  |  |  |  |
| ykkD | BSU13100 | similar to molecular chaperone |  |  |  |  |
| ykkE | BSU13110 | formyltetrahydrofolate deformylase |  |  |  |  |
| proB | BSU13120 | glutamate 5-kinase |  |  |  |  |
| proA | BSU13130 | glutamate-5-semialdehyde dehydrogenase |  |  |  |  |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ohrA | BSU13140 | peroxidase, protects the cell against organic peroxides | | | | |
| ohrR | BSU13150 | transcription repressor of the ohrA gene | | | | |
| ohrB | BSU13160 | general stress protein | | | | |
| ykzN | BSU13169 | unknown | | | | |
| guaD | BSU13170 | guanine deaminase, general stress protein | | | | |
| metE | BSU13180 | methionine synthase | | | | |
| ispA | BSU13190 | major intracellular serine protease | | | | |
| rsbRB | BSU13200 | probably part of the stressosome | | | | |
| thiX | BSU13210 | thiamine ABC transporter (membrane protein) | | | | |
| thiW | BSU13220 | thiamine ABC transporter (ATP-binding protein) | | | | |
| thiV | BSU13230 | thiamine ABC transporter (membrane protein) | | | | |
| thiU | BSU13240 | thiamine ABC transporter (binding protein) | | | | |
| ykoG | BSU13250 | two-component response regulator | | | | |
| ykoH | BSU13260 | two-component sensor kinase | | | | |
| ykoI | BSU13270 | unknown | | | | |
| ykoJ | BSU13280 | unknown | | | | |
| ykzD | BSU13290 | unknown | | | | |
| ykzO | BSU13299 | unknown, putative pseudogene | | | | |
| mgtE | BSU13300 | primary magnesium transporter | | | | |
| tnrA | BSU13310 | transcriptional pleiotropic regulator invoved in global nitrogen regulation | | | | |
| ykzB | BSU13320 | unknown | | 🟦 | 🟦 | 🟦 |
| ykoL | BSU13330 | unknown | | 🟦 | 🟦 | 🟦 |
| ykoM | BSU13340 | similar to transcriptional regulator (MarR family) | | 🟦 | 🟦 | 🟦 |
| ykoN | BSU13350 | unknown | | 🟦 | 🟦 | 🟦 |
| ykoP | BSU13360 | unknown | | 🟦 | 🟦 | 🟦 |
| ykoQ | BSU13370 | unknown | | 🟦 | 🟦 | 🟦 |
| ykoS | BSU13380 | unknown | | 🟦 | 🟦 | 🟦 |
| ykoT | BSU13390 | similar to dolichol phosphate mannose synthase | | 🟦 | 🟦 | 🟦 |
| ligD | BSU13400 | DNA repair polymerase/ ligase in non-homologous end joining DNA repair | | | | |
| ykoV | BSU13410 | DNA-end-binding protein Ku, recruits LigD to DNA ends, confers dry-heat resistance to dormant spores | | | | |
| dgcW | BSU13420 | diguanylate cyclase and potential phosphodiesterase | | | | |
| ykoX | BSU13430 | similar to alkaline phosphatase | | | | |
| ykoY | BSU13440 | similar to toxic anion resistance protein | | | | |
| sigI | BSU13450 | RNA polymerase sigma factor SigI | | | | |
| rsgI | BSU13460 | regulator of SigI activity | | | | |
| sspD | BSU13470 | small acid-soluble spore protein (minor alpha/beta-type SASP) | | | | |
| ykrK | BSU13480 | transcription regulator of htpX expression | | | | |
| htpX | BSU13490 | stress-responsive membrane protease | | | | |
| ktrD | BSU13500 | low affinity potassium transporter KtrCD, integral membrane subunit | | | | |
| ykzP | BSU13509 | unknown | | | | |
| ykzE | BSU13510 | unknown | | | | |
| ykrP | BSU13520 | unknown | | | | |
| kinE | BSU13530 | two-component sensor kinase, phosphorylates Spo0F, part of the phosphorelay | | | | |
| ogt | BSU13540 | O6-methylguanine DNA alkyltransferase | | | | |
| mtnA | BSU13550 | 5-methylthioribose-1-phosphate isomerase | | | | |
| mtnK | BSU13560 | 5-methylthioribose kinase | | | | |
| mtnU | BSU13570 | unknown | | | | |
| mtnE | BSU13580 | aminotransferase | | | | |
| mtnW | BSU13590 | 2,3-diketo-5-methylthiopentyl-1-phosphate enolase, Rubisco-like protein | | | | |
| mtnX | BSU13600 | 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase | | | | |
| mtnB | BSU13610 | methylthioribulose-1-phosphate dehydratase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| mtnD | BSU13620 | 1,2,-dihydroxy-3-keto-5-methylthiopentene dioxygenase | | | | |
| ykvA | BSU13630 | unknown | | | | |
| spo0E | BSU13640 | Spo0A-P phosphatase, control of the phosphorelay | | | | |
| eag | BSU13650 | small membrane protein | | | | |
| kinD | BSU13660 | two-component sensor kinase, phosphorylates Spo0F, part of the phosphorelay | | 🟦 | 🟦 | 🟦 |
| mhqR | BSU13670 | transcriptional repressor of dioxygenase/ glyoxalase genes | | 🟦 | 🟦 | 🟦 |
| motB | BSU13680 | H+-coupled MotAB flagellar stator | | 🟦 | 🟦 | 🟦 |
| motA | BSU13690 | H+-coupled MotAB flagellar stator | | 🟦 | 🟦 | 🟦 |
| clpE | BSU13700 | ATP-dependent Clp protease-like (class III stress gene) | | | | |
| ykvI | BSU13710 | unknown | | | | |
| queC | BSU13720 | synthesis of the modified ribonucleotide queuosine | | | | |
| queD | BSU13730 | 6-pyruvoyltetrahydropterin synthase, synthesis of the modified ribonucleotide queuosine | | | | |
| queE | BSU13740 | 7-carboxy-7-deazaguanine (CDG) synthase, required for the synthesis of the modified ribonucleotide queuosine | | | | |
| queF | BSU13750 | nitrile reductase, synthesis of the modified ribonucleotide queuosine | | | | |
| ykvN | BSU13760 | MarR/DUF24-family transcription regulator | | 🟦 | 🟦 | 🟦 |
| ykvO | BSU13770 | similar to glucose 1-dehydrogenase | | 🟦 | 🟦 | 🟦 |
| ykvP | BSU13780 | unknown | | 🟦 | 🟦 | 🟦 |
| ykzQ | BSU13789 | unknown | | 🟦 | 🟦 | 🟦 |
| ykvQ | BSU13790 | similar to chitinase | | 🟦 | 🟦 | 🟦 |
| ykzR | BSU13799 | unknown | | 🟦 | 🟦 | 🟦 |
| ykvR | BSU13800 | unknown | | 🟦 | 🟦 | 🟦 |
| ykvS | BSU13810 | unknown | | 🟦 | 🟦 | 🟦 |
| ykzS | BSU13819 | unknown | | 🟦 | 🟦 | 🟦 |
| ykvT | BSU13820 | similar to spore cortex-lytic enzyme | | 🟦 | 🟦 | 🟦 |
| ykvU | BSU13830 | spore cortex membrane protein, required for germination at high pressure | | 🟦 | 🟦 | 🟦 |
| stoA | BSU13840 | thiol-disulfide oxidoreductase, with thioredoxin-like domain | | | | |
| zosA | BSU13850 | zinc transporter | | | | |
| papB | BSU13860 | Xaa-Pro amino-peptidase | | | | |
| ykvZ | BSU13870 | similar to transcriptional regulator (LacI family) | | | | |
| glcT | BSU13880 | Transcriptional antiterminator , controls expression of the ptsG-ptsH-ptsI operon | | | | |
| ptsG | BSU13890 | trigger enzyme: major glucose permease of the PTS, EIICBA(Glc) and control of GlcT activity | | | | |
| ptsH | BSU13900 | HPr, General component of the sugar phosphotransferase system (PTS). | | | | |
| ptsI | BSU13910 | Enzyme I, general (non sugar-specific) component of the PTS | | | | |
| splA | BSU13920 | transcriptional repressor of the spore photoproduct lyase splA-splB operon | | | 🟦 | |
| splB | BSU13930 | spore photoproduct lyase | | | 🟦 | |
| ykwB | BSU13940 | unknown | | | 🟦 | |
| mcpC | BSU13950 | methyl-accepting chemotaxis protein | | | 🟦 | |
| ykwC | BSU13960 | putative beta-hydroxyacid dehydrogenase | | | 🟦 | |
| ykwD | BSU13970 | unknown | | | 🟦 | |
| pbpH | BSU13980 | penicillin-binding protein H | | | 🟦 | |
| kinA | BSU13990 | two-component sensor kinase, phosphorylates Spo0F, part of the phosphorelay | | | 🟦 | |
| patA | BSU14000 | aminotransferase | | | | |
| ykzT | BSU14009 | unknown | | partial | partial | partial |
| cheV | BSU14010 | modulation of CheA activity in response to attractants | | 🟦 | 🟦 | 🟦 |
| ykyB | BSU14020 | unknown | | 🟦 | 🟦 | 🟦 |
| ykuC | BSU14030 | similar to macrolide-efflux protein | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ldt | BSU14040 | L,D-transpeptidase involved in cell wall synthesis |  | 🟦 | 🟦 | 🟦 |
| ykuE | BSU14050 | Mn/ Zn-dependent phosphatase |  | 🟦 | 🟦 | 🟦 |
| fadH | BSU14060 | 2,4-dienoyl-CoA reductase |  | 🟦 | 🟦 | 🟦 |
| fadG | BSU14071 | fatty acid degradation |  | 🟦 | 🟦 | 🟦 |
| ykzU | BSU14072 | unknown |  | 🟦 | 🟦 | 🟦 |
| ykuH | BSU14080 | unknown |  | 🟦 | 🟦 | 🟦 |
| ykuI | BSU14090 | c-di-GMP binding protein |  | 🟦 | 🟦 | 🟦 |
| fsrA |  | regulatory RNA |  | 🟦 | 🟦 | 🟦 |
| ykuJ | BSU14100 | unknown |  | 🟦 | 🟦 | 🟦 |
| ykuK | BSU14110 | unknown |  | 🟦 | 🟦 | 🟦 |
| abbA | BSU14120 | inhibitor of AbrB activity |  | 🟦 | 🟦 | 🟦 |
| ykuL | BSU14130 | unknown |  | 🟦 | 🟦 | 🟦 |
| ccpC | BSU14140 | transcriptional repressor of citZ and citB |  |  |  |  |
| ykuN | BSU14150 | flavodoxin, binds FMN, replaces ferredoxin under conditions of iron limitation |  |  |  |  |
| ykuO | BSU14160 | unknown |  |  |  |  |
| ykuP | BSU14170 | flavodoxin, binds FMN, replaces ferredoxin under conditions of iron limitation |  |  |  |  |
| ykuQ | BSU14180 | similar to tetrahydrodipicolinate succinylase |  |  |  |  |
| dapI | BSU14190 | N-acetyl-diaminopimelate deacetylase |  |  |  |  |
| ykuS | BSU14200 | unknown |  |  |  |  |
| ykuT | BSU14210 | mechanosensitive channel, similar to MscS, general stress protein |  |  |  |  |
| ykuU | BSU14220 | similar to 2-cys peroxiredoxin |  |  |  |  |
| ykuV | BSU14230 | thiol disulfide oxidoreductase |  |  |  |  |
| rok | BSU14240 | repressor of comK |  |  |  |  |
| yknT | BSU14250 | spore coat protein |  |  |  |  |
| mobA | BSU14260 | molybdopterin-guanine dinucleotide biosynthesis |  |  |  |  |
| moeB | BSU14270 | molybdopterin biosynthesis protein |  |  |  |  |
| moeA | BSU14280 | molybdopterin biosynthesis protein |  |  |  |  |
| mobB | BSU14290 | molybdopterin-guanine dinucleotide biosynthesis |  |  |  |  |
| moaE | BSU14300 | molybdopterin synthase (large subunit) |  |  |  |  |
| moaD | BSU14310 | molybdopterin synthase (small subunit) |  |  |  |  |
| yknU | BSU14320 | similar to ABC transporter (ATP-binding protein) |  |  |  |  |
| yknV | BSU14330 | similar to ABC transporter (ATP-binding protein) |  |  |  |  |
| yknW | BSU14340 | ABC-type antimicrobial peptide transporter (permease) |  |  |  |  |
| yknX | BSU14350 | ABC-type antimicrobial peptide transporter (permease) |  |  |  |  |
| yknY | BSU14360 | ABC transporter (ATP-binding protein, exporter) |  |  |  |  |
| yknZ | BSU14370 | ABC transporter (permease) for resistance against SdpC |  |  |  |  |
| fruR | BSU14380 | transcription repressor of the fruR-fruK-fruA operon, DeoR family |  |  |  |  |
| fruK | BSU14390 | fructose-1-phosphate kinase |  |  |  |  |
| fruA | BSU14400 | fructose-specific phosphotransferase system, EIIABC of the PTS |  |  |  |  |
| sipT | BSU14410 | signal peptidase I |  |  |  |  |
| ykoA | BSU14420 | unknown |  |  |  |  |
| ykpA | BSU14430 | similar to ABC transporter (ATP-binding protein) |  |  |  |  |
| ykpB | BSU14440 | putative ketopantoate reductase |  |  |  |  |
| ampS | BSU14450 | aminopeptidase |  |  |  |  |
| ykpC | BSU14460 | unknown |  |  |  |  |
| mreBH | BSU14470 | cell-shape determining protein |  |  |  |  |
| abh | BSU14480 | transcriptional regulator of transition state genes |  |  |  |  |
| kinC | BSU14490 | two-component sensor kinase, phosphorylates Spo0F and Spo0A, part of the phosphorelay |  |  |  |  |
| ykqA | BSU14500 | unknown |  |  |  |  |
| ktrC | BSU14510 | low affinity potassium transporter KtrCD, peripheric membrane component |  |  |  |  |
| adeC | BSU14520 | adenine deaminase |  |  |  |  |
| rnjA | BSU14530 | RNase J1 |  |  |  |  |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ykzG | BSU14540 | epsilon subunit of RNA polymerase | | | | |
| ykrA | BSU14550 | unknown | | | | |
| defB | BSU14560 | N-formylcysteine deformylase, required for the conversion of S-methyl-cysteine to cysteine | | | | |
| ykzV | BSU14569 | unknown | | | | |
| ykyA | BSU14570 | unknown | | | | |
| pdhA | BSU14580 | pyruvate dehydrogenase (E1 alpha subunit) | | | | |
| pdhB | BSU14590 | pyruvate dehydrogenase (E1 beta subunit) | | | | |
| pdhC | BSU14600 | pyruvate dehydrogenase (dihydrolipoamide acetyltransferase E2 subunit) | | | | |
| pdhD | BSU14610 | dihydrolipoamide dehydrogenase E3 subunit of both pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase complexes | | | | |
| slp | BSU14620 | small peptidoglycan-associated lipoprotein | | | | |
| Sr1 | BSU14629 | small regulatory RNA controlling AhrC expression, regulatory peptide | | | | |
| speA | BSU14630 | arginine decarboxylase | | | | |
| yktA | BSU14640 | unknown | | 🟦 | 🟦 | 🟦 |
| yktB | BSU14650 | unknown | | 🟦 | 🟦 | 🟦 |
| ykzI | BSU14660 | general stress protein | | 🟦 | 🟦 | 🟦 |
| yktC | BSU14670 | unknown | | 🟦 | 🟦 | 🟦 |
| ykzC | BSU14680 | unknown | | 🟦 | 🟦 | 🟦 |
| yktD | BSU14690 | unknown | | 🟦 | 🟦 | 🟦 |
| nprE | BSU14700 | extracellular neutral protease B | | 🟦 | 🟦 | 🟦 |
| ylaA | BSU14710 | unknown | | | | |
| ylaB | BSU14720 | unknown | | | | |
| ylaC | BSU14730 | RNA polymerase ECF-type sigma factor YlaC | | | | |
| ylaD | BSU14740 | unknown | | | | |
| ylaE | BSU14750 | unknown | | | | |
| ylaF | BSU14760 | unknown | | | | |
| ylaG | BSU14770 | similar to GTP-binding elongation factor | | | | |
| ylaH | BSU14780 | unknown | | | | |
| ylaI | BSU14790 | unknown | | | | |
| ylaJ | BSU14800 | unknown | | | | |
| ylaK | BSU14810 | similar to phosphate starvation inducible protein PhoH | | | | |
| ylaL | BSU14820 | unknown | | | | |
| ylaM | BSU14830 | glutaminase, high affinity for glutamine | | | | |
| ylaN | BSU14840 | unknown | | | | |
| ftsW | BSU14850 | cell-division protein | | | | |
| pycA | BSU14860 | pyruvate carboxylase | | | | |
| ctaA | BSU14870 | heme A synthase | | | | |
| ctaB | BSU14880 | heme O synthase (major enzyme) | | | | |
| ctaC | BSU14890 | cytochrome-c oxidase (subunit II) | | | | |
| ctaD | BSU14900 | cytochrome-c oxidase (subunit I) | | | | |
| ctaE | BSU14910 | cytochrome-c oxidase (subunit III) | | | | |
| ctaF | BSU14920 | cytochrome-c oxidase (subunit IV) | | | | |
| ctaG | BSU14930 | formation of functional cytochrome C-oxidase (caa3) | | | | |
| ylbA | BSU14940 | unknown | | | | |
| ylbB | BSU14950 | similar to IMP dehydrogenase | | | | |
| ylbC | BSU14960 | unknown | | | | |
| ylbD | BSU14970 | outer spore coat protein | | | | |
| ylbE | BSU14980 | unknown | | | | |
| ylbF | BSU14990 | antagonist of biofilm repression by SinR, control of the phosphorelay | | | | |
| ylbG | BSU15000 | unknown | | | | |
| csfG | | sporulation specific ncRNA | | | | |
| ylbH | BSU15010 | predicted methyltransferase; 16S rRNA (G966) methyltransferase | | | | |
| ylbI | BSU15020 | pantetheine-phosphate adenylyltransferase | | | | |
| ylbJ | BSU15030 | unknown | | | | |

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| ylbK | BSU15040 | unknown | | | | |
| ylbL | BSU15050 | unknown | | | | |
| ylbM | BSU15060 | unknown | | | | |
| ylzH | BSU15069 | unknown | | | | |
| ylbN | BSU15070 | unknown | | | | |
| rpmF | BSU15080 | ribosomal protein L32 | | | | |
| gerR | BSU15090 | probably DNA-binding protein, regulates transcription of some spore coat genes | | | | |
| ylbP | BSU15100 | unknown | | | | |
| ylbQ | BSU15110 | 2-dehydropantoate 2-reductase | | | | |
| bshC | BSU15120 | cysteine-adding enzyme required for the synthesis of bacillithiol | | | | |
| mraZ | BSU15130 | unknown | | | | |
| mraW | BSU15140 | S-adenosyl-L-methionine-dependent methyltransferase | | | | |
| ftsL | BSU15150 | cell-division protein (septum formation), controls together with EzrA dynamics of the FtsZ ring | | | | |
| pbpB | BSU15160 | penicillin-binding protein 2B | | | | |
| spoVD | BSU15170 | mother-cell specific penicillin-binding protein (spore cortex) | | | | |
| murE | BSU15180 | UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelate synthetase | | | | |
| mraY | BSU15190 | phospho-N-acetylmuramoyl-pentapeptide-transferase (meso-2,6-diaminopimelate) | | | | |
| murD | BSU15200 | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase | | | | |
| spoVE | BSU15210 | required for spore cortex peptidoglycan synthesis | | | | |
| murG | BSU15220 | UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase | | | | |
| murB | BSU15230 | UDP-N-acetylenolpyruvoylglucosamine reductase | | | | |
| divIB | BSU15240 | cell-division initiation protein (septum formation) | | | | |
| ylxW | BSU15250 | unknown | | | | |
| ylxX | BSU15260 | unknown | | | | |
| sbp | BSU15270 | small basic protein | | | | |
| ftsA | BSU15280 | cell-division protein, membrane anchor for FtsZ | | | | |
| ftsZ | BSU15290 | cell-division initiation protein (septum formation) | | | | |
| bpr | BSU15300 | bacillopeptidase F | | 🟦 | 🟦 | 🟦 |
| spoIIGA | BSU15310 | Pro-SigE protease | | 🟦 | 🟦 | 🟦 |
| sigE | BSU15320 | RNA polymerase sporulation mother cell-specific (early) sigma factor SigE | | 🟦 | 🟦 | 🟦 |
| sigG | BSU15330 | RNA polymerase sporulation forespore-specific (late) sigma factor SigG | | 🟦 | 🟦 | 🟦 |
| ylmA | BSU15340 | similar to ABC transporter (ATP-binding protein) | | | | |
| ylmB | BSU15350 | N-formyl-4-amino-5-aminomethyl-2-methylpyrimidine deformylase | | | | |
| ylmC | BSU15360 | sporulation protein | | | | |
| ylmD | BSU15370 | unknown | | | | |
| ylmE | BSU15380 | enzyme involved in controlling the availability of coenzyme A | | | | |
| sepF | BSU15390 | part of the divisome | | | | |
| ylmG | BSU15400 | unknown | | | | |
| ylmH | BSU15410 | unknown | | | | |
| divIVA | BSU15420 | cell-division initiation protein (septum placement) | | | | |
| ileS | BSU15430 | isoleucyl-tRNA synthetase | | | | |
| ylyA | BSU15440 | modulator of SigG-containing RNA polymerase | | | | |
| lspA | BSU15450 | signal peptidase II | | | | |
| ylyB | BSU15460 | similar to pseudouridylate synthase | | | | |
| pyrR | BSU15470 | transcriptional antiterminator of the pyr operon | | | | |
| pyrP | BSU15480 | uracil permease | | | | |
| pyrB | BSU15490 | aspartate carbamoyltransferase | | | | |
| pyrC | BSU15500 | dihydroorotase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| pyrAA | BSU15510 | carbamoyl-phosphate synthetase (glutaminase subunit) | | | | |
| pyrAB | BSU15520 | carbamoyl-phosphate synthetase (catalytic subunit) | | | | |
| pyrK | BSU15530 | dihydroorotic acid dehydrogenase (electron transfer subunit) | | | | |
| pyrD | BSU15540 | dihydroorotic acid dehydrogenase (catalytic subunit) | | | | |
| pyrF | BSU15550 | orotidine 5'-phosphate decarboxylase | | | | |
| pyrE | BSU15560 | orotate phosphoribosyltransferase | | | | |
| cysH | BSU15570 | phosphoadenosine phosphosulfate sulfotransferase | | | 🟦 | |
| cysP | BSU15580 | sulfate transport in via proton symport | | | 🟦 | |
| sat | BSU15590 | sulfate adenylyltransferase | | | 🟦 | |
| cysC | BSU15600 | adenylyl-sulfate kinase | | | 🟦 | |
| ylnD | BSU15610 | probable uroporphyrin-III C-methyltransferase | | | 🟦 | |
| ylnE | BSU15620 | probable siroheme ferrochelatase | | | 🟦 | |
| ylnF | BSU15630 | probably precorrin-2 dehydrogenase | | | 🟦 | |
| yloA | BSU15640 | similar to fibronectin-binding protein | | | 🟦 | |
| yloB | BSU15650 | similar to MgtA magnesium transporter | | | 🟦 | |
| yloC | BSU15660 | unknown | | | | |
| remA | BSU15670 | transcriptional regulator of the extracellular matrix genes, acts in parallel to SinR, AbrB, and DegU | | | | |
| gmk | BSU15680 | guanylate kinase (GMP:dATP, dGMP:ATP) | | | | |
| yloH | BSU15690 | probably omega2 subunit of RNA polymerase | | | | |
| yloI | BSU15700 | Coenzyme A biosynthesis bifunctional protein CoaBC; putative phosphopantothenoylcysteine synthetase/decarboxylase | | | | |
| priA | BSU15710 | primosomal replication factor Y | | | | |
| defA | BSU15720 | formylmethionine deformylase | | | | |
| fmt | BSU15730 | methionyl-tRNA formyltransferase | | | | |
| yloM | BSU15740 | similar to RNA-binding Sun protein | | | | |
| yloN | BSU15750 | similar to rRNA adenosine methyltransferase for modification of 23S rRNA | | | | |
| prpC | BSU15760 | protein phosphatase | | | | |
| prkC | BSU15770 | protein kinase C | | | | |
| cpgA | BSU15780 | GTPase, activity stimulated by ribosomes, may be involved in ribosome maturation | | | | |
| rpe | BSU15790 | ribulose 5-phosphate 3-epimerase | | | | |
| yloS | BSU15800 | thiamine pyrophosphokinase | | | | |
| spoVM | BSU15810 | required for normal spore cortex and coat synthesis, inhibits the proteolytic activity of FtsH | | | | |
| rpmB | BSU15820 | ribosomal protein L28 | | | | |
| yloU | BSU15830 | similar to alkaline-shock protein | | | | |
| yloV | BSU15840 | unknown | | | | |
| sdaAB | BSU15850 | L-serine deaminase | | | | |
| sdaAA | BSU15860 | L-serine deaminase | | | | |
| recG | BSU15870 | ATP-dependent DNA helicase, branch migration translocase, required for DNA repair and chromosomal segregation | | | | |
| fapR | BSU15880 | repressor of fatty acid synthetic genes | | | | |
| plsX | BSU15890 | acyl-acyl carrier protein (ACP):phosphate acyltransferase | | | | |
| fabD | BSU15900 | malonyl CoA-acyl carrier protein transacylase | | | | |
| fabG | BSU15910 | beta-ketoacyl-acyl carrier protein reductase | | | | |
| acpA | BSU15920 | acyl carrier protein | | | | |
| rnc | BSU15930 | RNase III | | | | |
| smc | BSU15940 | chromosome condensation and segregation SMC protein | | | | |
| ftsY | BSU15950 | signal recognition particle | | | | |
| sivC | BSU15960 | inhibitor of entry into sporulation via KinB or KinC | | | | |
| ylxM | BSU15970 | unknown | | | | |
| ffh | BSU15980 | signal recognition particle (SRP) component | | | | |
| rpsP | BSU15990 | ribosomal protein S16 | | | | |
| ylqC | BSU16000 | unknown | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ylqD | BSU16010 | unknown | | | | |
| rimM | BSU16020 | 16S rRNA processing protein, RNase | | | | |
| trmD | BSU16030 | tRNA methyltransferase | | | | |
| rplS | BSU16040 | ribosomal protein L19 | | | | |
| rbgA | BSU16050 | assembly of the 50S subunit of the ribosome | | | | |
| rnhB | BSU16060 | RNase HII, endoribonuclease | | | | |
| ylqG | BSU16070 | unknown | | | | |
| ylqH | BSU16080 | similar to flagellar biosynthetic protein | | | | |
| sucC | BSU16090 | succinyl-CoA synthetase (beta subunit) | | | | |
| sucD | BSU16100 | succinyl-CoA synthetase (alpha subunit) | | | | |
| dprA | BSU16110 | conveys incoming ssDNA to RecA | | | | |
| topA | BSU16120 | DNA topoisomerase I | | | | |
| trmFO | BSU16130 | tRNA:m(5)U-54 methyltransferase, glucose-inhibited division protein | | | | |
| codV | BSU16140 | site-specific integrase/recombinase, partitioning of the terminus region after replication | | | | |
| clpQ | BSU16150 | two-component ATP-dependent protease | | | | |
| clpY | BSU16160 | two-component ATP-dependent protease, ATPase subunit | | | | |
| codY | BSU16170 | regulation of a large regulon in response to branched-chain amino acid limitation | | | | |
| flgB | BSU16180 | flagellar basal-body rod protein | | | | |
| flgC | BSU16190 | flagellar basal-body rod protein | | | | |
| fliE | BSU16200 | flagellar hook-basal body protein | | 🟦 | 🟦 | 🟦 |
| fliF | BSU16210 | flagellar basal-body M-ring protein | | 🟦 | 🟦 | 🟦 |
| fliG | BSU16220 | flagellar motor switch protein | | 🟦 | 🟦 | 🟦 |
| fliH | BSU16230 | flagellar assembly protein | | 🟦 | 🟦 | 🟦 |
| fliI | BSU16240 | flagellar-specific ATP synthase | | 🟦 | 🟦 | 🟦 |
| fliJ | BSU16250 | flagellar protein required for formation of basal body | | 🟦 | 🟦 | 🟦 |
| ylxF | BSU16260 | unknown | | 🟦 | 🟦 | 🟦 |
| fliK | BSU16270 | flagellar hook-length control | | 🟦 | 🟦 | 🟦 |
| flgD | BSU16280 | putative flagellar hook cap, required for hook assembly | | 🟦 | 🟦 | 🟦 |
| flgE | BSU16290 | flagellar hook protein | | 🟦 | 🟦 | 🟦 |
| ylzI | BSU16299 | unknown | | 🟦 | 🟦 | 🟦 |
| fliL | BSU16300 | flagellar protein required for flagellar formation , membrane protein | | 🟦 | 🟦 | 🟦 |
| fliM | BSU16310 | flagellar motor switch protein | | 🟦 | 🟦 | 🟦 |
| fliY | BSU16320 | flagellar motor switch protein | | 🟦 | 🟦 | 🟦 |
| cheY | BSU16330 | two-component response regulator, modulation of flagellar switch bias | | 🟦 | 🟦 | 🟦 |
| fliZ | BSU16340 | flagellar protein required for flagellar formation | | 🟦 | 🟦 | 🟦 |
| fliP | BSU16350 | flagellar protein required for flagellar formation | | 🟦 | 🟦 | 🟦 |
| fliQ | BSU16360 | flagellar protein required for flagellar formation | | 🟦 | 🟦 | 🟦 |
| fliR | BSU16370 | flagellar protein required for flagellar formation | | 🟦 | 🟦 | 🟦 |
| flhB | BSU16380 | flagella-associated protein | | 🟦 | 🟦 | 🟦 |
| flhA | BSU16390 | flagella-associated protein | | 🟦 | 🟦 | 🟦 |
| flhF | BSU16400 | signal recognition particle-like GTPase, placement and assembly of flagella | | 🟦 | 🟦 | 🟦 |
| flhG | BSU16410 | GTPase activating protein, activates FlhF | | 🟦 | 🟦 | 🟦 |
| cheB | BSU16420 | MCP-glutamate methylesterase / two-component response regulator-like | | 🟦 | 🟦 | 🟦 |
| cheA | BSU16430 | two-component sensor kinase, chemotactic signal modulator | | 🟦 | 🟦 | 🟦 |
| cheW | BSU16440 | modulation of CheA activity in response to attractants, subject to strong Clp-dependent proteolysis upon glucose starvation | | 🟦 | 🟦 | 🟦 |
| cheC | BSU16450 | CheY-P phosphatase, inhibition of CheR-mediated methylation of MCPs | | 🟦 | 🟦 | 🟦 |
| cheD | BSU16460 | protein deaminase, required for methylation of methyl-accepting chemotaxis proteins by CheR | | 🟦 | 🟦 | 🟦 |
| sigD | BSU16470 | RNA polymerase sigma factor SigD | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| swrB | BSU16480 | control of SigD activity, required for full SigD activity | | | | |
| rpsB | BSU16490 | ribosomal protein S2 | | | | |
| tsf | BSU16500 | elongation factor Ts | | | | |
| pyrH | BSU16510 | uridylate kinase | | | | |
| frr | BSU16520 | ribosome recycling factor | | | | |
| uppS | BSU16530 | probable undecaprenyl pyrophosphate synthetase | | | | |
| cdsA | BSU16540 | phosphatidate cytidylyltransferase | | | | |
| ispC | BSU16550 | 1-deoxy-D-xylulose-5-phosphate reductoisomerase, second step in the MEP pathway of isoprenoid biosynthesis | | | | |
| rasP | BSU16560 | intramembrane protease, cleaves FtsL, RsiV and RsiW as well as signal peptides after release of the secreted proteins | | | | |
| proS | BSU16570 | prolyl-tRNA synthetase | | | | |
| polC | BSU16580 | DNA polymerase III (alpha subunit) | | | | |
| ylxS | BSU16590 | similar to 30S ribosomal subunit maturation protein | | | | |
| nusA | BSU16600 | transcription termination factor | | | | |
| ylxR | BSU16610 | unknown | | | | |
| ylxQ | BSU16620 | similar to ribosomal protein, L7AE family | | | | |
| infB | BSU16630 | translation initiation factor IF-2 | | | | |
| ylxP | BSU16640 | general stress protein | | | | |
| rbfA | BSU16650 | ribosome-binding factor A | | | | |
| truB | BSU16660 | tRNA pseudouridine 5S synthase | | | | |
| ribC | BSU16670 | riboflavin kinase / FAD synthase | | | | |
| rpsO | BSU16680 | ribosomal protein S15 | | | | |
| pnpA | BSU16690 | polynucleotide phosphorylase, RNase, involved in double-strand break repair | | | | |
| ylxY | BSU16700 | similar to deacetylase | | | | |
| mlpA | BSU16710 | mitochondrial processing peptidase-like, involved in regulation of protease gene expression | | | | |
| ymxH | BSU16720 | sporulation protein | | | | |
| spoVFA | BSU16730 | dipicolinate synthase (subunit A) | | | | |
| spoVFB | BSU16740 | dipicolinate synthase (subunit B) | | | | |
| asd | BSU16750 | aspartate-semialdehyde dehydrogenase | | | | |
| dapG | BSU16760 | aspartokinase I (alpha and beta subunits) | | | | |
| dapA | BSU16770 | dihydrodipicolinate synthase | | | | |
| rnjB | BSU16780 | RNase J2 | | | | |
| tepA | BSU16790 | orphan ClpP-like germination protease, contributes to SASP degradation | | | | |
| ylzJ | BSU16799 | germination protein, required for TepA activity | | | | |
| spoIIIE | BSU16800 | ATP-dependent DNA translocase, resolution of chromosomal dimers after DNA replication, transports the forespore chromosome across the sporulation septum | | | | |
| ymfC | BSU16810 | similar to transcriptional regulator (GntR family) | | | | |
| ymfD | BSU16825 | exporter for the siderophore bacillibactin | | | | |
| ymfF | BSU16845 | unknown | | | | |
| ymfH | BSU16860 | similar to processing protease | | | | |
| ymfI | BSU16870 | similar to 3-oxoacyl- acyl-carrier protein reductase | | | | |
| ymfJ | BSU16880 | unknown | | | | |
| ymfK/1 | BSU16890 | part of the ymfK pseudogene | | | | |
| ymfK/2 | BSU16900 | part of the ymfK pseudogene | | | | |
| rodZ | BSU16910 | required for cell shape determination | | | | |
| pgsA | BSU16920 | phosphatidylglycerophosphate synthase | | | | |
| cinA | BSU16930 | competence-damage inducible protein | | | | |
| recA | BSU16940 | multifunctional protein involved in homologous recombination and DNA repair (LexA-autocleavage) | | | | |
| pbpX | BSU16950 | penicillin-binding protein X | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| rny | BSU16960 | RNase Y, 5' end sensitive endoribonuclease, involved in the degradation/processing of mRNA | | | | |
| ymdB | BSU16970 | unknown function | | | | |
| spoVS | BSU16980 | required for dehydratation of the spore core and assembly of the coat, mutation increases SigD-dependent gene expression, might act via SinR | | | | |
| tdh | BSU16990 | L-threonine dehydrogenase | | | | |
| kbl | BSU17000 | 2-amino-3-ketobutyrate CoA ligase | | | | |
| ymcB | BSU17010 | unknown | | | | |
| ymcA | BSU17020 | antagonist of biofilm repression by SinR, control of the phosphorelay | | | | |
| cotE | BSU17030 | outer spore coat morphogenetic protein | | | | |
| mutS | BSU17040 | DNA mismatch repair (recognition) | | | | |
| mutL | BSU17050 | DNA mismatch repair | | | | |
| ymzD | BSU17060 | unknown | | 🟦 | 🟦 | 🟦 |
| ymcC | BSU17070 | unknown | | 🟦 | 🟦 | 🟦 |
| pksA | BSU17080 | transcriptional regulator (TetR family), **not** involved in the regulation of the pks operon! | 🟦 | 🟦 | 🟦 | 🟦 |
| pksB | BSU17090 | involved in polyketide synthesis | 🟦 | 🟦 | 🟦 | 🟦 |
| pksC | BSU17100 | bacillaene synthase trans-acting acyltransferase | 🟦 | 🟦 | 🟦 | 🟦 |
| pksD | BSU17110 | involved in polyketide synthesis | 🟦 | 🟦 | 🟦 | 🟦 |
| pksE | BSU17120 | involved in polyketide synthesis | 🟦 | 🟦 | 🟦 | 🟦 |
| acpK | BSU17130 | acyl carrier protein | 🟦 | 🟦 | 🟦 | 🟦 |
| pksF | BSU17140 | involved in polyketide synthesis | 🟦 | 🟦 | 🟦 | 🟦 |
| pksG | BSU17150 | involved in polyketide synthesis | 🟦 | 🟦 | 🟦 | 🟦 |
| pksH | BSU17160 | involved in polyketide synthesis | 🟦 | 🟦 | 🟦 | 🟦 |
| pksI | BSU17170 | involved in polyketide synthesis | 🟦 | 🟦 | 🟦 | 🟦 |
| pksJ | BSU17180 | polyketide synthase | 🟦 | 🟦 | 🟦 | 🟦 |
| pksL | BSU17190 | polyketide synthase of type I | 🟦 | 🟦 | 🟦 | 🟦 |
| pksM | BSU17200 | polyketide synthase | 🟦 | 🟦 | 🟦 | 🟦 |
| pksN | BSU17210 | polyketide synthase of type I | 🟦 | 🟦 | 🟦 | 🟦 |
| pksR | BSU17220 | polyketide synthase | 🟦 | 🟦 | 🟦 | 🟦 |
| pksS | BSU17230 | hydroxylase of the polyketide produced by the pks cluster | | 🟦 | 🟦 | 🟦 |
| ymzB | BSU17240 | general stress protein, survival of ethanol and salt stresses | | 🟦 | 🟦 | 🟦 |
| ymaE | BSU17250 | unknown | | 🟦 | 🟦 | 🟦 |
| aprX | BSU17260 | intracellular alkaline serine protease | | 🟦 | 🟦 | 🟦 |
| ymzE/1 | BSU17266 | part of the ymzE pseudogene | | 🟦 | 🟦 | 🟦 |
| ymzE/2 | BSU17267 | part of the ymzE pseudogene | | 🟦 | 🟦 | 🟦 |
| ymaC | BSU17270 | similar to phage-related protein | | 🟦 | 🟦 | 🟦 |
| ymaD | BSU17280 | unknown | | 🟦 | 🟦 | 🟦 |
| ebrB | BSU17290 | multidrug efflux transporter | | 🟦 | 🟦 | 🟦 |
| ebrA | BSU17300 | multidrug efflux transporter | | 🟦 | 🟦 | 🟦 |
| ymaG | BSU17310 | spore coat protein | | | | |
| ymaF | BSU17320 | unknown | | | | |
| miaA | BSU17330 | tRNA isopentenylpyrophosphate transferase | | | | |
| hfq | BSU17340 | RNA chaperone | | | | |
| ymzC | BSU17350 | unknown | | | | |
| ymzA | BSU17360 | unknown | | | | |
| nrdI | BSU17370 | ribonucleoside-diphosphate reductase | | | | |
| nrdE | BSU17380 | ribonucleoside-diphosphate reductase (major subunit), control of DNA/cell mass ratio | | | | |
| nrdF | BSU17390 | ribonucleoside-diphosphate reductase (major subunit) | | | | |
| ymaB | BSU17400 | unknown | | | | |
| cwlC | BSU17410 | N-acetylmuramoyl-L-alanine amidase | | | | |
| spoVK | BSU17420 | required for spore maturation | | | | |
| ynbA | BSU17430 | GTP-binding protein | | | | |
| ynbB | BSU17440 | putative C-S lyase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| glnR | BSU17450 | transcriptional repressor of the glnR-glnA operon | | | | |
| glnA | BSU17460 | trigger enzyme: glutamine synthetase and effector of TnrA and GlnR | | | | |
| ynxB | BSU17470 | unknown | | 🟦 | 🟦 | 🟦 |
| ynzF | BSU17480 | similar to delta-endotoxin | | 🟦 | 🟦 | 🟦 |
| ynzG | BSU17490 | unknown | | 🟦 | 🟦 | 🟦 |
| ynaB | BSU17500 | unknown | | 🟦 | 🟦 | 🟦 |
| ynaC | BSU17510 | unknown | | 🟦 | 🟦 | 🟦 |
| ynaD | BSU17520 | similar to ribosomal-protein-alanine N-acetyltransferase | | 🟦 | 🟦 | 🟦 |
| ynaE | BSU17530 | unknown | | 🟦 | 🟦 | 🟦 |
| ynaF | BSU17540 | unknown | | 🟦 | 🟦 | 🟦 |
| ynaG | BSU17550 | unknown | | 🟦 | 🟦 | 🟦 |
| ynzI | BSU17559 | unknown | | 🟦 | 🟦 | 🟦 |
| ynaI | BSU17560 | similar to phosphoribosylanthranilate isomerase | | 🟦 | 🟦 | 🟦 |
| xynP | BSU17570 | beta-xyloside permease | | 🟦 | 🟦 | 🟦 |
| xynB | BSU17580 | xylan beta-1,4-xylosidase | | 🟦 | 🟦 | 🟦 |
| xylR | BSU17590 | transcriptional repressor of the xyl and xyn operons | | 🟦 | 🟦 | 🟦 |
| xylA | BSU17600 | xylose isomerase | | 🟦 | 🟦 | 🟦 |
| xylB | BSU17610 | xylulokinase | | 🟦 | 🟦 | 🟦 |
| yncB | BSU17620 | similar to micrococcal nuclease | | 🟦 | 🟦 | 🟦 |
| yncC | BSU17630 | similar to metabolite transport protein | | 🟦 | 🟦 | 🟦 |
| yncD | BSU17640 | alanine racemase | | 🟦 | 🟦 | 🟦 |
| yncE | BSU17650 | unknown | | 🟦 | 🟦 | 🟦 |
| yncF | BSU17660 | dUTP diphosphatase | | 🟦 | 🟦 | 🟦 |
| cotU | BSU17670 | spore coat protein | | 🟦 | 🟦 | 🟦 |
| ynzJ | BSU17678 | unknown, putative pseudogene | | 🟦 | 🟦 | 🟦 |
| thyA | BSU17680 | thymidylate synthase A | | | | |
| yncM | BSU17690 | unknown | | 🟦 | 🟦 | 🟦 |
| ynzK | BSU17699 | unknown | | 🟦 | 🟦 | 🟦 |
| cotC | BSU17700 | spore coat protein (outer) | | 🟦 | 🟦 | 🟦 |
| tatAC | BSU17710 | putative component of the twin-arginine translocation pathway | | 🟦 | 🟦 | 🟦 |
| yndA | BSU17720 | unknown | | 🟦 | 🟦 | 🟦 |
| yndB | BSU17730 | unknown | | 🟦 | 🟦 | 🟦 |
| ynzB | BSU17740 | potential D protein for the YndD-YndE-YndF germinant receptor of unknown specificity | | 🟦 | 🟦 | 🟦 |
| yndD | BSU17750 | part of the YndD-YndE-YndF germinant receptor of unknown specificity | | 🟦 | 🟦 | 🟦 |
| yndE | BSU17760 | part of the YndD-YndE-YndF germinant receptor of unknown specificity | | 🟦 | 🟦 | 🟦 |
| yndF | BSU17770 | part of the YndD-YndE-YndF germinant receptor of unknown specificity | | 🟦 | 🟦 | 🟦 |
| yndG | BSU17780 | unknown | | 🟦 | 🟦 | 🟦 |
| yndH | BSU17790 | unknown | | 🟦 | 🟦 | 🟦 |
| yndJ | BSU17800 | unknown | | 🟦 | 🟦 | 🟦 |
| yndK | BSU17810 | unknown | | 🟦 | 🟦 | 🟦 |
| surA | | small RNA | | 🟦 | 🟦 | 🟦 |
| yndL | BSU17820 | similar to phage-related replication protein | | 🟦 | 🟦 | 🟦 |
| yndM | BSU17830 | unknown | | 🟦 | 🟦 | 🟦 |
| fosB | BSU17840 | resistence against antimicrobial compounds from B. amyloliquefaciens | | 🟦 | 🟦 | 🟦 |
| lexA | BSU17850 | transcriptional repressor of the SOS regulon | | | | |
| yneA | BSU17860 | inhibits cell division during SOS response | | | | |
| yneB | BSU17870 | similar to resolvase | | | | |
| ynzC | BSU17880 | unknown | | | | |
| tkt | BSU17890 | transketolase | | | | |
| sirA | BSU17900 | sporulation protein, inhibits DNA replication | | | | |
| yneF | BSU17910 | membrane protein | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ynzD | BSU17920 | Spo0A-P phosphatase, control of the phosphorelay | | | | |
| ccdA | BSU17930 | membrane-embedded thiol-disulfide oxidoreductase | | | | |
| yneI | BSU17940 | two-component response regulator | | | | |
| yneJ | BSU17950 | unknown | | | | |
| yneK | BSU17960 | unknown | | | | |
| cotM | BSU17970 | spore coat protein (outer) | | | | |
| sspP | BSU17980 | probable small acid-soluble spore protein (minor) | | | | |
| sspO | BSU17990 | small acid-soluble spore protein (minor) | | | | |
| citB | BSU18000 | trigger enzyme: aconitase and RNA binding protein | | | | |
| yneN | BSU18010 | similar to thiol:disulfide interchange protein | | | | |
| ynzL | BSU18019 | unknown | | | | |
| sspN | BSU18020 | small acid-soluble spore protein (minor) | | | | |
| tlp | BSU18030 | thioredoxin-like protein | | | | |
| yneP | BSU18040 | unknown | | | | |
| yneQ | BSU18050 | unknown | | | | |
| yneR | BSU18060 | unknown | | | | |
| plsY | BSU18070 | acylphosphate:glycerol-phosphate acyltransferase | | | | |
| yneT | BSU18080 | unknown | | | | |
| parE | BSU18090 | subunit of DNA topoisomerase IV | | | | |
| parC | BSU18100 | subunit of DNA topoisomerase IV | | | | |
| ynfC | BSU18110 | unknown | | | | |
| alsT | BSU18120 | amino acid carrier protein | | | | |
| bglC | BSU18130 | endo-1,4-beta-glucanase | | | | |
| ynfE | BSU18140 | unknown | | | | |
| xynC | BSU18150 | endo-xylanase, preference for methylglucurono-xylan | | | | |
| xynD | BSU18160 | arabinoxylan arabinofuranohydrolase | | | | |
| yngA | BSU18170 | unknown | | | | |
| yngB | BSU18180 | similar to UTP-glucose-1-phosphate uridylyltransferase | | | | |
| yngC | BSU18190 | similar to alkaline phosphatase | | | | |
| nrnB | BSU18200 | oligoribonuclease (nano-RNase) | | | | |
| yngE | BSU18210 | methylcrotonoyl-CoA carboxylase, subunit | | | | |
| yngF | BSU18220 | methylglutaconyl-CoA hydratase | | | | |
| yngG | BSU18230 | 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) lyase | | | | |
| yngHB | BSU18239 | acyl-CoA carboxylase, biotinylated subunit | | | | |
| yngH | BSU18240 | methylcrotonoyl-CoA carboxylase | | | | |
| yngI | BSU18250 | aceto-acetate-CoA ligase | | | | |
| yngJ | BSU18260 | 3-methylbutanoyl-CoA dehydrogenase | | | | |
| ynzE | BSU18270 | unknown | | | | |
| yngK | BSU18280 | unknown | | | | |
| yngL | BSU18290 | unknown | | | | |
| ppsE | BSU18300 | plipastatin synthetase | | 🟦 | 🟦 | 🟦 |
| ppsD | BSU18310 | plipastatin synthetase | | 🟦 | 🟦 | 🟦 |
| ppsC | BSU18320 | plipastatin synthetase | | 🟦 | 🟦 | 🟦 |
| ppsB | BSU18330 | plipastatin synthetase | | 🟦 | 🟦 | 🟦 |
| ppsA | BSU18340 | plipastatin synthetase | | 🟦 | 🟦 | 🟦 |
| dacC | BSU18350 | penicillin-binding protein 4A, D-alanyl-D-alanine carboxypeptidase | | | | |
| galM | BSU18360 | aldose-1-epimerase | | | | |
| yoeA | BSU18370 | unknown | | | | |
| iseA | BSU18380 | inhibits in vitro activity of cell wall endopeptidases LytE and LytF, inhibits cell separation | | | | |
| trnSL-Arg1 | | | | | | |
| yoeC | BSU18390 | unknown | | | | |
| yoeD | BSU18400 | unknown | | | | |
| ggt | BSU18410 | gamma-glutamyltransferase | | | | |
| yofA | BSU18420 | transcriptional activator of ftsW-pycA at the onset of stationary phase | | | | |
| yogA | BSU18430 | unknown | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| gltB | BSU18440 | small subunit of glutamate synthase | | | | |
| gltA | BSU18450 | large subunit of glutamate synthase | | | | |
| gltC | BSU18460 | Transcriptional activator of the gltA-gltB operon. Activates expression of the operon in the absence of arginine. | | | | |
| proJ | BSU18470 | glutamate 5-kinase | | | | |
| proH | BSU18480 | pyrroline-5-carboxylate reductase | | | | |
| rtp | BSU18490 | replication terminator protein | | | | |
| yoxD | BSU18500 | similar to 3-oxoacyl- acyl-carrier protein reductase | | | | |
| yoxC | BSU18510 | general stress protein, survival of ethanol stress | | 🟦 | 🟦 | 🟦 |
| yoxB | BSU18520 | general stress protein | | 🟦 | 🟦 | 🟦 |
| yoaA | BSU18530 | similar to ribosomal-protein-alanine N-acetyltransferase | | 🟦 | 🟦 | 🟦 |
| yoaB | BSU18540 | 2-oxoglutarate permease (proton symporter) | | 🟦 | 🟦 | 🟦 |
| yoaC | BSU18550 | similar to xylulokinase | | 🟦 | 🟦 | 🟦 |
| yoaD | BSU18560 | similar to phosphoglycerate dehydrogenase | | 🟦 | 🟦 | 🟦 |
| yoaE | BSU18570 | formate dehydrogenase | | 🟦 | 🟦 | 🟦 |
| yoaF | BSU18580 | unknown | | 🟦 | 🟦 | 🟦 |
| yoaG | BSU18590 | unknown | | 🟦 | 🟦 | 🟦 |
| yozQ | BSU18600 | unknown | | 🟦 | 🟦 | 🟦 |
| yoaH | BSU18610 | membrane-bound chemotaxis receptor, similar to methyl-accepting chemotaxis protein | | 🟦 | 🟦 | 🟦 |
| yoaI | BSU18620 | similar to 4-hydroxyphenylacetate-3-hydroxylase | | 🟦 | 🟦 | 🟦 |
| yoaJ | BSU18630 | bacterial expansin, required for the colonization of maize roots | | 🟦 | 🟦 | 🟦 |
| yoaK | BSU18640 | unknown | | 🟦 | 🟦 | 🟦 |
| pelB | BSU18650 | pectate lyase | | 🟦 | 🟦 | 🟦 |
| yoaM | BSU18660 | unknown | | 🟦 | 🟦 | 🟦 |
| yozS | BSU18669 | unknown | | 🟦 | 🟦 | 🟦 |
| oxdD | BSU18670 | oxalate decarboxylase, spore coat protein | | 🟦 | 🟦 | 🟦 |
| yoaO | BSU18680 | unknown | | 🟦 | 🟦 | 🟦 |
| yoaP | BSU18690 | unknown | | 🟦 | 🟦 | 🟦 |
| yoaQ | BSU18700 | unknown | | 🟦 | 🟦 | 🟦 |
| yozT | BSU18709 | unknown | | 🟦 | 🟦 | 🟦 |
| yozF | BSU18710 | unknown | | 🟦 | 🟦 | 🟦 |
| yoaR | BSU18720 | unknown | | 🟦 | 🟦 | 🟦 |
| yoaS | BSU18730 | unknown | | 🟦 | 🟦 | 🟦 |
| yozG | BSU18740 | similar to transcriptional regulator | | 🟦 | 🟦 | 🟦 |
| yoaT | BSU18750 | unknown | | 🟦 | 🟦 | 🟦 |
| yoaU | BSU18760 | similar to transcriptional regulator (LysR family) | | 🟦 | 🟦 | 🟦 |
| yoaV | BSU18770 | putative cysteine and O-acetyl serine efflux permease | | 🟦 | 🟦 | 🟦 |
| yoaW | BSU18780 | unknown | | 🟦 | 🟦 | 🟦 |
| yoaZ | BSU18790 | unknown | | 🟦 | 🟦 | 🟦 |
| penP | BSU18800 | beta-lactamase | | 🟦 | 🟦 | 🟦 |
| yobA | BSU18810 | unknown | | 🟦 | 🟦 | 🟦 |
| yozU | BSU18819 | unknown, putative pseudogene | | 🟦 | 🟦 | 🟦 |
| yobB | BSU18820 | unknown | | 🟦 | 🟦 | 🟦 |
| pps | BSU18830 | similar to phosphoenolpyruvate synthase | | | | |
| xynA | BSU18840 | endo-1,4-beta-xylanase | | | | |
| yozV | BSU18849 | unknown | | 🟦 | 🟦 | 🟦 |
| yobD | BSU18850 | similar to transcriptional regulator (phage-related) (Xre family) | | 🟦 | 🟦 | 🟦 |
| yozH | BSU18860 | unknown | | 🟦 | 🟦 | 🟦 |
| yozI | BSU18870 | unknown | | 🟦 | 🟦 | 🟦 |
| yobE | BSU18880 | similar to general secretion pathway | | 🟦 | 🟦 | 🟦 |
| yobF | BSU18890 | unknown | | 🟦 | 🟦 | 🟦 |
| yozW | BSU18898 | unknown | | 🟦 | 🟦 | 🟦 |
| yozX | BSU18899 | unknown | | 🟦 | 🟦 | 🟦 |
| yozJ | BSU18900 | unknown | | 🟦 | 🟦 | 🟦 |
| yozY | BSU18908 | unknown | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yozZ | BSU18909 | unknown, putative pseudogene | | 🟦 | 🟦 | 🟦 |
| rapK | BSU18910 | response regulator aspartate phosphatase, controls ComA activity | | 🟦 | 🟦 | 🟦 |
| phrK | BSU18920 | response regulator aspartate phosphatase (RapK) regulator, controls ComA activity | | 🟦 | 🟦 | 🟦 |
| yobH | BSU18930 | similar to Uvr repair protein | | 🟦 | 🟦 | 🟦 |
| yozK | BSU18940 | similar to DNA repair protein | | 🟦 | 🟦 | 🟦 |
| yozL | BSU18950 | unknown | | 🟦 | 🟦 | 🟦 |
| yozM | BSU18960 | unknown | | 🟦 | 🟦 | 🟦 |
| yobI | BSU18970 | unknown | | 🟦 | 🟦 | 🟦 |
| yoyA | BSU18979 | unknown, putative pseudogene | | 🟦 | 🟦 | 🟦 |
| yobJ | BSU18980 | unknown | | 🟦 | 🟦 | 🟦 |
| yobK | BSU18990 | antitoxin | | 🟦 | 🟦 | 🟦 |
| yobL | BSU19000 | toxin | | 🟦 | 🟦 | 🟦 |
| yobM | BSU19010 | unknown | | 🟦 | 🟦 | 🟦 |
| yobN | BSU19020 | similar to L-amino acid oxidase | | 🟦 | 🟦 | 🟦 |
| yobO | BSU19030 | similar to phage-related pre-neck appendage protein | | 🟦 | 🟦 | 🟦 |
| csaA | BSU19040 | molecular chaperone involved in protein secretion | | | | |
| yobQ | BSU19050 | similar to transcriptional regulator (AraC family) | | | | |
| yobR | BSU19060 | unknown | | | | |
| yobS | BSU19070 | unknown | | | | |
| yobT | BSU19080 | unknown | | | | |
| yobU | BSU19090 | unknown | | | | |
| yobV | BSU19100 | unknown | | | | |
| yobW | BSU19110 | sporulation membrane protein | | | | |
| czrA | BSU19120 | transcriptional repressor of cadA and czcD | | | | |
| yocA | BSU19130 | similar to transposon-related protein | | | | |
| yozB | BSU19140 | unknown | | | | |
| yocB | BSU19150 | general stress protein, survival of stress conditions | | | | |
| yocC | BSU19160 | unknown | | | | |
| yocD | BSU19170 | similar to immunity to bacteriotoxins | | | | |
| des | BSU19180 | phospholipid desaturase | | | | |
| desK | BSU19190 | two-component sensor kinase, regulation of cold shock expression of des | | | | |
| desR | BSU19200 | two-component response regulator, regulation of cold shock expression of des | | | | |
| yocH | BSU19210 | peptidoglycan hydrolase (amidase) | | 🟦 | 🟦 | 🟦 |
| yocI | BSU19220 | similar to ATP-dependent DNA helicase | | 🟦 | 🟦 | 🟦 |
| bsrB | BSU_misc_RNA_32 | 6S RNA | | 🟦 | 🟦 | 🟦 |
| azoR1 | BSU19230 | azoreductase, involved in quinone detoxification | | 🟦 | 🟦 | 🟦 |
| yocK | BSU19240 | general stress protein | | 🟦 | 🟦 | 🟦 |
| yocL | BSU19250 | unknown | | 🟦 | 🟦 | 🟦 |
| yoyB | BSU19259 | unknown | | 🟦 | 🟦 | 🟦 |
| yocM | BSU19260 | similar to small heat-shock protein | | 🟦 | 🟦 | 🟦 |
| yozN | BSU19270 | unknown | | 🟦 | 🟦 | 🟦 |
| yocN | BSU19280 | similar to permease | | 🟦 | 🟦 | 🟦 |
| yozO | BSU19290 | unknown | | 🟦 | 🟦 | 🟦 |
| yozC | BSU19300 | unknown | | 🟦 | 🟦 | 🟦 |
| dhaS | BSU19310 | aldehyde dehydrogenase (NAD) | | | | |
| sqhC | BSU19320 | squalene-hopene cyclase, biosynthesis of sporulenes, protection of the spore against oxidative stress | | | | |
| sodF | BSU19330 | superoxide dismutase | | | | |
| yocR | BSU19340 | similar to sodium-dependent transporter | | | | |
| yocS | BSU19350 | putative sodium-dependent transporter | | | | |
| odhB | BSU19360 | 2-oxoglutarate dehydrogenase complex (dihydrolipoamide transsuccinylase, E2 subunit) | | | | |
| odhA | BSU19370 | 2-oxoglutarate dehydrogenase (E1 subunit) | | | | |

| Gene | BSU_number [1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yojO | BSU19380 | unknown | | | | |
| yojN | BSU19390 | similar to nitric-oxide reductase | | | | |
| yojM | BSU19400 | superoxide dismutase | | | | |
| cwlS | BSU19410 | D,L-endopeptidase, peptidoglycan hydrolase for cell separation | | | | |
| yojK | BSU19420 | similar to macrolide glycosyltransferase | | | | |
| cdaS | BSU19430 | sporulation-specific diadenylate cyclase, synthesis of c-di-AMP | | | | |
| yojI | BSU19440 | unknown | | | | |
| rsbRC | BSU19450 | probably part of the stressosome | | | | |
| bshB2 | BSU19460 | N-acetylglucosamine-malate deacetylase, minor enzyme involved in bacillithiol synthesis | | ■ | ■ | ■ |
| yojF | BSU19470 | unknown | | ■ | ■ | ■ |
| yoyC | BSU19479 | unknown | | ■ | ■ | ■ |
| yojE | BSU19480 | unknown | | ■ | ■ | ■ |
| gerT | BSU19490 | spore coat protein, involved in germination | | ■ | ■ | ■ |
| yojB | BSU19510 | unknown | | ■ | ■ | ■ |
| yojA | BSU19520 | similar to gluconate permease | | ■ | ■ | ■ |
| yodA | BSU19530 | unknown | | ■ | ■ | ■ |
| yodB | BSU19540 | repressor (MarR-type) of spx, yodC and azoR1 expression | | ■ | ■ | ■ |
| yodC | BSU19550 | similar to nitroreductase | | ■ | ■ | ■ |
| mhqD | BSU19560 | may be involved in protection against methyl-hydroquinone | | ■ | ■ | ■ |
| mhqE | BSU19570 | dioxygenase/glyoxalase | | ■ | ■ | ■ |
| yoyD | BSU19579 | unknown | | ■ | ■ | ■ |
| yodF | BSU19580 | similar to proline permease | | ■ | ■ | ■ |
| ctpA | BSU19590 | carboxy-terminal processing protease | | ■ | ■ | ■ |
| yodH | BSU19600 | unknown | | ■ | ■ | ■ |
| yodI | BSU19610 | unknown | | ■ | ■ | ■ |
| yodJ | BSU19620 | similar to D-alanyl-D-alanine carboxypeptidase | | ■ | ■ | ■ |
| deoD | BSU19630 | purine nucleoside phosphorylase | | | | |
| yoyE | BSU19639 | unknown | | ■ | ■ | ■ |
| yodL | BSU19640 | unknown | | ■ | ■ | ■ |
| yodM | BSU19650 | unknown | | ■ | ■ | ■ |
| yozD | BSU19660 | unknown | | ■ | ■ | ■ |
| yoyF | BSU19669 | unknown | | ■ | ■ | ■ |
| yodN | BSU19670 | unknown | | ■ | ■ | ■ |
| yozE | BSU19680 | unknown | | ■ | ■ | ■ |
| yokU | BSU19689 | unknown | | ■ | ■ | ■ |
| kamA | BSU19690 | lysine 2,3-aminomutase | | ■ | ■ | ■ |
| yodP | BSU19700 | beta-lysine acetyltransferase | | ■ | ■ | ■ |
| yodQ | BSU19710 | putative deacylase | | ■ | ■ | ■ |
| yodR | BSU19720 | similar to butyrate-acetoacetate CoA-transferase | | ■ | ■ | ■ |
| yodS | BSU19730 | similar to 3-oxoadipate CoA-transferase | | ■ | ■ | ■ |
| yodT | BSU19740 | similar to adenosylmethionine-8-amino-7-oxononanoate aminotransferase | | ■ | ■ | ■ |
| yoyG | BSU19749 | unknown | | ■ | ■ | ■ |
| cgeE | BSU19750 | maturation of the outermost layer of the spore | | ■ | ■ | ■ |
| cgeD | BSU19760 | maturation of the outermost layer of the spore | | ■ | ■ | ■ |
| cgeC | BSU19770 | maturation of the outermost layer of the spore | | ■ | ■ | ■ |
| cgeA | BSU19780 | spore coat protein, maturation of the outermost layer of the spore | | ■ | ■ | ■ |
| cgeB | BSU19790 | maturation of the outermost layer of the spore | | ■ | ■ | ■ |
| phy | BSU19800 | phytase | | ■ | ■ | ■ |
| yodU | BSU19810 | similar to capsular polysaccharide biosynthesis, in B. subtilis 168 the gene is disrupted by the SP-beta prophage | | ■ | ■ | ■ |
| yotN | BSU19820 | excision of prophage SP-beta prophage | ■ | ■ | ■ | ■ |
| yotM | BSU19830 | unknown | ■ | ■ | ■ | ■ |
| yotL | BSU19840 | similar to transcription regulator (Xre family) | ■ | ■ | ■ | ■ |
| yotK | BSU19850 | unknown | ■ | ■ | ■ | ■ |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yotJ | BSU19860 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yotI | BSU19870 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yotH | BSU19880 | similar to propionyl-CoA carboxylase | 🟦 | 🟦 | 🟦 | 🟦 |
| yotG | BSU19890 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yotF | BSU19900 | similar to 3-hydroxy-3-methylglutaryl-CoA lyase | 🟦 | 🟦 | 🟦 | 🟦 |
| yotE | BSU19910 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yotD | BSU19920 | similar to acyl-CoA synthetase | 🟦 | 🟦 | 🟦 | 🟦 |
| yotC | BSU19930 | similar to acyl-CoA dehydrogenase | 🟦 | 🟦 | 🟦 | 🟦 |
| yotB | BSU19940 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| sspC | BSU19950 | small acid-soluble spore protein (minor alpha/beta-type SASP) | 🟦 | 🟦 | 🟦 | 🟦 |
| yosX | BSU19970 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosW | BSU19980 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosV | BSU19990 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yojW | BSU19999 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosU | BSU20000 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosT | BSU20010 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosS | BSU20020 | dUTP diphosphatase | 🟦 | 🟦 | 🟦 | 🟦 |
| yosR | BSU20030 | glutaredoxin-like thioredoxin | 🟦 | 🟦 | 🟦 | 🟦 |
| yosP | BSU20040 | similar to ribonucleoside-diphosphate reductase (beta subunit) | 🟦 | 🟦 | 🟦 | 🟦 |
| yosQ | BSU20050 | similar to phage-related endodeoxyribonuclease | 🟦 | 🟦 | 🟦 | 🟦 |
|  |  | confers resistance to infection with phage SP10 | 🟦 | 🟦 | 🟦 | 🟦 |
| nrdEB | BSU20060 | similar to ribonucleoside-diphosphate reductase (alpha subunit) | 🟦 | 🟦 | 🟦 | 🟦 |
| yosM | BSU20070 | putative SPbeta phage subunit of nucleoside diphosphate reductase | 🟦 | 🟦 | 🟦 | 🟦 |
| yosL | BSU20080 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosK | BSU20090 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosJ | BSU20100 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosI | BSU20110 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosH | BSU20120 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosG | BSU20130 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosF | BSU20140 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosE | BSU20150 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosD | BSU20160 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosC | BSU20170 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosB | BSU20180 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yosA | BSU20190 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorZ | BSU20200 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorY | BSU20210 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorX | BSU20220 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorW | BSU20230 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorV | BSU20240 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| mtbP | BSU20250 | DNA (cytosine-5-)-methyltransferase | 🟦 | 🟦 | 🟦 | 🟦 |
| yorT | BSU20260 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorS | BSU20270 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorR | BSU20280 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorQ | BSU20290 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorP | BSU20300 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorO | BSU20310 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorN | BSU20320 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorM | BSU20330 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorL | BSU20340 | similar to DNA polymerase III (alpha subunit) | 🟦 | 🟦 | 🟦 | 🟦 |
| yorK | BSU20350 | similar to single-strand DNA-specific exonuclease | 🟦 | 🟦 | 🟦 | 🟦 |
| yorJ | BSU20360 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorI | BSU20370 | similar to putative replicative DNA helicase | 🟦 | 🟦 | 🟦 | 🟦 |
| yorH | BSU20380 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorG | BSU20390 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorF | BSU20400 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yorE | BSU20410 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorD | BSU20420 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorC | BSU20430 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorB | BSU20440 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yorA | BSU20450 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqZ | BSU20460 | phage-derived gamma polyglutamic acid hydrolase | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqY | BSU20470 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqX | BSU20480 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqW | BSU20490 | similar to general secretion pathway protein | 🟦 | 🟦 | 🟦 | 🟦 |
| ligB | BSU20500 | DNA ligase (ATP-dependent) | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqU | BSU20510 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqT | BSU20520 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqS | BSU20530 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqR | BSU20540 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqP | BSU20550 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqO | BSU20560 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqN | BSU20570 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqM | BSU20580 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqL | BSU20590 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqK | BSU20600 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqJ | BSU20610 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqI | BSU20620 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqH | BSU20630 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqG | BSU20640 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqF | BSU20650 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqE | BSU20660 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqD | BSU20670 | similar to phage-related DNA-binding protein anti-repressor | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqC | BSU20680 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqB | BSU20690 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoqA | BSU20700 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopZ | BSU20710 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopY | BSU20720 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopX | BSU20730 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopW | BSU20740 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopV | BSU20750 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopU | BSU20760 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopT | BSU20770 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopS | BSU20780 | similar to transcription regulator (Xre family) | 🟦 | 🟦 | 🟦 | 🟦 |
| yopR | BSU20790 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopQ | BSU20800 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopP | BSU20810 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopO | BSU20820 | similar to transcription regulator (Xre family) | 🟦 | 🟦 | 🟦 | 🟦 |
| yopN | BSU20830 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopM | BSU20840 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopL | BSU20850 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopK | BSU20860 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopJ | BSU20870 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopI | BSU20880 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopH | BSU20890 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopG | BSU20900 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopF | BSU20910 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopE | BSU20920 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoyH | BSU20928 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoyI | BSU20929 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopD | BSU20930 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopC | BSU20940 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yopB | BSU20950 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yopA | BSU20960 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonX | BSU20970 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonV | BSU20980 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonU | BSU20990 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoyJ | BSU20999 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonT | BSU21000 | toxin | 🟦 | 🟦 | 🟦 | 🟦 |
| yonS | BSU21010 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonR | BSU21020 | similar to transcription regulator (Xre family) | 🟦 | 🟦 | 🟦 | 🟦 |
| yonP | BSU21030 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonO | BSU21040 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonN | BSU21050 | similar to HU-related DNA-binding protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yonK | BSU21060 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonJ | BSU21070 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonI | BSU21080 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonH | BSU21090 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonG | BSU21100 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonF | BSU21110 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonE | BSU21120 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonD | BSU21130 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonC | BSU21140 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonB | BSU21150 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yonA | BSU21160 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomZ | BSU21170 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomY | BSU21180 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomX | BSU21190 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomW | BSU21200 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomV | BSU21210 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomU | BSU21220 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| youA | BSU21229 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomT | BSU21230 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomS | BSU21240 | similar to phage-related lytic exoenzyme | 🟦 | 🟦 | 🟦 | 🟦 |
| yomR | BSU21250 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yomQ | BSU21260 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomP | BSU21270 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yomO | BSU21280 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomN | BSU21290 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomM | BSU21300 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yozP | BSU21310 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomL | BSU21320 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| youB | BSU21329 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomK | BSU21330 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomJ | BSU21340 | similar to phage-related immunity protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yomI | BSU21350 | cell wall hydrolase of the SP-beta prophage region | 🟦 | 🟦 | 🟦 | 🟦 |
| yomH | BSU21360 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomG | BSU21370 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomF | BSU21380 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomE | BSU21390 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yomD | BSU21400 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| blyA | BSU21410 | N-acetylmuramoyl-L-alanine amidase | 🟦 | 🟦 | 🟦 | 🟦 |
| bhlA | BSU21420 | holin-like protein | 🟦 | 🟦 | 🟦 | 🟦 |
| bhlB | BSU21430 | holin-like protein | 🟦 | 🟦 | 🟦 | 🟦 |
| bdbB | BSU21440 | thiol-disulfide oxidoreductase | 🟦 | 🟦 | 🟦 | 🟦 |
| yolJ | BSU21450 | sublancin S-glycosyltransferase | 🟦 | 🟦 | 🟦 | 🟦 |
| bdbA | BSU21460 | thiol-disulfide oxidoreductase | 🟦 | 🟦 | 🟦 | 🟦 |
| sunT | BSU21470 | sublancin 168 lantibiotic ABC transporter | 🟦 | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| sunA | BSU21480 | sublancin 168 lantibiotic antimicrobial precursor peptide | 🟦 | 🟦 | 🟦 | 🟦 |
| sunI | BSU21490 | bacteriocin producer immunity protein | 🟦 | 🟦 | 🟦 | 🟦 |
| uvrX | BSU21500 | UV-damage repair protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yolD | BSU21510 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yolC | BSU21520 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yolB | BSU21530 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yolA | BSU21540 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yokL | BSU21550 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yokK | BSU21560 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yokJ | BSU21570 | putative antitoxin | 🟦 | 🟦 | 🟦 | 🟦 |
| yokI | BSU21580 | putative toxin | 🟦 | 🟦 | 🟦 | 🟦 |
| yokH | BSU21590 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yoyK/1 | BSU21598 | part of the yoyK pseudogene | 🟦 | 🟦 | 🟦 | 🟦 |
| yoyK/2 | BSU21599 | part of the yoyK pseudogene | 🟦 | 🟦 | 🟦 | 🟦 |
| yokG | BSU21600 | similar to delta-endotoxin | 🟦 | 🟦 | 🟦 | 🟦 |
| yokF | BSU21610 | similar to micrococcal nuclease | 🟦 | 🟦 | 🟦 | 🟦 |
| yokE | BSU21620 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yokD | BSU21630 | similar to aminoglycoside N3'-acetyltransferase | 🟦 | 🟦 | 🟦 | 🟦 |
| yokC | BSU21640 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yokB | BSU21650 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yokA | BSU21660 | DNA recombinase, SP-beta prophage site-specific recombination factor A | 🟦 | 🟦 | 🟦 | 🟦 |
| ypqP | BSU21670 | similar to capsular polysaccharide biosynthesis, in B. subtilis 168 the gene is disrupted by the SP-beta prophage |  | 🟦 | 🟦 | 🟦 |
| msrB | BSU21680 | peptide methionine sulfoxide reductase |  | 🟦 | 🟦 | 🟦 |
| msrA | BSU21690 | peptide methionine sulfoxide reductase |  | 🟦 | 🟦 | 🟦 |
| ypoP | BSU21700 | similar to transcriptional regulator (MarR family) |  | 🟦 | 🟦 | 🟦 |
| ypnP | BSU21710 | putative damage inducible, Na+ driven multidrug efflux pump |  | 🟦 | 🟦 | 🟦 |
| ypmT | BSU21720 | unknown |  | 🟦 | 🟦 | 🟦 |
| ypmS | BSU21730 | unknown |  | 🟦 | 🟦 | 🟦 |
| ypmR | BSU21740 | unknown |  | 🟦 | 🟦 | 🟦 |
| sco | BSU21750 | accessory protein required for assembly of the Cu(A) center of cytochrome c oxidase caa3 |  |  |  |  |
| ypmP | BSU21760 | unknown |  |  |  |  |
| ilvA | BSU21770 | threonine dehydratase |  |  |  |  |
| yplP | BSU21780 | transcriptional activator (for SigL-dependent promoter) |  |  |  |  |
| yplQ | BSU21790 | similar to hemolysin III homolog |  |  |  |  |
| ypkP | BSU21800 | unknown |  |  |  |  |
| dfrA | BSU21810 | dihydrofolate reductase |  |  |  |  |
| thyB | BSU21820 | thymidylate synthase B |  |  |  |  |
| ypjQ | BSU21830 | similar to low temperature requirement C protein |  |  |  |  |
| ypjP | BSU21840 | unknown |  |  |  |  |
| ypiP | BSU21850 | unknown |  |  |  |  |
| brxA | BSU21860 | bacilliredoxin |  |  |  |  |
| ilvD | BSU21870 | dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylbutanoate, 2,3-dihydroxy-3-methylpentanoate) |  |  |  |  |
| ypgR | BSU21880 | unknown |  |  |  |  |
| ypgQ | BSU21890 | unknown |  |  |  |  |
| bsaA | BSU21900 | similar to glutathione peroxidase |  |  |  |  |
| metA | BSU21910 | homoserine O-succinyltransferase |  |  |  |  |
| ugtP | BSU21920 | UDP-glucose diacylglycerol glucosyltransferase, growth-rate dpendent inhibitor of cell division |  |  |  |  |
| cspD | BSU21930 | cold shock protein |  |  |  |  |
| degR | BSU21940 | regulation of degradative enzyme production |  |  |  |  |
| ypzA | BSU21950 | unknown |  |  |  |  |
| ypeQ | BSU21960 | unknown |  |  |  |  |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ypeP | BSU21970 | unknown | | | | |
| ypdP | BSU21980 | unknown | | | | |
| ypdQ | BSU21990 | similar to RNase HI | | | | |
| sspL | BSU22000 | small acid-soluble spore protein (minor SASP) | | | | |
| ypcP | BSU22010 | similar to DNA polymerase I | | | | |
| ypzF | BSU22019 | unknown | | | | |
| ypbS | BSU22020 | unknown | | | | |
| dynA | BSU22030 | dynamin-like protein, mediates membrane fusion | | | | |
| fbpC | | small protein, acts as RNA chaperone for fsrA | | | | |
| bpsB | BSU22040 | methyltransferase, involved in polyketide synthesis | | | | |
| bpsA | BSU22050 | type III polyketide synthase | | | | |
| pbuX | BSU22060 | xanthine transport in/out via proton symport | | | | |
| xpt | BSU22070 | xanthine phosphoribosyltransferase | | | | |
| ypwA | BSU22080 | carboxypeptidase, metalloprotease | | 🟦 | 🟦 | 🟦 |
| kdgT | BSU22090 | 2-keto-3-deoxygluconate permease | | 🟦 | 🟦 | 🟦 |
| kdgA | BSU22100 | 2-dehydro-3-deoxy-phosphogluconate aldolase | | 🟦 | 🟦 | 🟦 |
| kdgK | BSU22110 | 2-dehydro-3-deoxygluconokinase | | 🟦 | 🟦 | 🟦 |
| kdgR | BSU22120 | transcriptional repressor of the pectin utilization operon (LacI family) | | 🟦 | 🟦 | 🟦 |
| kduI | BSU22130 | 5-keto-4-deoxyuronate isomerase | | 🟦 | 🟦 | 🟦 |
| kduD | BSU22140 | 2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase | | 🟦 | 🟦 | 🟦 |
| ypvA | BSU22150 | similar to ATP-dependent helicase | | 🟦 | 🟦 | 🟦 |
| yptA | BSU22160 | unknown | | 🟦 | 🟦 | 🟦 |
| ypzG | BSU22169 | unknown | | 🟦 | 🟦 | 🟦 |
| ypsC | BSU22170 | similar to SAM-dependent 23S rRNA methyltransferase | | | | |
| rnpB | BSU_misc_RNA_35 | RNA component of RNase P | | | | |
| gpsB | BSU22180 | required for removal of PBP1 from the cell pole after completion of cell pole maturation | | | | |
| ypsA | BSU22190 | unknown | | 🟦 | 🟦 | 🟦 |
| cotD | BSU22200 | spore coat protein (inner) | | 🟦 | 🟦 | 🟦 |
| yprB | BSU22210 | unknown | | 🟦 | 🟦 | 🟦 |
| yprA | BSU22220 | similar to ATP-dependent helicase | | 🟦 | 🟦 | 🟦 |
| ypqE | BSU22230 | similar to PTS, EIIA component | | 🟦 | 🟦 | 🟦 |
| ypqA | BSU22240 | unknown | | 🟦 | 🟦 | 🟦 |
| yppG | BSU22250 | spore coat protein | | 🟦 | 🟦 | 🟦 |
| yppF | BSU22260 | unknown | | 🟦 | 🟦 | 🟦 |
| yppE | BSU22270 | unknown | | 🟦 | 🟦 | 🟦 |
| yppD | BSU22280 | unknown | | 🟦 | 🟦 | 🟦 |
| sspM | BSU22290 | small acid-soluble spore protein (minor SASP) | | 🟦 | 🟦 | 🟦 |
| yppC | BSU22300 | unknown | | | | |
| | | | | | | |
| recU | BSU22310 | DNA repair, homologous recombination and chromosome segregation | | | | |
| ponA | BSU22320 | penicillin-binding proteins 1A/1B | | | | |
| ypoC | BSU22330 | unknown | | | | |
| nth | BSU22340 | endonuclease III | | | | |
| dnaD | BSU22350 | initiation of chromosome replication | | | | |
| asnS | BSU22360 | asparagyl-tRNA synthetase | | | | |
| aspB | BSU22370 | aspartate transaminase | | | | |
| ypmB | BSU22380 | unknown | | | | |
| ypmA | BSU22390 | unknown | | | | |
| dinG | BSU22400 | ATP-dependent DNA helicase | | | | |
| panD | BSU22410 | aspartate 1-decarboxylase | | | | |
| panC | BSU22420 | pantothenate synthase | | | | |
| panB | BSU22430 | 3-methyl-2-oxobutanoate hydroxymethyltransferase | | | | |
| birA | BSU22440 | trigger enzyme: transcriptional repressor of the biotin operon / biotin-protein ligase | | | | |
| cca | BSU22450 | tRNA nucleotidyltransferase | | | | |

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| bshA | BSU22460 | L-malic acid glycosyltransferase, involved in bacillithiol synthesis | | | | |
| bshB1 | BSU22470 | N-acetylglucosamin-malate deacetylase, involved in bacillithiol synthesis (major enzyme) | | | | |
| mgsA | BSU22480 | methylglyoxal synthase | | | | |
| dapB | BSU22490 | dihydrodipicolinate reductase (NADPH) | | | | |
| ypjD | BSU22500 | putative pyrophosphatase | | | | |
| ypjC | BSU22510 | unknown | | | | |
| ypjB | BSU22520 | unknown | | | | |
| ypjA | BSU22530 | unknown | | | | |
| qcrC | BSU22540 | component of the cytochrome bc complex, cytochrome-c reductase | | | | |
| qcrB | BSU22550 | component of the cytochrome bc complex, cytochrome-c reductase | | | | |
| qcrA | BSU22560 | component of the cytochrome bc complex, cytochrome-c reductase | | | | |
| ypiF | BSU22570 | unknown | | | | |
| ypiB | BSU22580 | unknown | | | | |
| ypiA | BSU22590 | unknown | | | | |
| aroE | BSU22600 | 3-phosphoshikimate 1-carboxyvinyltransferase | | | | |
| tyrA | BSU22610 | prephenate dehydrogenase | | | | |
| hisC | BSU22620 | histidinol-phosphate aminotransferase / tyrosine and phenylalanine aminotransferase | | | | |
| trpA | BSU22630 | tryptophan synthase (alpha subunit) | | | | |
| trpB | BSU22640 | tryptophan synthase (beta subunit) | | | | |
| trpF | BSU22650 | phosphoribosylanthranilate isomerase | | | | |
| trpC | BSU22660 | indole-3-glycerol-phosphate synthase | | | | |
| trpD | BSU22670 | anthranilate phosphoribosyltransferase | | | | |
| trpE | BSU22680 | anthranilate synthase (subunit I) | | | | |
| aroH | BSU22690 | chorismate mutase (isozymes 1 and 2) | | | | |
| aroB | BSU22700 | 3-dehydroquinate synthase | | | | |
| aroF | BSU22710 | chorismate synthase | | | | |
| cheR | BSU22720 | MCPs methyltransferase | | | | |
| ndk | BSU22730 | nucleoside diphosphate kinase | | | | |
| hepT | BSU22740 | heptaprenyl diphosphate synthase component II | | | | |
| menH | BSU22750 | menaquinone biosynthesis methyltransferase | | | | |
| hepS | BSU22760 | heptaprenyl diphosphate synthase component I | | | | |
| mtrB | BSU22770 | tryptophan operon RNA-binding attenuation protein (TRAP) | | | | |
| folE | BSU22780 | GTP cyclohydrolase I | | | | |
| hbs | BSU22790 | non-specific DNA-binding protein Hbsu | | | | |
| spoIVA | BSU22800 | ATPase, spore coat morphogenetic protein, anchors the spore coat to the spore surface via SpoVM | | | | |
| yphF | BSU22810 | unknown | | | | |
| yphE | BSU22820 | unknown | | | | |
| gpsA | BSU22830 | glycerol-3-phosphate dehydrogenase (NAD) | | | | |
| engA | BSU22840 | GTPase essential for ribosome 50S subunit assembly | | | | |
| ypzH | BSU22849 | unknown | | | | |
| seaA | BSU22850 | involved in spore envelope assembly | | | | |
| yphA | BSU22860 | unknown | | | | |
| ypzI | BSU22869 | unknown | | | | |
| fni | BSU22870 | isopentenyl diphosphate isomerase, last (8th) step in the MEP pathway of isoprenoid biosynthesis | | | | |
| ypfD | BSU22880 | similar to ribosomal protein S1 | | | | |
| cmk | BSU22890 | cytidylate kinase (CMP, dCMP) | | | | |
| ypfB | BSU22900 | unknown | | | | |
| dgrA | BSU22910 | c-di-GMP receptor protein, inhibits motility at high c-di-GMP concentrations | | | | |
| ypeB | BSU22920 | unknown | | | | |
| sleB | BSU22930 | spore cortex-lytic enzyme | | | | |
| prsW | BSU22940 | protease, cleaves RsiW in the presence of antimicrobial peptides | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ypdA | BSU22950 | similar to thioredoxin reductase | | | | |
| gudB | BSU22960 | trigger enzyme: glutamate dehydrogenase (cryptic in 168 and derivatives) | | | | |
| ypbH | BSU22970 | putative adaptor protein | | | | |
| ypbG | BSU22980 | unknown | | | | |
| ypbF | BSU22990 | unknown | | | | |
| ypbE | BSU23000 | unknown | | | | |
| ypbD | BSU23010 | unknown | | | | |
| recQ | BSU23020 | ATP-dependent DNA helicase | | | | |
| ypbB | BSU23030 | unknown | | | | |
| fer | BSU23040 | ferredoxin | | | | |
| ribU | BSU23050 | riboflavin ECF transporter, S protein | | | | |
| ypzE | BSU23060 | unknown | | | | |
| serA | BSU23070 | phosphoglycerate dehydrogenase | | | | |
| aroC | BSU23080 | 3-dehydroquinate dehydratase | | | | |
| rsiX | BSU23090 | anti-SigX | | | | |
| sigX | BSU23100 | RNA polymerase ECF-type sigma factor SigX | | | | |
| resE | BSU23110 | two-component sensor kinase, regulation of aerobic and anaerobic respiration | | | | |
| resD | BSU23120 | two-component response regulator, regulation of aerobic and anaerobic respiration | | | | |
| resC | BSU23130 | part of heam translocase, required for cytochrome c synthesis | | | | |
| resB | BSU23140 | part of haem translocase, required for cytochrome c synthesis | | | | |
| resA | BSU23150 | extracytoplasmic thioredoxin, cytochrome c biogenesis, reduces disulfide bonds in apo-cytochrome prior to the attachment of heme | | | | |
| rluB | BSU23160 | pseudouridine synthase | | | | |
| spmB | BSU23170 | spore maturation protein (spore core dehydratation) | | | | |
| spmA | BSU23180 | spore maturation protein (spore core dehydratation) | | | | |
| dacB | BSU23190 | penicillin-binding protein 5, D-alanyl-D-alanine carboxypeptidase | | | | |
| ypuI | BSU23200 | rRNA pseudouridine 2633 synthase | | | | |
| scpB | BSU23210 | DNA segregation and condensation protein | | | | |
| scpA | BSU23220 | DNA segregation and condensation protein | | | | |
| ypuF | BSU23230 | SMC interacting protein | | | | |
| ribT | BSU23240 | reductase | | | | |
| ribH | BSU23250 | riboflavin synthase (beta subunit) | | | | |
| ribA | BSU23260 | GTP cyclohydrolase II/ 3,4-dihydroxy-2-butanone 4-phosphate synthase | | | | |
| ribE | BSU23270 | riboflavin synthase (alpha subunit) | | | | |
| ribD | BSU23280 | 5-amino-6-(5-phosphoribosylamino)uracil reductase | | | | |
| | BSU_misc_RNA_36 | FMN box | | | | |
| ypuD | BSU23300 | unknown | | | | |
| sipS | BSU23310 | signal peptidase I | | | | |
| ypzC | BSU23320 | unknown | | | | |
| ypzJ | BSU23328 | unknown | | | | |
| ypuC/1 | BSU23329 | part of the ypuC pseudogene | | | | |
| ypuC/2 | BSU23330 | part of the ypuC pseudogene | | | | |
| ypuB | BSU23340 | unknown | | | | |
| ypzD | BSU23350 | unknown | | | | |
| ppiB | BSU23360 | peptidyl-prolyl isomerase | | | | |
| ypuA | BSU23370 | unknown | | | | |
| lysA | BSU23380 | diaminopimelate decarboxylase | | | | |
| spoVAF | BSU23390 | essential for the uptake of the 1:1 chelate of pyridine-2,6-dicarboxylic acid (DPA(2,6)) and Ca(2+) into developing spores, required for spore maturation | | partial | partial | partial |
| spoVAEA | BSU23401 | stage V sporulation germinant protein | | | | |
| spoVAEB | BSU23402 | spore germinant protein | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| spoVAD | BSU23410 | essential for the uptake of the 1:1 chelate of pyridine-2,6-dicarboxylic acid (DPA(2,6)) and Ca(2+) into developing spores |  | 🟦 | 🟦 | 🟦 |
| spoVAC | BSU23420 | essential for the uptake of the 1:1 chelate of pyridine-2,6-dicarboxylic acid (DPA(2,6)) and Ca(2+) into developing spores |  | 🟦 | 🟦 | 🟦 |
| spoVAB | BSU23430 | essential for the uptake of the 1:1 chelate of pyridine-2,6-dicarboxylic acid (DPA(2,6)) and Ca(2+) into developing spores |  | 🟦 | 🟦 | 🟦 |
| spoVAA | BSU23440 | essential for the uptake of the 1:1 chelate of pyridine-2,6-dicarboxylic acid (DPA(2,6)) and Ca(2+) into developing spores |  | 🟦 | 🟦 | 🟦 |
| sigF | BSU23450 | RNA polymerase forespore-specific (early) sigma factor SigF |  | 🟦 | 🟦 | 🟦 |
| spoIIAB | BSU23460 | anti-SigF/ protein serine kinase |  | 🟦 | 🟦 | 🟦 |
| spoIIAA | BSU23470 | anti-anti-SigF |  | 🟦 | 🟦 | 🟦 |
| dacF | BSU23480 | penicillin-binding protein I, D-alanyl-D-alanine carboxypeptidase |  |  |  |  |
| pupG | BSU23490 | purine nucleoside phosphorylase |  |  |  |  |
| drm | BSU23500 | phosphopentomutase |  |  |  |  |
| ripX | BSU23510 | site-specific integrase/recombinase, partitioning of the terminus region after replication |  |  |  |  |
| yqzK | BSU23519 | unknown |  |  |  |  |
| fur | BSU23520 | transcription regulator of iron homoeostasis |  |  |  |  |
| spoIIM | BSU23530 | required for dissolution of the septal cell wall |  |  |  |  |
| yqkK | BSU23540 | unknown |  |  |  |  |
| mleA | BSU23550 | malic enzyme |  |  |  |  |
| mleN | BSU23560 | malate-H+/Na+-lactate antiporter |  |  |  |  |
| ansB | BSU23570 | L-aspartase |  |  |  |  |
| ansA | BSU23580 | L-asparaginase |  |  |  |  |
| ansR | BSU23590 | transcription repressor of the ansA-ansB operon |  |  |  |  |
| yqxK | BSU23600 | unknown |  |  |  |  |
| nudF | BSU23610 | involved in isopentenol (isoprenoid) biosynthesis |  |  |  |  |
| mciZ |  | FtsZ inhibtition peptide |  |  |  |  |
| yqkF | BSU23620 | similar to oxidoreductase |  |  |  |  |
| yqkE | BSU23630 | unknown |  |  |  |  |
| yqkD | BSU23640 | unknown |  |  |  |  |
| yqkC | BSU23650 | unknown |  |  |  |  |
| yqkB | BSU23660 | unknown |  |  |  |  |
| yqkA | BSU23670 | unknown |  |  |  |  |
| yqjZ | BSU23680 | unknown |  |  |  |  |
| yqjY | BSU23690 | probable acetyltransferase |  |  |  |  |
| yqjX | BSU23700 | unknown |  |  |  |  |
| polY2 | BSU23710 | translesion synthesis (TLS-) DNA polymerase Y2 |  |  |  |  |
| yqzH | BSU23720 | unknown |  |  |  |  |
| yqjV | BSU23730 | similar to multidrug resistance protein |  |  |  |  |
| yqjU | BSU23740 | unknown |  |  |  |  |
| yqjT | BSU23750 | unknown |  |  |  |  |
| coaA | BSU23760 | probable pantothenate kinase |  |  |  |  |
| dsdA | BSU23770 | D-serine deaminase |  |  |  |  |
| yqjQ | BSU23780 | similar to ketoacyl reductase |  |  |  |  |
| yqjP | BSU23790 | unknown |  |  |  |  |
| proI | BSU23800 | pyrroline-5-carboxylate reductase |  |  |  |  |
| yqjN | BSU23810 | similar to amino acid degradation |  |  |  |  |
| yqjM | BSU23820 | NADPH-dependent flavin oxidoreductase |  |  |  |  |
| yqjL | BSU23830 | general stress protein, putative hydrolase involved in oxidative stress resistance |  |  |  |  |
| rnz | BSU23840 | RNase Z |  |  |  |  |
| zwf | BSU23850 | glucose 6-phosphate dehydrogenase, pentose-phosphate pathway |  |  |  |  |
| gndA | BSU23860 | NADP-dependent phosphogluconate dehydrogenase |  |  |  |  |
| polY1 | BSU23870 | translesion synthesis (TLS-) DNA polymerase Y1 |  |  |  |  |
| mifM | BSU23880 | ribosome-nascent chain sensor of membrane protein biogenesis |  |  |  |  |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yidC2 | BSU23890 | Sec-independent membrane protein translocase | | | | |
| yqjF | BSU23900 | unknown | | | | |
| yqjE | BSU23910 | similar to tripeptidase | | | | |
| yqjD | BSU23920 | propionyl-CoA carboxylase | | | | |
| yqjC | BSU23930 | inner spore coat protein | | | | |
| yqjB | BSU23940 | unknown | | | | |
| yqjA | BSU23950 | unknown | | | | |
| artR | BSU23960 | high affinity arginine ABC transporter (ATP-binding protein) | | | | |
| artQ | BSU23970 | high affinity arginine ABC transporter (permease) | | | | |
| artP | BSU23980 | high affinity arginine ABC transporter (ATP-binding protein) | | | | |
| brxB | BSU23990 | bacilliredoxin | | | | |
| bmrU | BSU24000 | general stress protein, multidrug resistance protein | | | | |
| bmr | BSU24010 | general stress protein, multidrug-efflux transporter | | | | |
| bmrR | BSU24020 | general stress protein, transcriptional activator of the bmrU-bmr-bmrR operon | | | | |
| bkdB | BSU24030 | 2-oxoisovalerate dehydrogenase (E2 subunit, lipoamide acyltransferase) | | | | |
| bkdAB | BSU24040 | 2-oxoisovalerate dehydrogenase (E1 beta subunit) | | | | |
| bkdAA | BSU24050 | 2-oxoisovalerate dehydrogenase (E1 alpha subunit) | | | | |
| lpdV | BSU24060 | 2-oxoisovalerate dehydrogenase (E3 subunit, dihydrolipoamide dehydrogenase) | | | | |
| buk | BSU24070 | butyrate kinase | | | | |
| bcd | BSU24080 | valine dehydrogenase, isoleucine dehydrogenase, L-leucine dehydrogenase | | | | |
| ptb | BSU24090 | phosphate butyryltransferase | | | | |
| bkdR | BSU24100 | transcriptional activator of the ptb-bcd-buk-lpdV-bkdAA-bkdAB-bkdB operon | | | | |
| yqzF | BSU24110 | unknown | | | | |
| yqiQ | BSU24120 | methylisocitrate lyase | | | | |
| mmgE | BSU24130 | putative methyl-cis-aconitase | | | | |
| mmgD | BSU24140 | 2-methylcitrate synthase | | | | |
| mmgC | BSU24150 | acyl-CoA dehydrogenase | | | | |
| mmgB | BSU24160 | 3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) | | | | |
| mmgA | BSU24170 | degradative acetoacetyl-CoA thiolase | | | | |
| yqiK | BSU24180 | cytoplasmic glycerophosphodiester phosphodiesterase | | | | |
| yqiI | BSU24190 | secreted N-acetylmuramoyl-L-alanine amidase | | | | |
| yqiH | BSU24200 | extracellular lipoprotein | | | | |
| yqiG | BSU24210 | similar to NADH-dependent flavin oxidoreductase | | | | |
| spo0A | BSU24220 | phosphorelay regulator, initiation of sporulation | | | | |
| spoIVB | BSU24230 | serine protease, cleaves SpoIVFA, this results in pro-SigK processing/activation in the mother-cell | | 🟦 | 🟦 | 🟦 |
| recN | BSU24240 | DNA repair and genetic recombination | | | | |
| ahrC | BSU24250 | AhrC represses the genes for arginine biosynthesis and activates the genes for arginine catabolism. | | | | |
| yqxC | BSU24260 | similar to hemolysin-like | | | | |
| dxs | BSU24270 | 1-deoxyxylulose-5-phosphate synthase, first step in the MEP pathway of isoprenoid biosynthesis | | | | |
| yqiD | BSU24280 | geranyltransferase | | | | |
| yqiC | BSU24290 | similar to exodeoxyribonuclease VII (small subunit) | | | | |
| yqiB | BSU24300 | similar to exodeoxyribonuclease VII (large subunit) | | | | |
| folD | BSU24310 | methylenetetrahydrofolate dehydrogenase (NADP) | | | | |
| nusB | BSU24320 | probable transcription termination | | | | |
| yqhY | BSU24330 | unknown | | | | |
| accC | BSU24340 | acetyl-CoA carboxylase (biotin carboxylase subunit) | | | | |
| accB | BSU24350 | acetyl-CoA carboxylase (biotin carboxyl carrier subunit) | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| spoIIIAH | BSU24360 | component of the SpoIIIA-SpoIIQ type III secretion system residing in the forespore membrane | | | | |
| spoIIIAG | BSU24370 | component of the SpoIIIA-SpoIIQ type III secretion system residing in the forespore membrane | | | | 🟦 |
| spoIIIAF | BSU24380 | component of the SpoIIIA-SpoIIQ type III secretion system residing in the forespore membrane | | | | 🟦 |
| spoIIIAE | BSU24390 | component of the SpoIIIA-SpoIIQ type III secretion system residing in the forespore membrane | | | | 🟦 |
| spoIIIAD | BSU24400 | component of the SpoIIIA-SpoIIQ type III secretion system residing in the forespore membrane | | | | 🟦 |
| spoIIIAC | BSU24410 | component of the SpoIIIA-SpoIIQ type III secretion system residing in the forespore membrane | | | | 🟦 |
| spoIIIAB | BSU24420 | component of the SpoIIIA-SpoIIQ type III secretion system residing in the forespore membrane | | | | 🟦 |
| spoIIIAA | BSU24430 | AAA protease, required for SigG activation | | | | 🟦 |
| yqhV | BSU24440 | unknown | | | | 🟦 |
| efp | BSU24450 | elongation factor P | | | | |
| papA | BSU24460 | Xaa-Pro amino-peptidase | | | | |
| yqhS | BSU24470 | similar to 3-dehydroquinate dehydratase | | | | |
| yqhR | BSU24480 | unknown | | | | |
| yqhQ | BSU24490 | general stress protein, survival of stress conditions | | | | |
| yqhP | BSU24500 | unknown | | | | |
| yqhO | BSU24510 | unknown | | | | |
| mntR | BSU24520 | transcriptional regulator, (repression of mntH in high Mn(II) conditions, activation of mntA-mntB-mntC-mntD under low Mn(II) conditions) | | | | |
| lipM | BSU24530 | octanoyltransferase | | | | |
| yqhL | BSU24540 | membrane protein | | | | |
| gcvPB | BSU24550 | glycine decarboxylase (subunit 2) | | | | |
| gcvPA | BSU24560 | glycine decarboxylase (subunit 1) | | | | |
| gcvT | BSU24570 | aminomethyltransferase (glycine cleavage system protein T) | | | | |
| yqhH | BSU24580 | similar to SNF2 helicase | | | | |
| yqhG | BSU24590 | unknown | | | | |
| sinI | BSU24600 | antagonist of SinR | | | | |
| sinR | BSU24610 | transcriptional regulator of post-exponential-phase responses genes | | | | |
| tasA | BSU24620 | major component of biofilm matrix, forms amyloid fibers | | 🟦 | 🟦 | 🟦 |
| sipW | BSU24630 | signal peptidase I | | 🟦 | 🟦 | 🟦 |
| tapA | BSU24640 | TasA anchoring/assembly protein | | 🟦 | 🟦 | 🟦 |
| yqzG | BSU24650 | unknown | | | | |
| yqzE | BSU24660 | unknown | | | | |
| comGG | BSU24670 | DNA transport machinery, minor pseudopilin | | | | |
| comGF | BSU24680 | DNA transport machinery | | | | |
| comGE | BSU24690 | DNA transport machinery, minor pseudopilin | | | | |
| comGD | BSU24700 | DNA transport machinery, minor pseudopilin | | | | |
| comGC | BSU24710 | DNA uptake, major pseudopilin | | | | |
| comGB | BSU24720 | polytopic membrane protein, DNA transport machinery | | | | |
| comGA | BSU24730 | late competence gene, traffic ATPase | | | | |
| corA | BSU24740 | general stress protein, magnesium transporter | | | | |
| yqhB | BSU24750 | general stress protein, similar to hemolysin | | | | |
| rsbRD | BSU24760 | probably part of the stressosome | | | | |
| trnSL-Gln1 | | | | | | |
| mgsR | BSU24770 | transcriptional regulator of a subset of the SigB general stress regulon | | | | |
| yqgY | BSU24780 | unknown | | | | |
| yqgX | BSU24790 | unknown | | | | |
| yqgW | BSU24800 | unknown | | | | |
| yqgV | BSU24810 | unknown | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yqgU | BSU24820 | unknown | | | | |
| yqgT | BSU24830 | similar to gamma-D-glutamyl-L-diamino acid endopeptidase I | | | | |
| yqgS | BSU24840 | minor lipoteichoic acid synthase (stationary phase) | | | | |
| glcK | BSU24850 | glucose kinase (D-glucose:ATP) | | | | |
| yqgQ | BSU24860 | putative single-stranded nucleic acid binding protein | | | | |
| yqgP | BSU24870 | intramembrane protease | | | | |
| yqgO | BSU24880 | unknown | | | | |
| yqgN | BSU24890 | similar to 5-formyltetrahydrofolate cyclo-ligase | | | | |
| rpmGA | BSU24900 | ribosomal protein | | | | |
| yqgM | BSU24910 | unknown | | | | |
| yqgL | BSU24920 | unknown | | | | |
| yqzD | BSU24930 | unknown | | | | |
| yqzC | BSU24940 | unknown | | | | |
| pstBB | BSU24950 | phosphate ABC transporter (ATP-binding protein) | | | | |
| pstBA | BSU24960 | phosphate ABC transporter (ATP-binding protein) | | | | |
| pstA | BSU24970 | phosphate ABC transporter (permease) | | | | |
| pstC | BSU24980 | phosphate ABC transporter (permease) | | | | |
| pstS | BSU24990 | phosphate ABC transporter (binding protein) | | | | |
| pbpA | BSU25000 | penicillin-binding protein PBP 2A | | | | |
| yqgE | BSU25010 | unknown | | | | |
| sodA | BSU25020 | superoxide dismutase, general stress protein | | | | |
| yqgC | BSU25030 | unknown | | | | |
| yqgB | BSU25040 | unknown | | | | |
| yqgA | BSU25050 | unknown | | | | |
| yqfZ | BSU25060 | unknown | | | | |
| ispG | BSU25070 | similar to peptidoglycan acetylation, 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate synthase | | | | |
| yqfX | BSU25080 | unknown | | | | |
| yqfW | BSU25090 | unknown | | | | |
| zur | BSU25100 | transcriptional repressor, regulates zinc homeostasis | | | | |
| yqfU | BSU25110 | unknown | | | | |
| yqfT | BSU25120 | unknown | | | | |
| nfo | BSU25130 | type IV apurinic/apyrimidinic endonuclease | | | | |
| cshB | BSU25140 | DEAD-box RNA helicase | | | | |
| yqfQ | BSU25150 | late sporulation protein | | | | |
| ispH | BSU25160 | (E)-4-hydroxy-3-methylbut-2-enyl diphosphate reductase, 7th step in the MEP pathway of isoprenoid biosynthesis | | | | |
| yqfO | BSU25170 | unknown | | | | |
| trmK | BSU25180 | tRNA:m1A22 methyl transferase | | | | |
| cccA | BSU25190 | cytochrome c550 | | | | |
| sigA | BSU25200 | RNA polymerase major sigma factor SigA | | | | |
| dnaG | BSU25210 | DNA primase | | | | |
| antE | BSU25220 | dnaG overlapping gene of unknown function | | | | |
| yqxD | BSU25230 | unknown | | | | |
| yqfL | BSU25240 | Modulator of CcpN activity | | | | |
| ccpN | BSU25250 | transcriptional repressor of gluconeogenetic genes and of sr1. repression in the presence of glucose | | | | |
| glyS | BSU25260 | glycyl-tRNA synthetase (beta subunit) | | | | |
| glyQ | BSU25270 | glycyl-tRNA synthetase (alpha subunit) | | | | |
| recO | BSU25280 | mediator of RecA binding to ssDNA | | | | |
| yqzL | BSU25289 | unknown | | | | |
| era | BSU25290 | GTP-binding protein | | | | |
| cdd | BSU25300 | cytidine deaminase | | | | |
| dgkA | BSU25310 | undecaprenol kinase | | | | |
| yqfG | BSU25320 | unknown | | | | |
| yqfF | BSU25330 | unknown | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| phoH | BSU25340 | phosphate starvation-induced protein | | | | |
| yqfD | BSU25350 | SigE-dependent sporulation gene, similar to UDP-glucose 4-epimerase | | | | |
| yqfC | BSU25360 | sporulation protein | | | | |
| yqfB | BSU25370 | resistence protein (against sublancin) | | | | |
| floA | BSU25380 | resistence protein (against sublancin), accessory role in resistance to cefuroxime, second bacterial flottilin-like protein | | | | |
| yqeZ | BSU25390 | resistence protein (against sublancin), accessory role in resistance to cefuroxime, NfeD family protein | | | | |
| yqeY | BSU25400 | unknown | | | | |
| rpsU | BSU25410 | ribosomal protein S21 | | | | |
| yqeW | BSU25420 | phosphate transport in via three Na+ symporter | | | | |
| yqeV | BSU25430 | putative methylthiotransferase for ribosomal protein S12 | | | | |
| yqeU | BSU25440 | unknown | | | | |
| yqeT | BSU25450 | similar to ribosomal protein L11 methyltransferase | | | | |
| dnaJ | BSU25460 | heat-shock protein (activation of DnaK) | | | | |
| surC | | small RNA | | | | |
| dnaK | BSU25470 | class I heat-shock protein (molecular chaperone) | | | | |
| grpE | BSU25480 | heat-shock protein (activation of DnaK) | | | | |
| hrcA | BSU25490 | transcriptional repressor of class I heat-shock genes | | | | |
| hemN | BSU25500 | anaerobic coproporphyrinogen III oxidase | | | | |
| lepA | BSU25510 | GTP-binding protein | | | | |
| yqxA | BSU25520 | sporulation protein | | | | |
| spoIIP | BSU25530 | required for dissolution of the septal cell wall | | | | |
| gpr | BSU25540 | spore protease (degradation of SASPs) | | | | |
| rpsT | BSU25550 | ribosomal protein S20 | | | | |
| holA | BSU25560 | DNA polymerase III, delta subunit | | | | |
| yqzM | BSU25569 | unknown | | | | |
| comEC | BSU25570 | late competence operon required for DNA binding and uptake | | | | |
| comEB | BSU25580 | late competence protein required for DNA binding and uptake | | | | |
| comEA | BSU25590 | exogenous DNA-binding protein | | | | |
| comER | BSU25600 | non-essential gene for competence | | | | |
| yqeM | BSU25610 | unknown | | | | |
| yqeL | BSU25620 | ribosomal silencing factor | | | | |
| yqeK | BSU25630 | unknown | | | | |
| nadD | BSU25640 | nicotinamide-nucleotide adenylyltransferase | | | | |
| yqeI | BSU25650 | similar to predicted RNA-binding protein | | | | |
| aroD | BSU25660 | shikimate dehydrogenase | | | | |
| yqeH | BSU25670 | assembly/ stability of the 30S subunit of the ribosome, assembly of the 70S ribosome | | | | |
| yqeG | BSU25680 | unknown | | | | |
| sda | BSU25690 | developmental checkpoint protein, inhibits the autokinase activity of KinA and KinB | | | | |
| yqeF | BSU25700 | unknown | | 🟦 | 🟦 | 🟦 |
| cwlH | BSU25710 | N-acetylmuramoyl-L-alanine amidase | | 🟦 | 🟦 | 🟦 |
| yqeD | BSU25720 | unknown | | 🟦 | 🟦 | 🟦 |
| yqeC | BSU25730 | similar to 3-hydroxyisobutyrate dehydrogenase | | 🟦 | 🟦 | 🟦 |
| yqeB | BSU25740 | unknown | | 🟦 | 🟦 | 🟦 |
| nucB | BSU25750 | sporulation-specific extracellular nuclease | | 🟦 | 🟦 | 🟦 |
| spoIVCB | BSU25760 | sporulation-specific sigma factor (SigK) (N-terminal half), other part: spoIIIC | | 🟦 | 🟦 | 🟦 |
| spoIVCA | BSU25770 | site-specific DNA recombinase required for creating the sigK gene (excision of the skin element) | | 🟦 | 🟦 | 🟦 |
| arsC | BSU25780 | arsenate reductase | | 🟦 | 🟦 | 🟦 |
| arsB | BSU25790 | extrusion of arsenite | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcK | BSU25800 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| arsR | BSU25810 | arsenic resistance operon repressor | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcI | BSU25820 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| rapE | BSU25830 | response regulator aspartate phosphatase, dephosphorylates Spo0F-P, control of the phosphorelay | 🟦 | 🟦 | 🟦 | 🟦 |
| phrE | BSU25840 | response regulator aspartate phosphatase (RapE) regulator, control of the phosphorelay | 🟦 | 🟦 | 🟦 | 🟦 |
| yqzI | BSU25850 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcG | BSU25860 | toxin | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcF | BSU25870 | antitoxin | 🟦 | 🟦 | 🟦 | 🟦 |
| yqxJ | BSU25880 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqxI | BSU25890 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| cwlA | BSU25900 | N-acetylmuramoyl-L-alanine amidase | 🟦 | 🟦 | 🟦 | 🟦 |
| yqxH | BSU25910 | similar to holin | 🟦 | 🟦 | 🟦 | 🟦 |
| yqxG | BSU25920 | similar to phage-related lytic exoenzyme | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcE | BSU25930 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcD | BSU25940 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcC | BSU25950 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcB | BSU25960 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqcA | BSU25970 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbT | BSU25980 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbS | BSU25990 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbR | BSU26000 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbQ | BSU26010 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbP | BSU26020 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbO | BSU26030 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbN/1 | BSU26039 | part of the yqbN pseudogene | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbN/2 | BSU26040 | similar to phage-related protein, part of the yqbN pseudogene | 🟦 | 🟦 | 🟦 | 🟦 |
| txpA | BSU26050 | toxic peptide | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbM | BSU26060 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbK | BSU26075 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqzN | BSU26089 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbJ | BSU26090 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbI | BSU26100 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbH | BSU26110 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbG | BSU26120 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbF | BSU26130 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbE | BSU26140 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbD | BSU26150 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbC | BSU26160 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbB | BSU26170 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqbA | BSU26180 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaT | BSU26190 | similar to phage-related terminase | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaS | BSU26200 | similar to phage-related terminase | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaR | BSU26210 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaQ | BSU26220 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaP | BSU26230 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaO | BSU26240 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaN | BSU26250 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqzO | BSU26259 | unknown, Skin element | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaM | BSU26260 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaL | BSU26270 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaK | BSU26280 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaJ | BSU26290 | similar to phage-related protein | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaI | BSU26300 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaH | BSU26310 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaG | BSU26320 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yqdA | BSU26330 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaF | BSU26340 | similar to transcription regulator (Xre family) | 🟦 | 🟦 | 🟦 | 🟦 |
| sknR | BSU26350 | transcription repressor of the yqaF-yqdA-yqaG-yqaH-yqaI-yqaJ-yqaK-yqaL-yqaM-yqaN operon of the skin element | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaD | BSU26360 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaC | BSU26370 | unknown | 🟦 | 🟦 | 🟦 | 🟦 |
| yqaB | BSU26380 | similar to phage-related protein | 🟦 partial | 🟦 | 🟦 | 🟦 |
| spoIIIC | BSU26390 | RNA polymerase sporulation-specific sigma factor (SigK) (C-terminal half), other part: spoIVCB |  | 🟦 | 🟦 | 🟦 |
| yrkS | BSU26400 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrkR | BSU26410 | unknown |  |  |  |  |
| yrkQ | BSU26420 | two-component sensor kinase |  |  |  |  |
| yrkP | BSU26430 | two-component response regulator |  |  |  |  |
| yrkO | BSU26440 | unknown |  |  |  |  |
| yrkN | BSU26450 | unknown |  |  |  |  |
| yrkL | BSU26470 | similar to NAD(P)H oxidoreductase |  |  |  |  |
| yrkK | BSU26480 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrkJ | BSU26490 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrkI | BSU26500 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrkH | BSU26510 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrkF | BSU26530 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrkE | BSU26540 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrkD | BSU26550 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrzM | BSU26558 | unknown, putative pseudogene |  | 🟦 | 🟦 | 🟦 |
| yrzN | BSU26559 | unknown, putative pseudogene |  | 🟦 | 🟦 | 🟦 |
| yrkC | BSU26560 | mother cell-specific sporulation protein |  | 🟦 | 🟦 | 🟦 |
| yrkB | BSU26570 | unknown |  | 🟦 | 🟦 | 🟦 |
| bltR | BSU26580 | transcriptional regulator of the blt-bltD operon |  | 🟦 | 🟦 | 🟦 |
| blt | BSU26590 | spermidine-efflux transporter |  | 🟦 | 🟦 | 🟦 |
| bltD | BSU26600 | spermidine/ spermine acetyltransferase |  | 🟦 | 🟦 | 🟦 |
| yrkA | BSU26610 | similar to hemolysin-like |  | 🟦 | 🟦 | 🟦 |
| yrzO | BSU26619 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrdR | BSU26620 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrdQ | BSU26630 | similar to transcriptional regulator (LysR family) |  | 🟦 | 🟦 | 🟦 |
| trkA | BSU26640 | cation transport via proton symporter |  | 🟦 | 🟦 | 🟦 |
| czcD | BSU26650 | cation diffusion facilitator |  | 🟦 | 🟦 | 🟦 |
| yrdN | BSU26660 | unknown |  | 🟦 | 🟦 | 🟦 |
| gltR | BSU26670 | transcriptional regulator (LysR family) |  | 🟦 | 🟦 | 🟦 |
| yrdK | BSU26680 | unknown |  | 🟦 | 🟦 | 🟦 |
| brnQ | BSU26690 | branched-chain amino acid transporter |  | 🟦 | 🟦 | 🟦 |
| azlD | BSU26700 | branched-chain amino acid transport |  | 🟦 | 🟦 | 🟦 |
| azlC | BSU26710 | branched-chain amino acid transport |  | 🟦 | 🟦 | 🟦 |
| azlB | BSU26720 | transcriptional repressor of the azlB-azlC-azlD-brnQ-yrdK operon |  | 🟦 | 🟦 | 🟦 |
| yrdF | BSU26730 | similar to ribonuclease inhibitor |  | 🟦 | 🟦 | 🟦 |
| cypA | BSU26740 | cytochrome P450-like enzyme |  | 🟦 | 🟦 | 🟦 |
| yrdD/1 | BSU26748 | part of the yrdD pseudogene |  | 🟦 | 🟦 | 🟦 |
| yrdD/2 | BSU26749 | part of the yrdD pseudogene |  | 🟦 | 🟦 | 🟦 |
| yrdD/3 | BSU26750 | part of the yrdD pseudogene |  | 🟦 | 🟦 | 🟦 |
| yrdC | BSU26760 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrdB | BSU26770 | unknown |  | 🟦 | 🟦 | 🟦 |
| yrdA | BSU26780 | unknown |  | 🟦 | 🟦 | 🟦 |
| aadK | BSU26790 | aminoglycoside 6-adenylyltransferase |  | 🟦 | 🟦 | 🟦 |
| yrpB | BSU26800 | similar to 2-nitropropane dioxygenase |  | 🟦 | 🟦 | 🟦 |
| yrpC | BSU26810 | glutamate racemase |  | 🟦 | 🟦 | 🟦 |
| yrpD | BSU26820 | unknown |  | 🟦 | 🟦 | 🟦 |
| zinT | BSU26830 | unknown |  | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| sigZ | BSU26840 | RNA polymerase ECF-type sigma factor SigZ | | | | |
| yrpG | BSU26850 | similar to sugar-phosphate dehydrogenase | | | | |
| yraO | BSU26860 | citrate uptake via proton symport | | | | |
| yraN | BSU26870 | similar to transcriptional regulator (LysR family) | | 🟦 | 🟦 | 🟦 |
| yraM | BSU26880 | unknown | | 🟦 | 🟦 | 🟦 |
| csn | BSU26890 | chitosanase | | 🟦 | 🟦 | 🟦 |
| yraL | BSU26900 | unknown | | 🟦 | 🟦 | 🟦 |
| yraK | BSU26910 | unknown | | 🟦 | 🟦 | 🟦 |
| yraJ | BSU26920 | unknown | | 🟦 | 🟦 | 🟦 |
| yraI | BSU26930 | unknown | | 🟦 | 🟦 | 🟦 |
| yraH | BSU26940 | unknown | | 🟦 | 🟦 | 🟦 |
| yraG | BSU26950 | forespore-specific sporulation protein,similar to spore coat protein | | 🟦 | 🟦 | 🟦 |
| yraF | BSU26960 | forespore-specific sporulation protein, similar to spore coat protein | | 🟦 | 🟦 | 🟦 |
| adhB | BSU26970 | forespore-specific protein, similar to alcohol dehydrogenase | | 🟦 | 🟦 | 🟦 |
| yraE | BSU26980 | forespore-specific sporulation protein, similar to spore coat protein | | 🟦 | 🟦 | 🟦 |
| yraD | BSU26990 | forespore-specific sporulation protein, similar to spore coat protein | | 🟦 | 🟦 | 🟦 |
| adhR | BSU27000 | transcriptional activator of adhA-yraA | | 🟦 | 🟦 | 🟦 |
| yrzP | BSU27009 | unknown, putative pseudogene | | 🟦 | 🟦 | 🟦 |
| adhA | BSU27010 | thiol-dependent aldehyde dehydrogenase, repair of damaged thiol-containing proteins | | 🟦 | 🟦 | 🟦 |
| yraA | BSU27020 | general stress protein, degradation of damaged thiol-containing proteins, glyoxalase III-like enzyme | | 🟦 | 🟦 | 🟦 |
| sacC | BSU27030 | levanase | | 🟦 | 🟦 | 🟦 |
| levG | BSU27040 | fructose-specific phosphotransferase system, EIID component of the PTS | | 🟦 | 🟦 | 🟦 |
| levF | BSU27050 | fructose-specific phosphotransferase system, EIIC component of the PTS | | 🟦 | 🟦 | 🟦 |
| levE | BSU27060 | trigger enzyme: fructose-specific phosphotransferase system, EIIB component of the PTS | | 🟦 | 🟦 | 🟦 |
| levD | BSU27070 | fructose-specific phosphotransferase system, EIIA component of the PTS | | 🟦 | 🟦 | 🟦 |
| levR | BSU27080 | transcriptional activator of the levD-levE-levF-levG-sacC operon | | 🟦 | 🟦 | 🟦 |
| aapA | BSU27090 | amino acid permease | | | | |
| yrhP | BSU27100 | similar to efflux protein | | | | |
| yrhO | BSU27110 | similar to cyclodextrin metabolism | | | | |
| sigV | BSU27120 | RNA polymerase ECF-type sigma factor SigV | | | | |
| rsiV | BSU27130 | anti-sigma factor to SigV | | | | |
| oatA | BSU27140 | O-acetyl transferase | | | | |
| yrhK | BSU27150 | unknown | | | | 🟦 |
| yrhJ | BSU27160 | similar to cytochrome P450 / NADPH-cytochrome P450 reductase | | | | 🟦 |
| fatR | BSU27170 | transcriptional repressor of the fatR-yrhJ operon | | | | 🟦 |
| yrhH | BSU27180 | similar to methyltransferase | | | | 🟦 |
| yrzI | BSU27190 | unknown | | | | 🟦 |
| yrhG | BSU27200 | similar to formate dehydrogenase | | | | 🟦 |
| yrhF | BSU27210 | unknown | | | | 🟦 |
| yrhE | BSU27220 | unknown, similar to formate dehydrogenase | | | | 🟦 |
| yrhD | BSU27230 | unknown | | | | 🟦 |
| yrhC | BSU27240 | unknown | | | | 🟦 |
| mccB | BSU27250 | cystathionine lyase/ homocysteine gamma-lyase | | | | |
| mccA | BSU27260 | O-acetylserine-thiol-lyase | | | | |
| mtnN | BSU27270 | methylthioadenosine nucleosidase | | | | |
| yrrT | BSU27280 | putative AdoMet-dependent methyltransferase | | | | |
| yrzA | BSU27290 | unknown | | | | |
| yrrS | BSU27300 | sporulation protein | | | | |
| pbpI | BSU27310 | sporulation-specific penicillin-binding protein 4b | | | | |
| greA | BSU27320 | transcription elongation factor | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| udk | BSU27330 | uridine kinase | | | | |
| yrrO | BSU27340 | similar to protease | | | | |
| yrrN | BSU27350 | similar to protease | | | | |
| yrrM | BSU27360 | similar to caffeoyl-CoA O-methyltransferase | | | | |
| yrrL | BSU27370 | similar to folate metabolism | | | | |
| yrzB | BSU27380 | unknown | | | | |
| yrrK | BSU27390 | unknown | | | | |
| yrzL | BSU27400 | unknown | | | | |
| alaS | BSU27410 | alanine-tRNA synthetase | | | | |
| yrrI | BSU27420 | unknown | | | | |
| glnQ | BSU27430 | glutamine ABC transporter (ATP-binding protein) , | | | | |
| glnH | BSU27440 | glutamine ABC transporter (binding protein) | | | | |
| glnM | BSU27450 | glutamine ABC transporter (membrane protein) | | | | |
| glnP | BSU27460 | glutamine ABC transporter (membrane protein) | | | | |
| yrzQ | BSU27468 | unknown | | | | |
| yrzR | BSU27469 | unknown | | | | |
| yrrD | BSU27470 | forespore-specific sporulation protein | | | | |
| recD2 | BSU27480 | 5'-3' DNA helicase replication fork progression | | | | |
| yrrB | BSU27490 | unknown | | | | |
| trmU | BSU27500 | tRNA (5-methylaminomethyl-2-thiouridylate) methyltransferase | | | | |
| yrvO | BSU27510 | cysteine desulfurase | | | | |
| cymR | BSU27520 | pleiotropic regulator of sulphur metabolism | | | | |
| yrvN | BSU27530 | unknown | | | | |
| yrvM | BSU27540 | similar to E. coli enzyme that catalyzes ATP-dependent dehydration of N6-threonylcarbamoyladenosine (t6A) | | | | |
| bsrA | BSU_misc_RNA_41 | 6S RNA | | | | |
| aspS | BSU27550 | aspartyl-tRNA synthetase | | | | |
| hisS | BSU27560 | histidyl-tRNA synthetase | | | | |
| yrzK | BSU27570 | unknown | | | | |
| yrvJ | BSU27580 | similar to N-acetylmuramoyl-L-alanine amidase | | | | |
| dtd | BSU27590 | D-aminoacyl-tRNA deacylase | | | | |
| relA | BSU27600 | GTP pyrophosphokinase (stringent response) | | | | |
| apt | BSU27610 | adenine phosphoribosyltransferase, universally conserved protein | | | | |
| yrvE | BSU27620 | similar to single-strand DNA-specific exonuclease | | | | |
| yrvD | BSU27630 | unknown | | | | |
| yrvC | BSU27640 | unknown | | | | |
| secDF | BSU27650 | preprotein translocase subunit (ATPase) | | | | |
| comN | BSU27660 | mediates post-transcriptional control of comE operon expression | | | | |
| spoVB | BSU27670 | involved in spore cortex synthesis | | | | |
| yrbG | BSU27680 | unknown | | | | |
| yrzE | BSU27690 | unknown | | | | |
| yrbF | BSU27700 | unknown | | | | |
| tgt | BSU27710 | tRNA-guanine transglycosylase | | | | |
| yrzS | BSU27729 | unknown | | | | |
| ruvB | BSU27730 | Holliday junction DNA helicase | | | | |
| ruvA | BSU27740 | Holliday junction DNA helicase | | | | |
| bofC | BSU27750 | general stress protein, controls processing of pro-SigK by SpoIVFB | | | | |
| csbX | BSU27760 | general stress protein | | | | |
| yrbE | BSU27770 | similar to dehydrogenase | | | | |
| yrzF | BSU27785 | unknown | | | | |
| yrzH | BSU27800 | unknown | | | | |
| yrzT | BSU27809 | unknown | | | | |
| yrbD | BSU27810 | sodium/proton-dependent alanine transporter | | | | |
| yrbC | BSU27820 | similar to spore cortex protein | | | | |
| coxA | BSU27830 | spore cortex protein | | | | |
| safA | BSU27840 | morphogenetic protein associated with SpoVID | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| nadA | BSU27850 | quinolinate synthetase | | | | |
| nadC | BSU27860 | nicotinate-nucleotide diphosphorylase (carboxylating) | | | | |
| nadB | BSU27870 | L-aspartate oxidase | | | | |
| nifS | BSU27880 | cysteine desulfurase, required for NAD biosynthesis | | | | |
| nadR | BSU27890 | transcriptional repressor of genes involved in NAD biosynthesis | | | | |
| pheA | BSU27900 | prephenate dehydratase | | | | |
| pheB | BSU27910 | chorismate mutase | | | | |
| obg | BSU27920 | GTP-binding protein involved in initiation of sporulation | | | | |
| spo0B | BSU27930 | sporulation initiation phosphotransferase of the phosphorelay | | | | |
| rpmA | BSU27940 | ribosomal protein L27 | | | | |
| ysxB | BSU27950 | unknown | | | | |
| rplU | BSU27960 | ribosomal protein L21 | | | | |
| | | | | | | |
| spoIVFB | BSU27970 | intramembrane metalloprotease, processing of pro-sigma-K to active SigK | | | | |
| spoIVFA | BSU27980 | inhibitor of SpoIVFB metalloprotease | | | | |
| minD | BSU27990 | cell-division inhibitor (septum placement) | | | | |
| minC | BSU28000 | cell-division inhibitor (septum placement), destabilizes FtsZ-rings at new cell poles | | | | |
| mreD | BSU28010 | MreD is a cell shape determining protein and is associated with the MreB cytoskeleton in B. subtilis | | | | |
| mreC | BSU28020 | MreC is a cell shape determining protein and is associated with the MreB cytoskeleton in B. subtilis and | | | | |
| mreB | BSU28030 | cell-shape determining protein | | | | |
| radC | BSU28040 | probable DNA repair protein | | | | |
| maf | BSU28050 | cell division inhibitor in competent cells, blocks septation during the escape from competence | | | | |
| spoIIB | BSU28060 | spatial and temporal regulation of the dissolution of septal peptidoglycan during engulfment | | | | |
| comC | BSU28070 | late competence gene required for processing and translocation of ComGC, ComGD, ComGE and ComGG | | | | |
| folC | BSU28080 | folyl-polyglutamate synthetase | | | | |
| valS | BSU28090 | valyl-tRNA synthetase | | | | |
| yszA | BSU28099 | unknown | | | | |
| ysxE | BSU28100 | inner spore coat protein | | | | |
| | | | | | | |
| spoVID | BSU28110 | spore coat morphogenetic protein, promotes encasement of the spore | | | | |
| hemL | BSU28120 | glutamate-1-semialdehyde aminotransferase | | | | |
| hemB | BSU28130 | porphobilinogen synthase | | | | |
| hemD | BSU28140 | uroporphyrinogen-III synthase | | | | |
| hemC | BSU28150 | hydroxymethylbilane synthase | | | | |
| hemX | BSU28160 | negative effector of the concentration of HemA | | | | |
| hemA | BSU28170 | glutamyl-tRNA reductase | | | | |
| ysxD | BSU28180 | unknown | | | | |
| ysxC | BSU28190 | assembly of the 50S subunit of the ribosome | | | | |
| lonA | BSU28200 | class III heat-shock ATP-dependent protease | | | | |
| lonB | BSU28210 | Lon-like ATP-dependent protease | | | | |
| | | | | | | |
| clpX | BSU28220 | ATP-dependent Clp protease ATP-binding subunit (class III heat-shock protein) | | | | |
| tig | BSU28230 | trigger factor (prolyl isomerase) | | | | |
| ysoA | BSU28240 | unknown | | | | |
| leuD | BSU28250 | 3-isopropylmalate dehydratase (small subunit) | | | | |
| leuC | BSU28260 | 3-isopropylmalate dehydratase (large subunit) | | | | |
| leuA | BSU28280 | 2-isopropylmalate synthase | | | | |
| ilvC | BSU28290 | ketol-acid reductoisomerase (2,3-dihydroxy-3-methylbutanoate, 2-acetolactate) | | | | |
| ilvH | BSU28300 | acetolactate synthase (small subunit) | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ilvB | BSU28310 | acetolactate synthase (large subunit) | | | | |
| ysnD | BSU28320 | inner spore coat protein | | | | |
| ysnE | BSU28330 | similar to acetyltransferase | | | | |
| ysnF | BSU28340 | general stress protein, survival of ethanol stress | | | | |
| trnSL-Arg2 | | | | | | |
| ysnB | BSU28350 | unknown | | | | |
| ysnA | BSU28360 | ITPase | | | | |
| rph | BSU28370 | RNase PH | | | | |
| gerM | BSU28380 | germination (cortex hydrolysis) and sporulation | | | | |
| racE | BSU28390 | glutamate racemase | | | | |
| ysmB | BSU28400 | similar to transcriptional regulator (MarR family) | | | | |
| gerE | BSU28410 | transcriptional regulator (repressor or activator) of a subset of sigma-K-dependent late spore coat genes | | | | |
| ysmA | BSU28420 | unknown | | | | |
| sdhB | BSU28430 | succinate dehydrogenase | | | | |
| sdhA | BSU28440 | succinate dehydrogenase (flavoprotein subunit) | | | | |
| sdhC | BSU28450 | succinate dehydrogenase(cytochrome b558 subunit) | | | | |
| yslB | BSU28460 | unknown | | | | |
| lysC | BSU28470 | aspartokinase II (alpha and beta subunits) | | | | |
| | BSU_misc_RNA_46 | L box | | | | |
| uvrC | BSU28490 | excinuclease ABC (subunit C) | | | | |
| trxA | BSU28500 | antioxidative action by facilitating the reduction of other proteins by cysteine thiol-disulfide exchange | | | | |
| abf2 | BSU28510 | alpha-L-arabinofuranosidase | | | | |
| etfA | BSU28520 | electron transfer flavoprotein (alpha subunit) | | | | |
| etfB | BSU28530 | electron transfer flavoprotein (beta subunit) | | | | |
| fadB | BSU28540 | 3-hydroxyacyl-CoA dehydratase | | | | |
| fadR | BSU28550 | transcriptional repressor, regulation of fatty acid degradation | | | | |
| lcfA | BSU28560 | long chain acyl-CoA synthetase | | | | |
| yshE | BSU28570 | unknown | | | | |
| mutSB | BSU28580 | probable DNA mismatch repair protein | | | | |
| polX | BSU28590 | DNA polymerase X, involved in DNA repair | | | | |
| yshB | BSU28600 | unknown | | | | |
| zapA | BSU28610 | positive modulator of FtsZ Z ring assembly and stability | | | | |
| rnhC | BSU28620 | RNase HIII, endoribonuclease | | | | |
| pheT | BSU28630 | phenylalanyl-tRNA synthetase (beta subunit) | | | | |
| pheS | BSU28640 | phenylalanyl-tRNA synthetase (alpha subunit), universally conserved protein | | | | |
| ysgA | BSU28650 | similar to rRNA methylase | | | | |
| sspI | BSU28660 | small acid-soluble spore protein (minor), SASP | | 🟦 | 🟦 | 🟦 |
| ysfB | BSU28670 | unknown | | 🟦 | 🟦 | 🟦 |
| ysfC | BSU28680 | unknown | | 🟦 | 🟦 | 🟦 |
| ysfD | BSU28690 | similar to glycolate oxidase subunit | | 🟦 | 🟦 | 🟦 |
| ysfE | BSU28700 | unknown | | 🟦 | 🟦 | 🟦 |
| cstA | BSU28710 | putative peptide transporter, carbon starvation-induced protein | | 🟦 | 🟦 | 🟦 |
| abfA | BSU28720 | alpha-L-arabinofuranosidase | | 🟦 | 🟦 | 🟦 |
| araQ | BSU28730 | L-arabinose ABC transporter (integral membrane protein) | | 🟦 | 🟦 | 🟦 |
| araP | BSU28740 | L-arabinose ABC transporter (integral membrane protein) | | 🟦 | 🟦 | 🟦 |
| araN | BSU28750 | L-arabinose ABC transporter (sugar-binding protein) | | 🟦 | 🟦 | 🟦 |
| araM | BSU28760 | glycerol-1-phosphate dehydrogenase, L-arabinose operon | | 🟦 | 🟦 | 🟦 |
| araL | BSU28770 | sugar phosphate phosphatase, L-arabinose operon | | 🟦 | 🟦 | 🟦 |
| araD | BSU28780 | L-ribulose-phosphate 4-epimerase | | 🟦 | 🟦 | 🟦 |
| araB | BSU28790 | L-ribulokinase | | 🟦 | 🟦 | 🟦 |
| araA | BSU28800 | L-arabinose isomerase | | 🟦 | 🟦 | 🟦 |
| abnA | BSU28810 | endo-1,5-alpha-L-arabinosidase | | 🟦 | 🟦 | 🟦 |
| ysdC | BSU28820 | similar to endo-1,4-beta-glucanase | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ysdA | BSU28840 | unknown | | | | |
| rplT | BSU28850 | ribosomal protein L20 | | | | |
| rpmI | BSU28860 | ribosomal protein L35 | | | | |
| infC | BSU28870 | translation initiation factor IF-3 | | | | |
| yscB | BSU28890 | unknown | | | | |
| ysbB | BSU28900 | putative peptidoglycan hydrolase, probably involved in cell wall turnover | | | | |
| ysbA | BSU28910 | putative anti-holin | | | | |
| lytT | BSU28920 | two-component response regulator, regulation of the rate of autolysis | | | | |
| lytS | BSU28930 | two-component sensor kinase, regulation of rate of autolysis | | | | |
| ysaA | BSU28940 | unknown | | | | |
| thrS | BSU28950 | threonyl-tRNA synthetase (major) | | | | |
| ytxC | BSU28960 | unknown | | | | |
| ytxB | BSU28970 | unknown | | | | |
| dnaI | BSU28980 | primosome component (helicase loader) | | | | |
| dnaB | BSU28990 | initiation of chromosome replication/ membrane attachment protein | | | | |
| ytcG | BSU29000 | putative negative regulator of transcription of ribonucleotide reductase nrd genes and operons | | | | |
| speD | BSU29010 | S-adenosylmethionine decarboxylase | | | | |
| gapB | BSU29020 | glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent, gluconeogenic enzyme | | | | |
| ytcD | BSU29030 | MarR/DUF24-family transcription regulator | | | | |
| ytbD | BSU29040 | similar to antibiotic resistance protein | | | | |
| ytbE | BSU29050 | putative aldo/keto reductase, may be involved in detoxification | | | | |
| ytaG | BSU29060 | dephospho-CoA kinase | | | | |
| ytaF | BSU29070 | sporulation protein | | | | |
| mutM | BSU29080 | formamidopyrimidine-DNA glycosidase | | | | |
| polA | BSU29090 | DNA polymerase I | | | | |
| phoR | BSU29100 | two-component sensor kinase, regulation of phosphate metabolism | | | | |
| phoP | BSU29110 | two-component response regulator, regulation of phosphate metabolism | | | | |
| mdh | BSU29120 | malate dehydrogenase | | | | |
| icd | BSU29130 | isocitrate dehydrogenase | | | | |
| citZ | BSU29140 | citrate synthase | | | | |
| ytwI | BSU29150 | unknown | | | | |
| ytvI | BSU29160 | sporulation protein | | | | |
| ytzA | BSU29170 | unknown | | | | |
| pyk | BSU29180 | pyruvate kinase, glycolytic enzyme | | | | |
| pfkA | BSU29190 | phosphofructokinase, glycolytic enzyme | | | | |
| accA | BSU29200 | acetyl-CoA carboxylase (alpha subunit) | | | | |
| accD | BSU29210 | acetyl-CoA carboxylase (beta subunit) | | | | |
| ytsJ | BSU29220 | malic enzyme | | | | |
| dnaE | BSU29230 | DNA polymerase III (alpha subunit) | | | | |
| ytrH | BSU29239 | sporulation protein | | | | |
| ytrI | BSU29240 | spore cortex formation | | | | |
| ytzJ | BSU29249 | unknown | | | | |
| nrnA | BSU29250 | oligoribonuclease (nanoRNase), 3',5'-bisphosphate nucleotidase | | | | |
| ytpI | BSU29260 | unknown | | | | |
| ytoI | BSU29270 | unknown | | | | |
| ytnM | BSU29280 | unknown | | | | |
| sndA | BSU29290 | sulphur compound N-deacetylase, required for the conversion of S-methyl-cysteine to cysteine | | | | |
| ribR | BSU29300 | cryptic riboflavin kinase, binds leader (RFN) rib operon mRNA, may have a regulatory role | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| cmoJ | BSU29310 | alkylmonooxygenase, required for the conversion of S-methyl-cysteine to cysteine | | | | |
| cmoI | BSU29320 | required for the conversion of S-methyl-cysteine to cysteine | | | | |
| cmoO | BSU29330 | monooxygenase, required for the conversion of S-methyl-cysteine to cysteine | | | | |
| tcyN | BSU29340 | cystine ABC transporter (ATP-binding protein) | | | | |
| tcyM | BSU29350 | cystine ABC transporter (permease) | | | | |
| tcyL | BSU29360 | cystine ABC transporter (permease) | | | | |
| tcyK | BSU29370 | cystine ABC transporter (binding protein) | | | | |
| tcyJ | BSU29380 | cystine ABC transporter (binding protein) | | | | |
| ascR | BSU29400 | alkyl-sulphur catabolism regulator | | | | |
| ytkL | BSU29410 | general stress protein | | | | |
| ytkK | BSU29420 | similar to 3-oxoacyl- acyl-carrier protein reductase | | | | |
| ytzD | BSU29430 | unknown | | | | |
| argH | BSU29440 | argininosuccinate lyase | | | | |
| argG | BSU29450 | argininosuccinate synthase, reversible | | | | |
| moaB | BSU29460 | molybdopterin precursor biosynthesis | | | | |
| ackA | BSU29470 | acetate kinase | | | | |
| ytxK | BSU29480 | unknown | | | | |
| tpx | BSU29490 | probable thiol peroxidase | | | | |
| gerW | BSU29500 | germination protein, essential for germination in response to L-alanine | | | | |
| ytfI | BSU29510 | sporulation protein | | | | |
| yteJ | BSU29520 | stress protein | | | | |
| sppA | BSU29530 | signal peptide peptidase required for efficient processing of pre-proteins | | | | |
| ytdI | BSU29540 | inorganic polyphosphate/ATP-NAD kinase | | | | |
| ytcJ | BSU29550 | unknown | | | | |
| ytcI | BSU29560 | similar to acetate-CoA ligase | | | | |
| sspA | BSU29570 | small acid-soluble spore protein (major alpha-type SASP) | | | | |
| thiI | BSU29580 | sulfuryl transferase, biosynthesis of 4-thiouridine in tRNA | | | | |
| nifZ | BSU29590 | cysteine desulfurase, biosynthesis of 4-thiouridine in tRNA | | | | |
| braB | BSU29600 | branched-chain amino acid transporter | | | | |
| ezrA | BSU29610 | negative regulator of FtsZ ring formation | | | | |
| hisJ | BSU29620 | histidinol phosphate phosphatase | | | | |
| refZ | BSU29630 | regulator of FtsZ, facilitates switch from medial to polar FtsZ ring placement during sporulation | | | | |
| ytsP | BSU29640 | unknown | | | | |
| dgcP | BSU29650 | diguanylate cyclase | | | | |
| rpsD | BSU29660 | ribosomal protein S4 | | | | |
| tyrS | BSU29670 | tyrosly-tRNA synthetase (major) | | | | |
| ytzK | BSU29679 | unknown | | | | |
| acsA | BSU29680 | acetyl-CoA synthetase | | | | |
| acuA | BSU29690 | protein acetylase for the control of AcsA activity | | | | |
| acuB | BSU29700 | unknown | | | | |
| acuC | BSU29710 | protein deacetylase for the control of AcsA activity | | | | |
| motS | BSU29720 | Na+-coupled MotP-MotS flagellar stator | | | | |
| motP | BSU29730 | Na+-coupled MotP-MotS flagellar stator | | | | |
| ccpA | BSU29740 | Carbon catabolite control protein A | | | | |
| aroA | BSU29750 | 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase / chorismate mutase-isozyme 3 | | | | |
| ytxJ | BSU29760 | general stress protein | | | | |
| ytxH | BSU29770 | general stress protein | | | | |
| ytxG | BSU29780 | general stress protein | | | | |
| murC | BSU29790 | UDP-N-acetylmuramoyl-L-alanine synthetase | | | | |
| sftA | BSU29805 | DNA translocase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ytpR | BSU29820 | similar to Phe-tRNA synthetase (beta subunit) | | | | |
| ytpQ | BSU29830 | unknown | | | | |
| ytpP | BSU29840 | similar to thioredoxin H1 | | | | |
| ytoQ | BSU29850 | unknown | | | | |
| ytoP | BSU29860 | similar to endo-1,4-beta-glucanase | | | | |
| ytzB | BSU29870 | unknown | | | | |
| malS | BSU29880 | malate dehydrogenase (decarboxylating) | | | | |
| ytnP | BSU29890 | unknown | | | | |
| trmB | BSU29900 | tRNA (m7G46) methyltransferase | | | | |
| ytzH | BSU29910 | unknown | | | | 🟦 |
| ytmP | BSU29920 | unknown | | | | 🟦 |
| amyX | BSU29930 | pullulanase (debranching enzyme) | | | | 🟦 |
| ytlR | BSU29940 | unknown | | | | 🟦 |
| ytlQ | BSU29950 | unknown | | | | 🟦 |
| ytkP | BSU29970 | similar to cysteine synthase | | | | 🟦 |
| ytjP | BSU29980 | similar to Xaa-His dipeptidase | | | | 🟦 |
| pbuO | BSU29990 | similar to hypoxanthine/guanine permease PbuG | | | | 🟦 |
| ythQ | BSU30000 | similar to ABC transporter (membrane protein) | | | | 🟦 |
| ythP | BSU30010 | similar to ABC transporter (ATP-binding protein) | | | | 🟦 |
| ytzE | BSU30020 | similar to transcriptional regulator (DeoR family) | | | | 🟦 |
| ytzG | BSU30035 | similar to 16S pseudouridylate synthase | | | | 🟦 |
| murJ | BSU30050 | Lipid II flippase | | | | 🟦 |
| ytfP | BSU30060 | unknown | | | | 🟦 |
| opuD | BSU30070 | glycine betaine transporter | | | | 🟦 |
| yteV | BSU30080 | sporulation protein | | | | 🟦 |
| yteU | BSU30090 | unknown | | | | 🟦 |
| yteT | BSU30100 | unknown | | | | 🟦 |
| yteS | BSU30110 | unknown | | | | 🟦 |
| yteR | BSU30120 | galacturonyl hydrolase, catalyses intracellular degradation of disaccharides generated by YesX | | | | 🟦 |
| yteP | BSU30135 | similar to ABC transporter (transmembrane lipoprotein) | | | | 🟦 |
| ytdP | BSU30150 | similar to transcriptional regulator (AraC family) | | | | 🟦 |
| ytcQ | BSU30160 | similar to ABC transporter (solute-binding lipoprotein) | | | | 🟦 |
| ytcP | BSU30170 | similar to ABC transporter (permease) | | | | 🟦 |
| ytbQ | BSU30180 | unknown | | | | |
| bioI | BSU30190 | cytochrome P450 enzyme | | | | |
| bioB | BSU30200 | biotin synthase | | | | |
| bioD | BSU30210 | dethiobiotin synthase | | | | |
| bioF | BSU30220 | 8-amino-7-oxononanoate synthase | | | | |
| bioA | BSU30230 | lysine-8-amino-7-oxononanoate aminotransferase | | | | |
| bioW | BSU30240 | 6-carboxyhexanoate-CoA ligase | | | | |
| ytaP | BSU30250 | unknown | | | | |
| msmR | BSU30260 | transcriptional regulator of the msmR-msmE-amyD-amyC-melA operon | | | | |
| msmE | BSU30270 | probably ABC transporter for melibiose (binding protein) | | | | |
| amyD | BSU30280 | probably ABC transporter for melibiose (permease) | | | | |
| amyC | BSU30290 | probably ABC transporter for melibiose | | | | |
| melA | BSU30300 | alpha-galactosidase | | | | |
| ytwF | BSU30310 | unknown | | | | |
| leuS | BSU30320 | Leu-tRNA synthetase | | | | |
| ytvB | BSU30330 | unknown | | | | |
| ytvA | BSU30340 | positive regulation of SigB activity under conditions of blue light | | | | |
| yttB | BSU30350 | similar to multidrug resistance protein | | partial | partial | partial |
| yttA | BSU30360 | unknown | | 🟦 | 🟦 | 🟦 |
| bceB | BSU30370 | bacitracin ABC transporter (permease) for bacitracin export | | 🟦 | 🟦 | 🟦 |
| bceA | BSU30380 | bacitracin ABC transporter (ATP-binding protein) for bacitracin export | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| bceS | BSU30390 | two-component sensor kinase, regulation of bceA-bceB in response to bacitracin | | ■ | ■ | ■ |
| bceR | BSU30400 | two-component response regulator, regulation of bceA-bceB in response to bacitracin | | ■ | ■ | ■ |
| ytrF | BSU30410 | ABC transporter (substrate-binding lipoprotein) | | ■ | ■ | ■ |
| ytrE | BSU30420 | ABC transporter (ATP-binding protein) | | ■ | ■ | ■ |
| ytrD | BSU30430 | ABC transporter (hydrophobic protein, probably channel protein) | | ■ | ■ | ■ |
| ytrC | BSU30440 | ABC transporter (hydrophobic protein, probably channel protein) | | ■ | ■ | ■ |
| ytrB | BSU30450 | ABC transporter (ATP-binding protein) | | ■ | ■ | ■ |
| ytrA | BSU30460 | transcriptional repressor, GntR family, control of cell envelope stress responses in response to ramoplanin | | ■ | ■ | ■ |
| ytrG | BSU_CDS_3119273 | unknown | | ■ | ■ | ■ |
| ytzC | BSU30470 | unknown | | ■ | ■ | ■ |
| ytqA | BSU30480 | unknown | | ■ | ■ | ■ |
| ytqB | BSU30490 | unknown | | ■ | ■ | ■ |
| ytpB | BSU30500 | salt stress protein | | ■ | ■ | ■ |
| ytpA | BSU30510 | similar to lysophospholipase | | ■ | ■ | ■ |
| ytoA | BSU30520 | similar to ferripyochelin binding protein | | ■ | ■ | ■ |
| ytnA | BSU30530 | similar to proline permease | | | | |
| metK | BSU30550 | S-adenosylmethionine synthetase | | | | |
| pckA | BSU30560 | phosphoenolpyruvate carboxykinase | | | | |
| ytmB | BSU30570 | unknown | | | | |
| ytmA | BSU30580 | unknown | | | | |
| ytlA | BSU30595 | similar to ABC transporter (binding protein) | | | | |
| ytlC | BSU30610 | similar to anion transport ABC transporter (ATP-binding protein) | | | | |
| ytlD | BSU30620 | similar to ABC transporter (permease) | | | | |
| mutTA | BSU30630 | error prevention oxidized guanine system, confers protection against oxidative stress to vegetative cells | | | | |
| ytkC | BSU30640 | similar to autolytic amidase | | | | |
| dps | BSU30650 | iron storage protein, general stress protein, resistance against ethanol stress and survival at low temperatures | | | | |
| ytzI | BSU30659 | unknown | | | | |
| ytkA | BSU30660 | unknown | | | | |
| luxS | BSU30670 | S-ribosylhomocysteine lyase, autoinducer-2 production protein | | | | |
| ytjA | BSU30680 | hemolysin | | | | |
| ytiB | BSU30690 | similar to carbonic anhydrase | | | | |
| ytiA | BSU30700 | general stress protein, binds in the stationary phase to the ribosome, replaces RpmE under conditions of zinc limitation | | | | |
| ythA | BSU30710 | cytochrome bd2, menaquinol oxidase (7:1 protons) | | | | |
| ythB | BSU30720 | cytochrome bd2, menaquinol oxidase (7:1 protons) | | | | |
| ytzL | BSU30739 | unknown | | | | |
| mntD | BSU30740 | manganese ABC transporter (permease) | | | | |
| mntC | BSU30750 | manganese ABC transporter (membrane protein) | | | | |
| mntB | BSU30760 | manganese ABC transporter (ATP-binding protein) | | | | |
| mntA | BSU30770 | manganese ABC transporter (membrane protein) | | | | |
| menC | BSU30780 | O-succinylbenzoate-CoA synthase | | | | |
| menE | BSU30790 | o-succinylbenzoate-CoA ligase | | | | |
| menB | BSU30800 | naphthoate synthase | | | | |
| ytxM | BSU30810 | similar to prolyl aminopeptidase | | | | |
| menD | BSU30820 | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase / 2-oxoglutarate decarboxylase | | | | |
| menF | BSU30830 | menaquinone-specific isochorismate synthase | | | | |
| yteA | BSU30840 | sporulation protein | | | | ■ |
| ytdA | BSU30850 | similar to UTP-glucose-1-phosphate uridylyltransferase | | | | ■ |
| ytcA | BSU30860 | similar to to NDP-sugar dehydrogenase | | | | ■ |
| ytcB | BSU30870 | putative UDP-glucose epimerase | | | | ■ |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ytcC | BSU30880 | sporulation protein, similar to lipopolysaccharide N-acetylglucosaminyltransferase | | | | 🟦 |
| ytxO | BSU30890 | spore coat protein | | | | 🟦 |
| cotS | BSU30900 | spore coat protein | | | | 🟦 |
| cotSA | BSU30910 | spore coat protein | | | | 🟦 |
| cotI | BSU30920 | spore coat protein | | | | 🟦 |
| ytaB | BSU30930 | general stress protein, survival of ethanol and salt stresses | | | | 🟦 |
| glgP | BSU30940 | glycogen phosphorylase | | | | |
| glgA | BSU30950 | glycogen synthase (ADPGlc) | | | | |
| glgD | BSU30960 | glucose-1-phosphate adenylyltransferase | | | | |
| glgC | BSU30970 | glucose-1-phosphate adenylyltransferase | | | | |
| glgB | BSU30980 | 1,4-alpha-glucan branching enzyme | | | | |
| rrnB-16S- rrnB-23S- rrnB-5S - trnB-Ala- trnB-Arg- trnB-Asn- trnB-Asp- trnB-Glu- trnB-Gly1- trnB-Gly2- trnB-His- trnB-Ile2- trnB-Leu1- trnB-Leu2- trnB-Lys- trnB-Met1- trnB-Met2- trnB-Met3- trnB-Phe- trnB-Pro- trnB-Ser1- trnB-Ser2- | | | | | | |
| thiT | BSU30990 | S protein of thiamine ECF transporter | | | | |
| yuaI | BSU31000 | unknown | | | | |
| floT | BSU31010 | similar to flottilin 1, orchestration of physiological processes in lipid microdomains, | | | | |
| yuaF | BSU31020 | role in maintaining membrane integrity during conditions of cellular stress | | | | |
| yuaE | BSU31030 | unknown | | | | |
| yuaD | BSU31040 | unknown | | | | |
| gbsB | BSU31050 | choline dehydrogenase (FAD-dependent), glycine betaine synthesis | | | | |
| gbsA | BSU31060 | glycine betaine-aldehyde dehydrogenase, glycine betaine synthesis | | | | |
| gbsR | BSU31070 | unknown | | | | |
| bslA | BSU31080 | amphiphilic protein, forms water-repellent surface layer of the biofilm, inhibitor of KinA autophosphorylation | | 🟦 | 🟦 | 🟦 |
| ktrA | BSU31090 | high affinity potassium transporter KtrAB, peripheric membrane component (proton symport) | | | | |
| ktrB | BSU31100 | high affinity potassium transporter KtrAB, integral membrane subunit | | | | |
| yubF | BSU31110 | unknown | | | | |
| lytG | BSU31120 | similar to N-acetylmuramoyl-L-alanine amidase | | | | |
| yubD | BSU31130 | similar to multidrug resistance protein | | | | |
| yubC | BSU31140 | similar to cysteine dioxygenase | | | | |
| trnSL-Ala1 | | | | | | |
| yubB | BSU31150 | minor undecaprenyl pyrophosphate phosphatase | | | | |
| yubA | BSU31160 | membrane protein | | | | |
| yulF | BSU31170 | unknown | | | | |
| yulE | BSU31180 | L-rhamnose isomerase | | 🟦 | 🟦 | 🟦 |
| yulD | BSU31190 | unknown | | 🟦 | 🟦 | 🟦 |
| yulC | BSU31200 | rhamnulokinase | | 🟦 | 🟦 | 🟦 |
| yulB | BSU31210 | similar to transcriptional regulator (DeoR family) | | 🟦 | 🟦 | 🟦 |
| yuxG | BSU31220 | similar to sorbitol-6-phosphate 2-dehydrogenase | | 🟦 | 🟦 | 🟦 |
| tlpB | BSU31230 | methyl-accepting chemotaxis protein | | 🟦 | 🟦 | 🟦 |
| mcpA | BSU31240 | methyl-accepting chemotaxis protein | | 🟦 | 🟦 | 🟦 |
| tlpA | BSU31250 | methyl-accepting chemotaxis protein | | 🟦 | 🟦 | 🟦 |
| mcpB | BSU31260 | methyl-accepting chemotaxis protein | | 🟦 | 🟦 | 🟦 |
| tgl | BSU31270 | outer spore coat protein, spore associated transglutaminase | | 🟦 | 🟦 | 🟦 |
| yuzH | BSU31279 | unknown | | 🟦 | 🟦 | 🟦 |
| yugU | BSU31280 | general stress protein, survival of ethanol stress | | 🟦 | 🟦 | 🟦 |
| yugT | BSU31290 | similar to exo-alpha-1,4-glucosidase | | 🟦 | 🟦 | 🟦 |
| yugS | BSU31300 | similar to hemolysin | | 🟦 | 🟦 | 🟦 |
| yugP | BSU31310 | unknown | | 🟦 | 🟦 | 🟦 |
| yuzI | BSU31319 | unknown | | 🟦 | 🟦 | 🟦 |
| mstX | BSU31321 | membrane-integrating protein for membrane protein expression, MISTIC | | 🟦 | 🟦 | 🟦 |

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| yugO | BSU31322 | putative potassium channel protein | | 🟦 | 🟦 | 🟦 |
| yugN | BSU31330 | unknown | | 🟦 | 🟦 | 🟦 |
| yugM | BSU31340 | unknown | | 🟦 | 🟦 | 🟦 |
| pgi | BSU31350 | glucose 6-phosphate isomerase, glycolytic / gluconeogenic enzyme | | | | |
| yugK | BSU31360 | similar to NADH-dependent butanol dehydrogenase | | | | |
| yugJ | BSU31370 | similar to NADH-dependent butanol dehydrogenase | | | | |
| yuzA | BSU31380 | general stress protein | | | | |
| yugI | BSU31390 | similar to polyribonucleotide nucleotidyl transferase, general stress protein with a RNA-binding surface | | | | |
| alaT | BSU31400 | similar to PLP-dependent methionine aminotransferase | | | | |
| alaR | BSU31410 | transcriptional regulator of the alaR-alaT operon | | | | |
| yugF | BSU31420 | similar to dihydrolipoamide S-acetyltransferase | | | | |
| yugE | BSU31430 | unknown | | | | |
| patB | BSU31440 | cystathione-beta-lyase | | | | |
| kinB | BSU31450 | two-component sensor kinase, phosphorylates Spo0F, part of the phosphorelay | | | | |
| kapB | BSU31460 | activator of KinB, control of the phosphorelay | | | | |
| kapD | BSU31470 | inhibitor of the KinA pathway to sporulation | | | | |
| yuxJ | BSU31480 | similar to multidrug-efflux transporter | | | | |
| pbpD | BSU31490 | penicillin-binding protein 4 | | | | |
| yuxK | BSU31500 | unknown | | | | |
| yufK | BSU31510 | unknown | | | | |
| malK | BSU31520 | two-component sensor kinase, regulation of malate uptake | | | | |
| malR | BSU31530 | two-component response regulator, regulation of malate uptake | | | | |
| nupN | BSU31540 | lipoprotein, part of guanosine transporter | | | | |
| nupO | BSU31550 | ABC transporter for guanosine (ATP-binding protein) | | | | |
| nupP | BSU31560 | ABC transporter for guanosine (membrane protein) | | | | |
| nupQ | BSU31570 | ABC transporter for guanosine (membrane protein) | | | | |
| maeN | BSU31580 | Na+/malate symporter | | | | |
| yufS | BSU31590 | unknown | | | | |
| mrpA | BSU31600 | Na+/H+ antiporter subunit, multiple resistance and pH homeostasis | | | | |
| mrpC | BSU31620 | Na+/H+ antiporter subunit, multiple resistance and pH homeostasis | | | | |
| mrpD | BSU31630 | Na+/H+ antiporter subunit, multiple resistance and pH homeostasis | | | | |
| mrpE | BSU31640 | Na+/H+ antiporter subunit, multiple resistance and pH homeostasis | | | | |
| mrpF | BSU31650 | Na+/H+ antiporter subunit, multiple resistance and pH homeostasis | | | | |
| mrpG | BSU31660 | Na+/H+ antiporter subunit, multiple resistance and pH homeostasis | | | | |
| yuxO | BSU31670 | unknown | | | | |
| comA | BSU31680 | two-component system response regulator, controls gene expression in response to cell density | | 🟦 | 🟦 | 🟦 |
| comP | BSU31690 | two-component sensor kinase, detects extracellular ComX | | 🟦 | 🟦 | 🟦 |
| comX | BSU31700 | competence pheromone precursor, transfers cell density signal to ComP; triggers the production of surfactin | | 🟦 | 🟦 | 🟦 |
| comQ | BSU31710 | prenyltransferase, prenylation of ComX, regulator of late competence operon (comG) and surfactin expression (srfA) | | 🟦 | 🟦 | 🟦 |
| degQ | BSU31720 | stimulates production of degradative enzymes and of extracellular poly-gamma-glutamate | | | | |
| yuzC | BSU31730 | spore coat protein | | | | |
| pdeH | BSU31740 | c-di-GMP degrading phosphodiesterase | | | | |
| pncB | BSU31750 | putative nicotinate phosphoribosyltransferase | | | | |
| pncA | BSU31760 | putative nicotinamidase | | | | |
| yueI | BSU31770 | unknown | | 🟦 | 🟦 | 🟦 |
| yueH | BSU31780 | unknown | | 🟦 | 🟦 | 🟦 |
| yueG | BSU31790 | unknown | | 🟦 | 🟦 | 🟦 |
| yueF | BSU31800 | membrane protein | | 🟦 | 🟦 | 🟦 |
| yuzE | BSU31810 | unknown | | 🟦 | 🟦 | 🟦 |
| yuzF | BSU31820 | unknown | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yueE | BSU31830 | unknown | | 🟦 | 🟦 | 🟦 |
| yueD | BSU31840 | similar to sepiapterin reductase | | 🟦 | 🟦 | 🟦 |
| yueC | BSU31850 | membrane protein, part of the type VII protein secretion system YukD-YukC-YukB-YueB-**YueC** | | 🟦 | 🟦 | 🟦 |
| yueB | BSU31860 | membrane protein, part of the type VII protein secretion system YukD-YukC-YukB-**YueB**-YueC | | 🟦 | 🟦 | 🟦 |
| yukB | BSU31875 | membrane FtsK/SpoIIIE-like ATPase, part of the type VII protein secretion system YukD-YukC-**YukB**-YueB-YueC | | 🟦 | 🟦 | 🟦 |
| yukC | BSU31890 | membrane pseudokinase-like protein, part of the type VII protein secretion system YukD-**YukC**-YukB-YueB-YueC | | 🟦 | 🟦 | 🟦 |
| yukD | BSU31900 | Ubiquitin-like protein, part of the type VII protein secretion system **YukD**-YukC-YukB-YueB-YueC | | 🟦 | 🟦 | 🟦 |
| yukE | BSU31910 | secreted protein of the WXG100 superfamily | | 🟦 | 🟦 | 🟦 |
| adeR | BSU31920 | transcription activator (PucR family) for ald gene expression | | 🟦 | 🟦 | 🟦 |
| ald | BSU31930 | L-alanine dehydrogenase | | 🟦 | 🟦 | 🟦 |
| yukJ | BSU31945 | unknown | | 🟦 | 🟦 | 🟦 |
| ybdZ | BSU31959 | unknown | | | | |
| dhbF | BSU31960 | involved in 2,3-dihydroxybenzoate biosynthesis | | | | |
| dhbB | BSU31970 | isochorismatase | | | | |
| dhbE | BSU31980 | 2,3-dihydroxybenzoate-AMP ligase (enterobactin synthetase component E) | | | | |
| dhbC | BSU31990 | isochorismate synthase | | | | |
| dhbA | BSU32000 | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase | | | | |
| besA | BSU32010 | trilactone hydrolase, catalyses ferri-bacillibactin hydrolysis leading to cytosolic iron release | | | | |
| yuiH | BSU32020 | similar to sulfite oxidase | | | | |
| yuiG | BSU32030 | putative S protein of a second biotin ECF transporter | | | | |
| yuiF | BSU32040 | membrane protein | | | | |
| yuiE | BSU32050 | similar to leucyl aminopeptidase | | | | |
| yuiD | BSU32060 | unknown | | | | |
| yuiC | BSU32070 | sporulation protein | | | | |
| yuiB | BSU32080 | unknown | | | | |
| yuiA | BSU32090 | unknown | | | | |
| yumB | BSU32100 | unknown | | | | |
| yumC | BSU32110 | ferredoxin-NAD(P)+ oxidoreductase | | | | |
| yuzG | BSU32120 | unknown | | | | |
| guaC | BSU32130 | GMP reductase | | | | |
| paiB | BSU32140 | transcriptional repressor of sporulation and degradative enzyme genes | | | | |
| paiA | BSU32150 | spermine/spermidine-N-acetyltransferase | | | | |
| sufA | BSU32160 | putative iron-sulfur cluster scaffold protein | | | | |
| dapF | BSU32170 | diaminopimelate epimerase | | | | |
| yutK | BSU32180 | similar to Na+/nucleoside cotransporter | | | | |
| yutJ | BSU32200 | putative NADH dehydrogenase | | | | |
| yuzD | BSU32210 | unknown | | | | |
| yutI | BSU32220 | similar to NifU protein homolog | | | | |
| yuxL | BSU32230 | similar to acylaminoacyl-peptidase | | | | |
| thrB | BSU32240 | homoserine kinase | | | | |
| thrC | BSU32250 | threonine synthase | | | | |
| hom | BSU32260 | homoserine dehydrogenase (NADPH) | | | | |
| yutH | BSU32270 | spore coat protein | | | | |
| yutG | BSU32280 | similar to low temperature requirement C protein | | | | |
| yutF | BSU32290 | similar to p-nitrophenyl phosphatase | | | | |
| yutE | BSU32300 | unknown | | | | |
| yutD | BSU32310 | unknown | | | | |
| yutC | BSU32320 | unknown | | | | |

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| lipA | BSU32330 | trigger enzyme: lipoic acid synthase and regulator of comE operon expression | | | | |
| lytH | BSU32340 | unknown | | | 🟦 | 🟦 |
| fisB | BSU32350 | membrane fission protein, mediates membrane fission during sporulation | | | 🟦 | 🟦 |
| yunC | BSU32360 | unknown | | | 🟦 | 🟦 |
| yunD | BSU32370 | unknown | | | 🟦 | 🟦 |
| yunE | BSU32380 | unknown | | | 🟦 | 🟦 |
| yunF | BSU32390 | unknown | | | 🟦 | 🟦 |
| yunG | BSU32400 | unknown | | | 🟦 | 🟦 |
| pucH | BSU32410 | allantoinase | | | 🟦 | 🟦 |
| pucR | BSU32420 | transcriptional regulator of puc genes | | | 🟦 | 🟦 |
| pucJ | BSU32430 | uric acid permease | | | 🟦 | 🟦 |
| pucK | BSU32440 | uric acid permease | | | 🟦 | 🟦 |
| pucL | BSU32450 | uricase | | | 🟦 | 🟦 |
| pucM | BSU32460 | uricase | | | 🟦 | 🟦 |
| yuzJ | BSU32469 | unknown | | | 🟦 | 🟦 |
| pucE | BSU32470 | xanthine dehydrogenase | | | 🟦 | 🟦 |
| pucD | BSU32480 | xanthine dehydrogenase | | | 🟦 | 🟦 |
| pucC | BSU32490 | xanthine dehydrogenase | | | 🟦 | 🟦 |
| pucB | BSU32500 | xanthine dehydrogenase | | | 🟦 | 🟦 |
| pucA | BSU32510 | xanthine dehydrogenase | | | 🟦 | 🟦 |
| pucG | BSU32520 | similar to aspartate aminotransferase | | | 🟦 | 🟦 |
| pucF | BSU32530 | allantoate amidohydrolase | | | 🟦 | 🟦 |
| yurI | BSU32540 | ribonuclease, extracellular RNase Bsn | | | 🟦 | 🟦 |
| yurJ | BSU32550 | aminosugar ABC transporter (ATP-binding protein) | | | 🟦 | 🟦 |
| frlR | BSU32560 | transcriptional regulator (GntR family) | | | 🟦 | 🟦 |
| frlD | BSU32570 | fructosamine kinase | | | 🟦 | 🟦 |
| frlM | BSU32580 | aminosugar ABC transporter (permease) | | | 🟦 | 🟦 |
| frlN | BSU32590 | aminosugar ABC transporter (permease) | | | 🟦 | 🟦 |
| frlO | BSU32600 | aminosugar ABC transporter (binding protein) | | | 🟦 | 🟦 |
| frlB | BSU32610 | fructoselysine-6-P-glycosidase | | | 🟦 | 🟦 |
| yurQ | BSU32620 | unknown | | | 🟦 | 🟦 |
| yurR | BSU32630 | similar to glycine oxidase | | | 🟦 | 🟦 |
| sspG | BSU32640 | small acid-soluble spore protein (minor) | | | 🟦 | 🟦 |
| yurS | BSU32650 | sporulation protein | | | 🟦 | 🟦 |
| glxB | BSU32660 | glyoxalase II | | | 🟦 | 🟦 |
| yuzN | BSU32669 | unknown | | | | |
| sufB | BSU32670 | synthesis of Fe-S-clusters | | | | |
| sufU | BSU32680 | iron-sulfur cluster scaffold protein, synthesis of Fe-S clusters | | | | |
| sufS | BSU32690 | cysteine desulfurase | | | | |
| sufD | BSU32700 | synthesis of Fe-S-clusters | | | | |
| sufC | BSU32710 | ABC transporter (ATP-binding protein), synthesis of Fe-S clusters | | | | |
| bsrI | | small RNA | | | | |
| yuzK | BSU32719 | unknown | | | | |
| metQ | BSU32730 | methionine ABC transporter (binding lipoprotein) | | | | |
| metP | BSU32740 | methionine ABC transporter, permease | | | | |
| metN | BSU32750 | methionine ABC transporter (ATP-binding protein) | | | | |
| yusD | BSU32760 | unknown | | | | |
| yusE | BSU32770 | similar to thioredoxin | | | | |
| yusF | BSU32780 | unknown | | | | |
| yusG | BSU32790 | unknown | | | | |
| gcvH | BSU32800 | glycine cleavage system protein H, 2-oxo acid dehydrogenase, lipoyl-binding site | | | | |
| yusI | BSU32810 | similar to arsenate reductase | | | | |
| fadE | BSU32820 | acyl-CoA dehydrogenase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| fadA | BSU32830 | acetyl-CoA C-acyltransferase | | | | |
| fadN | BSU32840 | 3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) | | | | |
| yuzL | BSU32849 | unknown | | | | |
| fadM | BSU32850 | fatty acid degradation, similar to proline dehydrogenase | | | | |
| yuzM | BSU32859 | unknown | | | | |
| yusN | BSU32860 | unknown | | | | |
| | | | | | | |
| mdtR | BSU32870 | transcription repressor of the multidrug-resistance mdtR-mdtP operon | | | | |
| mdtP | BSU32880 | multidrug-efflux transporter | | | | |
| yusQ | BSU32890 | similar to acyloate catabolism | | | | |
| yusR | BSU32900 | similar to 3-oxoacyl- acyl-carrier protein reductase | | | | |
| yusS | BSU32910 | similar to 3-oxoacyl- acyl-carrier protein reductase | | | | |
| yusT | BSU32920 | similar to transcriptional regulator (LysR family) | | | | |
| yusU | BSU32930 | unknown | | | | |
| yusV | BSU32940 | ABC transporter for the siderophores Fe-enterobactin and Fe-bacillibactin(ATPase) | | | | |
| yusW | BSU32950 | unknown | | | | |
| yusY/1 | BSU32960 | similar to oligoendopeptidase, inactive pseudogene | | | | |
| yusY/2 | BSU32970 | similar to oligoendopeptidase, inactive pseudogene | | | | |
| yusZ | BSU32980 | similar to retinol dehydrogenase | | | | |
| mrgA | BSU32990 | iron storage protein, DNA-binding stress protein | | | | |
| htrB | BSU33000 | serine protease, response to secretion and heat stresses | | | | |
| cssR | BSU33010 | two-component response regulator, control of cellular responses to protein secretion stress | | | | |
| cssS | BSU33020 | two-component sensor kinase, control of cellular responses to protein secretion stress | | | | |
| yirB | BSU33029 | anti-adaptor protein, inhibits YjbH | | | | |
| yuxN | BSU33030 | unknown | | | | |
| citG | BSU33040 | fumarase | | | | |
| yvzF | BSU33049 | unknown | | 🟦 | 🟦 | 🟦 |
| gerAA | BSU33050 | nutrient receptor, germination response to L-alanine | | 🟦 | 🟦 | 🟦 |
| gerAB | BSU33060 | nutrient receptor, germination response to L-alanine | | 🟦 | 🟦 | 🟦 |
| gerAC | BSU33070 | nutrient receptor, germination response to L-alanine | | 🟦 | 🟦 | 🟦 |
| liaR | BSU33080 | two-component response regulator, regulation of the liaI-liaH-liaG-liaF-liaS-liaR operon in response to bacitracin | | | | |
| liaS | BSU33090 | two-component sensor kinase, response to bacitracin | | | | |
| liaF | BSU33100 | negative effector of LiaR | | | | |
| liaG | BSU33110 | maybe involved in resistance to bacitracin | | | | |
| liaH | BSU33120 | similar to phage shock protein, resistance against oxidative stress and cell wall antibiotics (such as daptamycin) | | | | |
| liaI | BSU33130 | resistance against oxidative stress and cell wall antibiotics, may act as membrane anchor for LiaH | | | | |
| yvqJ | BSU33140 | similar to to macrolide-efflux protein | | | | |
| yvqK | BSU33150 | ATP:cob(I)alamin adenosyltransferase | | | | |
| | | | | | | |
| yvrA | BSU33160 | ABC transporter (ATP binding domain), similar to iron transport system | | | | |
| yvrB | BSU33170 | ABC transporter (ATP binding domain), similar to iron permease | | | | |
| yvrC | BSU33180 | ABC transporter (binding protein), similar to iron-binding protein | | | | |
| yvrD | BSU33190 | similar to ketoacyl-carrier protein reductase | | | | |
| yvrE | BSU33200 | general stress protein, similar to senescence marker protein-30 | | | | |
| | | | | | | |
| yvrG | BSU33210 | two-component sensor kinase of the YvrG-YvrHb two-component system | | | | |
| yvrHb | BSU33221 | two-component response regulator | | | | |
| yvrHa | BSU33222 | co-sigma factor (with YvrI) | | | | |
| yvrI | BSU33230 | RNA polymerase sigma factor YvrI | | | | |
| oxdC | BSU33240 | oxalate decarboxylase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yvrL | BSU33250 | anti-Sig(YvrI-YvrHa) | | | | |
| yvrN | BSU33260 | similar to ABC transporter (membrane protein) | | | | |
| yvrO | BSU33270 | similar to amino acid ABC transporter (ATP-binding protein) | | | | |
| yvrP | BSU33280 | unknown | | | | |
| fhuC | BSU33290 | hydroxamate siderophore ABC transporter (ATP-binding protein) (ferrichrome und ferrioxamine) | | | | |
| fhuG | BSU33300 | hydroxamate siderophore ABC transporter (ferrichrome und ferrioxamine) (permease) | | | | |
| fhuB | BSU33310 | hydroxamate siderophore ABC transporter (ferrichrome und ferrioxamine) (permease) | | | | |
| fhuD | BSU33320 | hydroxamate siderophore ABC transporter (only ferrichrome) (binding protein) | | | | |
| yvsH | BSU33330 | putative lysine transporter | | | | |
| sspJ | BSU33340 | small acid-soluble spore protein (minor) | | | | |
| yvsG | BSU33350 | unknown | | | | |
| yvgJ | BSU33360 | minor lipoteichoic acid synthase (stationary phase) | | | | |
| yvgK | BSU33370 | similar to molybdenum-binding protein | | | | |
| yvgL | BSU33380 | similar to ABC transporter for molybdenum uptake (binding protein) | | | | |
| yvgM | BSU33390 | similar to ABC transporter for molybdenum uptake (permease) | | | | |
| yvgN | BSU33400 | glyoxal reductase, general stress protein | | | 🟦 | |
| yvgO | BSU33410 | general stress protein, survival of ethanol stress | | | 🟦 | |
| nhaK | BSU33420 | cation/H+ antiporter | | | 🟦 | |
| cysI | BSU33430 | sulfite reductase (NADPH2) | | | 🟦 | |
| cysJ | BSU33440 | sulfite reductase (NADPH2) | | | 🟦 | |
| helD | BSU33450 | DNA 3'-5' helicase IV | | | 🟦 | |
| yvgT | BSU33460 | potential TRIC transporter | | | 🟦 | |
| bdbC | BSU33470 | thiol-disulfide oxidoreductase, required for the formation of thiol disulfide bonds in ComGC | | | | |
| bdbD | BSU33480 | thiol-disulfide oxidoreductase, required for the formation of thiol disulfide bonds in ComGC | | | | |
| cadA | BSU33490 | cadmium transporting ATPase, resistance to cadmium | | | | |
| copA | BSU33500 | copper-transporting ATPase, resistance to copper | | | | |
| copZ | BSU33510 | copper transport protein, metallochaperone | | | | |
| csoR | BSU33520 | transcription repressor of copZ-copA and of ycnJ | | | | |
| iolW | BSU33530 | scyllo-inositol dehydrogenase, general stress protein | | | | |
| azoR2 | BSU33540 | similar to NAD(P)H dehydrogenase (quinone) | | | | |
| yvaC | BSU33550 | unknown | | | | |
| yvaD | BSU33560 | unknown | | | | |
| yvaE | BSU33570 | similar to multidrug-efflux transporter | | | | |
| yvaF | BSU33580 | unknown | | | | |
| yvaG | BSU33590 | similar to 3-oxoacyl- acyl-carrier protein reductase | | | | |
| ssrA | BSU_misc_RNA_55 | tmRNA | | | | |
| smpB | BSU33600 | tmRNA-binding protein | | | | |
| rnr | BSU33610 | RNase R | | | | |
| yvaK | BSU33620 | general stress protein, carboxylesterase | | | | |
| secG | BSU33630 | preprotein translocase subunit | | | | |
| yvaM | BSU33640 | similar to hydrolase | | | | |
| yvzC | BSU33650 | unknown | | | | |
| rghR | BSU33660 | repressor of rapD, rapG, rapH and yvaM | | | | |
| yvaO | BSU33670 | similar to immunity repressor protein | | | | |
| catR | BSU33680 | transcription repressor of the catD-catE operon | | | | |
| yvaQ | BSU33690 | membrane-bound chemotaxis receptor, similar to methyl-accepting chemotaxis protein | | | | |
| opuBD | BSU33700 | choline ABC transporter (membane protein) | | | | |
| opuBC | BSU33710 | choline ABC transporter (binding protein) | | | | |
| opuBB | BSU33720 | choline ABC transporter (membrane protein) | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| opuBA | BSU33730 | choline ABC transporter (ATP-binding protein) | | | | |
| yvaV | BSU33740 | unknown, similar to transcription factor OpcR | | | | |
| sdpA | BSU33750 | required for SdpC toxin maturation | | 🟦 | 🟦 | 🟦 |
| sdpB | BSU33760 | membrane protein, required for SdpC toxin maturation | | 🟦 | 🟦 | 🟦 |
| sdpC | BSU33770 | toxin, kills non-sporulating cells, induces activity of SigW | | 🟦 | 🟦 | 🟦 |
| sdpI | BSU33780 | immunity protein, protection against SdpC | | 🟦 | 🟦 | 🟦 |
| opuCD | BSU33800 | glycine betaine/carnitine/choline ABC transporter | | | | |
| opuCC | BSU33810 | glycine betaine/carnitine/choline ABC transporter (binding protein) | | | | |
| opuCB | BSU33820 | glycine betaine/carnitine/choline ABC transporter | | | | |
| opuCA | BSU33830 | glycine betaine/carnitine/choline ABC transporter (ATP-binding protein) | | | | |
| opcR | BSU33840 | transcriptional repressor of the *opuBA-opuBB-opuBC-opuBD* and *opuCA-opuCB-opuCC-opuCD* operons | | | | |
| yvbG | BSU33850 | unknown | | | | |
| yvbH | BSU33860 | unknown | | | | |
| yvbI | BSU33870 | unknown | | | | |
| yvbJ | BSU33880 | unknown | | | | |
| yvbK | BSU33890 | unknown | | | | |
| eno | BSU33900 | enolase, glycolytic/ gluconeogenic enzyme, universally conserved protein | | | | |
| pgm | BSU33910 | phosphoglycerate mutase, glycolytic / gluconeogenic enzyme | | | | |
| tpi | BSU33920 | triose phosphate isomerase, glycolytic/ gluconeogenic enzyme | | | | |
| pgk | BSU33930 | phosphoglycerate kinase, glycolytic/ gluconeogenic enzyme, universally conserved protein | | | | |
| gapA | BSU33940 | Glyceraldehyde 3-phosphate dehydrogenase, NAD-dependent, glycolytic enzyme | | | | |
| cggR | BSU33950 | repressor of the glycolytic gapA operon, DeoR family | | | | |
| araE | BSU33960 | L-arabinose permease | | 🟦 | 🟦 | 🟦 |
| araR | BSU33970 | repressor of the arabinose utilization genes | | 🟦 | 🟦 | 🟦 |
| yvbT | BSU33980 | similar to alkanal monooxygenase | | 🟦 | 🟦 | 🟦 |
| yvbU | BSU33990 | similar to transcriptional regulator (LysR family) | | 🟦 | 🟦 | 🟦 |
| yvbV | BSU34000 | putative cysteine and O-acetyl serine efflux permease | | 🟦 | 🟦 | 🟦 |
| yvbW | BSU34010 | putative leucine permease | | 🟦 | 🟦 | 🟦 |
| yvbX | BSU34020 | unknown | | 🟦 | 🟦 | 🟦 |
| lutC | BSU34030 | lactate catabolic enzyme | | 🟦 | 🟦 | 🟦 |
| lutB | BSU34040 | lactate catabolic enzyme | | 🟦 | 🟦 | 🟦 |
| lutA | BSU34050 | lactate catabolic enzyme | | 🟦 | 🟦 | 🟦 |
| yvfU | BSU34060 | two-component response regulator | | 🟦 | 🟦 | 🟦 |
| yvfT | BSU34070 | two-component sensor kinase | | 🟦 | 🟦 | 🟦 |
| yvfS | BSU34080 | similar to ABC transporter (transmembrane subunit) | | 🟦 | 🟦 | 🟦 |
| yvfR | BSU34090 | similar to ABC transporter (ATP-binding protein) | | 🟦 | 🟦 | 🟦 |
| rsbQ | BSU34100 | protein serine phosphatase, energy PP2C, dephosphorylates RsbV | | 🟦 | 🟦 | 🟦 |
| rsbP | BSU34110 | protein serine phosphatase, energy PP2C, dephosphorylates RsbV | | 🟦 | 🟦 | 🟦 |
| ganB | BSU34120 | arabinogalactan endo-1,4-beta-galactosidase | | 🟦 | 🟦 | 🟦 |
| ganA | BSU34130 | beta-galactosidase | | 🟦 | 🟦 | 🟦 |
| ganQ | BSU34140 | galactotriose ABC transporter (permease) | | 🟦 | 🟦 | 🟦 |
| ganP | BSU34150 | galactotriose ABC transporter (permease) | | 🟦 | 🟦 | 🟦 |
| cycB | BSU34160 | galactotriose ABC transporter, binding protein | | 🟦 | 🟦 | 🟦 |
| lacR | BSU34170 | transcriptional repressor of the galactan utilization operon | | 🟦 | 🟦 | 🟦 |
| lutR | BSU34180 | repressor of the lutA-lutB-lutC operon | | 🟦 | 🟦 | 🟦 |
| lutP | BSU34190 | lactate permease | | 🟦 | 🟦 | 🟦 |
| sigL | BSU34200 | sigma factor of the RNA polymerase, Sigma-54, Sigma L | | | | |
| yvfG | BSU34210 | unknown | | | | |
| epsO | BSU34220 | extracellular polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| epsN | BSU34230 | extracellular polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| epsM | BSU34240 | similar to serine O-acetyltransferase, extracellular polysaccharide synthesis |  | ■ | ■ | ■ |
| epsL | BSU34250 | similar to UDP-galactose phosphate transferase, extracellular polysaccharide synthesis |  | ■ | ■ | ■ |
| epsK | BSU34265 | extracellular polysaccharide synthesis |  | ■ | ■ | ■ |
| epsJ | BSU34280 | similar to 1,4-galactosyltransferase |  | ■ | ■ | ■ |
| epsI | BSU34290 | extracellular polysaccharide synthesis |  | ■ | ■ | ■ |
| epsH | BSU34300 | extracellular polysaccharide synthesis |  | ■ | ■ | ■ |
| epsG | BSU34310 | extracellular polysaccharide synthesis |  | ■ | ■ | ■ |
| epsF | BSU34320 | similar to glycosyltransferase |  | ■ | ■ | ■ |
| epsE | BSU34330 | inhibitor of motility and glycosyltransferase required for EPS biosynthesis |  | ■ | ■ | ■ |
| epsD | BSU34340 | extracellular polysaccharide synthesis |  | ■ | ■ | ■ |
| epsC | BSU34350 | extracellular polysaccharide synthesis |  | ■ | ■ | ■ |
| epsB | BSU34360 | extracellular polysaccharide synthesis, putative protein tyrosine kinase |  | ■ | ■ | ■ |
| slrR | BSU34380 | transcriptional activator of competence development and sporulation genes |  | ■ | ■ | ■ |
| pnbA | BSU34390 | para-nitrobenzyl esterase |  |  |  |  |
| padC | BSU34400 | phenolic acid decarboxylase |  | ■ | ■ | ■ |
| yveG | BSU34410 | unknown |  | ■ | ■ | ■ |
| yveF | BSU34420 | unknown |  | ■ | ■ | ■ |
| racX | BSU34430 | amino acid racemase |  | ■ | ■ | ■ |
| pbpE | BSU34440 | penicillin-binding protein PBP 4* (spore cortex) |  | ■ | ■ | ■ |
| sacB | BSU34450 | levansucrase |  | ■ | ■ | ■ |
| levB | BSU34460 | endolevanase |  | ■ | ■ | ■ |
| yveA | BSU34470 | aspartate/ glutamate transporter |  | ■ | ■ | ■ |
| yvdT | BSU34480 | similar to transcriptional regulator (TetR family) |  | ■ | ■ | ■ |
| yvdS | BSU34490 | similar to molecular chaperone |  | ■ | ■ | ■ |
| yvdR | BSU34500 | similar to molecular chaperone |  | ■ | ■ | ■ |
| yvdQ | BSU34510 | unknown |  | ■ | ■ | ■ |
| cotQ | BSU34520 | spore coat protein |  | ■ | ■ | ■ |
| cotR | BSU34530 | spore protein |  | partial | partial | partial |
| trnQ-Arg |  |  |  |  |  |  |
| clpP | BSU34540 | ATP-dependent Clp protease proteolytic subunit (class III heat-shock protein) |  |  |  |  |
| pgcM | BSU34550 | beta-phosphoglucomutase |  | ■ | ■ | ■ |
| malL | BSU34560 | alpha-glucosidase |  | ■ | ■ | ■ |
| yvdK | BSU34570 | maltose phosphorylase |  | ■ | ■ | ■ |
| yvdJ | BSU34580 | unknown |  | ■ | ■ | ■ |
| mdxG | BSU34590 | maltodextrin ABC transporter, permease |  | ■ | ■ | ■ |
| mdxF | BSU34600 | maltodextrin ABC transporter, permease |  | ■ | ■ | ■ |
| mdxE | BSU34610 | maltodextrin ABC transporter, binding protein |  | ■ | ■ | ■ |
| yvdF | BSU34620 | glucan 1,4-alpha-maltohydrolase, neopullulanase, maltogenic amylase |  | ■ | ■ | ■ |
| yvdE | BSU34630 | similar to transcriptional regulator (LacI family), probably regulator of starch and maltodextrin utilization |  | ■ | ■ | ■ |
| yvdD | BSU34640 | putative lysine decarboxylase |  | ■ | ■ | ■ |
| yvdC | BSU34650 | unknown |  | ■ | ■ | ■ |
| yvdB | BSU34660 | putative anion transporter |  | ■ | ■ | ■ |
| yvdA | BSU34670 | similar to carbonic anhydrase |  | ■ | ■ | ■ |
| yvcT | BSU34680 | unknown |  | ■ | ■ | ■ |
| psdB | BSU34690 | ABC transporter (permease) for the export of lipid II-binding lantibiotics, such as nisin and gallidermin |  | ■ | ■ | ■ |
| psdA | BSU34700 | ABC transporter (ATP-binding protein) for the export of lipid II-binding lantibiotics, such as nisin and gallidermin |  | ■ | ■ | ■ |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| psdS | BSU34710 | two-component sensor kinase, control of psdA-psdB in response to lipid II-binding lantibiotics |  | 🟦 | 🟦 | 🟦 |
| psdR | BSU34720 | two-component response regulator, induction of psdA-psdB in response to lipid II-binding lantibiotics |  | 🟦 | 🟦 | 🟦 |
| yvzJ | BSU34729 | unknown |  | 🟦 | 🟦 | 🟦 |
| yvcN | BSU34730 | unknown |  | 🟦 | 🟦 | 🟦 |
| crh | BSU34740 | "Catabolite repression HPr-like protein", control of flux through the methylglyoxal pathway |  | 🟦 | 🟦 | 🟦 |
| yvcL | BSU34750 | WhiA family protein conserved and ubiquitous among gram-positive bacteria with unknown function |  |  |  |  |
| yvcK | BSU34760 | essential for growth under gluconeogenetic conditions |  |  |  |  |
| yvcJ | BSU34770 | GTPase, nucleotide-binding protein |  |  |  |  |
| yvcI | BSU34780 | Nudix hydrolase |  |  |  |  |
| trxB | BSU34790 | thioredoxin reductase (NADPH) |  |  |  |  |
| cwlO | BSU34800 | D,L-endopeptidase-type autolysin, primary autolytic pathway for cell elongation |  |  |  |  |
| yvcD | BSU34810 | unknown |  |  |  |  |
| bmrA | BSU34820 | multidrug ABC transporter (ATP-binding protein) |  |  |  |  |
| yvzA | BSU34830 | unknown |  |  |  |  |
| yvcB | BSU34840 | unknown |  |  |  |  |
| yvcA | BSU34850 | required for complex colony development |  | partial | partial | partial |
| $P_{mtlA}$-*comK-comS* |  | inserted in IIG-Bs27-24 |  |  |  |  |
| hisI | BSU34860 | phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphohydrolase |  |  |  |  |
| hisF | BSU34870 | cyclase-like protein |  |  |  |  |
| hisA | BSU34880 | phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase, homologue to HisF |  |  |  |  |
| hisH | BSU34890 | tyrosine transaminase |  |  |  |  |
| hisB | BSU34900 | imidazoleglycerol-phosphate dehydratase |  |  |  |  |
| hisD | BSU34910 | histidinol dehydrogenase |  |  |  |  |
| hisG | BSU34920 | ATP phosphoribosyltransferase |  |  |  |  |
| hisZ | BSU34930 | histidyl-tRNA synthetase |  |  |  |  |
| yvpB | BSU34940 | unknown |  |  |  |  |
| pelC | BSU34950 | pectate lyase C |  |  |  |  |
| yvoF | BSU34960 | similar to O-acetyltransferase |  |  |  |  |
| yvoE | BSU34970 | unknown (has been mis-annotated as HPr-P phosphatase) |  |  |  |  |
| yvoD | BSU34980 | unknown |  |  |  |  |
| lgt | BSU34990 | prolipoprotein diacylglyceryl transferase |  |  |  |  |
| hprK | BSU35000 | HPr kinase/ phosphorylase |  |  |  |  |
| nagA | BSU35010 | N-acetylglucosamine-6-phosphate deacetylase |  | 🟦 | 🟦 | 🟦 |
| nagB | BSU35020 | glucosamine-6-phosphate deaminase |  | 🟦 | 🟦 | 🟦 |
| nagR | BSU35030 | transcriptional regulator (GntR family) |  | 🟦 | 🟦 | 🟦 |
| yvnB | BSU35040 | unknown |  | 🟦 | 🟦 | 🟦 |
| yvnA | BSU35050 | unknown |  | 🟦 | 🟦 | 🟦 |
| cypX | BSU35060 | cytochrome P450-like enzyme |  | 🟦 | 🟦 | 🟦 |
| yvmC | BSU35070 | unknown |  | 🟦 | 🟦 | 🟦 |
| yvmB | BSU35080 | unknown |  | 🟦 | 🟦 | 🟦 |
| yvmA | BSU35090 | similar to multidrug transporter |  | 🟦 | 🟦 | 🟦 |
| yvlD | BSU35100 | unknown |  | 🟦 | 🟦 | 🟦 |
| yvlC | BSU35110 | similar to phage shock protein C, involved in resistance to nisin |  | 🟦 | 🟦 | 🟦 |
| yvlB | BSU35120 | unknown |  | 🟦 | 🟦 | 🟦 |
| yvlA | BSU35130 | unknown |  | 🟦 | 🟦 | 🟦 |
| yvkN | BSU35140 | unknown |  | 🟦 | 🟦 | 🟦 |
| yvzB | BSU35150 | similar to flagellin |  | 🟦 | 🟦 | 🟦 |
| uvrA | BSU35160 | excinuclease ABC (subunit A) |  |  |  |  |
| uvrB | BSU35170 | excinuclease ABC (subunit B) |  |  |  |  |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| csbA | BSU35180 | general stress protein | | | | |
| yvkC | BSU35190 | similar to pyruvate water dikinase | | | | |
| yvkB | BSU35200 | similar to transcriptional regulator (TetR family) | | | | |
| yvkA | BSU35210 | similar to multidrug-efflux transporter | | | | |
| minJ | BSU35220 | topological determinant of cell division | | | | |
| swrAA/1 | BSU35230 | control of DegU activity, enhances *sigD* transcription, part of the swrAA pseudogene in 168 | | | | |
| swrAA/2 | BSU35239 | control of DegU activity, enhances *sigD* transcription, part of the swrAA pseudogene in 168 | | | | |
| ctpB | BSU35240 | carboxy-terminal processing serine protease, cleaves SpoIVFA, this results in processing of pro-SigK | | | | |
| ftsX | BSU35250 | ABC transporter (membrane protein) (FtsE-FtsX), required for proper activation of Spo0A and initiation of sporulation | | | | |
| ftsE | BSU35260 | ABC transporter (ATP-binding protein) (FtsE-FtsX), required for proper activation of Spo0A and initiation of sporulation | | | | |
| cccB | BSU35270 | cytochrome c551 | | | | |
| yvjA | BSU35280 | unknown | | | | |
| prfB | BSU35290 | peptide chain release factor 2 | | | | |
| secA | BSU35300 | preprotein translocase subunit (ATPase) | | | | |
| yvyD | BSU35310 | general stress protein, required for ribosome dimerization in the stationary phase | | | | |
| smiA | BSU35319 | inhibitor of swarming motility | | 🟦 | 🟦 | 🟦 |
| fliT | BSU35320 | flagellar protein | | 🟦 | 🟦 | 🟦 |
| fliS | BSU35330 | flagellar protein | | 🟦 | 🟦 | 🟦 |
| fliD | BSU35340 | flagellar hook-associated protein 2 (HAP2) | | 🟦 | 🟦 | 🟦 |
| yvyC | BSU35350 | similar to flagellar protein | | 🟦 | 🟦 | 🟦 |
| hag | BSU35360 | flagellin protein | | 🟦 | 🟦 | 🟦 |
| csrA | BSU35370 | motility regulator, binds to the hag mRNA to inhibit its translation | | 🟦 | 🟦 | 🟦 |
| fliW | BSU35380 | checkpoint protein for *hag* expression, CsrA anatagonist | | 🟦 | 🟦 | 🟦 |
| yviE | BSU35390 | unknown | | 🟦 | 🟦 | 🟦 |
| flgL | BSU35400 | flagellar hook-associated protein 3 (HAP3) | | 🟦 | 🟦 | 🟦 |
| flgK | BSU35410 | flagellar hook-associated protein 1 (HAP1) | | 🟦 | 🟦 | 🟦 |
| yvyG | BSU35420 | similar to flagellar protein | | | | |
| flgM | BSU35430 | anti-SigD, regulation of flagellin, motility, and chemotaxis | | | | |
| yvyF | BSU35440 | similar to flagellar protein | | | | |
| comFC | BSU35450 | late competence gene | | | | |
| comFB | BSU35460 | late competence gene | | | | |
| comFA | BSU35470 | ATP-binding protein, late competence protein required for DNA binding and uptake | | | | |
| degV | BSU35480 | fatty acid binding protein | | | | |
| degU | BSU35490 | two-component response regulator, regulation of degradative enzyme and genetic competence | | | | |
| degS | BSU35500 | two-component sensor kinase for exoenzyme and competence regulation | | | | |
| yvyE | BSU35510 | unknown | | | | |
| tagV | BSU35520 | phosphotransferase, attachment of anionic polymers to peptidoglycan | | | | |
| tagO | BSU35530 | undecaprenyl-phosphate-GlcNAc-1-phosphate transferase, teichoic acid linkage unit synthesis | | | | |
| tuaH | BSU35540 | sugar transferase | | | | |
| tuaG | BSU35550 | sugar transferase | | | | |
| tuaF | BSU35560 | biosynthesis of teichuronic acid | | | | |
| tuaE | BSU35570 | repeating unit formation | | | | |
| tuaD | BSU35580 | UDP glucose 6-dehydrogenase | | | | |
| tuaC | BSU35590 | sugar transferase | | | | |
| tuaB | BSU35600 | polymer export | | | | |

| Gene | BSU_number [1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| tuaA/1 | BSU35609 | lipid carrier sugar transferase, disrupted pseudogene in B. subtilis 168 | | | | |
| tuaA/2 | BSU35610 | lipid carrier sugar transferase, disrupted pseudogene in B. subtilis 168 | | | | |
| lytC | BSU35620 | N-acetylmuramoyl-L-alanine amidase, required for flagellar function | | | | |
| lytB | BSU35630 | modifier protein of major autolysin LytC | | | | |
| lytA | BSU35640 | secretion of major autolysin LytC | | | | |
| tagU | BSU35650 | phosphotransferase, attachment of anionic polymers to peptidoglycan | | | | |
| mnaA | BSU35660 | UDP-N-acetylglucosamine 2-epimerase | | | | |
| gtaB | BSU35670 | UTP-glucose-1-phosphate uridylyltransferase, general stress protein | | | | |
| yvzH | BSU35679 | putative teichoic acid translocation permease protein (fragment) | | | | |
| ggaB | BSU35680 | galactosamine-containing minor teichoic acid biosynthesis, membrane protein | | | | |
| ggaA | BSU35690 | galactosamine-containing minor teichoic acid biosynthesis | | | | |
| yvzI | BSU35698 | putative CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase (fragment) | | | | |
| yvzE | BSU35699 | putative UTP-glucose-1-phosphate uridylyltransferase (UDP-glucose pyrophosphorylase) (UDPGP) (fragment) | | | | |
| tagH | BSU35700 | ABC transporter for teichoic acid translocation (ATP-binding protein) | | | | |
| tagG | BSU35710 | ABC transporter for teichoic acid translocation (permease) | | | | |
| tagF | BSU35720 | CDP-glycerol:polyglycerol phosphate glycero-phosphotransferase | | | | |
| tagE | BSU35730 | UDP-glucose:polyglycerol phosphate glucosyltransferase | | | | |
| tagD | BSU35740 | glycerol-3-phosphate cytidylyltransferase | | | | |
| tagA | BSU35750 | UDP-N-acetyl-D-mannosamine transferase | | | | |
| tagB | BSU35760 | putative CDP-glycerol:glycerol phosphate glycerophosphotransferase | | | | |
| tagC | BSU35770 | possibly involved in polyglycerol phosphate teichoic acid biosynthesis | | | | |
| lytD | BSU35780 | glucosaminidase | | 🟦 | 🟦 | 🟦 |
| pmi | BSU35790 | mannose-6-phosphate isomerase | | 🟦 | 🟦 | 🟦 |
| gerBA | BSU35800 | nutrient receptor, germination response to the combination of glucose, fructose, and KCl | | 🟦 | 🟦 | 🟦 |
| gerBB | BSU35810 | nutrient receptor | | 🟦 | 🟦 | 🟦 |
| gerBC | BSU35820 | nutrient receptor | | 🟦 | 🟦 | 🟦 |
| ywtG | BSU35830 | general stress protein, similar to metabolite transport protein | | 🟦 | 🟦 | 🟦 |
| tagT | BSU35840 | phosphotransferase, attachment of anionic polymers to peptidoglycan | | 🟦 | 🟦 | 🟦 |
| ywtE | BSU35850 | unknown | | 🟦 | 🟦 | 🟦 |
| pgdS | BSU35860 | gamma-DL-glutamyl hydrolase | | 🟦 | 🟦 | 🟦 |
| capE | BSU35870 | unknown | | 🟦 | 🟦 | 🟦 |
| capA | BSU35880 | similar to capsular polyglutamate biosynthesis | | 🟦 | 🟦 | 🟦 |
| capC | BSU35890 | capsular polyglutamate biosynthesis | | 🟦 | 🟦 | 🟦 |
| capB | BSU35900 | capsular polyglutamate biosynthesis | | 🟦 | 🟦 | 🟦 |
| rbsR | BSU35910 | transcriptional repressor of the ribose operon | | 🟦 | 🟦 | 🟦 |
| rbsK | BSU35920 | ribokinase | | 🟦 | 🟦 | 🟦 |
| rbsD | BSU35930 | ribose ABC transporter (membrane protein) | | 🟦 | 🟦 | 🟦 |
| rbsA | BSU35940 | ribose ABC transporter (ATP-binding protein) | | 🟦 | 🟦 | 🟦 |
| rbsC | BSU35950 | ribose ABC transporter (permease) | | 🟦 | 🟦 | 🟦 |
| rbsB | BSU35960 | ribose ABC transporter (binding protein) | | 🟦 | 🟦 | 🟦 |
| ywsB | BSU35970 | general stress protein, survival of ethanol and salt stresses | | 🟦 | 🟦 | 🟦 |
| ywsA | BSU35980 | unknown | | 🟦 | 🟦 | 🟦 |
| ywrO | BSU35990 | similar to NAD(P)H oxidoreductase | | | | |
| alsD | BSU36000 | acetolactate decarboxylase | | | | |
| alsS | BSU36010 | acetolactate synthase | | | | |
| alsR | BSU36020 | transcriptional activator of the alsS-alsD operon | | | | |
| ywrK | BSU36030 | similar to arsenical pump membrane protein | | | | |
| ywrJ | BSU36040 | unknown | | 🟦 | 🟦 | 🟦 |
| cotB | BSU36050 | spore coat protein (outer) | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| cotH | BSU36060 | spore coat protein (inner) |  | ■ | ■ | ■ |
| cotG | BSU36070 | spore coat protein |  | ■ | ■ | ■ |
| ywrF | BSU36080 | unknown |  | ■ | ■ | ■ |
| ywrE | BSU36090 | unknown |  | ■ | ■ | ■ |
| ywrD | BSU36100 | unknown |  | ■ | ■ | ■ |
| chrS | BSU36110 | transcriptional repressor (Lrp family) of the ***chrS***-*ywrB-ywrA* operon |  | ■ | ■ | ■ |
| ywrB | BSU36120 | subunit of chromate exporter (with YwrA) |  | ■ | ■ | ■ |
| ywrA | BSU36130 | subunit of chromate exporter (with YwrB) |  | ■ | ■ | ■ |
| ywqO | BSU36140 | unknown |  | ■ | ■ | ■ |
| ywqN | BSU36150 | unknown |  | ■ | ■ | ■ |
| ywqM | BSU36160 | similar to transcriptional regulator (LysR family) |  | ■ | ■ | ■ |
| ywqL | BSU36170 | endonuclease V |  | ■ | ■ | ■ |
| ywqK | BSU36180 | unknown |  | ■ | ■ | ■ |
| ywqJ | BSU36190 | putative toxin |  | ■ | ■ | ■ |
| ywqI | BSU36200 | unknown |  | ■ | ■ | ■ |
| ywqH | BSU36210 | unknown |  | ■ | ■ | ■ |
| ywqG | BSU36220 | unknown |  | ■ | ■ | ■ |
| ugd | BSU36230 | UDP-glucose dehydrogenase |  |  |  |  |
| ptpZ | BSU36240 | phosphotyrosin protein phosphatase, antagonist to PtkA |  |  |  |  |
| ptkA | BSU36250 | protein tyrosine kinase |  |  |  |  |
| tkmA | BSU36260 | transmembrane modulator of PtkA activity, activates PtkA autophosphorylation and substrate phosphorylation |  |  |  |  |
| ywzD | BSU36269 | unknown |  |  |  |  |
| ywqB | BSU36270 | unknown |  |  |  |  |
| ywqA | BSU36280 | similar to SNF2 helicase |  |  |  |  |
| ywpJ | BSU36290 | unknown |  |  |  |  |
| glcR | BSU36300 | transcriptional repressor (DeoR family) |  |  |  |  |
| ssbB | BSU36310 | single-strand DNA-binding protein |  |  |  |  |
| ywpG | BSU36320 | unknown |  |  |  |  |
| ywpF | BSU36330 | unknown |  |  |  |  |
| ywpE | BSU36340 | similar to sortase, but lacking the membrane anchor |  |  |  |  |
| ywpD | BSU36350 | two-component orphan sensor kinase |  |  |  |  |
| mscL | BSU36360 | large conductance mechanosensitive channel protein, prevents selective release of cytoplasmic proteins in a hypotonic environment |  |  |  |  |
| ywpB | BSU36370 | β-hydroxyacyl-(acyl carrier protein) dehydratase |  |  |  |  |
| rapD | BSU36380 | response regulator aspartate phosphatase, controls ComA activity |  |  |  |  |
| flhP | BSU36390 | flagellar hook-basal body protein, required for hook assembly |  |  |  |  |
| flhO | BSU36400 | flagellar basal-body rod protein, required for hook assembly |  |  |  |  |
| mbl | BSU36410 | cell-shape determining protein |  |  |  |  |
| spoIIID | BSU36420 | transcriptional regulator (repressor or activator) of a subset of sigma-E-dependent genes |  |  |  |  |
| usd | BSU36430 | putative spoIIID leader peptide |  |  |  |  |
| ywoH | BSU36440 | similar to transcriptional regulator (MarR family) |  |  |  |  |
| ywoG | BSU36450 | similar to antibiotic resistance protein |  |  |  |  |
| ywoF | BSU36460 | unknown |  |  |  |  |
| pucI | BSU36470 | allantoin permease |  |  |  |  |
| ywoD | BSU36480 | similar to transporter |  |  |  |  |
| ywoC | BSU36490 | unknown |  |  |  |  |
| ywoB | BSU36500 | unknown |  |  |  |  |
| nrgA | BSU36510 | ammonium transporter, required at low ammonium concentration |  |  |  |  |
| nrgB | BSU36520 | nitrogen-regulated PII-like protein |  |  |  |  |
| bcrC | BSU36530 | undecaprenyl pyrophosphate phosphatase, bacitracin resistance |  |  |  |  |
| ywnJ | BSU36540 | unknown |  |  |  |  |
| spoIIQ | BSU36550 | component of the SpoIIIA-SpoIIQ type III secretion system residing in the forespore membrane |  |  |  |  |
| ywnH | BSU36560 | similar to phosphinothricin acetyltransferase |  |  |  |  |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ywnG | BSU36570 | unknown | | | | |
| ywnF | BSU36580 | unknown | | | | |
| clsA | BSU36590 | cardiolipin synthase, major enzyme | | | | |
| mta | BSU36600 | transcriptional activator of multidrug-efflux transporter genes, activates ymfD expression | | | | 🟦 |
| ywnC | BSU36610 | unknown | | | | 🟦 |
| ywnB | BSU36620 | unknown | | | | 🟦 |
| ywnA | BSU36630 | unknown | | | | 🟦 |
| ureC | BSU36640 | urease (alpha subunit) | | | | 🟦 |
| ureB | BSU36650 | urease (beta subunit) | | | | 🟦 |
| ureA | BSU36660 | urease (gamma subunit) | | | | 🟦 |
| ywzE | BSU36668 | unknown, putative pseudogene | | | | 🟦 |
| ywzF | BSU36669 | unknown, putative pseudogene | | | | 🟦 |
| csbD | BSU36670 | general stress protein | | | | 🟦 |
| ywmF | BSU36680 | unknown | | | | 🟦 |
| rapB | BSU36690 | response regulator aspartate phosphatase, dephosphorylates Spo0F-P, control of the phosphorelay | | | | 🟦 |
| moaA | BSU36700 | molybdopterin precursor biosynthesis | | | | |
| fdhD | BSU36710 | putative subunit of an respiration oxidoreductase | | | | |
| ywmE | BSU36720 | general stress protein, survival of ethanol stress | | | | |
| ywmD | BSU36730 | unknown | | | | |
| ywmC | BSU36740 | unknown | | | | |
| spoIID | BSU36750 | required for complete dissolution of the asymmetric septum | | | | |
| murAA | BSU36760 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | | | | |
| ywmB | BSU36770 | unknown | | | | |
| ywzB | BSU36780 | unknown | | | | |
| ywmA | BSU36790 | unknown | | | | |
| atpC | BSU36800 | ATP synthase, F1 complex (subunit epsilon) | | | | |
| atpD | BSU36810 | ATP synthase, F1 complex (subunit beta) | | | | |
| atpG | BSU36820 | ATP synthase, F1 complex (subunit gamma) | | | | |
| atpA | BSU36830 | ATP synthase, F1 complex (subunit alpha) | | | | |
| atpH | BSU36840 | ATP synthase, F1 complex (subunit delta) | | | | |
| atpF | BSU36850 | ATP synthase, Fo complex (subunit b) | | | | |
| atpE | BSU36860 | ATP synthase, Fo complex (subunit c) | | | | |
| atpB | BSU36870 | ATP synthase, Fo complex (subunit a) | | | | |
| atpI | BSU36880 | ATP synthase (subunit i) | | | | |
| upp | BSU36890 | uracil phosphoribosyltransferase | | | | |
| glyA | BSU36900 | serine hydroxymethyltransferase | | | | |
| ywlG | BSU36910 | unknown | | | | |
| ywlF | BSU36920 | ribose-5-phosphate isomerase | | | | |
| ywlE | BSU36930 | protein tyrosine phosphatase | | | | |
| ywlD | BSU36940 | unknown | | | | |
| tsaC | BSU36950 | L-threonylcarbamoyl-AMP synthase, biosynthesis of the hypermodified base threonylcarbamoyladenosine (t(6)A) | | | | |
| ywlB | BSU36960 | general stress protein | | | | |
| spoIIR | BSU36970 | required for processing of pro-SigE | | | | |
| ywlA | BSU36980 | unknown | | | | |
| ywkF | BSU36990 | unknown | | | | |
| ywkE | BSU37000 | similar to N5-glutamine methyltransferase that modifies peptide release factors | | | | |
| prfA | BSU37010 | peptide chain release factor 1 | | | | |
| ywkD | BSU37020 | unknown | | | | |
| racA | BSU37030 | cell division protein: attaches the chromosome to the cell pole | | | | |
| ywkB | BSU37040 | unknown | | | | |
| maeA | BSU37050 | malic enzyme | | | | |
| tdk | BSU37060 | thymidine kinase | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| rpmE | BSU37070 | ribosomal protein L31 | | | | |
| rho | BSU37080 | transcriptional termination protein | | | | |
| glpX | BSU37090 | class II fructose-1,6-bisphosphatase, gluconeogenesis | | | | |
| murAB | BSU37100 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | | | | |
| ywjH | BSU37110 | transaldolase | | | | |
| | | | | | | |
| fbaA | BSU37120 | fructose 1,6-bisphosphate aldolase, glycolytic/ gluconeogenic enzyme | | | | |
| spo0F | BSU37130 | phosphotransferase of the sporulation initiation phosphorelay | | | | |
| ywjG | BSU37140 | unknown | | | | |
| pyrG | BSU37150 | CTP synthase (NH3, glutamine) | | | | |
| rpoE | BSU37160 | RNA polymerase delta subunit | | | | |
| acdA | BSU37170 | acyl-CoA dehydrogenase | | | | |
| fadF | BSU37180 | similar to iron-sulphur-binding reductase | | | | |
| ywjE | BSU37190 | minor cardiolipin synthetase | | | | |
| ywjD | BSU37200 | sporulation specific UV-damage-endonuclease | | | | |
| ywjC | BSU37210 | general stress protein | | | | |
| ywjB | BSU37220 | unknown | | | | |
| ywjA | BSU37230 | similar to ABC transporter (ATP-binding protein) | | | | |
| ywiE | BSU37240 | minor cardiolipin synthetase, general stress protein | | | | |
| narI | BSU37250 | nitrate reductase (gamma subunit) | | | | |
| narJ | BSU37260 | nitrate reductase (protein J) | | | | |
| narH | BSU37270 | nitrate reductase (beta subunit) | | | | |
| narG | BSU37280 | nitrate reductase (alpha subunit) | | | | |
| arfM | BSU37290 | regulation of anaerobic genes | | | | |
| ywiC | BSU37300 | unknown | | | | |
| fnr | BSU37310 | transcriptional regulator of anaerobic genes | | | | |
| narK | BSU37320 | nitrite extrusion protein | | | | |
| argS | BSU37330 | arginyl-tRNA synthetase, universally conserved protein | | | | |
| ywiB | BSU37340 | unknown | | | | |
| sboA | BSU37350 | subtilosin A | | 🟦 | 🟦 | 🟦 |
| sboX | BSU37360 | bacteriocin-like product | | 🟦 | 🟦 | 🟦 |
| albA | BSU37370 | radical S-adenosylmethionine enzyme, antilisterial bacteriocin (subtilosin) production | | 🟦 | 🟦 | 🟦 |
| albB | BSU37380 | antilisterial bacteriocin (subtilosin) production | | 🟦 | 🟦 | 🟦 |
| albC | BSU37390 | ABC transporter (ATP-binding protein), export of antilisterial bacteriocin (subtilosin) | | 🟦 | 🟦 | 🟦 |
| albD | BSU37400 | ABC transporter (membrane protein), export of antilisterial bacteriocin (subtilosin) | | 🟦 | 🟦 | 🟦 |
| albE | BSU37410 | antilisterial bacteriocin (subtilosin) production | | 🟦 | 🟦 | 🟦 |
| albF | BSU37420 | antilisterial bacteriocin (subtilosin) production | | 🟦 | 🟦 | 🟦 |
| albG | BSU37430 | antilisterial bacteriocin (subtilosin) production | | 🟦 | 🟦 | 🟦 |
| ywhL | BSU37440 | unknown | | | | |
| ywhK | BSU37450 | unknown | | | | |
| rapF | BSU37460 | response regulator aspartate phosphatase, controls ComA activity | | | | |
| phrF | BSU37470 | response regulator aspartate phosphatase (RapF) regulator | | | | |
| ywhH | BSU37480 | unknown | | | | |
| speB | BSU37490 | agmatinase | | | | |
| speE | BSU37500 | spermidine synthase | | | | |
| pbpG | BSU37510 | penicillin-binding protein 2d | | | | |
| ywhD | BSU37520 | unknown | | | | |
| ywhC | BSU37530 | unknown | | | | |
| ywhB | BSU37540 | similar to 4-oxalocrotonate tautomerase | | | | |
| ywhA | BSU37550 | similar to transcriptional regulator (MarR family) | | | | |
| thrZ | BSU37560 | threonyl-tRNA synthetase (minor) | | | | |
| mmr | BSU37570 | methylenomycin A resistance protein | | | | |
| ywgB | BSU37580 | unknown | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ywgA | BSU37590 | unknown | | | | |
| ywfO | BSU37600 | unknown | | | | |
| ywzC | BSU37610 | unknown | | | | |
| rsfA | BSU37620 | probable regulator of transcription of SigF-dependent genes | | | | |
| ywfM | BSU37630 | unknown | | | | |
| lipL | BSU37640 | GcvH:E2 amidotransferase | | | | |
| cysL | BSU37650 | transcriptional activator of the cysJ-cysI operon | | | | |
| pta | BSU37660 | phosphotransacetylase | | | | |
| hemQ | BSU37670 | heme-binding protein, essential for heme biosynthesis | | | | |
| bacG | BSU37680 | short chain reductase involved in bacilysin synthesis | | 🟦 | 🟦 | 🟦 |
| bacF | BSU37690 | aminotransferase involved in bacilysin synthesis | | 🟦 | 🟦 | 🟦 |
| bacE | BSU37700 | efflux protein for bacilysin excretion, self-protection against bacilysin | | 🟦 | 🟦 | 🟦 |
| bacD | BSU37710 | alanine-anticapsin ligase | | 🟦 | 🟦 | 🟦 |
| bacC | BSU37720 | bacilysin biosynthesis oxidoreductase | | 🟦 | 🟦 | 🟦 |
| bacB | BSU37730 | oxidase that catalyzes the synthesis of 2-oxo-3-(4-oxocyclohexa-2,5-dienyl)propanoic acid | | 🟦 | 🟦 | 🟦 |
| bacA | BSU37740 | bacilysin biosynthesis protein, prephenate decarboxylase | | 🟦 | 🟦 | 🟦 |
| ywfA | BSU37750 | similar to chloramphenicol resistance | | | | |
| rocC | BSU37760 | amino acid permease | | | | |
| rocB | BSU37770 | involved in arginine and ornithine utilization | | | | |
| rocA | BSU37780 | 3-hydroxy-1-pyrroline-5-carboxylate dehydrogenase | | | | |
| rocG | BSU37790 | trigger enzyme: catabolic glutamate dehydrogenase induced by arginine, ornithine or proline | | | | |
| sivA | BSU37800 | inhibitor of KinA autophosphorylation, and subsequently of entry into sporulation | | 🟦 | 🟦 | 🟦 |
| spsL | BSU37810 | dTDP-4-dehydrorhamnose-3,5-epimerase, spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsK | BSU37820 | dTDP-4-dehydrorhamnose reductase, spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsJ | BSU37830 | dTDP-glucose-4,6-dehydratase, spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsI | BSU37840 | glucose-1-phosphate thymidylyltransferase, spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsG | BSU37850 | spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsF | BSU37860 | spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsE | BSU37870 | spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsD | BSU37880 | spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsC | BSU37890 | spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsB | BSU37900 | spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| spsA | BSU37910 | spore coat polysaccharide synthesis | | 🟦 | 🟦 | 🟦 |
| gerQ | BSU37920 | spore coat protein, necessary for the proper localization of CwlJ | | 🟦 | 🟦 | 🟦 |
| ywdK | BSU37930 | unknown | | 🟦 | 🟦 | 🟦 |
| ywdJ | BSU37940 | unknown | | 🟦 | 🟦 | 🟦 |
| ywdI | BSU37950 | unknown | | 🟦 | 🟦 | 🟦 |
| ywdH | BSU37960 | similar to aldehyde dehydrogenase | | 🟦 | 🟦 | 🟦 |
| ung | BSU37970 | uracil-DNA glycosylase | | | | |
| ywdF | BSU37980 | unknown | | | | |
| ywdE | BSU37990 | unknown | | | | |
| ywdD | BSU38000 | unknown | | | | |
| ywzG | BSU38018 | unknown | | | | |
| pdxK | BSU38020 | pyridoxine, pyridoxal, and pyridoxamine kinase | | | | |
| ywdA | BSU38030 | unknown | | | | |
| sacA | BSU38040 | phosphosucrase | | | | |
| sacP | BSU38050 | trigger enzyme: sucrose-specific phosphotransferase system, EIIBC component of the PTS | | | | |
| ywcJ | BSU38060 | similar to nitrite transporter | | | | |
| sacT | BSU38070 | transcriptional antiterminator for the sacP-sacA operon | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| ywcI | BSU38080 | unknown | | | | |
| vpr | BSU38090 | minor extracellular serine protease | | 🟦 | 🟦 | 🟦 |
| ywcH | BSU38100 | similar to monooxygenase | | | | |
| nfrA | BSU38110 | Spx-dependent FMN-containing NADPH-linked nitro/flavin reductase, stress protein | | | | |
| rodA | BSU38120 | control of cell shape and elongation | | | | |
| ywcE | BSU38130 | holin, required for spore morphogenesis and germination | | | | |
| qoxD | BSU38140 | cytochrome aa3 quinol oxidase (subunit IV) | | | | |
| qoxC | BSU38150 | cytochrome aa3 quinol oxidase (subunit III) | | | | |
| qoxB | BSU38160 | cytochrome aa3 quinol oxidase (subunit I) | | | | |
| qoxA | BSU38170 | cytochrome aa3 quinol oxidase (subunit II) | | | | |
| ywzA | BSU38180 | general stress protein | | | | |
| galT | BSU38190 | galactose-1-phosphate uridylyltransferase | | | | |
| galK | BSU38200 | galactokinase | | | | |
| gtaC | BSU38210 | teichoic acid glycosylation protein | | | | |
| ywcC | BSU38220 | transcription repressor (TetR family), controls SlrA expression | | | | |
| slrA | BSU38229 | anti-repressor, antagonist of SinR, involved in control of flagellar genes and eps and yqxM-sipW-tasA operons | | | | |
| ywcB | BSU38230 | unknown | | | | |
| ywcA | BSU38240 | similar to Na+-dependent symport | | | | |
| ywbO | BSU38250 | unknown | | | | |
| efeB | BSU38260 | elemental iron uptake system, heme peroxidase | | | | |
| efeO | BSU38270 | lipoprotein, elemental iron uptake system (binding protein), high affinity uptake of ferric iron (Fe(III)) | | | | |
| efeU | BSU38280 | elemental iron uptake system (permease), high affinity uptake of ferric iron (Fe(III)) | | | | |
| thiE | BSU38290 | thiamine-phosphate diphosphorylase | | | | |
| thiM | BSU38300 | hydroxyethylthiazole kinase | | | | |
| ywbI | BSU38310 | similar to transcriptional regulator (LysR family) | | | | |
| ywbH | BSU38320 | putative holin | | | | |
| ywbG | BSU38330 | unknown | | | | |
| ywbF | BSU38340 | unknown | | | | |
| ywbE | BSU38350 | unknown | | | | |
| ywbD | BSU38360 | unknown | | | | |
| glxA | BSU38370 | glyoxalase I | | | | |
| ywbB | BSU38380 | unknown | | 🟦 | 🟦 | 🟦 |
| ywbA | BSU38390 | PTS, putative EIIC component | | 🟦 | 🟦 | 🟦 |
| epr | BSU38400 | minor extracellular serine protease, involved in control of swarming motility | | 🟦 | 🟦 | 🟦 |
| sacX | BSU38410 | trigger enzyme: sucrose-specific phosphotransferase system, EIIBC component of the PTS (low affinity) | | | | |
| sacY | BSU38420 | transcriptional antiterminator for sacB and sacX-sacY (acts at high sucrose concentrations) | | | | |
| gspA | BSU38430 | general stress protein | | | | |
| ywaF | BSU38440 | unknown | | | | |
| ywaE | BSU38450 | similar to transcriptional regulator (MarR family) | | | | |
| tyrZ | BSU38460 | tyrosyl-tRNA synthetase (minor) | | | | |
| ywaD | BSU38470 | double-zinc aminopeptidase | | | | |
| sasA | BSU38480 | (p)ppGpp synthetase, small alarmone synthetase | | | | |
| menA | BSU38490 | probable 1,4-dihydroxy-2-naphthoate octaprenyltransferase | | | | |
| ywzH | BSU38499 | unknown | | | | 🟦 |
| dltA | BSU38500 | D-alanyl-D-alanine carrier protein ligase | | | | 🟦 |
| dltB | BSU38510 | D-alanine transfer from Dcp to undecaprenol-phosphate | | | | 🟦 |
| dltC | BSU38520 | D-alanine carrier protein | | | | 🟦 |
| dltD | BSU38530 | D-alanine transfer from undecaprenol-phosphate to the poly(glycerophosphate) chain | | | | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| dltE | BSU38540 | D-alanine transfer from undecaprenol-phosphate to the poly(glycerophosphate) chain | | | | ■ |
| ywaA | BSU38550 | branched-chain amino acid aminotransferase | | | | |
| licH | BSU38560 | 6-phospho-beta-glucosidase | | | ■ | ■ |
| licA | BSU38570 | lichenan-specific phosphotransferase system, EIIA component of the PTS | | | ■ | ■ |
| licC | BSU38580 | lichenan-specific phosphotransferase system, EIIC component of the PTS | | | ■ | ■ |
| licB | BSU38590 | trigger enzyme: lichenan-specific phosphotransferase system, EIIB component of the PTS | | | ■ | ■ |
| licR | BSU38600 | transcriptional activator of the licB-licC-licA-licH operon | | | ■ | ■ |
| yxzF | BSU38610 | general stress protein | | | ■ | ■ |
| aag | BSU38620 | general stress protein, similar to DNA-3-methyladenine glycosidase II | | | ■ | ■ |
| katX | BSU38630 | catalase, general stress protein | | | ■ | ■ |
| yxlH | BSU38640 | similar to multidrug-efflux transporter | | | ■ | ■ |
| yxlG | BSU38650 | similar to ABC transporter (membrane protein) | | | ■ | ■ |
| yxlF | BSU38660 | similar to ABC transporter (ATP-binding protein) | | | ■ | ■ |
| yxlE | BSU38670 | unknown | | | ■ | ■ |
| yxlD | BSU38680 | negative regulation of SigY-directed transcription of the sigY operon | | | ■ | ■ |
| yxlC | BSU38690 | putative anti-SigY protein | | | ■ | ■ |
| sigY | BSU38700 | RNA polymerase ECF-type sigma factor SigY | | | ■ | ■ |
| yxlA | BSU38710 | similar to purine-cytosine permease | | | ■ | ■ |
| yxkO | BSU38720 | ADP/ATP-dependent NAD(P)H-hydrate dehydratase, general stress protein, survival of ethanol stress | | | ■ | ■ |
| cydD | BSU38730 | ABC transporter required for expression of cytochrome bd (ATP-binding protein) | | | | |
| cydC | BSU38740 | ABC transporter required for expression of cytochrome bd (ATP-binding protein) | | | | |
| cydB | BSU38750 | cytochrome bd ubiquinol oxidase (subunit II), high affinity terminal oxidase | | | | |
| cydA | BSU38760 | cytochrome bd ubiquinol oxidase (subunit I), high affinity terminal oxidase | | | | |
| cimH | BSU38770 | transporter for citrate (proton symport) | | | ■ | |
| yxkI | BSU38780 | similar to heat shock protein | | | ■ | |
| yxzE | BSU38790 | unknown | | | ■ | |
| yxkH | BSU38800 | unknown | | ■ | ■ | ■ |
| msmX | BSU38810 | multiple sugar ABC transporter (ATP-binding protein) | | ■ | ■ | ■ |
| yxkF | BSU38820 | unknown | | ■ | ■ | ■ |
| aldY | BSU38830 | aldehyde dehydrogenase (NAD), general stress protein | | ■ | ■ | ■ |
| yxkD | BSU38840 | unknown | | ■ | ■ | ■ |
| yxkC | BSU38850 | unknown | | ■ | ■ | ■ |
| galE | BSU38860 | UDP glucose 4-epimerase | | ■ | ■ | ■ |
| yxkA | BSU38870 | unknown | | ■ | ■ | ■ |
| yxjO | BSU38880 | similar to transcriptional regulator (LysR family) | | ■ | ■ | ■ |
| yxjN | BSU38890 | unknown | | ■ | ■ | ■ |
| yxjM | BSU38900 | two-component sensor kinase | | ■ | ■ | ■ |
| yxjL | BSU38910 | two-component response regulator | | ■ | ■ | ■ |
| pepT | BSU38920 | peptidase T (tripeptidase), zinc-dependent | | ■ | ■ | ■ |
| yxjJ | BSU38930 | general stress protein, survival of ethanol and salt stresses | | | ■ | |
| yxjI | BSU38940 | unknown | | | ■ | |
| yxjH | BSU38950 | putative methionine synthase | | | ■ | |
| yxjG | BSU38960 | putative methionine synthase | | | ■ | |
| yxjF | BSU38970 | similar to gluconate 5-dehydrogenase | | | ■ | |
| scoB | BSU38980 | probable succinyl CoA:3-oxoacid CoA-transferase (subunit B) | | | ■ | |
| scoA | BSU38990 | probable succinyl CoA:3-oxoacid CoA-transferase (subunit A) | | | ■ | |
| yxjC | BSU39000 | unknown | | | ■ | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yxjB | BSU39010 | unknown | | | ■ | |
| nupG | BSU39020 | purine nucleoside transporter | | | ■ | |
| yxiT/1 | BSU39029 | part of the yxiT pseudogene | | | ■ | |
| yxiT/2 | BSU39030 | part of the yxiT pseudogene | | | ■ | |
| yxiS | BSU39040 | general stress protein, survival of ethanol and salt stresses | | | ■ | |
| katE | BSU39050 | catalase, general stress protein | | | ■ | |
| citH | BSU39060 | sporulation-specific secondary transporter of divalent metal ions/citrate complexes | | | ■ | |
| bglS | BSU39070 | endo-beta-1,3-1,4 glucanase | | ■ | ■ | ■ |
| licT | BSU39080 | transcriptional antiterminator of the bglP-bglH operon and the bglS gene | | ■ | ■ | ■ |
| yxiP | BSU39090 | unknown | | ■ | ■ | ■ |
| yxiO | BSU39100 | unknown | | ■ | ■ | ■ |
| deaD | BSU39110 | DEAD-box RNA helicase | | ■ | ■ | ■ |
| yxiM | BSU39120 | similar to rhamnogalacturonan acetylesterase | | ■ | ■ | ■ |
| yxzI | BSU39129 | unknown, putative pseudogene | | ■ | ■ | ■ |
| yxzJ | BSU39139 | unknown | | ■ | ■ | ■ |
| yxiK | BSU39140 | unknown | | ■ | ■ | ■ |
| yxiJ | BSU39150 | unknown | | ■ | ■ | ■ |
| yxiI | BSU39160 | unknown | | ■ | ■ | ■ |
| yxzG | BSU39170 | unknown | | ■ | ■ | ■ |
| yxiH | BSU39180 | unknown | | ■ | ■ | ■ |
| yxiG | BSU39190 | unknown | | ■ | ■ | ■ |
| yxzC | BSU39200 | unknown | | ■ | ■ | ■ |
| yxiF | BSU39210 | unknown | | ■ | ■ | ■ |
| yxxG | BSU39220 | immunity protein, protects the cell against the toxic activity of WapA | | | ■ | |
| wapA | BSU39230 | cell wall-associated protein precursor, contact-dependent growth inhibition protein | | | ■ | |
| yxxF | BSU39240 | unknown | | | ■ | ■ |
| yxiE | BSU39250 | unknown | | | ■ | ■ |
| bglH | BSU39260 | phospho-beta-glucosidase | | | ■ | ■ |
| bglP | BSU39270 | trigger enzyme: beta-glucoside-specific phosphotransferase system, EIIBCA of the PTS | | | ■ | ■ |
| yxxE | BSU39280 | unknown | | | ■ | ■ |
| yxxD | BSU39290 | antitoxin | | | ■ | ■ |
| yxiD | BSU39300 | toxin | | | ■ | ■ |
| yxiC | BSU39310 | unknown | | | ■ | ■ |
| yxiB | BSU39320 | unknown | | | ■ | ■ |
| abn2 | BSU39330 | endo-1,5-alpha-L-arabinosidase | | | ■ | ■ |
| yxzL | BSU39339 | unknown | | | ■ | ■ |
| hutP | BSU39340 | transcriptional antiterminator of the hut operon | | | ■ | ■ |
| hutH | BSU39350 | histidase | | | | ■ |
| hutU | BSU39360 | urocanase | | | | ■ |
| hutI | BSU39370 | imidazolone-5-propionate hydrolase | | | | ■ |
| hutG | BSU39380 | formiminoglutamate hydrolase | | | | ■ |
| hutM | BSU39390 | histidine permease | | | | ■ |
| pdp | BSU39400 | pyrimidine nucleoside phosphorylase | | | | |
| nupC | BSU39410 | pyrimidine nucleoside transport protein | | | | |
| dra | BSU39420 | deoxyribose-phosphate aldolase | | | | |
| deoR | BSU39430 | transcriptional repressor of the dra-nupC-pdp operon | | | | |
| yxxB | BSU39440 | unknown | | ■ | ■ | ■ |
| yxeR | BSU39450 | ethanolamine transporter in/out via proton symport | | ■ | ■ | ■ |
| yxeQ | BSU39460 | unknown | | ■ | ■ | ■ |
| sndB | BSU39470 | sulphur compound N-deacetylase | | ■ | ■ | ■ |
| yxeO | BSU39480 | putative cysteine ABC transporter (ATP-binding protein) | | ■ | ■ | ■ |
| yxeN | BSU39490 | putative cysteine ABC transporter (permease) | | ■ | ■ | ■ |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yxeM | BSU39500 | putative cysteine ABC transporter (binding protein) | | 🟦 | 🟦 | 🟦 |
| snaB | BSU39510 | N-formylcysteine deformylase | | 🟦 | 🟦 | 🟦 |
| yxeK | BSU39520 | similar to monooxygenase | | 🟦 | 🟦 | 🟦 |
| yxeJ | BSU39530 | unknown | | 🟦 | 🟦 | 🟦 |
| yxeI | BSU39540 | penicillin acylase | | 🟦 | 🟦 | 🟦 |
| yxeH | BSU39550 | unknown | | 🟦 | 🟦 | 🟦 |
| yxeG | BSU39560 | unknown | | 🟦 | 🟦 | 🟦 |
| yxeF | BSU39570 | unknown | | 🟦 | 🟦 | 🟦 |
| yxeE | BSU39580 | spore coat protein | | 🟦 | 🟦 | 🟦 |
| yxeD | BSU39590 | unknown | | 🟦 | 🟦 | 🟦 |
| yxeC | BSU39600 | unknown | | 🟦 | 🟦 | 🟦 |
| yxeB | BSU39610 | hydroxamate siderophore ABC transporter (only ferrioxamine) (binding protein) | | 🟦 | 🟦 | 🟦 |
| yxeA | BSU39620 | unknown | | 🟦 | 🟦 | 🟦 |
| yxdM | BSU39630 | similar to ABC transporter (permease) | | 🟦 | 🟦 | 🟦 |
| yxdL | BSU39640 | similar to ABC transporter (ATP-binding protein) | | 🟦 | 🟦 | 🟦 |
| yxdK | BSU39650 | two-component sensor kinase | | 🟦 | 🟦 | 🟦 |
| yxdJ | BSU39660 | two-component response regulator, regulation of the ABC transporter YxdL-YxdM | | 🟦 | 🟦 | 🟦 |
| iolJ | BSU39670 | 2-deoxy-5-keto-gluconic acid-6-phosphate aldolase | | 🟦 | 🟦 | 🟦 |
| iolI | BSU39680 | inosose isomerase, converts 2KMI to 1-keto-D-chiro-inositol | | 🟦 | 🟦 | 🟦 |
| iolH | BSU39690 | unknown, may be involved in myo-inositol catabolism | | 🟦 | 🟦 | 🟦 |
| iolG | BSU39700 | inositol 2-dehydrogenase | | 🟦 | 🟦 | 🟦 |
| iolF | BSU39710 | inositol transport protein | | 🟦 | 🟦 | 🟦 |
| iolE | BSU39720 | 2-keto-myo-inositol dehydratase, dehydration of 2-keto-myo-inositol (2nd reaction) | | 🟦 | 🟦 | 🟦 |
| iolD | BSU39730 | formation of 5-deoxy-D-glucuronic acid (3rd reaction) | | 🟦 | 🟦 | 🟦 |
| iolC | BSU39740 | formation of 2-deoxy-5-keto-gluconic acid-6-phosphate (5th reaction) | | 🟦 | 🟦 | 🟦 |
| iolB | BSU39750 | formation of 2-deoxy-5-keto-gluconic acid (4th reaction) | | 🟦 | 🟦 | 🟦 |
| iolA | BSU39760 | methylmalonate-semialdehyde dehydrogenase (acylating) | | 🟦 | 🟦 | 🟦 |
| iolR | BSU39770 | transcriptional repressor of the iol operon, DeoR family | | 🟦 | 🟦 | 🟦 |
| iolS | BSU39780 | unknown, may be involved in myo-inositol catabolism | | 🟦 | 🟦 | 🟦 |
| yxcE | BSU39790 | unknown | | 🟦 | 🟦 | 🟦 |
| yxcD | BSU39800 | unknown | | 🟦 | 🟦 | 🟦 |
| csbC | BSU39810 | general stress protein, putative sugar transporter | | | | |
| htpG | BSU39820 | class III heat-shock protein (molecular chaperone) | | | | |
| yxcA | BSU39830 | unknown | | | | |
| yxbG | BSU39840 | general stress protein, similar to glucose 1-dehydrogenase | | | | |
| yxbF | BSU39850 | unknown | | | | |
| aldX | BSU39860 | aldehyde dehydrogenase (NAD) | | | | |
| yxbD | BSU39870 | unknown | | | | |
| yxbC | BSU39880 | unknown | | | | |
| yxbB | BSU39890 | unknown | | | | |
| yxbA | BSU39900 | putative D-aspartate ligase | | | | |
| yxnB | BSU39910 | unknown | | | | |
| asnH | BSU39920 | asparagine synthase (glutamine-hydrolysing) | | | | |
| yxaM | BSU39930 | similar to antibiotic resistance protein | | 🟦 | 🟦 | 🟦 |
| yxaL | BSU39940 | similar to Ser/Thr kinase, increases the processivity of the PcrA helicase | | 🟦 | 🟦 | 🟦 |
| yxaJ | BSU39950 | unknown | | 🟦 | 🟦 | 🟦 |
| yxaI | BSU39960 | membrane protein | | 🟦 | 🟦 | 🟦 |
| yxaH | BSU39970 | putative transporter | | 🟦 | 🟦 | 🟦 |
| qdoI | BSU39980 | Fe-containing quercetin 2,3-dioxygenase | | 🟦 | 🟦 | 🟦 |
| qdoR | BSU39990 | transcriptional regulator, control of yxaG-yxaH and lmrA-lmrB | | 🟦 | 🟦 | 🟦 |
| yxnA | BSU40000 | general stress protein, similar to glucose 1-dehydrogenase, survival of ethanol stress | | 🟦 | 🟦 | 🟦 |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| yxaD | BSU40010 | similar to transcriptional regulator (MarR family) | | 🟦 | 🟦 | 🟦 |
| yxzK | BSU40021 | unknown | | 🟦 | 🟦 | 🟦 |
| yxaC | BSU40022 | unknown | | 🟦 | 🟦 | 🟦 |
| yxaB | BSU40030 | general stress protein, putative exopolysaccaride synthase, important for biofilm formation | | 🟦 | 🟦 | 🟦 |
| yxaA | BSU40040 | putative glycerate kinase | | | | |
| gntR | BSU40050 | transcriptional repressor of the gluconate operon | | | | 🟦 |
| gntK | BSU40060 | gluconokinase | | | | 🟦 |
| gntP | BSU40070 | gluconate permease | | | | 🟦 |
| gntZ | BSU40080 | 6-phosphogluconate dehydrogenase | | | | 🟦 |
| ahpC | BSU40090 | alkyl hydroperoxide reductase (small subunit) | | | | 🟦 |
| ahpF | BSU40100 | alkyl hydroperoxide reductase (large subunit) / NADH dehydrogenase | | | | 🟦 |
| bglA | BSU40110 | 6-phospho-beta-glucosidase | | | | 🟦 |
| yyzE | BSU40120 | similar to PTS, EIIA component (truncated) | | | | 🟦 |
| yydK | BSU40130 | similar to transcriptional regulator (GntR family) | | | | 🟦 |
| yyzN | BSU40139 | unknown | | | | 🟦 |
| yydJ | BSU40140 | ABC transporter (resistance), permease, export of YydF | | | | 🟦 |
| yydI | BSU40150 | ABC transporter (resistance), ATP-binding protein, export of YydF | | | | 🟦 |
| yydH | BSU40160 | similar to ABC transporter (membrane protein), processing of YydF | | | | 🟦 |
| yydG | BSU40170 | oxidoreductase, modification of YydF | | | | 🟦 |
| yydF | BSU40180 | secreted peptide, controls LiaRS activity | | | | 🟦 |
| fbp | BSU40190 | fructose-1,6-bisphosphatase, involved in gluconeogenesis | | | | |
| yydD | BSU40200 | unknown | | 🟦 | 🟦 | 🟦 |
| yydC | BSU40210 | unknown | | 🟦 | 🟦 | 🟦 |
| yydB | BSU40220 | unknown | | 🟦 | 🟦 | 🟦 |
| yydA | BSU40230 | unknown | | 🟦 | 🟦 | 🟦 |
| yyzF | BSU40239 | unknown | | 🟦 | 🟦 | 🟦 |
| yycS | BSU40240 | unknown | | 🟦 | 🟦 | 🟦 |
| yycR | BSU40250 | similar to formaldehyde dehydrogenase | | 🟦 | 🟦 | 🟦 |
| yyzG | BSU40259 | unknown | | 🟦 | 🟦 | 🟦 |
| yycQ | BSU40260 | unknown | | 🟦 | 🟦 | 🟦 |
| yycP | BSU40270 | unknown | | 🟦 | 🟦 | 🟦 |
| yycO | BSU40280 | unknown | | 🟦 | 🟦 | 🟦 |
| yycN | BSU40290 | putative acetyltransferase | | 🟦 | 🟦 | 🟦 |
| rapG | BSU40300 | response regulator aspartate phosphatase, controls DegU activity | | 🟦 | 🟦 | 🟦 |
| phrG | BSU40310 | response regulator aspartate phosphatase (RapG) regulator | | 🟦 | 🟦 | 🟦 |
| rocF | BSU40320 | arginase | | | | |
| rocE | BSU40330 | amino acid permease | | | | |
| rocD | BSU40340 | ornithine transaminase | | | | |
| rocR | BSU40350 | transcriptional activator of arginine utilization operons | | | | |
| yyzO | BSU40359 | unknown, putative pseudogene | | | | |
| htrC | BSU40360 | similar to quality control membrane serine protease HtrA | | | | |
| walJ | BSU40370 | coordination of cell division with DNA replication | | | | |
| yycI | BSU40380 | negative effector of WalK, controls cell wall metabolism | | | | |
| yycH | BSU40390 | negative effector of WalK, controls cell wall metabolism | | | | |
| walK | BSU40400 | two-component sensor kinase, controls cell wall metabolism | | | | |
| walR | BSU40410 | two-component response regulator, controls cell wall metabolism | | | | |
| trnY-Asp- trnY-Glu- trnY-Lys- trnY-Phe | | | | | | |
| purA | BSU40420 | adenylosuccinate synthetase | | | | |
| yycE | BSU40430 | unknown | | | | |
| dnaC | BSU40440 | replicative DNA helicase | | | | |
| yycD | BSU40450 | general stress protein, survival of ethanol stress | | | | |
| yyzB | BSU40460 | unknown | | | | |
| yycC | BSU40470 | unknown | | | | |
| yycB | BSU40480 | similar to ABC transporter (permease) | | | | |
| yycA | BSU40490 | unknown | | | | |

| Gene | BSU_number[1] | Function | Δ6 | IIG-Bs27-47-24 | PG10 | PS38 |
|---|---|---|---|---|---|---|
| rplI | BSU40500 | ribosomal protein L9 | | | | |
| gdpP | BSU40510 | c-di-AMP phosphodiesterase, involved in stress signaling and response | | | | |
| yybS | BSU40520 | unknown | | | | |
| yyzH | BSU40529 | unknown | | | | |
| cotF | BSU40530 | spore coat protein | | | | |
| hypR | BSU40540 | MarR/DUF24-family transcription regulator, positively controls the nitroreductase gene (hypO) | | | | |
| ppaC | BSU40550 | inorganic pyrophosphatase | | | | |
| yybP | BSU40560 | unknown | | ■ | ■ | ■ |
| yybO | BSU40570 | similar to ABC transporter (permease) | | ■ | ■ | ■ |
| yyzI | BSU40573 | unknown, putative pseudogene | | ■ | ■ | ■ |
| yyzJ | BSU40574 | unknown, putative pseudogene | | ■ | ■ | ■ |
| yyzK | BSU40578 | unknown, putative pseudogene | | ■ | ■ | ■ |
| yyzL | BSU40579 | unknown, putative pseudogene | | ■ | ■ | ■ |
| yybN | BSU40580 | unknown | | ■ | ■ | ■ |
| yybM | BSU40590 | unknown | | ■ | ■ | ■ |
| yybL | BSU40600 | similar to ABC transporter (permease) | | ■ | ■ | ■ |
| yybK | BSU40610 | similar to ABC transporter (membrane protein) | | ■ | ■ | ■ |
| yybJ | BSU40620 | similar to ABC transporter (ATP-binding protein) | | ■ | ■ | ■ |
| yybI | BSU40630 | inner spore coat protein | | ■ | ■ | ■ |
| yybH | BSU40640 | unknown | | ■ | ■ | ■ |
| yybG | BSU40650 | unknown | | ■ | ■ | ■ |
| yybF | BSU40660 | similar to antibiotic resistance protein | | ■ | ■ | ■ |
| yybE | BSU40670 | similar to transcriptional regulator (LysR family) | | ■ | ■ | ■ |
| yybD | BSU40680 | unknown | | ■ | ■ | ■ |
| yybC | BSU40690 | unknown | | ■ | ■ | ■ |
| yybB | BSU40700 | unknown | | ■ | ■ | ■ |
| yybA | BSU40710 | similar to to transcriptional regulator (MarR family) | | ■ | ■ | ■ |
| yyaT | BSU40720 | unknown | | ■ | ■ | ■ |
| yyaS | BSU40730 | unknown | | ■ | ■ | ■ |
| yyaR | BSU40740 | similar to streptothricine acetyl-transferase | | ■ | ■ | ■ |
| yyaQ | BSU40750 | unknown | | ■ | ■ | ■ |
| yyaP | BSU40760 | unknown | | ■ | ■ | ■ |
| tetB | BSU40770 | multifunctional tetracycline/Na+ resistance protein | | ■ | ■ | ■ |
| tetL | BSU40780 | tetracycline resistance leader peptide | | ■ | ■ | ■ |
| yyaO | BSU40790 | unknown | | ■ | ■ | ■ |
| yyaN | BSU40800 | similar to transcriptional regulator (MerR family) | | ■ | ■ | ■ |
| yyaM | BSU40810 | unknown | | ■ | ■ | ■ |
| yyaL | BSU40820 | unknown | | ■ | ■ | ■ |
| yyaK | BSU40830 | unknown | | ■ | ■ | ■ |
| yyaJ | BSU40840 | unknown | | ■ | ■ | ■ |
| maa | BSU40850 | maltose O-acetyltransferase | | | | |
| yyaH | BSU40860 | unknown | | | | |
| ccpB | BSU40870 | transcriptional regulator (LacI family) | | | | |
| exoA | BSU40880 | apurinic/apyrimidinic endonuclease, multifunctional DNA-repair enzyme, important for spore dormance | | | | |
| rpsR | BSU40890 | ribosomal protein S18 | | | | |
| ssbA | BSU40900 | single-strand DNA-binding protein | | | | |
| rpsF | BSU40910 | ribosomal protein S6 | | | | |
| yyaF | BSU40920 | GTP-binding protein/ GTPase | | | | |
| yyaE | BSU40930 | similar to formate dehydrogenase | | | | |
| yyzM | BSU40939 | unknown | | | | |
| yyaD | BSU40940 | unknown | | | | |
| yyaC | BSU40950 | unknown | | | | |

| **Gene** | **BSU_number**[1] | **Function** | **Δ6** | **IIG-Bs27-47-24** | **PG10** | **PS38** |
|---|---|---|---|---|---|---|
| spo0J | BSU40960 | chromosome positioning near the pole and transport through the polar septum | | | | |
| soj | BSU40970 | centromere-like function involved in forespore chromosome partitioning / negative regulation of sporulation initiation | | | | |
| yyaB | BSU40980 | unknown | | | | |
| noc | BSU40990 | DNA-binding protein, spatial regulator of cell division to protect the nucleoid | | | | |
| rsmG | BSU41000 | 7-methylguanosine methyltransferase specific for the 16S rRNA, glucose-inhibited division protein | | | | |
| gidA | BSU41010 | glucose-inhibited division protein, tRNA uridine 5-carboxymethylaminomethyl modification enzyme | | | | |
| thdF | BSU41020 | GTP-binding protein, putative tRNA modification GTPase | | | | |
| jag | BSU41030 | SpoIIIJ-associated protein | | | | |
| spoIIIJ | BSU41040 | Sec-independent membrane protein translocase, essential for SigG activity at stage III | | | | |
| rnpA | BSU41050 | protein component of RNase P | | | | |
| rpmH | BSU41060 | ribosomal protein L34 | | | | |