

The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*

F. Kunst¹, N. Ogasawara², I. Moszer³, A. M. Albertini⁴, G. Alloni⁴, V. Azevedo⁵, M. G. Bertero^{3,4}, P. Bessières⁵, A. Bolotin⁵, S. Borchert⁶, R. Borriss⁷, L. Boursier³, A. Brans⁸, M. Braun⁹, S. C. Brignelli¹⁰, S. Bron¹¹, S. Brouillet^{3,12}, C. V. Bruschi¹³, B. Caldwell¹⁴, V. Capuano⁵, N. M. Carter¹⁰, S.-K. Choi¹⁵, J.-J. Codani¹⁶, I. F. Connerton¹⁷, N. J. Cummings¹⁷, R. A. Daniel¹⁸, F. Denizot¹⁹, K. M. Devine²⁰, A. Düsterhöft⁹, S. D. Ehrlich⁵, P. T. Emmerson²¹, K. D. Entian⁶, J. Errington¹⁸, C. Fabret¹⁹, E. Ferrari¹⁴, D. Foulger¹⁸, C. Fritz⁹, M. Fujita²², Y. Fujita²³, S. Fuma²⁴, A. Galizzi⁴, N. Galleron⁵, S.-Y. Ghim¹⁵, P. Glaser³, A. Goffeau²⁵, E. J. Golightly²⁶, G. Grandi²⁷, G. Guiseppi¹⁹, B. J. Guy¹⁰, K. Haga²⁸, J. Haiech¹⁹, C. R. Harwood¹⁰, A. Hénaut²⁹, H. Hilbert⁹, S. Holsappel¹¹, S. Hosono³⁰, M.-F. Hullo³, M. Itaya³¹, L. Jones³², B. Joris⁸, D. Karamata³³, Y. Kasahara², M. Klaerr-Blanchard³, C. Klein⁶, Y. Kobayashi³⁰, P. Koetter⁶, G. Koningstein³⁴, S. Krogh²⁰, M. Kumano²⁴, K. Kurita²⁴, A. Lapidus⁵, S. Lardinio⁸, J. Lauber⁹, V. Lazarevic³³, S.-M. Lee³⁵, A. Levine³⁶, H. Liu²⁸, S. Masuda³⁰, C. Mauël³³, C. Médigue^{3,12}, N. Medina³⁶, R. P. Mellado³⁷, M. Mizuno³⁰, D. Moestl³, S. Nakai², M. Noback¹¹, D. Noone²⁰, M. O'Reilly²⁰, K. Ogawa²⁴, A. Ogiwara³⁸, B. Oudega³⁴, S.-H. Park¹⁵, V. Parro³⁷, T. M. Pohl³⁹, D. Portetelle⁴⁰, S. Porwollik⁷, A. M. Prescott¹⁸, E. Presecan³, P. Pujic⁵, B. Purnelle²⁵, G. Rapoport¹, M. Rey²⁶, S. Reynolds³³, M. Rieger⁴¹, C. Rivolta³³, E. Rocha^{3,12}, B. Roche³⁶, M. Rose⁶, Y. Sadaie²², T. Sato³⁰, E. Scanlan²⁰, S. Schleich³, R. Schroeter⁷, F. Scoffone⁴, J. Sekiguchi⁴², A. Sekowska³, S. J. Seror³⁶, P. Serror⁵, B.-S. Shin¹⁵, B. Soldo³³, A. Sorokin⁵, E. Tacconi⁴, T. Takagi⁴³, H. Takahashi²⁸, K. Takemaru³⁰, M. Takeuchi³⁰, A. Tamakoshi²⁴, T. Tanaka⁴⁴, P. Terpstra¹¹, A. Tognoni²⁷, V. Tosato¹³, S. Uchiyama⁴², M. Vandenberg⁴⁰, F. Vannier⁴⁶, A. Vassarotti⁴⁵, A. Viari¹², R. Wambutt⁴⁶, E. Wedler⁴⁶, H. Wedler⁴⁶, T. Weitzenegger³⁹, P. Winters¹⁴, A. Wipat¹⁰, H. Yamamoto⁴², K. Yamane²⁴, K. Yasumoto²⁸, K. Yata²², K. Yoshida²³, H.-F. Yoshikawa²⁸, E. Zumstein⁵, H. Yoshikawa² & A. Danchin³

¹ Institut Pasteur, Unité de Biochimie Microbienne, 25 rue du Docteur Roux, 75724 Paris Cedex 15, France

² Nara Institute of Science and Technology, Graduate School of Biological Sciences, Ikoma, Nara 630-01, Japan

³ Institut Pasteur, Unité de Régulation de l'Expression Génétique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France

⁴ Dipartimento di Genetica e Microbiologia, Università di Pavia, Via Abbategrasso 207, 27100 Pavia, Italy

⁵ INRA, Génétique Microbienne, Domaine de Vilvert, 78352 Jouy-en-Josas Cedex, France

⁶ Institut für Mikrobiologie, J. W. Goethe-Universität, Marie Curie Strasse 9, 60439 Frankfurt/Maine, Germany

⁷ Institut für Genetik und Mikrobiologie, Humboldt Universität, Chausseestrasse 17, D-10115 Berlin, Germany

⁸ Centre d'Ingénierie des Protéines, Université de Liège, Institut de Chimie B6, Sart Tilman, B-4000 Liège, Belgium

⁹ QIAGEN GmbH, Max-Volmer-Strasse 4, D-40724 Hilden, Germany

¹⁰ Department of Microbiological, Immunological and Virological Sciences, The Medical School, University of Newcastle, Framlington Place, Newcastle upon Tyne NE2 4HH, UK

¹¹ Department of Genetics, University of Groningen, Kerklaan 30, 9751 NN Haren, The Netherlands

¹² Atelier de Bioinformatique, Université Paris VI, 12 rue Cuvier, 75005 Paris, France

¹³ ICGEB, AREA Science Park, Padriciano 99, I-34012 Trieste, Italy

¹⁴ Genencor International, 925 Page Mill Road, Palo Alto, California 94304-1013, USA

¹⁵ Bacterial Molecular Genetics Research Unit, Applied Microbiology Research Division, KRIBB, PO Box 115, Yusong, Taejeon 305-600, Korea

¹⁶ INRIA, Domaine de Voluceau, PB 105, 78153 Le Chesnay Cedex, France

¹⁷ Institute of Food Research, Department of Food Macromolecular Science, Reading Laboratory, Earley Gate, Whiteknights Road, Reading RG6 6BZ, UK

¹⁸ Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE, UK

¹⁹ Laboratoire de Chimie Bactérienne, CNRS BP 71, 31 Chemin Joseph Aiguier, 13402 Marseille Cedex 09, France

²⁰ Department of Genetics, Trinity College, Lincoln Place Gate, Dublin 2, Republic of Ireland

²¹ Department of Biochemistry and Genetics, The Medical School, University of Newcastle, Framlington Place, Newcastle upon Tyne, NE2 4HH, UK

²² Radioisotope Center, National Institute of Genetics, Mishima, Shizuoka-ken 411, Japan

²³ Department of Biotechnology, Faculty of Engineering, Fukuyama University, Higashimura-cho, Fukuyama-shi, Hiroshima 729-02, Japan

²⁴ Institute of Biological Sciences, Tsukuba University, Tsuiuba-shi, Ibaraki 305, Japan

²⁵ Faculté des Sciences Agronomiques, Unité de Biochimie Physiologique, Université Catholique de Louvain, Place Croix du Sud, 2-20 B-1348 Louvain-la-Neuve, Belgium

²⁶ Novo Nordisk Biotech, 1445 Drew Avenue, Davis, California 95616-4880, USA

²⁷ Eniricerca, Via Maritano 26, San Donato Milanese, 20097 Milan, Italy

²⁸ Institute of Molecular and Cellular Biology, The University of Tokyo, Bunkyo-ku, Tokyo 113, Japan

²⁹ Laboratoire Génome et Informatique, Université de Versailles, Bâtiment Buffon, 45 Avenue des États-Unis, 78035 Versailles Cedex, France

³⁰ Faculty of Agriculture, Tokyo University of Agriculture and Technology, Fuchu, Tokyo 183, Japan

³¹ Mitsubishi Kasei Institute of Life Sciences, 11 Minamiooia, Machida-shi, Tokyo 194, Japan

³² Institut Pasteur, Service d'Informatique Scientifique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France

³³ Institut de Génétique et Biologie Microbiennes, Université de Lausanne, 19 rue César Roux, 1005 Lausanne, Switzerland

³⁴ Department of Molecular Microbiology, MBW/BCA, Faculty of Biology, Vrije Universiteit Amsterdam, De Boelelaan 1087, 1081 HV Amsterdam, The Netherlands

³⁵ Chongju University College of Science and Engineering, Chongju City, Korea

³⁶ Institut de Génétique et Microbiologie, Université Paris Sud, URA CNRS 2225, Université Paris XI—Bâtiment 409, 91405 Orsay Cedex, France

³⁷ Centro Nacional de Biotecnología (CSIC), Campus Universidad Autónoma, Cantoblanco, 28049 Madrid, Spain

³⁸ National Institute of Basic Biology, 38 Nishigounaka, Myoudaiji-chou, Okazaki 444, Japan

³⁹ Gesellschaft für Analyse-Technik und Consulting mbH, Fritz-Arnold Straße 23, D-78467 Konstanz, Germany

⁴⁰ Department of Microbiology, Faculty of Agronomy, 6 Avenue du Maréchal Juin, B-5030 Gembloux, Belgium

⁴¹ Biotech Research, BMF, Wilhelmsfeld, Klingelstrasse 35, D-69434 Hirschhorn, Germany

⁴² Department of Applied Biology, Faculty of Textile Science and Technology, Shinshu University 3-15-1, Tokida, Ueda-shi, Nagano 386, Japan

⁴³ Human Genome Center, Institute of Medical Science, University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108, Japan

⁴⁴ Department of Marine Science, School of Marine Science and Technology, Tokai University, 3-20-1 Orido Shimizu, Shizuoka 424, Japan

⁴⁵ European Commission, DG XII-E-1, SDME 8/78, Rue de la Loi 200, B-1049 Brussels, Belgium

⁴⁶ AGOWA GmbH, Glienicke Weg 185, 12489 Berlin, Germany

***Bacillus subtilis* is the best-characterized member of the Gram-positive bacteria. Its genome of 4,214,810 base pairs comprises 4,100 protein-coding genes. Of these protein-coding genes, 53% are represented once, while a quarter of the genome corresponds to several gene families that have been greatly expanded by gene duplication, the largest family containing 77 putative ATP-binding transport proteins. In addition, a large proportion of the genetic capacity is devoted to the utilization of a variety of carbon sources, including many plant-derived molecules. The identification of five signal peptidase genes, as well as several genes for components of the secretion apparatus, is important given the capacity of *Bacillus* strains to secrete large amounts of industrially important enzymes. Many of the genes are involved in the synthesis of secondary metabolites, including antibiotics, that are more typically associated with *Streptomyces* species. The genome contains at least ten prophages or remnants of prophages, indicating that bacteriophage infection has played an important evolutionary role in horizontal gene transfer, in particular in the propagation of bacterial pathogenesis.**

Techniques for large-scale DNA sequencing have brought about a revolution in our perception of genomes. Together with our understanding of intermediary metabolism, it is now realistic to envisage a time when it should be possible to provide an extensive chemical definition of many living organisms. During the past couple of years, the genome sequences of *Haemophilus influenzae*, *Mycoplasma genitalium*, *Synechocystis* PCC6803, *Methanococcus jannaschii*, *M. pneumoniae*, *Escherichia coli*, *Helicobacter pylori*, *Archaeoglobus fulgidus* and the yeast *Saccharomyces cerevisiae* have been published in their entirety¹⁻⁸, and at least 40 prokaryotic genomes are currently being sequenced. Regularly updated lists of genome sequencing projects are available at <http://www.mcs.anl.gov/home/gaasterl/genomes.html> (Argonne National Laboratory, Illinois, USA) and <http://www.tigr.org> (TIGR, Rockville, Maryland, USA).

The list of sequenced microorganisms does not currently include a paradigm for Gram-positive bacteria, which are known to be important for the environment, medicine and industry. *Bacillus subtilis* has been chosen to fill this gap^{9,10} as its biochemistry, physiology and genetics have been studied intensely for more than 40 years. *B. subtilis* is an aerobic, endospore-forming, rod-shaped bacterium commonly found in soil, water sources and in association with plants. *B. subtilis* and its close relatives are an important source of industrial enzymes (such as amylases and proteases), and much of the commercial interest in these bacteria arises from their capacity to secrete these enzymes at gram per litre concentrations. It has therefore been used for the study of protein secretion and for development as a host for the production of heterologous proteins¹¹. *B. subtilis* (*natto*) is also used in the production of Natto, a traditional Japanese dish of fermented soya beans.

Under conditions of nutritional starvation, *B. subtilis* stops growing and initiates responses to restore growth by increasing metabolic diversity. These responses include the induction of motility and chemotaxis, and the production of macromolecular hydrolases (proteases and carbohydrases) and antibiotics. If these responses fail to re-establish growth, the cells are induced to form chemically, irradiation- and desiccation-resistant endospores. Sporulation involves a perturbation of the normal cell cycle and the differentiation of a binucleate cell into two cell types. The division of the cell into a smaller forespore and a larger mother cell, each with an entire copy of the chromosome, is the first morphological indication of sporulation. The former is engulfed by the latter and differential expression of their respective genomes, coupled to a complex network of interconnected regulatory path-

ways and developmental checkpoints, culminates in the programmed death and lysis of the mother cell and release of the mature spore¹². In an alternative developmental process, *B. subtilis* is also able to differentiate into a physiological state, the competent state, that allows it to undergo genetic transformation¹³.

General features of the DNA sequence

Analysis at the replicon level. The *B. subtilis* chromosome has 4,214,810 base pairs (bp), with the origin of replication coinciding with the base numbering start point¹⁴, and the terminus at about 2,017 kilobases (kb)¹⁵. The average G + C ratio is 43.5%, but it varies considerably throughout the chromosome. This average is also different if one considers the nucleotide content of coding sequences, for which G and A (24% and 30%) are relatively more abundant than their counterparts C and T (20% and 26%). A significant inversion of the relative G - C/G + C ratio is visible at the origin of replication, indicating asymmetry of the nucleotide composition between the replication leading strand and the lagging strand¹⁶. Several A + T-rich islands are likely to reveal the signature of bacteriophage lysogens or other inserted elements (Fig. 1, see below).

We have analysed the abundance of oligonucleotides ('words') in the genome in various ways: absolute number of words in the genomic text, or comparison with the expected count derived from several models of the chromosome (for example, Markov models, or simulated sequences in which previously known features of the genome were conserved¹⁷). Comparing the experimental data with various models allowed us to define under- and overrepresentation of words in the experimental data set by reference to the model chosen. In general, the dinucleotide bias follows closely what has been described for other prokaryotes^{18,19}, in that the dinucleotides most overrepresented are AA, TT and GC, whereas those less represented are TA, AC and GT. Plots of the frequencies of AG, GA, CT and TC in sliding windows along the chromosome show dramatic decreases or increases around the origin and terminus of replication (data not shown). Trinucleotide frequency, directly related to the coding frame, will be discussed below. The distribution of words of four, five and six nucleotides shows significant correlations between the usage of some words and replication (several such oligonucleotides are very significantly overrepresented in one of the strands and underrepresented in the other one).

Setting a statistical cut-off for the significance of duplications at 10^{-3} , we expected duplication by chance of words longer than 24 nucleotides to be rare²⁰. In fact, the genome of *B. subtilis* contains a plethora of such duplications, some of them appearing more than

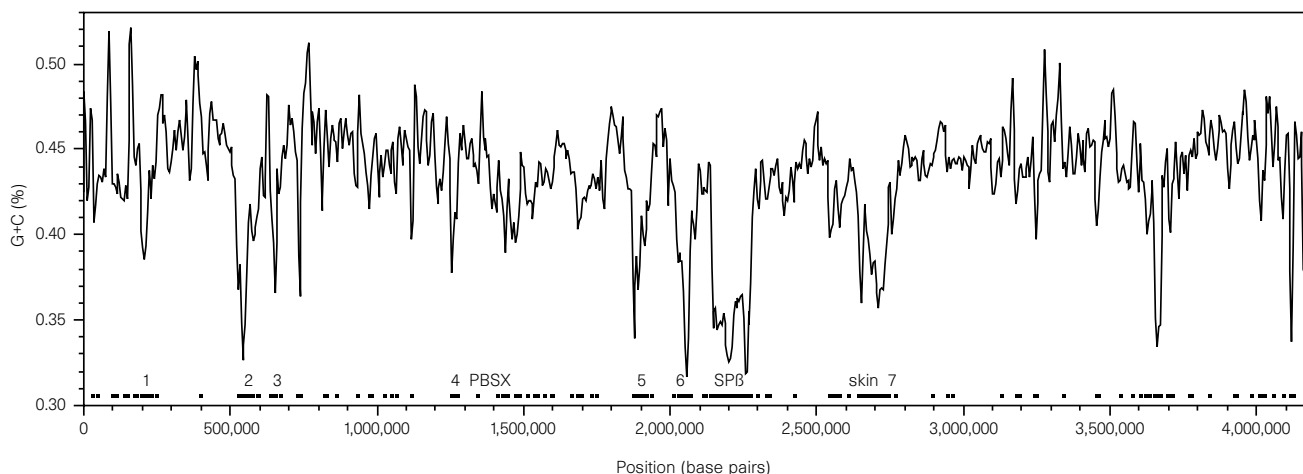


Figure 1 Distribution of A + T-rich islands along the chromosome of *B. subtilis*, in sliding windows of 10,000 nucleotides, with a step of 5,000 nucleotides. Location of genes from class 3 according to codon usage analysis (see Fig. 4) is indicated by dots at the bottom of the graph. Known prophages (PBSX, SP β and *skin*) are indicated by their names, and prophage-like elements are numbered from 1 to 7.

twice. Among the duplications, we identified, as expected, the ribosomal RNA genes and their flanking regions, but also regions known to correspond to genes comprising long sequence repeats (such as *pks* and *srf*). We also found several regions that were not expected: a 182-bp repetition within the *yyaL* and *yyaO* genes; a 410-bp repetition between the *yxaK* and *yxaL* genes; an internal duplication of 174 bp inside *ycdI*; and significant duplications in the regions involved in the transcriptional control of several genes (such as 118 bp repeated three times between *yxbB* and *yxbC*). Finally, we found several repetitions at the borders of regions that might be involved in bacteriophage integration.

The most prominent duplication was a 190-bp element that was repeated 10 times in the chromosome. Multiple alignment of the ten repeats showed that they could be classified into two subfamilies with six and three copies each, plus a copy of what appears to be a chimera. Similar sequences have also been described in the closely related species *Bacillus licheniformis*^{21,22}. A striking feature of these repeats is that they are only found in half of the chromosome, at either side of the origin of replication, with five repeats on each side. Furthermore, with the exception of the most distal repeat at position 737,062, they lie in the same orientation with respect to the movement of the replication fork (Figs 2 and 3). Putative secondary structures conserved by compensatory mutations, as well as an insert in three of the copies, suggest that this element could indicate a structural RNA molecule.

Analysis at the transcription and translation level. Over 4,000 putative protein coding sequences (CDSs) have been identified, with an average size of 890 bp, covering 87% of the genome sequence (Fig. 2). We found that 78% of the genes started with ATG, 13% with TTG and 9% with GTG, which compares with 85%, 3% and 14%, respectively, in *E. coli*⁸. Fifteen genes (eight in the predicted CDSs in bacteriophage SPβ) exhibiting unusual start codons (namely ATT and CTG) were also identified through their

similarities to known genes in other organisms or because they had a good GeneMark prediction (see Methods). This has not yet been substantiated experimentally. However, in the case of the gene coding for translation initiation factor 3, the similarity with its *E. coli* counterpart strongly suggests that the initiation codon is ATT, as is the case in *E. coli*.

We have not annotated CDSs that largely or entirely overlap existing genes, although such genes (for example, *comS* inside *srfAA*) certainly exist. It is also likely that some of the short CDSs present in the *B. subtilis* genome have been overlooked. For these reasons and possible sequencing errors, the estimated number of *B. subtilis* CDSs will fluctuate around the present figure of 4,100.

In several cases, in-frame termination codons or frameshifts were confirmed to be present on the chromosome (for example, an internal termination codon in *ywtF*, or the known programmed translational frameshift in *prfB*), indicating that the genes are either non-functional (pseudogenes) or subject to regulatory processes. It will therefore be of interest to determine whether these gene features are conserved in related *Bacillus* species, especially as strain 168 is derived from the Marburg strain that was subjected to X-ray irradiation²³.

A few regions do not have any identifiable feature indicating that they are transcribed: they could be 'grey holes' of the type described in *E. coli*²⁴. Preliminary studies involving all regions of more than 400 bp without annotated CDSs indicated that, of ~300 such regions, only 15% were likely to be really devoid of protein-coding sequences. One of the longest such regions, located between *yjfo* and *yjfn*, is 1,628 bp long. Grey holes seem generally to be clustered near the terminus of replication. However, a grey-hole cluster located at ~600 kb might be related to the temporary chromosome partition observed during the first stages of sporulation, when a segment of about one-third of the chromosome enters the prespore, and remains the sole part of the chromosome in the prespore for a significant transition period²⁵.

The codon usage of *B. subtilis* CDSs was analysed using factorial correspondence analysis¹⁷. We found that the CDSs of *B. subtilis* could be separated into three well-defined classes (Fig. 4). Class 1 comprises the majority of the *B. subtilis* genes (3,375 CDSs), including most of the genes involved in sporulation. Class 2 (188 CDSs) includes genes that are highly expressed under exponential growth conditions, such as genes encoding the transcription and translation machineries, core intermediary metabolism, stress proteins, and one-third of genes of unknown function. Class 3 (537 CDSs) contains a very high proportion of genes of unidentified function (84%), and the members of this class have codons enriched in A + T residues. These genes are usually clustered into groups between 15 and 160 genes (for example, bacteriophage SPβ) and correspond to the A + T-rich islands described above (Fig. 1). When they are of known function, or when their products display similarity to proteins of known function, they usually correspond to functions found in, or associated with, bacteriophages or transposons, as well as functions related to the cell envelope. This includes the region *ycd/ydd/yde* (40 genes that are missing in some *B. subtilis* strains²⁶), where gene products showing similarities to bacteriophage and transposon proteins are intertwined. Many of these genes are associated with virulence genes identified in pathogenic Gram-positive bacteria, suggesting that such virulence factors are transmitted horizontally among bacteria at a much higher frequency than previously thought. If we include these A + T-rich regions as possible cryptic phages, together with known bacteriophages or bacteriophage-like elements (SPβ, PBSX and the *skin* element), we find that the genome of *B. subtilis* 168 contains at least 10 such elements (Figs 2 and 3). Annotation of the corresponding regions often reveals the presence of genes that are similar to bacteriophage lytic enzymes, perhaps accounting for the observation that *B. subtilis* cultures are extremely prone to lysis.

The ribosomal RNA genes have been previously identified and

Table 1 Functional classification of the *Bacillus subtilis* protein-coding genes

The genes of known function or encoding products similar to known proteins in *B. subtilis* or in other organisms have been classified into functional categories (2,379 genes). The total number of genes in each category is indicated after the category title. Genes are listed in alphabetical order within each category, and their positions (in kilobases) on the *B. subtilis* chromosome are indicated after the gene names. A brief description is given for each gene. In some cases, interacting proteins have been indicated between brackets (for example, histidine kinases and response regulator, phosphatases and their substrates). More detailed and constantly updated information is available in the SubtiList database (see Methods). A preliminary assessment of the significance of sequence similarities was obtained through an automated procedure involving a combination between the BLAST2P probability and the percentage of amino-acid identity. Matches considered significant were re-examined manually. It should be emphasized that functions assigned to 'y' genes are based only on sequence similarity information with the best counterparts in protein databanks. Genes whose products are only similar to other unknown proteins, or not significantly similar to any other proteins in databanks (categories V and VI), were omitted.

Figure 2 General view of the *B. subtilis* chromosome. Arrows indicate the orientation of transcription. Genes are coloured according to their classification into six broad functional categories (blue, category I; green, category II; red, category III; orange, category IV; purple, category V; pink, category VI; see Table 1). Class 2 CDSs according to codon usage analysis are indicated by oblique hatches, and class 3 CDSs are indicated by vertical hatches. Ribosomal RNA genes are coloured in yellow. Transfer RNA genes are marked by triangles. Other RNA genes are represented as white arrows. Known genes (non-'y' genes) are printed in bold type. Putative transcription termination sites are represented as loops. Known prophages and prophage-like elements are indicated by brown hatches on the chromosome line. The 190-bp element repeated ten times is represented by hatched boxes.

shown to be organized into ten rRNA operons, mainly clustered around the origin of replication of the chromosome (Figs 2 and 3). In addition to the 84 previously identified tRNA genes, by using the Palingol²⁷ and tRNAscan²⁸ programs, we propose four putative new tRNA loci (at 1,262 kb, 1,945 kb, 2,003 kb and 2,899 kb), specific for lysine, proline and arginine (UUU, GGG, CCU and UCU anticodons, respectively). The 10S RNA involved in degradation of proteins made from truncated mRNA has been identified (*ssrA*), as well as the RNA component of RNase P (*rnpB*) and the 4.5S RNA involved in the secretion apparatus (*scr*).

There is a strong transcription orientation bias with respect to the movement of the replication fork: 75% of the predicted genes are transcribed in the direction of replication. Plotting the density of coding nucleotides in each strand along the chromosome readily identifies the replication origin and terminus (Fig. 3). To identify putative operons, we followed ref. 29 for describing Rho-independent transcription termination sites. This yielded ~1,630 putative terminators (340 of which were bidirectional). We retained only those that were located less than 100 bp downstream of a gene, or that were considered by the program to be 'very strong' (in order to account for possible erroneous CDSs). This yielded a total of ~1,250 terminators, with a mean operon size of three genes. A similar approach to the identification of promoters is problematical, especially because at least 14 sigma factors, recognizing different promoter sequences, have been identified in *B. subtilis*. Nevertheless, the consensus of the main vegetative sigma factor (σ^A) appears to be identical to its counterpart in *E. coli* (σ^{70}): 5'-TTGACA-*n*₁₇-TATAAT-3'. Relaxing the constraints of the similarity to sigma-specific consensus sequences led to an extremely high number of false-positive results, suggesting that the consensus-oriented approach to the identification of promoters should be replaced by another approach¹⁷.

Classification of gene products

Genes were classified according to ref. 14, based on the representation of cells as Turing machines in which one distinguishes between the machine and the program (Table 1). Using the BLAST2P software running against a composite protein databank compound of SWISS-PROT (release 34), TREMBL (release 3, update 1) and *B.*

subtilis proteins, we assigned at least one significant counterpart with a known function to 58% of the *B. subtilis* proteins. Thus for up to 42% of the gene products, the function cannot be predicted by similarity to proteins of known function: 4% of the proteins are similar only to other unknown proteins of *B. subtilis*; 12% are similar to unknown proteins from some other organism; and 26% of the proteins are not significantly similar to any other proteins in databanks. This preliminary analysis should be interpreted with caution, because only ~1,200 gene functions (30%) have been experimentally identified in *B. subtilis*. We used the 'y' prefix in gene names to emphasize that the function has not been ascertained (2,853 'y' genes, representing 70%).

Regulatory systems. Transcription regulatory proteins. Helix–turn–helix proteins form a large family of regulatory proteins found in both prokaryotes and eukaryotes. There are several classes, including repressors, activators and sigma factors. Using BLAST searches, we constructed consensus matrices for helix–turn–helix proteins to analyse the *B. subtilis* protein library. We identified 18 sigma or sigma-like factors, of which nine (including a new one) are of the SigA type. We also putatively identified 20 regulators (among which 18 were products of 'y' genes) of the GntR family, 19 regulators (15 'y' genes) of the LysR family, and 12 regulators (5 'y' genes) of the LacI family. Other transcription regulatory proteins were of the AraC family (11 members, 10 'y'), the Lrp family (7 members, 3 'y'), the DeoR family (6 members, 3 'y'), or additional families (such as the MarR, ArsR or TetR families). A puzzling observation is that several regulatory proteins display significant similarity to aminotransferases (seven such enzymes have been identified as showing similarity to repressors).

Two-component signal-transduction pathways. Two-component regulatory systems, consisting of a sensor protein kinase and a response regulator, are widespread among prokaryotes. We have identified 34 genes encoding response regulators in *B. subtilis*, most of which have adjacent genes encoding histidine kinases. Response regulators possess a well-conserved N-terminal phospho-acceptor domain³⁰, whereas their C-terminal DNA-binding domains share similarities with previously identified response regulators in *E. coli*, *Rhizobium meliloti*, *Klebsiella pneumoniae* or *Staphylococcus aureus*. Representatives of the four subfamilies recently identified in *E. coli*³¹

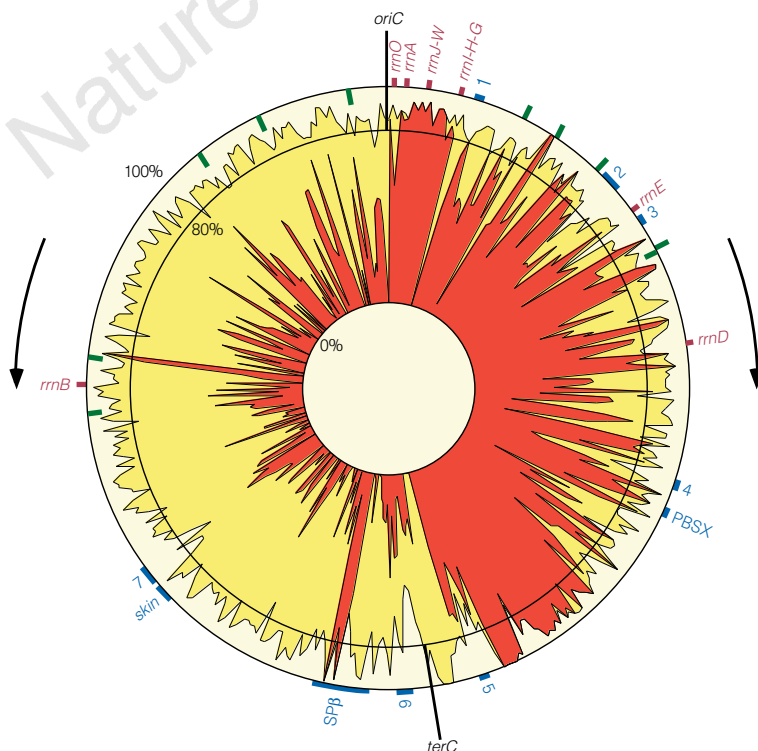


Figure 3 Density of coding nucleotides along the *B. subtilis* chromosome. Yellow stands for the density of coding nucleotides in both strands of the sequence; red indicates the density of coding nucleotides in the clockwise strand (nucleotides involved in genes transcribed in the clockwise orientation). The movement of the replication forks is represented by arrows. Ribosomal RNA operons are indicated by brown boxes. Known prophages and prophage-like elements are represented as blue lines. The 190-bp element repeated ten times is represented by green lines.

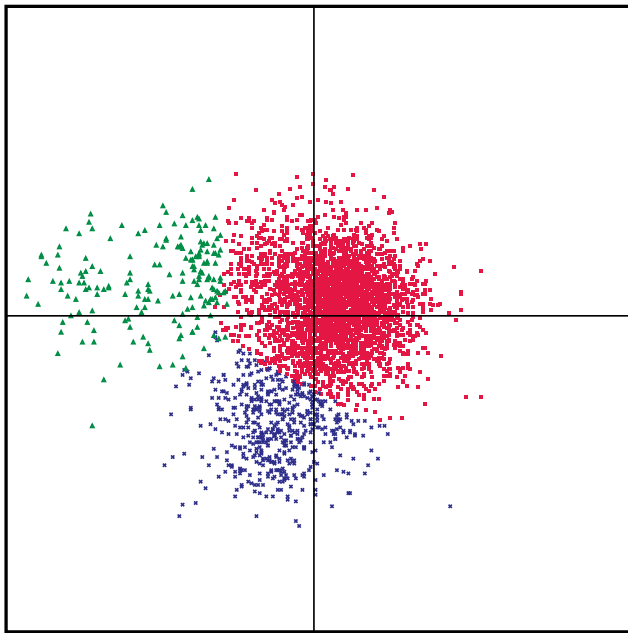


Figure 4 Factorial correspondence analysis of codon usage in the *B. subtilis* CDSs. Red dots, genes from class 1; green triangles, genes from class 2; blue crosses, genes from class 3. Class 2 contains genes coding for the translation and transcription machineries, and genes of the core intermediary metabolism. Class 3 genes correspond to codons strongly enriched in A or T in the wobble position; they generally belong to prophage-like inserts in the genome.

(OmpR, FixJ, CitB and LytR) have been identified in *B. subtilis*. In a fifth subfamily, CheY, the DNA-binding domain is absent. The DNA-binding domain of a single *B. subtilis* response regulator, YesN, shares similarity with regulatory proteins of the AraC family. **Quorum sensing.** The *B. subtilis* genome contains 11 aspartate phosphatase genes, whose products are involved in dephosphorylation of response regulators, that do not seem to have counterparts in Gram-negative bacteria such as *E. coli*. Downstream from the corresponding genes are some small genes, called *phr*, encoding regulatory peptides that may serve as quorum sensors³². Seven *phr* genes have been identified so far, including three new genes (*phrG*, *phrI* and *phrK*).

Protein secretion. It is known that *B. subtilis* and related *Bacillus* species, in particular *B. licheniformis* and *B. amyloliquefaciens*, have a high capacity to secrete proteins into the culture medium. Several genes encoding proteins of the major secretion pathway have been identified: *secA*, *secD*, *secE*, *secF*, *secY*, *ffh* and *ftsY*. Surprisingly, there is no gene for the SecB chaperone. It is thought that other chaperone(s) and targeting factor(s), such as Ffh and FtsY, may take over the SecB function. Further, although there is only one such gene in *E. coli*, five type I signal peptidase genes (*sipS*, *sipT*, *sipU*, *sipV* and *sipW*) have been found³³. The *lsp* gene, encoding a type II signal peptidase required for processing of lipo-modified precursors, was also identified. PrsA, located at the outer side of the membrane, is important for the refolding of several mature proteins after their translocation through the membrane.

Other families of proteins. ABC transporters were the most frequent class of proteins found in *B. subtilis*. They must be extremely important in Gram-positive bacteria, because they have an envelope comprising a single membrane. ABC transporters will therefore allow such bacteria to escape the toxic action of many compounds. We propose that 77 such transporters are encoded in the genome. In general they involve the interaction of at least three gene products, specified by genes organized into an operon. Other families comprised 47 transport proteins similar to facilitators (and perhaps sometimes part of the ABC transport systems), 18 amino-acid permeases (probably antiporters), and at least 16 sugar transporters belonging to the PEP-dependent phosphotransferase system.

General stress proteins are important for the survival of bacteria under a variety of environmental conditions. We identified 43 temperature-shock and general stress proteins displaying strong similarity to *E. coli* counterparts.

Missing genes. Histone-like proteins such as HU and H-NS have been identified in *E. coli*. We found that *B. subtilis* encodes two putative histone-like proteins that show similarity to *E. coli* HU, namely HBSu and YonN, but found no homologue to H-NS. It is known that the *hbs* gene encoding HBSu is essential, but we do not expect the *yonN* gene to be essential because it is present in the SP β prophage. IHF is similar to HU, and it is not known whether HBSu plays a similar role to that of IHF in *E. coli*. Similarly, no protein similar to FIS could be found.

Genes encoding products that interact with methylated DNA, such as *seqA* in *E. coli*, involved in the regulation of replication initiation timing, or *mutH*, the endonuclease recognizing the newly synthesized strand during mismatch repair at hemi-methylated

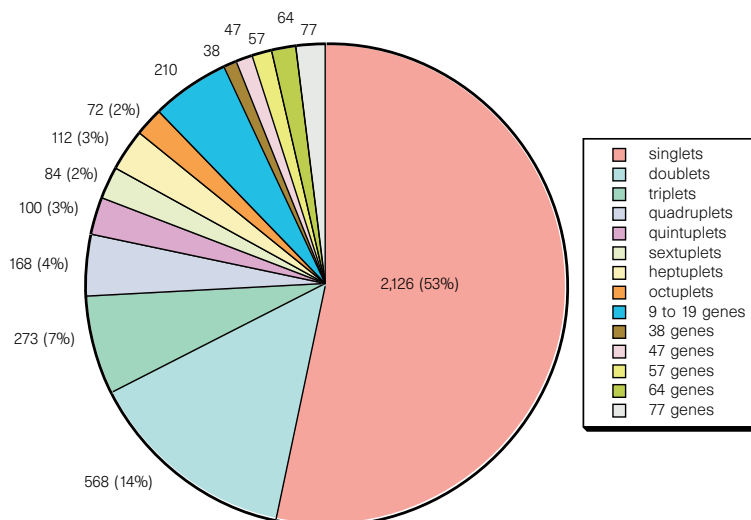


Figure 5 Gene paralogue distribution in the genome of *B. subtilis*. Each *B. subtilis* protein has been compared with all other proteins in the genome, using a Smith and Waterman algorithm. The baseline is established by making a similar

comparison using 100 independent random shuffles of the protein sequence (Z-score > 13).

GATC sites, are also missing. This is in line with the absence of known methylation in *B. subtilis*, equivalent to Dam methylation in *E. coli*. Similarly, *E. coli* *sfiA*, encoding an inhibitor of FtsZ action in the SOS response, has no counterpart in *B. subtilis*. In contrast, *B. subtilis* replication initiation-specific genes, such as *dnaB* and *dnaD*, are missing in *E. coli*. The exact counterpart of the *E. coli* *mukB* gene, involved in chromosome partitioning, does not exist in *B. subtilis*, but genes *spo0J* and *smc* (Smc is weakly similar to MukB), which are suggested to be involved in partitioning of the *B. subtilis* chromosome, are missing in *E. coli*.

Turnover of mRNA is controlled in *E. coli* by a 'degradosome' comprising RNase E. It has a counterpart in *B. subtilis*, but we failed to find a clear homologue of RNase E in this organism. Whether this is related to the role of ribosomal protein S1 as an RNA helicase involved in mRNA turnover in *E. coli* requires further investigation. In particular, a homologue of *rpsA* (S1 structural gene), *yfpD*, might be involved in a structure homologous to the degradosome³⁴.

Structurally unrelated genes of similar function. Several genes encode products that have similar functions in *E. coli* and *B. subtilis*, but have no evident common structure. This is the case for the helicase loader genes, *E. coli* *dnaC* and *B. subtilis* *dnaI*; the genes coding for the replication termination protein, *E. coli* *tus* and *B. subtilis* *rtp*; and the division topology specifier genes, *E. coli* *minE* and *B. subtilis* *divIVA*. The situation may even be more complex in multisubunit enzymes: *B. subtilis* synthesizes two DNA polymerase III α chains, one having 3'–5' proofreading exonuclease activity (PolC) and the other without the exonuclease activity (DnaE); in *E. coli*, only the latter exists. *E. coli* DNA polymerase II is structurally related to DNA polymerase α of eukaryotes, whereas *B. subtilis* YshC is related to DNA polymerase β .

Metabolism of small molecules

The type and range of metabolism used for the interconversion of low-molecular-weight compounds provide important clues to an organism's natural environment(s) and its biological activity. Here we briefly outline the main metabolic pathways of *B. subtilis* before the reconstruction of these pathways *in silico*, the correlation of genes with specific steps in the pathway, and ultimately the prediction of patterns of gene expression.

Intermediary metabolism. It has long been known that *B. subtilis* can use a variety of carbohydrates. As expected, it encodes an Embden–Meyerhof–Parnas glycolytic pathway, coupled to a functional tricarboxylic acid cycle. Further, *B. subtilis* is also able to grow anaerobically in the presence of nitrate as an electron acceptor. This metabolism is, at least in part, regulated by the FNR protein, binding to sites upstream of at least eight genes (four sites experimentally confirmed and four putative sites). A noteworthy feature of *B. subtilis* metabolism is an apparent requirement of branched short-chain carboxylic acids for lipid biosynthesis³⁵. Branched-chain 2-keto acid decarboxylase activity exists and may be linked to a variety of genes, suggesting that *B. subtilis* can synthesize and utilize linear branched short-chain carboxylic acids and alcohols.

Amino-acid and nucleotide metabolism. Pyrimidine metabolism of *B. subtilis* seems to be regulated in a way fundamentally different from that of *E. coli*, as it has two carbamylphosphate synthetases (one specific for arginine synthesis, the other for pyrimidine). Additionally, the aspartate transcarbamylase of *B. subtilis* does not act as an allosteric regulator as it does in *E. coli*. As in other microorganisms, pyrimidine deoxyribonucleotides are synthesized from ribonucleoside diphosphates, not triphosphates. The cytidine diphosphate required for DNA synthesis is derived from either the salvage pathway of mRNA turnover or from the synthesis of phospholipids and components of the cell wall. This means that polynucleotide phosphorylase is of fundamental importance in nucleic acid metabolism, and may account for its important role in competence³⁶. Two ribonucleoside reductases, both of class I, NrdEF type, are encoded by the *B. subtilis* chromosome, in one case

from within the SP β genome. In this latter case, the gene corresponding to the large subunit both contains an intron and codes for an intein (V.L., unpublished data). The gene of the small subunit of this enzyme also contains an intron, encoding an endonuclease, as was found for the homologue in bacteriophage T4.

By similarity with genes from other organisms, there appears to be, in addition to genes involved in amino-acid degradation (such as the *roc* operon, which degrades arginine and related amino acids), a large number of genes involved in the degradation of molecules such as opines and related molecules, derived from plants. This is also in line with the fact that *B. subtilis* degrades polygalacturonate, and suggests that, in its biotope, it forms specific relations with plants.

Secondary metabolism. In addition to many genes coding for degradative enzymes, almost 4% of the *B. subtilis* genome codes for large multifunctional enzymes (for example, the *srf*, *pps* and *pks* loci), similar to those involved in the synthesis of antibiotics in other genera of Gram-positive bacteria such as *Streptomyces*. Natural isolates of *B. subtilis* produce compounds with antibiotic activity, such as surfactin, fengycin and difficidin, that can be related to the above-mentioned loci. This bacterium therefore provides a simple and genetically amenable model in which to study the synthesis of antibiotics and its regulation. These pathways are often organized in very long operons (for example, the *pks* region spans 78.5 kb, about 2% of the genome). The corresponding sequences are mostly located near the terminus of replication, together with prophages and prophage-like sequences.

Paralogues and orthologues

It is important to relate intermediary metabolism to genome structure, function and evolution. We therefore compared the *B. subtilis* proteins with themselves, as well as with proteins from known complete genomes, using a consistent statistical method that allows the evaluation of unbiased probabilities of similarities between proteins^{37,38}. For *Z*-scores higher than 13, the number of proteins similar to each given protein does not vary, indicating that this cut-off value identifies sets of proteins that are significantly similar.

Families of paralogues. Many of the paralogues constitute large families of functionally related proteins, involved in the transport of compounds into and out of the cell, or involved in transcription regulation. Another part of the genome consists of gene doublets (568 genes), triplets (273 genes), quadruplets (168 genes) and quintuplets (100 genes). Finally, about half of the genome is made of genes coding for proteins with no apparent paralogues (Fig. 5). No large family comprises only proteins without any similarity to proteins of known function.

The process by which paralogues are generated is not well understood, but we might find clues by studying some of the duplications in the genome. Several approximate DNA repetitions, associated with very high levels of protein identity, were found, mainly within regions putatively or previously identified as prophages. This is in line with previous observations about PBSX and the *skin* element^{39,40}, and suggests that these prophage-like elements share a common ancestor and have diverged relatively recently. In addition, several protein duplications are in genes that are located very close to each other, such as *yukL* and *dhbF* (the corresponding proteins are 65% identical in an overlap of 580 amino acids), *yugJ* and *yugK* (proteins 73% identical), *yxjG* and *yxjH* (proteins 70% identical), and the entire *opuB* operon, which is duplicated 3 kb away (*opuC* operon, yielding ~80% of amino-acid identity in the corresponding proteins).

The study of paralogues showed that, as in other genomes, a few classes of genes have been highly expanded. This argues against the idea of the genome evolving through a series of duplications of ancestral genomes, but rather for the idea of genes as living organisms, subject to evolutionary constraints, some being sub-

mitted to expansion and natural selection, and others to local duplications of DNA regions.

Among paralogue doublets, some were unexpected, such as the three aminoacyl tRNA synthetases doublets (*hisS* (2,817 kb) and *hisZ* (3,588 kb); *thrS* (2,960 kb) and *thrZ* (3,855 kb); *tyrS* (3,036 kb) and *tyrZ* (3,945 kb)) or the two *mutS* paralogues (*mutS* and *yshD*). This latter situation is similar to that found in *Synechocystis*. In the case of *B. subtilis*, the presence of two MutS proteins could indicate that there are two different pathways for long-patch mismatch repair, possibly a consequence of the active genetic transformation mechanism of *B. subtilis*.

Families of orthologues. Because *Mycoplasma* spp. are thought to be derived from Gram-positive bacteria similar to *B. subtilis*, we compared the *B. subtilis* genome with that of *M. genitalium*. Among the 450 genes encoded by *M. genitalium*, the products of 300 are similar to proteins of *B. subtilis*. Among the 146 remaining gene products, a further 3 are similar to proteins of other *Bacillus* species, and 9 to proteins of other Gram-positive bacteria; 25 are similar to proteins of Gram-negative bacteria; and 19 are similar to proteins of other *Mycoplasma* spp. This leaves only 90 genes that would be specific to *M. genitalium* and might be involved in the interaction of this organism with its host.

The *B. subtilis* genome is similar in size to that of *E. coli*. Because these bacteria probably diverged more than one billion years ago, it is of evolutionary value to investigate their relative similarity. About 1,000 *B. subtilis* genes have clear orthologous counterparts in *E. coli* (one-quarter of the genome). These genes did not belong either to the prophage-like regions or to regions coding for secondary metabolism (~15% of the *B. subtilis* genome). This indicates that a large fraction of these genomes shared similar functions. At first sight, however, it seems that little of the operon structure has been conserved. We nevertheless found that ~100 putative operons or parts of operons were conserved between *E. coli* and *B. subtilis*. Among these, ~12 exhibited a reshuffled gene order (typically, the arabinose operon is *araABD* in *B. subtilis* and *araBAD* in *E. coli*). In addition to the core of the translation and transcription machinery, we identified other classes of operons that were well conserved between the two organisms, including major integrated functions such as ATP synthesis (*atp* operon) and electron transfer (*cta* and *qox* operons). As well as being well preserved, the murein biosynthetic region was partly duplicated, allowing creation of part of the genes required for the sporulation division machinery⁴¹. The amino-acid biosynthesis genes differ more in their organization: the *E. coli* genes for arginine biosynthesis are spread throughout the chromosome, whereas the arginine biosynthesis genes of *B. subtilis* form an operon. The same is true for purine biosynthetic genes. Genes responsible for the biosynthesis of coenzymes and prosthetic groups in *B. subtilis* are often clustered in operons that differ from those found in *E. coli*. Finally, several operons conserved in *E. coli* and *B. subtilis* correspond to unknown functions, and should therefore be priority targets for the functional analysis of these model genomes.

Comparison with *Synechocystis* PCC6803 revealed about 800 orthologues. However, in this case the putative operon structure is extremely poorly conserved, apart from four of the ribosomal protein operons, the *groES*–*groEL* operon, *yfnHG* (respectively in *Synechocystis* *rfbFG*), *rpsB*–*tsf*, *ylxS*–*nusA*–*infB*, *asd*–*dapGA*–*ymfA*, *spmAB*, *efp*–*accB*, *grpE*–*dnaK*, *yurXW*. The nine-gene *atp* operon of *B. subtilis* is split into two parts in *Synechocystis*: *atpBE* and *atpIHGFDAC*.

Conclusion

The biochemistry, physiology and molecular biology of *B. subtilis* have been extensively studied over the past 40 years. In particular, *B. subtilis* has been used to study postexponential phase phenomena such as sporulation and competence for DNA uptake. The genome sequences of *E. coli* and *B. subtilis* provide a means of studying the

evolutionary divergence, one billion years ago, of eubacteria into the Gram-positive and Gram-negative groups. The availability of powerful genetic tools will allow the *B. subtilis* genome sequence data to be exploited fully within the framework of a systematic functional analysis program, undertaken by a consortium of 19 European and 7 Japanese laboratories coordinated by S. D. Ehrlich (INRA, Jouy-en-Josas, France) and by N. Ogasawara and H. Yoshikawa (Nara Institute of Science and Technology, Nara, Japan). □

Methods

Genome cloning and sequencing. An international consortium was established to sequence the genome of *B. subtilis* strain 168 (refs 9, 10, 42). At its peak, 25 European, seven Japanese and one Korean laboratory participated in the program, together with two biotechnology companies. Five contiguous DNA regions totalling 0.94 Mb, and two additional regions of 0.28 and 0.14 Mb, were sequenced by the Japanese partners, while the European partners sequenced a total of 2.68 Mb. A few sequences from strain 168 published previously were not resequenced when long overlaps did not indicate differences.

A major technical difficulty was the inability to construct in *E. coli* gene banks representative of the entire *B. subtilis* chromosome using vectors that have proved efficient for other sources of bacterial DNA (such as bacteriophage or cosmid vectors). This was due to the generally very high level of expression of *B. subtilis* genes in *E. coli*, leading to toxic effects. This limitation was overcome by: cloning into a variety of vectors^{9,43,44}; using an *E. coli* strain maintaining low-copy number plasmids⁴⁴; using an integrative plasmid/marker rescue genome-walking strategy⁴⁴; and *in vitro* amplification using polymerase chain reaction (PCR) techniques^{45,46}.

Although cloning vectors were used in the early stages as templates for sequencing reactions, they were largely superseded in the later stages by long-range and inverse PCR techniques. To reduce sequencing errors resulting from PCR amplification artefacts, at least eight amplification reactions were performed independently and subsequently pooled. The various sequencing groups were free to choose their own strategy, except that all DNA sequences had to be determined entirely on both strands.

Sequence annotation and verification. The sequences were annotated by the groups, and sent to a central depository at the Institut Pasteur¹⁴. The Japanese sequences were also sent there through the Japanese depository at the Nara Institute of Science and Technology. The same procedures were used to identify CDSs and to detect frameshifts. They were embedded within a cooperative computer environment dedicated to automatic sequence annotation and analysis³⁹. In a first step, we identified in all six possible frames the open reading frames (ORFs) that were at least 100 codons in length. In a second step, three independent methods were used: the first method used the GeneMark coding-sequence prediction method⁴⁷ together with the search for CDSs preceded by typical translation initiation signals (5'-AAGGAGTG-3'), located 4–13 bases upstream of the putative start codons (ATG, TTG or GTG); the second method used the results of a BLAST2X analysis performed on the entire *B. subtilis* genome against the non-redundant protein database at the NCBI; and the third method was based on the distribution of non-overlapping trinucleotides or hexanucleotides in the three frames of an ORF⁴⁸.

In general, frameshifts and missense mutations generating termination codons or eliminating start codons are relatively easy to detect. We shall devise a procedure for detecting another type of error, GC instead of CG or vice versa, which are much more difficult to identify. It should be noted that putative frameshift errors should not be corrected automatically. The sequences of the flanking regions of a 500-bp fragment centred around a putative error were sent to an independent verification group, which performed PCR amplifications using chromosomal DNA as template, and sequenced the corresponding DNA products.

Organization and accessibility of data. The *B. subtilis* sequence data have been combined with data from other sources (biochemical, physiological and genetic) in a specialized database, SubtiList⁴⁹, available as a Macintosh or Windows stand-alone application (4th Dimension runtime) by anonymous FTP at ftp://ftp.pasteur.fr/pub/GenomeDB/SubtiList. SubtiList is also accessible through a World-Wide Web server at http://www.pasteur.fr/Bio/SubtiList.html,

where it has been implemented on a UNIX system using the Sybase relational database management system. A completely rewritten version of SubtiList is in preparation to facilitate browsing of the information of the whole chromosome. Flat files of the whole DNA and protein sequences in EMBL and FASTA format will be made available at the above ftp address. Another *B. subtilis* genome database is also under development at the Human Genome Center of Tokyo University (<http://www.genome.ad.jp>), and SubtiList will also be available there.

Received 16 July; 29 September 1997.

1. Fleischmann, R. D. *et al.* Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd. *Science* **269**, 496–512 (1995).
2. Fraser, C. M. *et al.* The minimal gene complement of *Mycoplasma genitalium*. *Science* **270**, 397–403 (1995).
3. Kaneko, T. *et al.* Sequence analysis of the genome of the unicellular Cyanobacterium *Synechocystis* sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions. *DNA Res.* **3**, 109–136 (1996).
4. Bult, C. J. *et al.* Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*. *Science* **273**, 1058–1073 (1996).
5. Himmelreich, R. *et al.* Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*. *Nucleic Acids Res.* **24**, 4420–4449 (1996).
6. Goffeau, A. *et al.* The yeast genome directory. *Nature* **387**, 5–105 (1997).
7. Tomb, J.-F. *et al.* The complete genome sequence of the gastric pathogen *Helicobacter pylori*. *Nature* **388**, 539–547 (1997).
8. Blattner, F. R. *et al.* The complete genome sequence of *Escherichia coli* K-12. *Science* **277**, 1453–1462 (1997).
9. Kunst, F., Vassarotti, A. & Danchin, A. Organization of the European *Bacillus subtilis* genome sequencing project. *Microbiology* **389**, 84–87 (1995).
10. Ogasawara, N. & Yoshikawa, H. The systematic sequencing of the *Bacillus subtilis* genome in Japan. *Microbiology* **142**, 2993–2994 (1996).
11. Harwood, C. R. *Bacillus subtilis* and its relatives: molecular biological and industrial workhorses. *Trends Biotechnol.* **10**, 247–256 (1992).
12. Stragier, P. & Losick, R. Molecular genetics of sporulation in *Bacillus subtilis*. *Annu. Rev. Genet.* **30**, 297–341 (1996).
13. Solomon, J. M. & Grossman, A. D. Who's competent and when: regulation of natural genetic competence in bacteria. *Trends Genet.* **12**, 150–155 (1996).
14. Moszer, I., Kunst, F. & Danchin, A. The European *Bacillus subtilis* genome sequencing project: current status and accessibility of the data from a new World Wide Web site. *Microbiology* **142**, 2987–2991 (1996).
15. Franks, A. H., Griffiths, A. A. & Wake, R. G. Identification and characterization of new DNA replication terminators in *Bacillus subtilis*. *Mol. Microbiol.* **17**, 13–23 (1995).
16. Lobry, J. R. Asymmetric substitution patterns in the two DNA strands of bacteria. *Mol. Biol. Evol.* **13**, 660–665 (1996).
17. Hénaut, A. & Danchin, A. in *Escherichia coli and Salmonella: Cellular and Molecular Biology* (eds Neidhardt, F. *et al.*) 2047–2066 (ASM, Washington DC, 1996).
18. Nussinov, R. The universal dinucleotide asymmetry rules in DNA and amino acid codon choice. *Nucleic Acids Res.* **17**, 237–244 (1989).
19. Karlin, S., Burge, C. & Campbell, A. M. Statistical analyses of counts and distributions of restriction sites in DNA sequences. *Nucleic Acids Res.* **20**, 1363–1370 (1992).
20. Burge, C., Campbell, A. M. & Karlin, S. Over- and under-representation of short oligonucleotides in DNA sequences. *Proc. Natl Acad. Sci. USA* **89**, 1358–1362 (1992).
21. Kasahara, Y., Nakai, S. & Ogasawara, H. Sequence analysis of the 36-kb region between *gntZ* and *trnY* genes of *Bacillus subtilis* genome. *DNA Res.* **4**, 155–159 (1997).
22. Presecan, E. *et al.* The *Bacillus subtilis* genome from *gerBC* (311°) to *licR* (334°). *Microbiology* **143**, 3313–3328 (1997).
23. Burkholder, P. R. & Giles, N. H. Induced biochemical mutations in *Bacillus subtilis*. *Am. J. Bot.* **33**, 345–348 (1947).
24. Daniels, D. L., Plunkett, G. III, Burland, V. & Blattner, F. R. Analysis of the *Escherichia coli* genome: DNA sequence of the region from 84.5 to 86.5 minutes. *Science* **257**, 771–778 (1992).
25. Wu, L. J. & Errington, J. *Bacillus subtilis* SpoIIIE protein required for DNA segregation during asymmetric cell division. *Science* **264**, 572–575 (1994).
26. Itaya, M. Stability and asymmetric replication of the *Bacillus subtilis* 168 chromosome structure. *J. Bacteriol.* **175**, 741–749 (1993).
27. Billoud, B., Kontic, M. & Viari, A. Palingol: a declarative programming language to describe nucleic acids' secondary structures and to scan sequence database. *Nucleic Acids Res.* **24**, 1395–1403 (1996).
28. Fichant, G. A. & Burks, C. Identifying potential tRNA genes in genomic DNA sequences. *J. Mol. Biol.* **220**, 659–671 (1991).
29. d'Aubenton Carafa, Y., Brody, E. & Thermes, C. Prediction of rho-independent *Escherichia coli* transcription terminators. A statistical analysis of their RNA stem-loop structures. *J. Mol. Biol.* **216**, 835–858 (1990).
30. Stock, J. B., Surette, M. G., Levitt, M. & Park, P. in *Two-Component Signal Transduction* (eds Hoch, J. A. & Silhavy, T. J.) 25–51 (ASM, Washington DC, 1995).
31. Mizuno, T. Compilation of all genes encoding two-component phosphotransfer signal transducers in the genome of *Escherichia coli*. *DNA Res.* **4**, 161–168 (1997).
32. Perego, M., Glaser, P. & Hoch, J. A. Aspartyl-phosphate phosphatases deactivate the response regulator components of the sporulation signal transduction system in *Bacillus subtilis*. *Mol. Microbiol.* **19**, 1151–1157 (1996).
33. Tjalsma, H. *et al.* *Bacillus subtilis* contains four closely related type I signal peptidases with overlapping substrate specificities: constitutive and temporally controlled expression of different *sip* genes. *J. Biol. Chem.* **272**, 25983–25992 (1997).
34. Danchin, A. Comparison between the *Escherichia coli* and *Bacillus subtilis* genomes suggests that a major function of polynucleotide phosphorylase is to synthesize CDP. *DNA Res.* **4**, 9–18 (1997).
35. Suutari, M. & Laakso, S. Unsaturated and branched chain-fatty acids in temperature adaptation of *Bacillus subtilis* and *Bacillus megaterium*. *Biochim. Biophys. Acta* **1126**, 119–124 (1992).
36. Luttinger, A., Hahn, J. & Dubnau, D. Polynucleotide phosphorylase is necessary for competence development in *Bacillus subtilis*. *Mol. Microbiol.* **19**, 343–356 (1996).
37. Landès, C., Hénaut, A. & Rislér, J.-L. A comparison of several similarity indices used in the classification of protein sequences: a multivariate analysis. *Nucleic Acids Res.* **20**, 3631–3637 (1992).
38. Glémet, E. & Codani, J.-J. LASSAP, a LARge Scale Sequence Comparison Package. *Comput. Appl. Biosci.* **13**, 137–143 (1997).
39. Médigue, C., Moszer, I., Viari, A. & Danchin, A. Analysis of a *Bacillus subtilis* genome fragment using a co-operative computer system prototype. *Gene* **165**, GC37–GC51 (1995).
40. Krogh, S., O'Reilly, M., Nolan, N. & Devine, K. M. The phage-like element PBSX and part of the *skin* element, which are resident at different locations on the *Bacillus subtilis* chromosome, are highly homologous. *Microbiology* **142**, 2031–2040 (1996).
41. Daniel, R. A., Drake, S., Buchanan, C. E., Scholle, R. & Errington, J. The *Bacillus subtilis* *spoVD* gene encodes a mother-cell-specific penicillin-binding protein required for spore morphogenesis. *J. Mol. Biol.* **235**, 209–220 (1994).
42. Anagnostopoulos, C. & Spizizen, J. Requirements for transformation in *Bacillus subtilis*. *J. Bacteriol.* **81**, 741–746 (1961).
43. Azevedo, V. *et al.* An ordered collection of *Bacillus subtilis* DNA segments cloned in yeast artificial chromosomes. *Proc. Natl Acad. Sci. USA* **90**, 6047–6051 (1993).
44. Glaser, P. *et al.* *Bacillus subtilis* genome project: cloning and sequencing of the 97 kb region from 325° to 333°. *Mol. Microbiol.* **10**, 371–384 (1993).
45. Ogasawara, N., Nakai, S. & Yoshikawa, H. Systematic sequencing of the 180 kilobase region of the *Bacillus subtilis* chromosome containing the replication origin. *DNA Res.* **1**, 1–14 (1994).
46. Sorokin, A. *et al.* A new approach using multiplex long accurate PCR and yeast artificial chromosomes for bacterial chromosome mapping and sequencing. *Genome Res.* **6**, 448–453 (1996).
47. Borodovsky, M. & McIninch, J. GENMARK: parallel gene recognition for both DNA strands. *Comput. Chem.* **17**, 123–133 (1993).
48. Fichant, G. A. & Quentin, Y. A frameshift error detection algorithm for DNA sequencing projects. *Nucleic Acids Res.* **23**, 2900–2908 (1995).
49. Moszer, I., Glaser, P. & Danchin, A. SubtiList: a relational database for the *Bacillus subtilis* genome. *Microbiology* **141**, 261–268 (1995).

Acknowledgements. We thank C. Anagnostopoulos, R. Dedonder and J. Hoch for their pioneering efforts, and A. Bairoch for advice in annotating *B. subtilis* protein data. The main funding of the European network was provided by the European Commission under the Biotechnology program. The Japanese project was included in the Human Genome Program, and supported by a research grant from the Ministry of Education, Science and Culture, and the Proposal-Based Advanced Industrial Technology R&D Program from New Energy and Industrial Technology Development Organization. The Swiss and Korean projects were funded by the Swiss National Fund and the Korean government, respectively. An industrial platform was set up to facilitate contacts between participants of the European consortium and some European biotechnology companies: DuPont de Nemours (France, USA), Frimond (Belgium), Genencor (Finland, USA), Gist Brocades (The Netherlands), Glaxo-Wellcome (UK, Italy), Hoechst Marion Roussel (France, Germany), F. Hoffmann-La Roche AG (Switzerland), Novo Nordisk (Denmark), SmithKline Beecham (UK).

Correspondence and requests for materials should be addressed to E.K. (e-mail: fkunst@pasteur.fr), N.O. (nogasawa@bs.aist-nara.ac.jp), H.Y. (hyoshika@bs.aist-nara.ac.jp) or A.D. (adanchin@pasteur.fr). The sequence has been deposited in EMBL/GenBank/DDJB with accession numbers from Z99104 to Z99124.

KNOW YOUR COPY RIGHTS RESPECT OURS

The publication you are reading is protected by copyright law. Photocopying copyright material without permission is no different from stealing a magazine from a newsagent, only it doesn't seem like theft.

If you take photocopies from books, magazines and periodicals at work your employer should be licensed with CLA. Make sure you are protected by a photocopying licence.



The Copyright Licensing Agency Limited
90 Tottenham Court Road, London W1P 0LP
Telephone: 0171 436 5931 Fax: 0171 436 3986

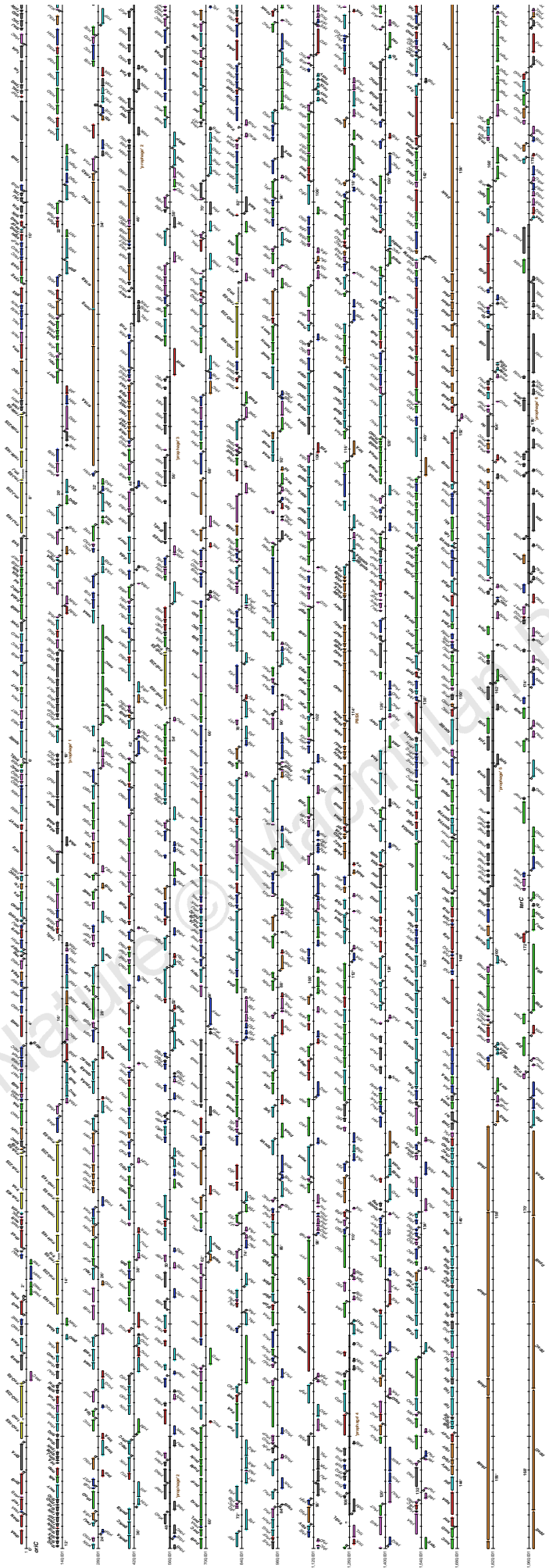
Table 1. Functional classification of the *Bacillus subtilis* protein-coding genes.

	CELL ENVELOPE AND CELLULAR PROCESSES 866					
		<i>xyfB</i>	1317	prophage-mediated lysis		specific enzyme IIC component
				<i>N</i> -acetylmuramoyl-L-alanine amidase (PBSX prophage-mediated lysis)	<i>lmrB</i>	290
					<i>lplA</i>	779
					<i>lplB</i>	781
					<i>lplC</i>	782
					<i>mdr</i>	334
						multidrug-efflux transporter (puromycin, nerfloxacin, tosofloxacin)
					<i>msmE</i>	3097
					<i>msmX</i>	3984
						multiple sugar-binding protein
						multiple sugar-binding transport ATP-binding protein
					<i>mtlA</i>	449
						phosphotransferase system (PTS) mannitol-specific enzyme I/ABC component
					<i>narK</i>	3833
					<i>nasA</i>	363
					<i>nata</i>	296
						Na ⁺ ABC transporter (extrusion) (ATP-binding protein)
					<i>natB</i>	297
						Na ⁺ ABC transporter (extrusion) (membrane protein)
					<i>ngaA</i>	3756
						ammonium transporter
					<i>nupC</i>	4050
						pyrimidine-nucleoside transport protein
					<i>oppA</i>	1219
						oligopeptide ABC transporter (binding protein) (initiation of sporulation, competence development)
					<i>oppB</i>	1221
						oligopeptide ABC transporter (permease) (initiation of sporulation, competence development)
					<i>oppC</i>	1222
						oligopeptide ABC transporter (permease) (initiation of sporulation, competence development)
					<i>oppD</i>	1223
						oligopeptide ABC transporter (ATP-binding protein) (initiation of sporulation, competence development)
					<i>oppF</i>	1224
						oligopeptide ABC transporter (ATP-binding protein) (initiation of sporulation, competence development)
					<i>opuAA</i>	321
						glycine betaine ABC transporter (ATP-binding protein) (osmoprotection)
					<i>opuAB</i>	322
						glycine betaine ABC transporter (permease) (osmoprotection)
					<i>opuAC</i>	323
						glycine betaine ABC transporter (glycine betaine-binding protein) (osmoprotection)
					<i>opuBA</i>	3462
						choline ABC transporter (ATP-binding protein) (osmoprotection)
					<i>opuBB</i>	3461
						choline ABC transporter (membrane protein) (osmoprotection)
					<i>opuBC</i>	3460
						choline ABC transporter (choline-binding protein) (osmoprotection)
					<i>opuBD</i>	3460
						choline ABC transporter (membrane protein) (osmoprotection)
					<i>opuCA</i>	3470
						glycine betaine/carnitine/choline ABC transporter (ATP-binding protein) (osmoprotection)
					<i>opuCB</i>	3469
						glycine betaine/carnitine/choline ABC transporter (membrane protein) (osmoprotection)
					<i>opuCC</i>	3468
						glycine betaine/carnitine/choline ABC transporter (osmoprotectant-binding protein) (osmoprotection)
					<i>opuCD</i>	3467
						glycine betaine/carnitine/choline ABC transporter (membrane protein) (osmoprotection)
					<i>opuD</i>	3076
						glycine betaine transporter (osmoprotection)
					<i>pbuX</i>	728
						proline transporter (osmoprotection)
					<i>ptsG</i>	1457
						xanthine permease
					<i>ptsI</i>	1459
						phosphotransferase system (PTS) glucose-specific enzyme I/ABC component
						phosphotransferase system (PTS) enzyme I (general energy coupling protein) of the PTS
					<i>pyrP</i>	1618
						uracil permease (pyrimidine biosynthesis)
					<i>rsaA</i>	3703
						ribose ABC transporter (ATP-binding protein)
					<i>rsaB</i>	3705
						ribose ABC transporter (ribose-binding protein)
					<i>rsaC</i>	3704
						ribose ABC transporter (permease)
					<i>rsaD</i>	3702
						ribose ABC transporter (membrane protein)
					<i>rocC</i>	3876
						amino acid permease (arginine and ornithine utilization)
					<i>rocE</i>	4143
						amino acid permease (arginine and ornithine utilization)
					<i>sacP</i>	3904
						phosphotransferase system (PTS) sucrose-specific enzyme I/ABC component
					<i>slp</i>	1533
						small peptidoglycan-associated lipoprotein
					<i>sunT</i>	2269
						sublancin 168 antibiotic transporter
					<i>tetB</i>	4188
						tetracycline resistance protein
					<i>trpE</i>	850
						phosphotransferase system (PTS) trehalose-specific enzyme I/ABC component
					<i>trkA</i>	2723
						potassium uptake
					<i>yabM</i>	65
						amino acid transporter
					<i>ybaE</i>	151
						ABC transporter (ATP-binding protein)
					<i>ybbF</i>	191
						sucrose phosphotransferase enzyme II
					<i>ybcL</i>	212
						chloramphenicol resistance enzyme
					<i>ybdA</i>	217
						ABC transporter (binding protein)
					<i>ybdB</i>	218
						ABC transporter (permease)
					<i>ybcC</i>	231
						amino acid transporter
					<i>ybfS</i>	257
						phosphotransferase system enzyme II
					<i>ybgF</i>	262
						histidine permease
					<i>ybgH</i>	264
						sodium/proton-dependent alanine transporter
					<i>ybxA</i>	150
						ABC transporter (ATP-binding protein)
					<i>ybxG</i>	227
						amino acid permease
					<i>ycbE</i>	270
						glucarate transporter
					<i>ycbK</i>	277
						efflux system
					<i>ycbN</i>	280
						ABC transporter (ATP-binding protein)
					<i>ycck</i>	298
						ion channel
					<i>yccl</i>	309
						ABC transporter (ATP-binding protein)
					<i>ycel</i>	317
						transporter
					<i>ycelJ</i>	320
						multidrug-efflux transporter
					<i>ycgH</i>	337
						amino acid transporter
					<i>ycgO</i>	347
						proline permease
					<i>ycKA</i>	368
						amino acid ABC transporter (permease)
					<i>ycKB</i>	368
						amino acid ABC transporter (binding protein)
					<i>ycKL</i>	410
						glutamine ABC transporter (ATP-binding protein)
					<i>ycKJ</i>	410
						glutamine ABC transporter (permease)
					<i>ycKK</i>	411
						glutamine ABC transporter (glutamine-binding protein)
					<i>yclF</i>	417
						di-tripeptide ABC transporter (membrane protein)
					<i>yclH</i>	424
						ABC transporter (permease)
					<i>yclI</i>	426
						transporter
					<i>yclN</i>	432
						ferrichrome ABC transporter (permease)
					<i>yclO</i>	433
						ferrichrome ABC transporter (permease)
					<i>yclP</i>	434
						ferrichrome ABC transporter (ATP-binding protein)
					<i>yclQ</i>	435
						ferrichrome ABC transporter (binding protein)
					<i>yclR</i>	437
						multidrug resistance protein
					<i>yclS</i>	448
						copper export protein
					<i>ycsG</i>	457
						branched chain amino acids transporter
					<i>ydbA</i>	493
						ABC transporter (binding protein)
					<i>ydbE</i>	497
						C4-dicarboxylate binding protein
					<i>ydbH</i>	500
						C4-dicarboxylate transport protein
					<i>ydbJ</i>	502
						ABC transporter (ATP-binding protein)
					<i>ydeG</i>	566
						metabolite transport protein

<i>ydeR</i>	578	antibiotic resistance protein	<i>ytmJ</i>	3007	amino acid ABC transporter (binding protein)	<i>yclK</i>	427	two-component sensor histidine kinase [YcIJ]
<i>ydeA</i>	580	arsenical pump membrane protein	<i>ytmK</i>	3006	amino acid ABC transporter (binding protein)	<i>ydbF</i>	437	two-component sensor histidine kinase [YdbG]
<i>ydfI</i>	583	antibiotic transport-associated protein	<i>ytmL</i>	3003	amino acid ABC transporter (permease)	<i>ydbG</i>	437	two-component sensor histidine kinase [YdbI]
<i>ydlH</i>	595	multidrug-efflux transporter regulator	<i>ytmM</i>	3005	amino acid ABC transporter (permease)	<i>yesM</i>	758	two-component sensor histidine kinase [YesN]
<i>ydlM</i>	596	cation efflux system	<i>ytmA</i>	3125	proline permease	<i>yfiJ</i>	903	two-component sensor histidine kinase [YfiK]
<i>ydlO</i>	597	ABC transporter (binding protein)	<i>ytrB</i>	3118	ABC transporter (ATP-binding protein)	<i>yhcY</i>	1008	two-component sensor histidine kinase [YhcZ]
<i>ydfF</i>	608	amino acid ABC transporter (permease)	<i>ytrE</i>	3115	ABC transporter (ATP-binding protein)	<i>yhlJ</i>	1129	sensory transduction pleiotropic regulatory protein
<i>ydgH</i>	609	transporter	<i>ytsC</i>	3111	ABC transporter (ATP-binding protein)	<i>ykoH</i>	1392	two-component sensor histidine kinase [YkoG]
<i>ydgK</i>	613	bicyclomycin resistance protein	<i>ytsD</i>	3110	ABC transporter (permease)	<i>ykrQ</i>	1419	two-component sensor histidine kinase
<i>ydhL</i>	626	chloramphenicol resistance protein	<i>ytsB</i>	3108	multidrug resistance protein	<i>ykvD</i>	1432	two-component sensor histidine kinase
<i>ydhM</i>	626	cellobiose phosphotransferase system enzyme II	<i>yubD</i>	3192	multidrug resistance protein	<i>yocF</i>	2090	two-component sensor histidine kinase [YocG]
<i>ydhN</i>	627	cellobiose phosphotransferase system enzyme II	<i>yubG</i>	3188	Na ⁺ -transporting ATP synthase	<i>yrcQ</i>	2704	two-component sensor histidine kinase [YrcP]
<i>ydhO</i>	627	cellobiose phosphotransferase system enzyme II	<i>yuinF</i>	3239	ABC transporter (lipoprotein)	<i>yrfP</i>	3035	two-component sensor histidine kinase
<i>ydfF</i>	648	ABC transporter (ATP-binding protein)	<i>yufO</i>	3240	ABC transporter (ATP-binding protein)	<i>ytsB</i>	3112	two-component sensor histidine kinase [YtsA]
<i>ydfD</i>	658	H ⁺ -symporter	<i>yufR</i>	3244	organic acid transport protein	<i>yufL</i>	3236	two-component sensor histidine kinase [YufM]
<i>ydgK</i>	676	sugar transporter	<i>yufU</i>	3248	Na ⁺ /H ⁺ antiporter	<i>yvcQ</i>	3566	two-component sensor histidine kinase [YvcP]
<i>yeaB</i>	687	cation efflux system membrane protein	<i>yufV</i>	3249	Na ⁺ /H ⁺ antiporter	<i>yvtT</i>	3497	two-component sensor histidine kinase [YvtU]
<i>yeaA</i>	712	amino acid permease	<i>yugO</i>	3218	potassium channel protein	<i>yvqB</i>	3385	two-component sensor histidine kinase [YvqA]
<i>yesO</i>	761	sugar-binding protein	<i>yurJ</i>	3330	purine permease	<i>yvqE</i>	3395	two-component sensor histidine kinase [YvqC]
<i>yesP</i>	762	lactose permease	<i>yurK</i>	3331	purine permease	<i>yvrG</i>	3407	two-component sensor histidine kinase [YvrH]
<i>yesQ</i>	763	lactose permease	<i>yurJ</i>	3345	multiple sugar ABC transporter (ATP-binding protein)	<i>ywpD</i>	3741	two-component sensor histidine kinase
<i>yfhA</i>	921	iron(III) dicitrate transport permease	<i>yurM</i>	3348	sugar permease	<i>yxdK</i>	4071	two-component sensor histidine kinase [YxdJ]
<i>yfhI</i>	926	antibiotic resistance protein	<i>yurN</i>	3349	sugar permease	<i>yxiM</i>	3992	two-component sensor histidine kinase [YxiL]
<i>yfiB</i>	893	ABC transporter (ATP-binding protein)	<i>yurO</i>	3350	multiple sugar-binding protein	<i>yycG</i>	4153	two-component sensor histidine kinase [YycF]
<i>yfiC</i>	895	ABC transporter (ATP-binding protein)	<i>yurY</i>	3360	ABC transporter (ATP-binding protein)			
<i>yfiD</i>	900	metalloidite transport protein	<i>yusC</i>	3363	ABC transporter (ATP-binding protein)			
<i>yfiL</i>	905	ABC transporter (ATP-binding protein)	<i>yusP</i>	3374	multidrug-efflux transporter			
<i>yfiM</i>	906	ABC transporter (ATP-binding protein)	<i>yusV</i>	3379	iron(III) dicitrate transport permease			
<i>yfiN</i>	907	ABC transporter (ATP-binding protein)	<i>yutK</i>	3307	Na ⁺ /nucleoside cotransporter			
<i>yfiS</i>	913	multidrug resistance protein	<i>yuxJ</i>	3232	multidrug-efflux transporter			
<i>yfiU</i>	916	multidrug-efflux transporter	<i>yvaE</i>	3448	multidrug-efflux transporter			
<i>yfiY</i>	920	iron(III) dicitrate transport permease	<i>yvbW</i>	3490	amino acid permease			
<i>yfiZ</i>	920	iron(III) dicitrate transport permease	<i>yvcC</i>	3579	ABC transporter (ATP-binding protein)			
<i>yfiQ</i>	872	divalent cation transport protein	<i>yvcR</i>	3565	ABC transporter (ATP-binding protein)			
<i>yjKE</i>	865	H ⁺ /Ca ²⁺ exchanger	<i>yvcS</i>	3565	ABC transporter (permease)			
<i>yjKF</i>	865	multidrug-efflux transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjKH</i>	865	multidrug-efflux transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjKL</i>	861	multidrug resistance protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjLA</i>	844	amino acid carrier protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjLE</i>	844	anion-binding protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjLF</i>	840	phosphotransferase system enzyme II	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjLS</i>	829	2-oxoglutarate/malate translocator	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmC</i>	826	ferrichrome ABC transporter (binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmD</i>	825	ferrichrome ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmE</i>	824	ferrichrome ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmF</i>	823	ferrichrome ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmM</i>	815	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmO</i>	812	multidrug-efflux transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmP</i>	805	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjnA</i>	806	metalloidite transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjaD</i>	939	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ygaL</i>	961	nitrate ABC transporter (binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ygaM</i>	963	ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ygaB</i>	962	ABC transporter (binding lipoprotein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhaQ</i>	1062	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhaU</i>	1060	Na ⁺ /H ⁺ antiporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhcA</i>	977	multidrug resistance protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhcG</i>	981	glycine betaine L-proline transport	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhcH</i>	983	iron transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhcI</i>	984	ABC transporter (binding lipoprotein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhcL</i>	986	sodium-glutamate symporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhdG</i>	1023	amino acid transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhdH</i>	1024	sodium-dependent transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yheH</i>	1047	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yheL</i>	1045	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yheM</i>	1044	Na ⁺ /H ⁺ antiporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhiQ</i>	1107	iron(III) dicitrate-binding protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhiB</i>	1120	metalloidite permease	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhiD</i>	1133	multidrug-efflux transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhiE</i>	1133	multidrug-efflux transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhiG</i>	1177	multidrug resistance protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yhiZ</i>	1194	multidrug resistance protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjbQ</i>	1240	Na ⁺ /H ⁺ antiporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjdD</i>	1272	fructose phosphotransferase system enzyme II	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjKB</i>	1296	amino acid ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmB</i>	1301	Na ⁺ /galactoside symporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yjmG</i>	1307	hexuronate transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykaB</i>	1350	low-affinity inorganic phosphate transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykaA</i>	1352	amino acid permease	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykaC</i>	1353	ABC transporter (binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykpE</i>	1393	xylopyruvate ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yknU</i>	1499	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yknV</i>	1501	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yknY</i>	1505	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykoD</i>	1390	cation ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykoK</i>	1395	Mg ²⁺ transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykpA</i>	1512	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykrM</i>	1416	Na ⁺ -transporting ATP synthase	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykuC</i>	1476	macrolide-efflux protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ykvW</i>	1451	heavy metal-transporting ATPase	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ylnA</i>	1606	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ylnB</i>	1630	anion permease	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ylnC</i>	1637	calcium-transporting ATPase	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ylnA</i>	1887	H ⁺ -symporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yocC</i>	1896	metalloidite transport protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yocN</i>	2098	permease	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yocR</i>	2106	sodium-dependent transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yocS</i>	2106	sodium-dependent transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yodE</i>	2129	aromatic metabolite transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yodF</i>	2130	proline permease	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yofA</i>	2125	glucuronate permease	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yopE</i>	2337	phosphotransferase system enzyme II	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqeiV</i>	2620	Na ⁺ /P _i cotransporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqgQ</i>	2559	phosphate ABC transporter (binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqgH</i>	2580	phosphate ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqjJ</i>	2579	phosphate ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqaj</i>	2578	phosphate ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqjK</i>	2577	phosphate ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqjH</i>	2515	lipoprotein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqjX</i>	2492	amino acid ABC transporter (binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqjY</i>	2491	amino acid ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqjZ</i>	2491	amino acid ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqjV</i>	2466	multidrug resistance protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yqjI</i>	2453	Na ⁺ /H ⁺ antiporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yraO</i>	2745	citrate transporter	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrbD</i>	2841	sodium/proton-dependent alanine carrier protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrbD</i>	2968	antibiotic resistance protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrcP</i>	3087	ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrcQ</i>	3086	lipoprotein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrcQ</i>	3082	sugar transport protein	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrgA</i>	3145	ABC transporter (membrane protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrgB</i>	3144	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrgC</i>	3143	ABC transporter (membrane protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yrfP</i>	3071	ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>yriC</i>	3132	anion transport ABC transporter (ATP-binding protein)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ytiD</i>	3133	ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
<i>ytiP</i>	3065	ABC transporter (permease)	<i>yvcb</i>	3561	ABC transporter (permease)			
			<i>ytmJ</i>	3007	amino acid ABC transporter (binding protein)			
			<i>ytmK</i>	3006	amino acid ABC transporter (binding protein)			
			<i>ytmL</i>	3003	amino acid ABC transporter (permease)			
			<i>ytmM</i>	3005	amino acid ABC transporter (permease)			
			<i>ytmA</i>	3125	proline permease			
			<i>ytrB</i>	3118	ABC transporter (ATP-binding protein)			
			<i>ytrE</i>	3115	ABC transporter (ATP-binding protein)			
			<i>ytsC</i>	3111	ABC transporter (ATP-binding protein)			
			<i>ytsD</i>	3110	ABC transporter (permease)			
			<i>ytsB</i>	3108	multidrug resistance protein			
			<i>yubD</i>	3192	multidrug resistance protein			
			<i>yubG</i>	3188	Na ⁺ -transporting ATP synthase			
			<i>yuinF</i>	3239	ABC transporter (lipoprotein)			
			<i>yufO</i>	3240	ABC transporter (ATP-binding protein)			
			<i>yufR</i>	3244	organic acid transport protein			
			<i>yufU</i>	3248	Na ⁺ /H ⁺ antiporter			
			<i>yufV</i>	3249	Na ⁺ /H ⁺ antiporter			
			<i>yugO</i>	3218	potassium channel protein			
			<i>yurJ</i>	3330	purine permease			
			<i>yurK</i>	3331	purine permease			
			<i>yurJ</i>	3345	multiple sugar ABC transporter (ATP-binding protein)			
			<i>yurM</i>	3348	sugar permease			
			<i>yurN</i>	3349	sugar permease			
			<i>yurO</i>	3350	multiple sugar-binding protein			
			<i>yurY</i>	3360	ABC transporter (ATP-binding protein)			
			<i>yusC</i>	3363	ABC transporter (ATP-binding protein)			
			<i>yusP</i>	3374	multidrug-efflux transporter			

<i>figE</i>	1700	flagellar hook protein	<i>cotX</i>	1251	spore coat protein (insoluble fraction)	SASP)		
<i>figK</i>	3639	flagellar hook-associated protein 1 (HAP1)	<i>cotY</i>	1250	spore coat protein (insoluble fraction)	<i>sspE</i>	937	small acid-soluble spore protein (major γ -type SASP)
<i>figL</i>	3637	flagellar hook-associated protein 3 (HAP3)	<i>cooZ</i>	1249	spore coat protein (insoluble fraction)	<i>sspF</i>	53	small acid-soluble spore protein (minor α/β -type SASP)
<i>figM</i>	3640	flagellin synthesis regulatory protein (anti-sigma factor (σ^F))	<i>cssA</i>	228	sporulation-specific SASP protein			
<i>flhA</i>	1707	flagella-associated protein	<i>jag</i>	4213	SpolII-associated protein			
<i>flhB</i>	1706	flagella-associated protein	<i>kapB</i>	3230	activator of KinB in the initiation of sporulation	<i>usd</i>	3748	required for translation of <i>spoIID</i>
<i>flhF</i>	1709	flagella-associated protein	<i>kapD</i>	3232	inhibitor of the KinA pathway to sporulation	<i>yknT</i>	1495	sporulation protein σ^F -controlled
<i>flhO</i>	3746	flagellar basal-body rod protein	<i>kbaA</i>	159	activation of the KinB signaling pathway to sporulation	<i>ykvU</i>	1449	spore cortex membrane protein
<i>flhP</i>	3745	flagellar hook-basal body protein			<i>ynzH</i>	1901	spore coat protein	
<i>flhD</i>	3633	flagellar hook-associated protein 2 (HAP2)	<i>obg</i>	2853	GTP-binding protein involved in initiation of sporulation (SpoA activation)	<i>yobW</i>	2063	membrane protein σ^F -controlled
<i>flhE</i>	1692	flagellar hook-basal body protein	<i>phrA</i>	1316	phosphatase (RapA) inhibitor (imported by Opp)	<i>yagT</i>	2568	γ -D-glutamyl-L-diamino acid endopeptidase I
<i>flhF</i>	1692	flagellar basal-body M-ring protein	<i>phrC</i>	430	phosphatase (RapC) regulator / competence and sporulation stimulating factor (CSF)	<i>yagG</i>	2483	lipoprotein SpoIIJ-like
<i>flhG</i>	1694	flagellar motor switch protein	<i>phrE</i>	2660	phosphatase (RapE) regulator	<i>yraD</i>	2754	spore coat protein
<i>flhH</i>	1695	flagellar assembly protein	<i>phrF</i>	3846	phosphatase (RapF) regulator	<i>yraE</i>	2752	spore coat protein
<i>flhI</i>	1695	flagellar-specific ATP synthase	<i>phrG</i>	4141	phosphatase (RapG) regulator	<i>yraG</i>	2752	spore coat protein
<i>flhJ</i>	1697	flagellar protein required for formation of basal body	<i>phrI</i>	548	phosphatase (RapI) regulator	<i>yrbA</i>	2845	spore coat protein
<i>flhK</i>	1698	flagellar hook-length control	<i>phrL</i>	548	phosphatase (RapL) regulator	<i>yrbB</i>	2844	spore coat protein
<i>flhL</i>	1701	flagellar protein required for flagellar formation	<i>phrK</i>	2063	phosphatase (RapK) regulator	<i>yrbC</i>	2843	spore coat protein
<i>flhM</i>	1701	flagellar motor switch protein	<i>phrP</i>	1315	response regulator aspartate phosphatase [SpoOF-P]	<i>ytaA</i>	3161	spore coat protein
<i>flhP</i>	1704	flagellar protein required for flagellar formation	<i>rapA</i>	3771	response regulator aspartate phosphatase [SpoOF-P]	<i>ytpT</i>	3074	spore cortex protein
<i>flhQ</i>	1705	flagellar protein required for flagellar formation	<i>rapB</i>	3771	response regulator aspartate phosphatase [SpoOF-P]	<i>ytpT</i>	3051	DNA translocase stage III sporulation protein
<i>flhR</i>	1705	flagellar protein required for flagellar formation	<i>rapC</i>	428	response regulator aspartate phosphatase	<i>ytaA</i>	4208	DNA-binding protein SpoIIJ-like
<i>flhS</i>	3632	flagellar protein	<i>rapD</i>	3743	response regulator aspartate phosphatase			
<i>flhT</i>	3632	flagellar protein	<i>rapE</i>	3758	response regulator aspartate phosphatase	1.9	GERMINATION	23
<i>flhY</i>	1702	flagellar motor switch protein	<i>rapF</i>	3845	response regulator aspartate phosphatase	<i>gerAA</i>	3390	germination response to L-alanine
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapG</i>	4139	response regulator aspartate phosphatase	<i>gerAB</i>	3391	germination response to L-alanine
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapG</i>	4139	response regulator aspartate phosphatase	<i>gerAC</i>	3392	germination response to L-alanine
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapH</i>	750	response regulator aspartate phosphatase	<i>gerBA</i>	3688	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapI</i>	547	response regulator aspartate phosphatase	<i>gerBB</i>	3689	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapJ</i>	304	response regulator aspartate phosphatase	<i>gerBC</i>	3690	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapK</i>	2061	response regulator aspartate phosphatase	<i>gerCA</i>	2384	heptaprenyl diphosphate synthase component I (menaquinone biosynthesis)
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapL</i>	2552	antagonist of SinR	<i>gerCB</i>	2383	menaquinone biosynthesis methyltransferase
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapM</i>	2552	antagonist of SinR	<i>gerCC</i>	2382	heptaprenyl diphosphate synthase component II (menaquinone biosynthesis)
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapN</i>	2552	antagonist of SinR	<i>gerD</i>	159	germination response to L-alanine and to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapO</i>	2552	antagonist of SinR	<i>gerKA</i>	420	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapP</i>	2552	antagonist of SinR	<i>gerKB</i>	423	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapQ</i>	2552	antagonist of SinR	<i>gerKC</i>	421	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapR</i>	2552	antagonist of SinR	<i>gerM</i>	2902	germination (cortex hydrolysis) and sporulation (stage II, multiple polar septa)
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapS</i>	2552	antagonist of SinR	<i>gpr</i>	2635	spore protease (degradation of SASPs)
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapT</i>	2552	antagonist of SinR	<i>sleB</i>	2399	spore cortex-lytic enzyme
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapU</i>	2552	antagonist of SinR	<i>ykqK</i>	850	spore germination response
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapV</i>	2552	antagonist of SinR	<i>ykqR</i>	848	spore germination protein
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapW</i>	2552	antagonist of SinR	<i>ykqT</i>	847	spore germination protein
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapX</i>	2552	antagonist of SinR	<i>ykqV</i>	1448	spore cortex-lytic enzyme
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapY</i>	2552	antagonist of SinR	<i>yndD</i>	1907	spore germination protein
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapZ</i>	2552	antagonist of SinR	<i>yndE</i>	1908	spore germination protein
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAA</i>	2552	antagonist of SinR	<i>yndF</i>	1909	spore germination protein
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAB</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAC</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAD</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAE</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAF</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAG</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAH</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAI</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAJ</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAK</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAL</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAM</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAN</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAO</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAP</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAQ</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAR</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAS</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAT</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAU</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAV</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAW</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAX</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAY</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapAZ</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBA</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBB</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBC</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBD</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBE</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBF</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBG</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBH</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBI</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBJ</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBK</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBL</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBM</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBN</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBO</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBP</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBQ</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBR</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBS</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBT</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBU</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBV</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBW</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBX</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBY</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapBZ</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCA</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCB</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCC</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCD</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCE</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCF</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCG</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCH</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCI</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCJ</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCK</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCL</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCM</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCN</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCO</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCP</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCQ</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCR</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCS</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCT</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCU</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCV</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation	<i>rapCW</i>	2552	antagonist of SinR			
<i>flhZ</i>	1704	flagellar protein required for flagellar formation						

<i>bgIH</i>	4033	β -glucosidase (cellulose degradation)	<i>yjmA</i>	1300	glucuronate isomerase	<i>mngD</i>	2510	citrate synthase III
<i>bgIS</i>	4011	endo-1,3-1,4 glucanase (lichen degradation)	<i>yjmD</i>	1304	sorbitol dehydrogenase	<i>odhA</i>	2111	2-oxoglutarate dehydrogenase (E1 subunit)
<i>crh</i>	3659	catabolite repression HPr-like protein	<i>yjmE</i>	1305	D-mannanase hydrolase	<i>odhB</i>	2108	2-oxoglutarate dehydrogenase (dihydroliipoamide transsuccinylase, E2 subunit)
<i>csrA</i>	2748	carbon storage regulator	<i>yjmF</i>	1306	2-deoxy-D-glucuronate 3-dehydrogenase			
<i>csrA</i>	3635	carbon storage regulator	<i>yjml</i>	1309	tagaturonate reductase	<i>sdhA</i>	2907	succinate dehydrogenase (flavoprotein subunit)
<i>frub</i>	1508	fructose 1-phosphate kinase	<i>yjml</i>	1311	altronate hydrolase	<i>sdhB</i>	2905	succinate dehydrogenase (iron-sulphur protein)
<i>galE</i>	3990	UDP-glucose 4-epimerase (galactose metabolism)	<i>ykC</i>	1356	dicolich phosphate mannose synthase	<i>sdhC</i>	2908	succinate dehydrogenase (cytochrome <i>b₅₅₈</i> subunit)
<i>galK</i>	3921	galactokinase (galactose metabolism)	<i>ykF</i>	1366	chloromuconate cyclisomerase	<i>sucC</i>	1680	succinyl-CoA synthetase (β subunit)
<i>galT</i>	3919	galactose-1-phosphate uridylyltransferase (galactose metabolism)	<i>ykG</i>	1367	polysugar degrading enzyme	<i>sucD</i>	1681	succinyl-CoA synthetase (α subunit)
<i>gdh</i>	445	glucose 1-dehydrogenase	<i>ykH</i>	1403	dicolich phosphate mannose synthase	<i>yjmC</i>	1303	malate dehydrogenase
<i>glcK</i>	2571	glucose kinase	<i>ykI</i>	1427	ribulose-bisphosphate carboxylase	<i>yqk</i>	2452	malate dehydrogenase
<i>glpA</i>	3167	starch (bacterial glycogen) synthase (glycogen biosynthesis)	<i>ykL</i>	1537	myo-inositol-1(or 4)-monophosphatase	<i>ytl</i>	2990	malate dehydrogenase
<i>glgB</i>	3171	1,4- α -glucan branching enzyme (glycogen biosynthesis)	<i>ykM</i>	1477	glucose 1-dehydrogenase	<i>ywkA</i>	3801	malate dehydrogenase
<i>glgC</i>	3169	glucose-1-phosphate adenylyltransferase (glycogen biosynthesis)	<i>ykO</i>	1442	glucose 1-dehydrogenase			
<i>glgD</i>	3168	required for glycogen biosynthesis	<i>ykP</i>	1445	chitinase			
<i>glpP</i>	3165	glycogen phosphorylase (glycogen metabolism)	<i>ykQ</i>	1445	chitinase			
<i>glpD</i>	1004	glycerol-3-phosphate dehydrogenase (glycerol utilization)	<i>ykR</i>	1445	chitinase			
<i>glpK</i>	1003	glycerol kinase (glycerol utilization)	<i>ykS</i>	1445	chitinase			
<i>glpA</i>	890	6-phospho- β -glucosidase (arbutin fermentation)	<i>ykT</i>	1477	glucose 1-dehydrogenase			
<i>gmK</i>	4113	gluconate kinase (gluconate utilization)	<i>ykU</i>	1477	glucose 1-dehydrogenase			
<i>gmZ</i>	4116	6-phosphogluconate dehydrogenase (gluconate utilization)	<i>ykV</i>	1477	glucose 1-dehydrogenase			
<i>gpsA</i>	2389	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	<i>ykW</i>	1427	ribulose-bisphosphate carboxylase			
<i>gutB</i>	667	sorbitol dehydrogenase	<i>ykX</i>	1741	deacetylase			
<i>iolB</i>	4082	myo-inositol catabolism	<i>ykY</i>	1741	deacetylase			
<i>iolC</i>	4081	myo-inositol catabolism	<i>ykZ</i>	1741	deacetylase			
<i>iolD</i>	4080	myo-inositol catabolism	<i>ynF</i>	1943	endo-xylianase	<i>ald</i>	3277	L-alanine dehydrogenase
<i>iolE</i>	4078	myo-inositol catabolism	<i>ynG</i>	1951	propionyl-CoA carboxylase	<i>ampS</i>	1516	aminopeptidase
<i>iolG</i>	4076	myo-inositol 2-dehydrogenase (inositol catabolism)	<i>yoaC</i>	2023	xylokinnase	<i>ansA</i>	2456	L-asparaginase
<i>iolH</i>	4075	myo-inositol catabolism	<i>yoaD</i>	2024	phosphoglycerate dehydrogenase	<i>ansB</i>	2455	L-asparaginase
<i>iolI</i>	4074	myo-inositol catabolism	<i>yoaE</i>	2025	formate dehydrogenase	<i>aprE</i>	1105	extracellular alkaline serine protease (subtilisin E)
<i>iolS</i>	4084	myo-inositol catabolism	<i>yoaF</i>	2031	4-hydroxyphenylacetate-3-hydroxylase	<i>aprX</i>	1862	intracellular alkaline serine protease
<i>kdgA</i>	2323	deoxyphosphogluconate aldolase (pectin utilization)	<i>yoaG</i>	2007	alcohol dehydrogenase	<i>argB</i>	1197	N-acetylglutamate 5-phosphotransferase (arginine biosynthesis)
<i>kdgK</i>	2324	2-keto-3-deoxygluconate kinase (pectin utilization)	<i>yqC</i>	2507	phosphoenolpyruvate mutase	<i>argC</i>	1195	N-acetylglutamate γ -semialdehyde dehydrogenase (arginine biosynthesis)
<i>kduD</i>	2326	2-keto-3-deoxygluconate oxidoreductase (pectin utilization)	<i>yqD</i>	2489	propionyl-CoA carboxylase	<i>argD</i>	1198	N-acetylornithine aminotransferase (arginine biosynthesis)
<i>kduI</i>	2325	5-keto-4-deoxyuronate isomerase (pectin utilization)	<i>yqE</i>	2780	formate dehydrogenase	<i>argE</i>	2142	acetylornithine deacetylase (arginine biosynthesis)
<i>lacA</i>	3504	β -galactosidase	<i>yqF</i>	2780	formate dehydrogenase	<i>argF</i>	1203	ornithine carbamoyltransferase (arginine biosynthesis)
<i>lctE</i>	329	L-lactate dehydrogenase	<i>yqG</i>	2780	formate dehydrogenase	<i>argG</i>	3013	argininosuccinate synthase (arginine biosynthesis)
<i>lchH</i>	3959	6-phospho- β -glucosidase	<i>yqH</i>	2780	formate dehydrogenase	<i>argH</i>	3012	argininosuccinate lyase (arginine biosynthesis)
<i>lplD</i>	782	hydrolytic enzyme	<i>yqI</i>	2780	formate dehydrogenase	<i>argI</i>	1196	ornithine acetyltransferase / amino-acid acetyltransferase (arginine biosynthesis)
<i>melA</i>	3100	α -D-galactoside galactohydrolase	<i>yqJ</i>	2780	formate dehydrogenase	<i>aroA</i>	3046	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase / chorismate mutase-isozyme 3 (shikimate pathway)
<i>mtlD</i>	451	mannitol-1-phosphate dehydrogenase	<i>yqK</i>	3155	UTP-glucose-1-phosphate uridylyltransferase	<i>aroB</i>	2378	3-dehydroquininate synthase (shikimate pathway)
<i>nagA</i>	3594	N-acetylglucosamine-6-phosphate deacetylase (N-acetylglucosamine utilization)	<i>yqL</i>	3138	carbonic anhydrase	<i>aroC</i>	2413	3-dehydroquininate dehydratase (shikimate pathway)
<i>nagB</i>	3596	N-acetylglucosamine-6-phosphate isomerase (N-acetylglucosamine utilization)	<i>yqM</i>	3055	endo-1,4-glucanase	<i>aroD</i>	2645	shikimate 5-dehydrogenase (shikimate pathway)
<i>narO</i>	3773	needed for formate dehydrogenase activity	<i>yqN</i>	2989	acetyl-CoA carboxylase	<i>aroE</i>	2368	5-enolpyruvylshikimate-3-phosphate synthase (shikimate pathway)
<i>pel</i>	828	pectate lyase	<i>yqO</i>	3227	dihydroliipoamide S-acetyltransferase	<i>aroF</i>	2380	chorismate synthase (shikimate pathway)
<i>pelB</i>	2034	pectate lyase	<i>yqP</i>	3224	NADH-dependent butanol dehydrogenase	<i>aroH</i>	2377	chorismate synthase (shikimate pathway) (aromatic amino acids biosynthesis)
<i>pni</i>	3688	mannose-6-phosphate isomerase	<i>yqQ</i>	3222	NADH-dependent butanol dehydrogenase	<i>aroI</i>	340	shikimate kinase (shikimate pathway)
<i>pps</i>	2053	phosphoenolpyruvate synthase	<i>yqR</i>	3215	exo-1,4-glucosidase	<i>asd</i>	2945	aspartate-semialdehyde dehydrogenase
<i>pta</i>	3865	phosphotransacetylase	<i>yqS</i>	3200	rhamnulokinase	<i>ask</i>	1710	aspartokinase II attenuator
<i>ptsH</i>	1459	histidine-containing phosphocarrier protein of the phosphotransferase system (PTS) (HPr protein)	<i>yqT</i>	3192	L-rhamnose isomerase	<i>asnB</i>	3127	asparagine synthetase
<i>rbsK</i>	3701	ribokinase (ribose metabolism)	<i>yqU</i>	3382	thiamulokinase	<i>asnH</i>	4098	asparagine synthetase
<i>sacA</i>	3902	sucrose-6-phosphate hydrolase	<i>yqV</i>	3382	rhamnulokinase	<i>aspB</i>	2348	aspartate aminotransferase
<i>sacB</i>	3535	levansucrase	<i>yqW</i>	3382	rhamnulokinase	<i>bcsA</i>	2317	naringenin-chalcone synthase (phenylalanine metabolism)
<i>sacC</i>	2759	sucrose-6-phosphate hydrolase	<i>yqX</i>	3382	rhamnulokinase	<i>bfmBAA</i>	2499	branched-chain α -keto acid dehydrogenase E1 (2-oxoisovalerate dehydrogenase α subunit)
<i>sacY</i>	3941	negative regulatory protein of SacY	<i>yqY</i>	3382	rhamnulokinase	<i>bfmBAB</i>	2498	branched-chain α -keto acid dehydrogenase E1 (2-oxoisovalerate dehydrogenase β subunit)
<i>traA</i>	851	trehalose-6-phosphate hydrolase	<i>yqZ</i>	3382	rhamnulokinase	<i>bfmBB</i>	2497	branched-chain α -keto acid dehydrogenase E2 subunit (lipoamide acyltransferase)
<i>xta</i>	2914	β -xylosidase / α -L-arabinosidase (xylan degradation)	<i>yqAA</i>	3382	rhamnulokinase	<i>bltD</i>	2718	spermine/spermidine acetyltransferase
<i>xyIA</i>	1891	xylose isomerase (xylose metabolism)	<i>yqAB</i>	3382	rhamnulokinase	<i>bpr</i>	1599	bacillopeptidase F
<i>xyIB</i>	1893	xylose kinase (xylose metabolism)	<i>yqAC</i>	3382	rhamnulokinase	<i>cad</i>	1535	lysine decarboxylase
<i>xyxA</i>	2054	endo-1,4-xylanase (xylan degradation)	<i>yqAD</i>	3382	rhamnulokinase	<i>carA</i>	1199	carbamoyl-phosphate transferase-arginine (subunit A) (arginine biosynthesis)
<i>xyxB</i>	1888	xylan β -1,4-xylosidase (xylan degradation)	<i>yqAE</i>	3382	rhamnulokinase	<i>carB</i>	1200	carbamoyl-phosphate transferase-arginine (subunit B) (arginine biosynthesis)
<i>xyxD</i>	1945	endo-1,4-xylanase (xylan degradation)	<i>yqAF</i>	3382	rhamnulokinase	<i>ctpA</i>	2133	carboxy-terminal processing protease
<i>ybbA</i>	161	polysaccharide deacetylase	<i>yqAG</i>	4091	glucose 1-dehydrogenase	<i>cysE</i>	113	serine acetyltransferase (cysteine biosynthesis)
<i>ybbB</i>	188	β -hexosaminidase	<i>yqAH</i>	4040	arabinan endo-15-L-arabinosidase	<i>cysH</i>	1630	phosphoadenosine phosphosulfate reductase (cysteine biosynthesis)
<i>ybcM</i>	213	glucosamine-fructose-6-phosphate aminotransferase	<i>yqAI</i>	4000	gluconate 5-dehydrogenase	<i>cysK</i>	82	cysteine synthetase A (cysteine biosynthesis)
<i>ybtT</i>	258	glucosamine-6-phosphate isomerase	<i>yqAJ</i>	4107	gluconate 1-dehydrogenase	<i>dal</i>	517	D-alanine racemase
<i>ybcB</i>	268	5-dehydro-4-deoxygluconate dehydratase	<i>yqAK</i>	4202	formate dehydrogenase	<i>dapA</i>	1748	dihydrodipicolinate synthase (diaminopimelate/lysine biosynthesis)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqAL</i>	4196	galactoside acetyltransferase	<i>dapB</i>	2359	dihydrodipicolinate reductase (diaminopimelate/lysine biosynthesis)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqAM</i>	4136	formaldehyde dehydrogenase	<i>dapG</i>	1787	aspartokinase I (α and β subunits)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqAN</i>	3664	UDP-N-acetylglucosamine 2-epimerase	<i>def</i>	1646	polypeptide deformylase
<i>ybcF</i>	272	gluconate dehydratase	<i>yqAO</i>	3695	aldehyde dehydrogenase	<i>epi</i>	3939	minor extracellular serine protease
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqAP</i>	3872	glucose 1-dehydrogenase	<i>glmS</i>	200	L-glutamine-D-fructose-6-phosphate amidotransferase
<i>ybcF</i>	272	gluconate dehydratase	<i>yqAQ</i>	3872	glucose 1-dehydrogenase	<i>glnA</i>	1878	glutamine synthetase
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqAR</i>	3872	glucose 1-dehydrogenase	<i>gltA</i>	2014	glutamate synthase (large subunit) (glutamate biosynthesis)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqAS</i>	3872	glucose 1-dehydrogenase	<i>gltB</i>	2009	glutamate synthase (small subunit) (glutamate biosynthesis)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqAT</i>	3872	glucose 1-dehydrogenase	<i>glyA</i>	3789	serine hydroxymethyltransferase (glycine/serine/threonine metabolism)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqAU</i>	3872	glucose 1-dehydrogenase	<i>hisA</i>	3584	phosphoribosylformimino-5-aminoimidazole carbamoyl ribotide isomerase (histidine biosynthesis)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqAV</i>	3872	glucose 1-dehydrogenase	<i>hisB</i>	3585	imidazoleglycerol-phosphate dehydratase (histidine biosynthesis)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqAW</i>	3872	glucose 1-dehydrogenase	<i>hisC</i>	2371	histidinol-phosphate aminotransferase (histidine biosynthesis) / tyrosine and phenylalanine aminotransferase
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqAX</i>	3872	glucose 1-dehydrogenase	<i>hisD</i>	3587	histidinol dehydrogenase (histidine biosynthesis)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqAY</i>	3872	glucose 1-dehydrogenase	<i>hisF</i>	3583	HISF cyclase-like protein (synthesis of D-erythroimidazole glycerol phosphate)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqAZ</i>	3872	glucose 1-dehydrogenase	<i>hisG</i>	3587	ATP phosphoribosyltransferase (histidine biosynthesis)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBA</i>	3872	glucose 1-dehydrogenase	<i>hisH</i>	3585	amidotransferase (histidine biosynthesis)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBB</i>	3872	glucose 1-dehydrogenase	<i>hisI</i>	3583	phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphorylase (histidine biosynthesis)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBC</i>	3872	glucose 1-dehydrogenase	<i>hom</i>	3315	homoserine dehydrogenase (threonine/methionine biosynthesis)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBD</i>	3872	glucose 1-dehydrogenase	<i>hutG</i>	4045	formiminoglutamate hydrolase (histidine utilization)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBE</i>	3872	glucose 1-dehydrogenase	<i>hutH</i>	4041	histidase (histidine utilization)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBF</i>	3872	glucose 1-dehydrogenase	<i>hutI</i>	4044	imidazole-5-propionate hydrolase (histidine utilization)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBG</i>	3872	glucose 1-dehydrogenase	<i>hutU</i>	4042	urocanase (histidine utilization)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBH</i>	3872	glucose 1-dehydrogenase	<i>ilvA</i>	2933	threonine dehydratase (isoleucine biosynthesis)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBI</i>	3872	glucose 1-dehydrogenase	<i>ilvB</i>	2896	acetolactate synthase (large subunit) (valine/isoleucine biosynthesis)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBJ</i>	3872	glucose 1-dehydrogenase	<i>ilvC</i>	2894	ketol-acid reductoisomerase (valine/isoleucine biosynthesis)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBK</i>	3872	glucose 1-dehydrogenase	<i>ilvD</i>	2302	dihydroxy-acid dehydratase (valine/isoleucine biosynthesis)
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBL</i>	3872	glucose 1-dehydrogenase	<i>ilvN</i>	2894	acetolactate synthase (small subunit)
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBM</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBN</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBO</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBP</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBQ</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBR</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBS</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBT</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBU</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBV</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBW</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBX</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqBY</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqBZ</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqCA</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqCB</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqCC</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqCD</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqCE</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqCF</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqCG</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqCH</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqCI</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqCJ</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqCK</i>	3872	glucose 1-dehydrogenase			
<i>ybcD</i>	269	aldehyde dehydrogenase	<i>yqCL</i>	3872	glucose 1-dehydrogenase			
<i>ybcF</i>	272	gluconate dehydratase	<i>yqCM</i>	3872	glucose 1-dehydrogenase</			



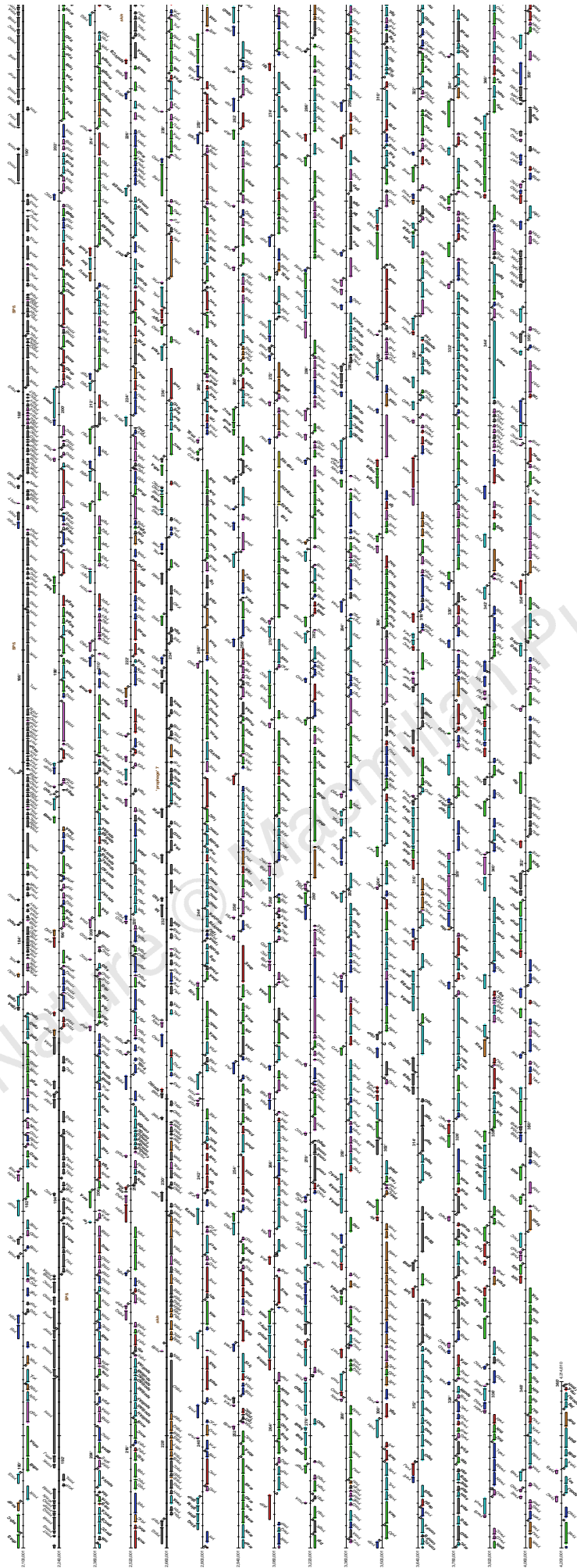


Table 1. (continuation) Functional classification of the *Bacillus subtilis* protein-coding genes.

<i>ioIA</i>	4083	(valine/isoleucine biosynthesis) methylmalonate-semialdehyde dehydrogenase (valine metabolism)	<i>yqjE</i>	2486	tripeptidase	<i>xpt</i>	2319	xanthine phosphoribosyltransferase (purine biosynthesis)
<i>ipi</i>	1189	intracellular proteinase inhibitor	<i>yqjN</i>	2475	amino acid degradation	<i>yaaF</i>	23	deoxyuridine kinase subunit
<i>ispA</i>	1386	major intracellular serine protease	<i>yqjO</i>	2472	pyrroline-5-carboxylate reductase	<i>yaaG</i>	24	deoxypurine kinase subunit
<i>kbl</i>	1771	2-amino-3-ketobutyrate CoA ligase	<i>yqjR</i>	2470	D-serine dehydratase	<i>yabR</i>	70	polyribonucleotide nucleotidyltransferase
<i>leuA</i>	2893	2-isopropylmalate synthase (leucine biosynthesis)	<i>yrbE</i>	2839	opine catabolism	<i>yera</i>	713	adenine deaminase
<i>leuB</i>	2891	3-isopropylmalate dehydrogenase (leucine biosynthesis)	<i>yrbF</i>	2786	cysteine synthase	<i>yfjM</i>	859	2'-3'-cyclic-nucleotide 2'-phosphodiesterase
<i>leuC</i>	2890	3-isopropylmalate dehydratase (large subunit) (leucine biosynthesis)	<i>yrbP</i>	2788	dihydrodipicolinate reductase	<i>yghM</i>	1069	CMP-binding factor
<i>leuD</i>	2889	3-isopropylmalate dehydratase (small subunit) (leucine biosynthesis)	<i>yrcC</i>	2738	glutamate racemase	<i>yhcR</i>	991	5'-nucleotidase
<i>lysA</i>	2437	diaminopimelate decarboxylase (lysine biosynthesis)	<i>yrcN</i>	2794	protease	<i>yirY</i>	1144	DNA exonuclease
<i>lysC</i>	2910	aspartokinase II (α and β subunits) (diaminopimelate/lysine biosynthesis)	<i>yrcO</i>	2793	protease	<i>yjbM</i>	1236	GTP pyrophosphokinase
<i>metB</i>	2305	homoserine O-succinyltransferase (methionine biosynthesis)	<i>ysnE</i>	2897	acetyltransferase	<i>yjbP</i>	1240	diadenosine tetraphosphatase
<i>metC</i>	1385	cobalamin-independent methionine synthase (methionine biosynthesis)	<i>ytdD</i>	3146	N-acetylamino acid racemase	<i>ykkE</i>	1377	formyltetrahydrofolate deformylase
<i>metK</i>	3128	S-adenosylmethionine synthetase	<i>ytkP</i>	3066	cysteine synthase	<i>yibB</i>	1565	IMP dehydrogenase
<i>mpr</i>	245	extracellular metalloprotease	<i>yubC</i>	3193	cysteine dioxygenase	<i>yioD</i>	1641	guanylate kinase
<i>nasB</i>	362	assimilatory nitrate reductase (electron transfer subunit)	<i>yugH</i>	3226	aspartate aminotransferase	<i>ymaA</i>	1868	ribonucleoprotein
<i>nasC</i>	360	assimilatory nitrate reductase (catalytic subunit)	<i>yurG</i>	3341	aspartate aminotransferase	<i>yrcB</i>	1836	micrococcal nuclease
<i>nasD</i>	358	assimilatory nitrite reductase (subunit)	<i>yurH</i>	3343	N-carbamyl-L-amino acid amidohydrolase	<i>yrcF</i>	1839	deoxyuridine 5'-triphosphate pyrophosphatase
<i>napE</i>	1196	extracellular neutral protease B	<i>yurI</i>	3347	opine catabolism	<i>ysnN</i>	2165	ribonucleoside-diphosphate reductase (α subunit)
<i>nprB</i>	1541	extracellular neutral metalloprotease	<i>yurP</i>	3351	opine catabolism	<i>yscO</i>	2164	ribonucleoside-diphosphate reductase (α subunit)
<i>nprE</i>	1541	extracellular neutral metalloprotease	<i>yurR</i>	3353	opine catabolism	<i>yscP</i>	2161	ribonucleoside-diphosphate reductase (β subunit)
<i>nrgB</i>	3757	nitrogen-regulated PII-like protein	<i>yurT</i>	3354	methylglyoxalase	<i>yscS</i>	2159	deoxyuridine 5'-triphosphate nucleotidohydrolyase
<i>patA</i>	1472	aminotransferase	<i>yusH</i>	3366	glycine cleavage system protein H	<i>yprD</i>	2395	ribosomal protein S1 homologue
<i>patB</i>	3228	aminotransferase	<i>yusM</i>	3373	proline dehydrogenase	<i>yqjB</i>	2528	exodeoxyribonuclease VII (large subunit)
<i>pepT</i>	3994	peptidase T	<i>yusX</i>	3381	oligoendopeptidase	<i>yqjC</i>	2526	exodeoxyribonuclease VII (small subunit)
<i>pheA</i>	2851	prephenate dehydratase (phenylalanine biosynthesis)	<i>yutL</i>	3306	diaminopimelate epimerase	<i>yrcD</i>	2730	ribonuclease inhibitor
<i>pheB</i>	2852	chorismate mutase (phenylalanine biosynthesis)	<i>yuxL</i>	3312	acylaminoacyl-peptidase	<i>yrrU</i>	2787	purine nucleoside phosphorylase
<i>proA</i>	1379	γ -glutamyl phosphate reductase (proline biosynthesis)	<i>yvaA</i>	3454	carboxylesterase	<i>yumD</i>	3302	GMP reductase
<i>proB</i>	1378	γ -glutamyl kinase (proline biosynthesis)	<i>yvaB</i>	3516	serine O-acetyltransferase	<i>yunH</i>	3328	allantoinase
<i>proH</i>	2017	involved in proline biosynthesis (salt-inducible)	<i>yidB</i>	3623	carboxy-terminal processing protease	<i>yunL</i>	3332	uricase
<i>proJ</i>	2016	glutamate 5-kinase (proline biosynthesis)	<i>yjb</i>	3623	carboxy-terminal processing protease	<i>yurI</i>	3343	ribonuclease
<i>racX</i>	3533	amino acid racemase	<i>ywaA</i>	3956	branched-chain amino acid aminotransferase	<i>ywaC</i>	3949	GTP-pyrophosphokinase
<i>rocA</i>	3879	pyrroline-5-carboxylate dehydrogenase (arginine and ornithine utilization)	<i>ywaD</i>	3947	aminopeptidase			
<i>rocB</i>	3878	involved in arginine and ornithine utilization	<i>yweB</i>	3881	glutamate dehydrogenase			
<i>rocD</i>	4146	ornithine aminotransferase (arginine and ornithine utilization)	<i>ywfG</i>	3868	aspartate aminotransferase			
<i>rocF</i>	4142	arginase (arginine and ornithine utilization)	<i>ywhF</i>	3849	spermidine synthase			
<i>serA</i>	2410	phosphoglycerate dehydrogenase (serine biosynthesis)	<i>ywhG</i>	3848	agmatinase			
<i>serC</i>	1076	phosphoserine aminotransferase (serine biosynthesis)	<i>ywrD</i>	3720	γ -glutamyltransferase			
<i>tdh</i>	1770	threonine 3-dehydrogenase (threonine catabolism)	<i>yxeP</i>	4057	aminoacylase			
<i>thrB</i>	3313	homoserine kinase (threonine biosynthesis)						
<i>thrC</i>	3314	threonine synthase (threonine biosynthesis)						
<i>trpA</i>	2372	tryptophan synthase (α subunit) (tryptophan biosynthesis)						
<i>trpB</i>	2373	tryptophan synthase (β subunit) (tryptophan biosynthesis)						
<i>trpC</i>	2374	indol-3-glycerol phosphate synthase (tryptophan biosynthesis)						
<i>trpD</i>	2375	anthranilate phosphoribosyltransferase (tryptophan biosynthesis)						
<i>trpE</i>	2377	anthranilate synthase (tryptophan biosynthesis)						
<i>trpF</i>	2373	phosphoribosyl anthranilate isomerase (tryptophan biosynthesis)						
<i>tyrA</i>	2370	prephenate dehydrogenase (tyrosine biosynthesis)						
<i>ureA</i>	3769	urease (γ subunit)						
<i>ureB</i>	3769	urease (β subunit)						
<i>ureC</i>	3767	urease (α subunit)						
<i>vpr</i>	3907	minor extracellular serine protease						
<i>yaaO</i>	38	lysine decarboxylase						
<i>ybgE</i>	259	branched-chain amino acid aminotransferase						
<i>ybgJ</i>	265	glutaminase						
<i>yccC</i>	290	asparaginase						
<i>ycgM</i>	344	proline oxidase						
<i>ycgN</i>	345	1-pyrroline-5-carboxylate dehydrogenase						
<i>yclE</i>	415	prolyl aminopeptidase						
<i>yclM</i>	422	homoserine dehydrogenase						
<i>ycnG</i>	441	4-aminobutyrate aminotransferase						
<i>ycnH</i>	443	succinate-semialdehyde dehydrogenase						
<i>ycaA</i>	452	3-isopropylmalate dehydrogenase						
<i>ycaS</i>	459	allophanate hydrolase						
<i>yedD</i>	718	glutamate synthase (ferredoxin)						
<i>yerM</i>	729	amidase						
<i>yhaA</i>	1081	aminoacylase						
<i>yhdR</i>	1034	aspartate aminotransferase						
<i>yheM</i>	1041	D-alanine aminotransferase						
<i>yisK</i>	1152	5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase						
<i>yisO</i>	1157	asparagine synthase						
<i>yisW</i>	1167	lysine aminotransferase						
<i>yjgB</i>	1231	oligoendopeptidase						
<i>yjgR</i>	1243	sarcosine oxidase						
<i>yjcl</i>	1258	cystathionine γ -synthase						
<i>yjcl</i>	1259	cystathionine β -lyase						
<i>ykeA</i>	1359	pyrroline-5-carboxylate reductase						
<i>ykrV</i>	1425	aspartate aminotransferase						
<i>ykuQ</i>	1488	tetrahydrodipicolinate succinylase						
<i>ykuR</i>	1489	hippurate hydrolase						
<i>yliM</i>	1551	glutaminase						
<i>ylnB</i>	1607	acetylornithine deacetylase						
<i>yliW</i>	1658	phosphoglycerate dehydrogenase						
<i>yliA</i>	1658	L-serine dehydratase						
<i>ymlG</i>	1757	processing protease						
<i>ymlH</i>	1758	processing protease						
<i>ymxG</i>	1742	processing protease						
<i>ynal</i>	1885	phosphoribosylanthranilate isomerase						
<i>yncD</i>	1898	alanine racemase						
<i>yobN</i>	2074	L-amino acid oxidase						
<i>yodT</i>	2145	adenosylmethionine-8-amino-7-oxononanoate aminotransferase						
<i>yocA</i>	2403	glutamate dehydrogenase						
<i>ywvA</i>	2321	carboxypeptidase						
<i>yael</i>	2844	dihydrodipicolinate reductase						
<i>yahl</i>	2549	aminomethyltransferase						
<i>yahJ</i>	2547	glycine dehydrogenase						
<i>yahK</i>	2546	glycine dehydrogenase						
<i>yahS</i>	2539	3-dehydroquininate dehydratase						
<i>yqIT</i>	2503	leucine dehydrogenase						
<i>adeC</i>	152	adenine deaminase						
<i>adk</i>	146	adenylate kinase						
<i>apt</i>	2823	adenine phosphoribosyltransferase						
<i>cdd</i>	2611	cytidine/deoxyuridine deaminase						
<i>cmk</i>	2396	cytidylate kinase						
<i>ctrA</i>	3811	CTP synthetase (pyrimidine biosynthesis)						
<i>deoD</i>	2135	purine nucleoside phosphorylase (purine nucleoside salvage)						
<i>dra</i>	4051	deoxyribose-phosphate aldolase (nucleotide/deoxyribonucleotide catabolism)						
<i>drm</i>	2448	phosphodeoxyribomutase (purine nucleoside salvage)						
<i>guaA</i>	692	GMP synthetase (GMP biosynthesis)						
<i>guaB</i>	16	inositol-monophosphate dehydrogenase (GMP biosynthesis)						
<i>hipO</i>	3000	hippurate hydrolase						
<i>hprT</i>	76	hypoxanthine-guanine phosphoribosyltransferase (purine salvage)						
<i>ndk</i>	2381	nucleoside diphosphate kinase						
<i>nin</i>	372	inhibitor of the DNA degrading activity of NucA subunit						
<i>nrdE</i>	1868	ribonucleoside-diphosphate reductase (major subunit)						
<i>nrdF</i>	1870	ribonucleoside-diphosphate reductase (minor subunit)						
<i>nucA</i>	372	membrane-associated nuclease						
<i>nucB</i>	2652	sporulation-specific extracellular nuclease						
<i>pdp</i>	4049	pyrimidine-nucleoside phosphorylase						
<i>pnp</i>	2446	purine nucleoside phosphorylase (purine nucleoside salvage)						
<i>pnpA</i>	1739	polynucleotide phosphorylase						
<i>prs</i>	58	phosphoribosyl pyrophosphate synthetase (nucleotide biosynthesis)						
<i>purA</i>	4156	adenylosuccinate synthetase (AMP biosynthesis)						
<i>purB</i>	700	adenylosuccinate lyase (purine biosynthesis)						
<i>purC</i>	701	phosphoribosylaminoimidazole succinocarboxamide synthetase (purine biosynthesis)						
<i>purD</i>	710	phosphoribosylglycinamide synthetase (purine biosynthesis)						
<i>purE</i>	698	phosphoribosylaminoimidazole carboxylase I (purine biosynthesis)						
<i>purF</i>	705	phosphoribosylpyrophosphate amidotransferase (purine biosynthesis)						
<i>purH</i>	708	phosphoribosylaminoimidazole carboxy formyl transferase / inosine-monophosphate cyclodiphase (purine biosynthesis)						
<i>purK</i>	699	phosphoribosylaminoimidazole carboxylase II (purine biosynthesis)						
<i>purL</i>	702	phosphoribosylformylglycinamide synthetase II (purine biosynthesis)						
<i>purM</i>	706	phosphoribosylaminoimidazole synthetase (purine biosynthesis)						
<i>purN</i>	708	phosphoribosylglycinamide formyltransferase (purine biosynthesis)						
<i>purQ</i>	703	phosphoribosylformylglycinamide synthetase I (purine biosynthesis)						
<i>purT</i>	244	phosphoribosylglycinamide formyltransferase 2 (purine biosynthesis)						
<i>pyrAA</i>	1622	carbamoyl-phosphate synthetase (glutaminase subunit) (pyrimidine biosynthesis)						
<i>pyrAB</i>	1623	carbamoyl-phosphate synthetase (catalytic subunit) (pyrimidine biosynthesis)						
<i>pyrB</i>	1620	aspartate carbamoyltransferase (pyrimidine biosynthesis)						
<i>pyrC</i>	1621	dihydroorotate (pyrimidine biosynthesis)						
<i>pyrD</i>	1622	dihydroorotate dehydrogenase (pyrimidine biosynthesis)						
<i>pyrDII</i>	1627	dihydroorotate dehydrogenase (electron transfer subunit) (pyrimidine biosynthesis)						
<i>pyrE</i>	1629	orotate phosphoribosyltransferase (pyrimidine biosynthesis)						
<i>pyrF</i>	1628	orotidine 5						

<i>ywpB</i>	3743	hydroxymyristoyl-(acyl carrier protein) dehydrogenase	<i>yjgT</i>	1245	thiamin biosynthesis	<i>recR</i>	29	DNA repair and genetic recombination
<i>yxjD</i>	4001	3-oxoadipate CoA-transferase	<i>yjgU</i>	1245	thiamin biosynthesis	<i>ruvA</i>	2636	Holliday junction DNA helicase
<i>yxjE</i>	4001	3-oxoadipate CoA-transferase	<i>yjgV</i>	1246	phosphomethylpyrimidine kinase	<i>ruvB</i>	2635	Holliday junction DNA helicase
II.5		METABOLISM OF COENZYMES AND PROSTHETIC GROUPS 99	<i>ykqB</i>	1513	thiamin biosynthesis	<i>sbpC</i>	1143	endonuclease SbcD homologue
<i>bioA</i>	3094	adenosylmethionine-8-amino-7-oxononanoate aminotransferase (biotin biosynthesis)	<i>ykxK</i>	1440	6-pyruvyl tetrahydropterin synthase	<i>yjgP</i>	1659	ATP-dependent DNA helicase
<i>bioB</i>	3091	biotin synthetase (biotin biosynthesis)	<i>ykxL</i>	1440	coenzyme-PMQ synthesis	<i>yocI</i>	2095	ATP-dependent DNA helicase
<i>bioD</i>	3091	dethiobiotin synthetase (biotin biosynthesis)	<i>yjgQ</i>	1577	pyrimidine-thiamine biosynthesis	<i>yorkQ</i>	2180	single-strand DNA-specific exonuclease
<i>bioF</i>	3092	8-amino-7-oxononanoate synthase (biotin biosynthesis)	<i>ylnD</i>	1633	uroporphyrin-III C-methyltransferase	<i>yqhH</i>	2549	SNF2 helicase
<i>bioI</i>	3089	cytochrome P450-like enzyme (biotin biosynthesis)	<i>ylnF</i>	1635	uroporphyrin-III C-methyltransferase	<i>yrrC</i>	2808	conjugation transfer protein
<i>bioW</i>	3094	6-carboxyhexanoate-CoA ligase (biotin biosynthesis)	<i>yloI</i>	1642	pantothenate metabolism flavoprotein	<i>yrvE</i>	2825	single-strand DNA-specific exonuclease
<i>dfrA</i>	2296	dihydrofolate reductase (glycine/purine/DNA precursor synthesis, conversion of dUMP to dTMP)	<i>yngH</i>	1954	nitro carboxylase	<i>yvwA</i>	3735	SNF2 helicase
<i>dhaS</i>	2100	aldehyde dehydrogenase	<i>yocD</i>	2127	nitroreductase	III.4		DNA PACKAGING AND SEGREGATION 10
<i>dhaA</i>	3291	2,3-dihydroxy-2,3-dihydroxybenzoate dehydrogenase (2,3-dihydroxybenzoate biosynthesis)	<i>yqgV</i>	2574	5-formyltetrahydrofolate cyclo-ligase	<i>grfA</i>	1935	DNA gyrase-like protein (subunit A)
<i>dhbB</i>	3288	isochorismatase (2,3-dihydroxybenzoate biosynthesis)	<i>yqjS</i>	2469	pantothenate kinase	<i>grfB</i>	1933	DNA gyrase-like protein (subunit B)
<i>dhbC</i>	3291	isochorismatase synthase (2,3-dihydroxybenzoate biosynthesis)	<i>yrrL</i>	2796	folate metabolism	<i>grfA</i>	7	DNA gyrase (subunit A)
<i>dhbE</i>	3289	2,3-dihydroxybenzoate-AMP ligase (enterobactin synthetase component E) (2,3-dihydroxybenzoate biosynthesis)	<i>yrrM</i>	2795	caffeoyl-CoA O-methyltransferase	<i>gyrB</i>	5	DNA gyrase (subunit B)
<i>dhbF</i>	3287	involved in 2,3-dihydroxybenzoate biosynthesis	<i>yueD</i>	3265	sepiapterin reductase	<i>hbs</i>	2385	non-specific DNA-binding protein HBSu
<i>folA</i>	87	7,8-dihydropterin aldolase (folate biosynthesis)	<i>yueJ</i>	3261	pyrazinamidase/nicotinamidase	<i>smc</i>	1666	chromosome segregation SMC protein homologue
<i>folC</i>	2866	folyl-polyglutamate synthetase (folate biosynthesis)	<i>yueK</i>	3260	nicotinate phosphoribosyltransferase	<i>smf</i>	1682	DNA processing Smf protein homologue
<i>folD</i>	2529	methylenetetrahydrofolate dehydrogenase / methylenetetrahydrofolate cyclohydrolase (purines and amino acids biosynthesis)	<i>yulG</i>	3293	biotin metabolism	<i>topA</i>	1683	DNA topoisomerase I
<i>folK</i>	87	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase (dihydrofolate biosynthesis)	<i>yurB</i>	3335	4-hydroxybenzoyl-CoA reductase	<i>topB</i>	476	DNA topoisomerase III
<i>ggt</i>	2004	γ -glutamyltranspeptidase (glutathione metabolism)	<i>yurC</i>	3338	4-hydroxybenzoyl-CoA reductase	<i>yopN</i>	2225	HU-related DNA-binding protein
<i>gsaB</i>	943	glutamate-1-semialdehyde aminotransferase	<i>yurD</i>	3338	4-hydroxybenzoyl-CoA reductase	III.5		RNA SYNTHESIS 244
<i>hemA</i>	2878	glutamyl-tRNA reductase (porphyrin biosynthesis)	<i>yutB</i>	3320	lipic acid synthetase	III.5.1		INITIATION 19
<i>hemB</i>	2874	8-aminolevulinic acid dehydratase (porphyrin biosynthesis)	<i>ywaB</i>	3950	quinone biosynthesis	<i>sigA</i>	2601	RNA polymerase major sigma factor (σ^70)
<i>hemC</i>	2876	porphobilinogen deaminase (porphyrin biosynthesis)	<i>ywbE</i>	3796	protoporphyrinogen oxidase	<i>sigB</i>	522	RNA polymerase general stress sigma factor (σ^32)
<i>hemD</i>	2875	uroporphyrinogen III cosynthase (porphyrin biosynthesis)	<i>ywcC</i>	3755	isochorismatase	<i>sigD</i>	1716	RNA polymerase flagella, motility, chemotaxis and autolysis sigma factor (σ^{54})
<i>hemE</i>	1086	uroporphyrinogen III decarboxylase (porphyrin biosynthesis)	II.6		METABOLISM OF PHOSPHATE 9	<i>sigE</i>	1604	RNA polymerase sporulation mother cell-specific (early) sigma factor (σ^S) (SpollGB)
<i>hemH</i>	1087	ferrochelatase (porphyrin biosynthesis)	<i>phoA</i>	1018	alkaline phosphatase A	<i>sigF</i>	2443	RNA polymerase sporulation forespore-specific (early) sigma factor (σ^S) (SpollAC)
<i>hemL</i>	2873	glutamate-1-semialdehyde 2,1-aminotransferase (porphyrin biosynthesis)	<i>phoB</i>	621	alkaline phosphatase III	<i>sigG</i>	1605	RNA polymerase sporulation forespore-specific (late) sigma factor (σ^S) (SpollIG)
<i>hemN</i>	2630	coproporphyrinogen III oxidase (porphyrin biosynthesis)	<i>phoD</i>	284	phosphodiesterase/alkaline phosphatase	<i>sigH</i>	117	RNA polymerase vegetative and early stationary-phase sigma factor (σ^70) (SpolH)
<i>hemX</i>	2877	negative effector of the concentration of HemA	<i>phoH</i>	2615	phosphate starvation-induced protein	<i>sigL</i>	3513	RNA polymerase sigma factor (σ^4)
<i>hemY</i>	1088	protoporphyrinogen IX oxidase (porphyrin biosynthesis)	<i>xpaC</i>	36	hydrolysis of 5-bromo-4-chloroindolyl phosphate	<i>sigV</i>	2769	RNA polymerase ECF-type sigma factor (σ^{54})
<i>menB</i>	3149	dihydroxynaphthoic acid synthetase (menaquinone biosynthesis)	<i>ybiM</i>	248	alkaline phosphatase	<i>sigW</i>	195	RNA polymerase ECF-type sigma factor (σ^{54})
<i>menD</i>	3151	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase / 2-oxoglutarate decarboxylase (menaquinone biosynthesis)	<i>ykoX</i>	1408	alkaline phosphatase	<i>sigX</i>	2414	RNA polymerase ECF-type sigma factor (σ^{54})
<i>menE</i>	3148	O-succinylbenzoic acid-CoA ligase (menaquinone biosynthesis)	<i>ykoX</i>	1408	alkaline phosphatase	<i>sigY</i>	3970	RNA polymerase ECF-type sigma factor (σ^{54})
<i>menF</i>	3153	menaquinone-specific isochorismatase (menaquinone biosynthesis)	<i>yiaK</i>	1549	phosphate starvation inducible protein	<i>sigZ</i>	2742	RNA polymerase ECF-type sigma factor (σ^{54})
<i>moaB</i>	3014	molybdopter precursor biosynthesis	<i>yngC</i>	1947	alkaline phosphatase	<i>spolIC</i>	2701	RNA polymerase sporulation mother cell-specific (late) sigma factor (σ^S) (C-terminal half)
<i>moaD</i>	1499	molybdopter converting factor (subunit 1)	II.7		METABOLISM OF SULPHUR 8	<i>spolVCB</i>	2652	RNA polymerase sporulation mother cell-specific (late) sigma factor (σ^S) (N-terminal half)
<i>moaE</i>	1498	molybdopter converting factor (subunit 2)	<i>yisZ</i>	1170	adenylsulfate kinase	<i>xpf</i>	1324	RNA polymerase PoxX sigma factor-like
<i>moaA</i>	1495	molybdopter-guanine dinucleotide biosynthesis	<i>yitA</i>	1171	sulfate adenyltransferase	<i>yhdM</i>	1030	RNA polymerase ECF-type sigma factor
<i>mobB</i>	1498	molybdopter-guanine dinucleotide biosynthesis	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>ykoZ</i>	1411	RNA polymerase sigma factor
<i>moaE</i>	1497	molybdopter biosynthesis protein	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>yiaC</i>	1543	RNA polymerase ECF-type sigma factor
<i>moaB</i>	1496	molybdopter biosynthesis protein	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	III.5.2		REGULATION 213
<i>mtA</i>	2385	GTP cyclohydrolase I (tetrahydrofolate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>abh</i>	1517	transcriptional regulator of transition state genes (AbrB-like)
<i>nadA</i>	2846	quinolinate synthetase (quinolinate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>abrB</i>	45	transcriptional pleiotropic regulator of transition state genes (<i>aprE</i> , <i>comK</i> , <i>ftsAZ</i> , <i>hpr</i> , <i>motAB</i> , <i>npfE</i> , <i>pbpE</i> , <i>rbS</i> , <i>spoOH</i> , <i>spoVG</i> , <i>spoVE</i> , <i>tycA</i>)
<i>nadB</i>	2849	L-aspartate oxidase (quinolinate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>acoR</i>	883	transcriptional activator of the acetoin dehydrogenase operon (<i>acoABC</i>)
<i>nadC</i>	2847	nicotinate-nucleotide pyrophosphorylase (NAD/NADP biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>ahrC</i>	2522	transcriptional regulator of arginine metabolism expression (<i>roc</i> operon)
<i>nadE</i>	338	NH ₄ ⁺ -dependent NAD ⁺ synthetase (NAD biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>alsR</i>	3711	transcriptional regulator of the α -acetolactate operon (<i>alsSD</i>)
<i>narA</i>	3772	molybdopter precursor biosynthesis	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>ansR</i>	2456	transcriptional repressor of the <i>ansAB</i> operon (<i>Xre</i> family)
<i>nasF</i>	355	uroporphyrin-III C-methyltransferase (porphyrin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>araR</i>	3485	transcriptional repressor of the arabinose operon (<i>araBDLMMNCP</i>)
<i>nifS</i>	2849	required for NAD biosynthesis	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>aziB</i>	2729	transcriptional repressor of the <i>aziBCD</i> operon
<i>pabA</i>	84	p-aminobenzoate synthase glutamine amidotransferase (subunit B) / anthranilate synthase (subunit II) (folate and tryptophan biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>birA</i>	2355	transcriptional repressor of the biotin operon (<i>bioWAFDBI</i>) / biotin acetyl-CoA-carboxylase synthetase
<i>pabB</i>	83	p-aminobenzoate synthase (subunit A) (folate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>bltR</i>	2716	transcriptional regulator of the <i>bltD</i> operon
<i>pabC</i>	85	aminodeoxychorismate lyase (folate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>bmrR</i>	2495	transcriptional activator of the <i>bmrUR</i> operon
<i>panB</i>	2354	ketopantoate hydroxymethyltransferase (pantothenate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>ccpA</i>	3044	transcriptional regulator involved in carbon catabolite control
<i>panC</i>	2353	pantothenate synthetase (pantothenate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>cheB</i>	1711	two-component response regulator-like [CheA] / methyl-accepting chemotaxis proteins-glycylate methyltransferase
<i>panD</i>	2352	aspartate 1-decarboxylase (pantothenate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>cheY</i>	1703	two-component response regulator [CheA] involved in modulation of flagellar switch bias (chemotaxis)
<i>ribA</i>	2429	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase (riboflavin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>citR</i>	1020	transcriptional repressor of the citrate synthase I gene (<i>citA</i>)
<i>ribB</i>	2429	riboflavin synthase (α subunit) (riboflavin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>citT</i>	832	two-component response regulator [CitS]
<i>ribC</i>	1737	riboflavin kinase / FAD synthase (riboflavin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>codY</i>	1690	transcriptional pleiotropic repressor (expression of <i>srfA</i> , <i>comK</i> , <i>dpp</i> , <i>gabP</i> , <i>hut</i> , <i>ureABC</i>)
<i>ribG</i>	2431	riboflavin-specific deaminase (riboflavin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>comA</i>	3253	two-component response regulator [ComP] of late competence genes / surfactin production competence transcription factor (CTF), final autoregulatory control switch prior to competence development
<i>ribH</i>	2428	riboflavin synthase (β subunit) (riboflavin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>comK</i>	1117	transcriptional regulator of late competence operon (<i>comG</i>) and surfactin expression (<i>srfA</i>)
<i>ribT</i>	2427	reductase (riboflavin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>comQ</i>	3256	transcriptional regulator of late competence operon (<i>comG</i>) and surfactin expression (<i>srfA</i>)
<i>sul</i>	86	dihydropterolate synthase (dihydrofolate biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>ctsR</i>	101	transcriptional repressor of class III stress genes (<i>clpC</i> , <i>clpP</i>)
<i>thiA</i>	955	synthesis of the pyrimidine moiety of thiamin (thiamin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>degA</i>	1163	transcriptional activator involved in the degradation of glutamine phosphoribosylpyrophosphate amidotransferase
<i>thiC</i>	3930	thiamine-phosphate pyrophosphorylase (thiamin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>degU</i>	3644	two-component response regulator [DegS] involved in degradative enzyme and competence regulation (<i>sacB</i> , <i>degQ</i> , <i>comK</i>)
<i>thiD</i>	3900	phosphomethylpyrimidine kinase (thiamin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>deoR</i>	4052	transcriptional repressor of the <i>dra</i> / <i>nupC</i> / <i>pdp</i> operon (deoxyribonucleoside)
<i>thiK</i>	3931	hydroxyethylthiazole kinase (thiamin biosynthesis)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>fnr</i>	3831	transcriptional regulator of anaerobic genes (<i>narK</i> , <i>narGHI</i>)
<i>yalA</i>	26	isochorismatase	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>fruR</i>	1507	transcriptional repressor of the fructose operon (<i>fruRBA</i>)
<i>ydiA</i>	640	thiamin-monophosphate kinase	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>gerE</i>	2904	transcriptional regulator required for expression of late spore coat genes
<i>ydiG</i>	646	molybdopter precursor biosynthesis	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>glcR</i>	3739	transcriptional repressor involved in the expression of the phosphotransferase system
<i>yhaV</i>	1058	coproporphyrinogen III oxidase	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>glcT</i>	1456	transcriptional antiterminal essential for the expression of the <i>ptsGHI</i> operon
<i>yhcB</i>	979	flavodoxin	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>glnR</i>	1877	transcriptional repressor of the glutamine synthetase gene (<i>glfA</i>)
<i>yhuU</i>	1112	biotin biosynthesis	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>glpP</i>	1001	transcriptional antiterminal and control of mRNA stability of <i>glpD</i>
<i>yhxA</i>	1000	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>glpC</i>	2014	transcriptional activator of the glutamate synthase operon (<i>gltAB</i>)
			<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>gltR</i>	2725	transcriptional repressor of the glutamate synthase operon (<i>gltAB</i>)
			<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>gntR</i>	4113	transcriptional repressor of the gluconate operon (<i>gntRKPZ</i>)
			III.1		DNA REPLICATION 22			
			<i>dnaA</i>	2965	initiation of chromosome replication			
			<i>dnaB</i>	2965	initiation of chromosome replication / membrane attachment protein			
			<i>dnaC</i>	4158	replicative DNA helicase			
			<i>dnaD</i>	2345	initiation of chromosome replication			
			<i>dnaE</i>	2994	DNA polymerase III (α subunit)			
			<i>dnaG</i>	2603	DNA primase			
			<i>dnaI</i>	2963	primosome component (helicase loader)			
			<i>dnaJ</i>	2	DNA polymerase III (β subunit)			
			<i>dnaK</i>	27	DNA polymerase III (γ and τ subunits)			
			<i>hoiB</i>	41	DNA polymerase III (δ subunit)			
			<i>polA</i>	2975	DNA polymerase I			
			<i>polC</i>	1727	DNA polymerase III (α subunit)			
			<i>priA</i>	1643	ribosomal replication factor Y			
			<i>mh</i>	1677	ribonuclease H			
			<i>rtp</i>	2018	replication terminator protein			
			<i>ssb</i>	4199	single-strand DNA-binding protein			
			<i>yerF</i>	719	ATP-dependent DNA helicase			
			<i>yerG</i>	721	DNA ligase			
			<i>yocV</i>	2192	DNA ligase			
			<i>yori</i>	2179	DNA polymerase III (α subunit)			
			<i>yrcP</i>	2311	5'-3' exonuclease			
			<i>ywpH</i>	3740	single-strand DNA-binding protein			
			III.2		DNA RESTRICTION/MODIFICATION AND REPAIR 39			
			<i>adaA</i>	204	methylphosphotriester-DNA alkyltransferase / transcriptional activator of the			

<i>gutR</i>	667	transcriptional activator of the sorbitol dehydrogenase gene (<i>gutA</i>)	<i>ydeC</i>	562	transcriptional regulator (AraC/XylS family)	III.5.4	TERMINATION.....4	
<i>hpr</i>	1073	transcriptional repressor of sporulation and extracellular proteases genes (<i>aprE</i> , <i>nprE</i> , <i>sin</i>)	<i>ydeE</i>	564	transcriptional regulator (AraC/XylS family)	<i>nusA</i>	1732	transcription termination
<i>hrcA</i>	2629	transcriptional repressor of class I heat-shock genes (<i>dnaK</i> , <i>groESL</i>)	<i>ydeF</i>	571	transcriptional regulator (GntR family) / amino-transferase (MocR-like)	<i>nusG</i>	118	transcription antitermination factor
<i>hutP</i>	4040	transcriptional activator of the histidine utilization operon (<i>hutPHUGM</i>)	<i>ydeL</i>	574	transcriptional regulator (GntR family) / amino-transferase (MocR-like)	<i>rho</i>	3904	transcriptional terminator Rho
<i>iolR</i>	4084	transcriptional repressor of the myo-inositol catabolism operon (<i>iolABCDEFGHIU/iosRS</i>)	<i>ydeS</i>	578	transcriptional regulator (TetR/AcrR family)	<i>yqhZ</i>	2529	transcription termination
<i>kdgR</i>	2325	transcriptional repressor of the pectin utilization operon (<i>kdgRKA1</i>)	<i>ydeT</i>	579	transcriptional regulator (ArsR family)			
<i>lacR</i>	3509	transcriptional repressor of the β -galactosidase gene (<i>lacA</i>)	<i>ydeY</i>	583	transcriptional regulator (GntR family) / amino-transferase (MocR-like)			
<i>levR</i>	2765	transcriptional activator of the levansucrase operon (<i>levDEFGLsacC</i>)	<i>ydfI</i>	589	two-component response regulator [YdfH]	III.6	RNA MODIFICATION.....19	
<i>lexA</i>	1918	transcriptional repressor of the SOS regulon	<i>ydgG</i>	609	transcriptional regulator (MarR family)	<i>cspR</i>	970	rRNA methylase homolog
<i>licR</i>	3963	transcriptional regulator (antiterminator) of the lichenan operon (<i>licBCAH</i>)	<i>ydgJ</i>	613	transcriptional regulator (MarR family)	<i>deaD</i>	4016	ATP-dependent RNA helicase
<i>licT</i>	4012	transcriptional antiterminator required for substrate-dependent induction and catabolite repression of <i>bglPH</i>	<i>ydhC</i>	616	transcriptional regulator (GntR family)	<i>miaA</i>	1866	tRNA isopentenylpyrophosphate transferase
<i>lmrA</i>	290	transcriptional repressor of the lincomycin operon (<i>lmrBA</i>)	<i>ydhI</i>	620	transcriptional regulator (GntR family)	<i>queA</i>	2834	S-adenosylmethionine tRNA ribosyltransferase (queuosine biosynthesis)
<i>lrpA</i>	551	transcriptional Lrp-like regulator (repression of <i>glyA</i> transcription and KinB-dependent sporulation)	<i>ydhJ</i>	622	transcriptional regulator (GntR family)	<i>rncS</i>	1665	ribonuclease III
<i>lrpB</i>	552	transcriptional Lrp-like regulator (repression of <i>glyA</i> transcription and KinB-dependent sporulation)	<i>ydhK</i>	630	transcriptional regulator (GntR family)	<i>rnpA</i>	4214	ribonuclease P (protein component)
<i>lrpC</i>	476	transcriptional regulator (Lrp/AsnC family)	<i>ydhL</i>	632	transcriptional regulator (GntR family)	<i>rph</i>	2901	ribonuclease PH
<i>lytR</i>	3662	attenuator role for <i>lytABC</i> and <i>lytR</i> expression	<i>ydhM</i>	636	transcriptional regulator (TetR/AcrR family)	<i>tgt</i>	2833	tRNA-guanine transglycosylase (queuosine biosynthesis)
<i>lysT</i>	2956	two-component response regulator [LysS] involved in the rate of autolysis	<i>ydhN</i>	638	transcriptional regulator (MarR family)	<i>trmD</i>	1675	tRNA methyltransferase
<i>msmR</i>	3096	transcriptional regulator (LacI family)	<i>ydhO</i>	639	transcriptional regulator (MarR family)	<i>truA</i>	153	pseudouridylyl synthase I
<i>mta</i>	3764	transcriptional activator of multidrug-efflux transfer genes (<i>mta</i> and <i>bit</i>)	<i>ydhP</i>	642	transcriptional regulator (MarR family)	<i>truB</i>	1736	tRNA pseudouridylyl 5S synthase
<i>mtb</i>	2384	hypothan operon RNA-binding attenuation protein (TRAP)	<i>ydhQ</i>	644	transcriptional regulator (MarR family)	<i>ydbR</i>	511	ATP-dependent RNA helicase
<i>paiA</i>	3304	transcriptional repressor of sporulation, septation and degradative enzyme genes (<i>aprE</i> , <i>nprE</i> , <i>phoA</i> , <i>sacB</i>)	<i>ydhR</i>	648	transcriptional regulator (GntR family)	<i>yefA</i>	737	RNA methyltransferase
<i>paiB</i>	3304	transcriptional repressor of sporulation and degradative enzyme genes	<i>ydhS</i>	650	two-component response regulator [YhcY]	<i>yfjO</i>	873	RNA methyltransferase
<i>phoP</i>	2978	two-component response regulator [PhoR] involved in phosphate regulation (<i>phoA</i> , <i>phoB</i> , <i>phoD</i> , <i>resABCDE</i>)	<i>ydhT</i>	652	transcriptional regulator (GntR family) / amino-transferase (MocR-like)	<i>yfmL</i>	816	RNA helicase
<i>pkcA</i>	1781	transcriptional regulator of the polyketide synthase operon (<i>pkcS</i>)	<i>ydhU</i>	654	transcriptional regulator (MerR family)	<i>yfmM</i>	1647	RNA-binding Sun protein
<i>purR</i>	54	transcriptional repressor of the purine operon (<i>purEKBCLQFMNH</i>)	<i>ydhV</i>	658	transcriptional regulator (TetR/AcrR family)	<i>yfmN</i>	2595	ATP-dependent RNA helicase
<i>pyrR</i>	1618	transcriptional attenuation of the pyrimidine operon (<i>pyrPBCADF</i>) / uracil phosphoribosyltransferase activity (minor) (pyrimidine biosynthesis)	<i>ydhW</i>	660	transcriptional regulator (GntR family) / amino-transferase (MocR-like)	<i>yfmO</i>	2311	rRNA methylase
<i>rbpR</i>	3700	transcriptional repressor of the ribose operon (<i>rbpRKDACB</i>)	<i>ydhX</i>	662	transcriptional regulator (GntR family) / amino-transferase (MocR-like)	<i>yugI</i>	3225	polyribonucleotide nucleotidyltransferase
<i>resD</i>	2417	two-component response regulator [ResE] involved in aerobic and anaerobic respiration (<i>resA</i> , <i>ctaA</i> , <i>qorABC</i> , <i>frj</i>)	<i>ydhY</i>	664	transcriptional regulator (MerR family)			
<i>ribR</i>	3001	transcriptional regulator of riboflavin biosynthesis genes	<i>ydhZ</i>	666	transcriptional regulator (MerR family)	III.7	PROTEIN SYNTHESIS.....96	
<i>rocR</i>	4145	transcriptional activator of arginine utilization operons (<i>rocABC</i> , <i>rocDEF</i>)	<i>ydh1</i>	668	transcriptional regulator (MerR family)	III.7.1	RIBOSOMAL PROTEINS.....56	
<i>sacT</i>	3906	transcriptional antiterminator involved in positive regulation of <i>sacA</i> and <i>sacP</i>	<i>ydh2</i>	670	transcriptional regulator (MerR family)	<i>rplA</i>	119	ribosomal protein L1 (BL1)
<i>sacV</i>	532	transcriptional regulator of the levansucrase gene (<i>sacB</i>)	<i>ydh3</i>	672	transcriptional regulator (MerR family)	<i>rplB</i>	137	ribosomal protein L2 (BL2)
<i>sacY</i>	3942	transcriptional antiterminator involved in positive regulation of levansucrase and sucrose synthesis	<i>ydh4</i>	674	transcriptional regulator (MerR family)	<i>rplC</i>	136	ribosomal protein L3 (BL3)
<i>senS</i>	959	transcriptional activator of extracellular enzyme genes (<i>amyE</i> , <i>aprE</i> , <i>nprE</i>)	<i>ydh5</i>	676	transcriptional regulator (MerR family)	<i>rplD</i>	136	ribosomal protein L4
<i>sinR</i>	2552	transcriptional regulator of post-exponential-phase responses genes (<i>aprE</i> , <i>comK</i> , <i>kinB</i> , <i>sigD</i> , <i>spo0A</i> , <i>spoIIA</i> , <i>spoIIE</i> , <i>spoIIG</i>)	<i>ydh6</i>	678	transcriptional regulator (MerR family)	<i>rplE</i>	141	ribosomal protein L5 (BL6)
<i>slr</i>	3529	transcriptional activator of competence development and sporulation genes	<i>ydh7</i>	680	transcriptional regulator (MerR family)	<i>rplF</i>	142	ribosomal protein L6 (BL8)
<i>spIA</i>	1461	transcriptional regulator of the spore photoproduct lyase operon (<i>spIAB</i>)	<i>ydh8</i>	682	transcriptional regulator (MerR family)	<i>rplG</i>	4163	ribosomal protein L9
<i>spo0A</i>	2518	two-component response regulator [KinC] central for the initiation of sporulation (<i>spo0A</i> , <i>abrB</i> , <i>kinA</i> , <i>kinB</i> , <i>spoIIA</i> , <i>spoIIE</i> , <i>spoIIG</i>) (part of phosphorylated Spo0B-P ₂ -Spo0B-P)	<i>ydh9</i>	684	transcriptional regulator (MerR family)	<i>rplH</i>	120	ribosomal protein L10 (BL5)
<i>spo0F</i>	3809	two-component response regulator [KinA, KinB] involved in the initiation of sporulation (part of phosphorylated Spo0F-P ₂ -Spo0B-P)	<i>ydh10</i>	686	transcriptional regulator (MerR family)	<i>rplK</i>	119	ribosomal protein L11 (BL11)
<i>spoIID</i>	3748	transcriptional regulator of σ^F - and σ^H -dependent genes	<i>ydh11</i>	688	transcriptional regulator (MerR family)	<i>rplL</i>	121	ribosomal protein L12 (BL9)
<i>spoVT</i>	64	transcriptional positive and negative regulator of σ^F -dependent genes	<i>ydh12</i>	690	transcriptional regulator (MerR family)	<i>rplM</i>	154	ribosomal protein L13
<i>tenA</i>	1242	transcriptional regulator of extracellular enzyme genes (<i>aprE</i> , <i>nprE</i> , <i>phoA</i> , <i>sacB</i>)	<i>ydh13</i>	692	transcriptional regulator (MerR family)	<i>rplN</i>	140	ribosomal protein L14
<i>tenI</i>	1243	transcriptional activator of extracellular enzyme genes	<i>ydh14</i>	694	transcriptional regulator (MerR family)	<i>rplO</i>	144	ribosomal protein L15
<i>tnrA</i>	1397	transcriptional pleiotropic regulator involved in global nitrogen regulation (expression of <i>nrpAB</i> , <i>nasB</i> , <i>gabP</i> , <i>ureABC</i> , <i>glnRA</i>)	<i>ydh15</i>	696	transcriptional regulator (MerR family)	<i>rplP</i>	139	ribosomal protein L16
<i>treR</i>	853	transcriptional repressor of the trehalose operon (<i>trePAR</i>)	<i>ydh16</i>	698	transcriptional regulator (MerR family)	<i>rplQ</i>	150	ribosomal protein L17 (BL15)
<i>xre</i>	1321	transcriptional repressor of PBXS genes	<i>ydh17</i>	700	transcriptional regulator (MerR family)	<i>rplR</i>	143	ribosomal protein L18
<i>xylR</i>	1891	transcriptional repressor of the xylose operon (<i>xylAB</i>)	<i>ydh18</i>	702	transcriptional regulator (MerR family)	<i>rplS</i>	1675	ribosomal protein L19
<i>yacF</i>	88	transcriptional regulator (nitrogen regulation protein)	<i>ydh19</i>	704	transcriptional regulator (MerR family)	<i>rplT</i>	2355	ribosomal protein L20
<i>ybbB</i>	185	transcriptional regulator (AraC/XylS family)	<i>ydh20</i>	706	transcriptional regulator (MerR family)	<i>rplU</i>	2855	ribosomal protein L21 (BL20)
<i>ybdD</i>	221	two-component response regulator [YbdK]	<i>ydh21</i>	708	transcriptional regulator (MerR family)	<i>rplV</i>	138	ribosomal protein L22 (BL17)
<i>ybfI</i>	244	transcriptional regulator (AraC/XylS family)	<i>ydh22</i>	710	transcriptional regulator (MerR family)	<i>rplW</i>	137	ribosomal protein L23
<i>ybpP</i>	251	transcriptional regulator (AraC/XylS family)	<i>ydh23</i>	712	transcriptional regulator (MerR family)	<i>rplX</i>	141	ribosomal protein L24 (BL23) (histone-like protein HPB12)
<i>ybgA</i>	258	transcriptional regulator (GntR family)	<i>ydh24</i>	714	transcriptional regulator (MerR family)	<i>rpmA</i>	2854	ribosomal protein L27 (BL24)
<i>ycbB</i>	267	two-component response regulator [YcbA]	<i>ydh25</i>	716	transcriptional regulator (MerR family)	<i>rpmB</i>	1655	ribosomal protein L28
<i>ycbG</i>	273	transcriptional regulator (GntR family)	<i>ydh26</i>	718	transcriptional regulator (MerR family)	<i>rpmC</i>	140	ribosomal protein L29
<i>yclL</i>	278	two-component response regulator [YcbM]	<i>ydh27</i>	720	transcriptional regulator (MerR family)	<i>rpmD</i>	144	ribosomal protein L30 (BL27)
<i>yccH</i>	296	two-component response regulator [YccG]	<i>ydh28</i>	722	transcriptional regulator (MerR family)	<i>rpmE</i>	3602	ribosomal protein L31
<i>yceK</i>	320	transcriptional regulator (ArsR family)	<i>ydh29</i>	724	transcriptional regulator (MerR family)	<i>rpmF</i>	1575	ribosomal protein L32
<i>ycgK</i>	341	transcriptional regulator (LysR family)	<i>ydh30</i>	726	transcriptional regulator (MerR family)	<i>rpmG</i>	171	ribosomal protein L33
<i>yclA</i>	412	transcriptional regulator (LysR family)	<i>ydh31</i>	728	transcriptional regulator (MerR family)	<i>rpmH</i>	4215	ribosomal protein L34
<i>yclU</i>	426	two-component response regulator [YclK]	<i>ydh32</i>	730	transcriptional regulator (MerR family)	<i>rpmI</i>	2952	ribosomal protein L35
<i>ycnC</i>	438	transcriptional regulator (TetR/AcrR family)	<i>ydh33</i>	732	transcriptional regulator (MerR family)	<i>rpmJ</i>	148	ribosomal protein L36 (ribosomal protein B)
<i>ycnF</i>	441	transcriptional regulator (GntR family) / amino-transferase (MocR-like)	<i>ydh34</i>	734	transcriptional regulator (MerR family)	<i>rpmK</i>	1717	ribosomal protein S2
<i>ycnK</i>	449	transcriptional regulator (DeoR family)	<i>ydh35</i>	736	transcriptional regulator (MerR family)	<i>rpmL</i>	139	ribosomal protein S3 (BS3)
<i>ycsO</i>	461	transcriptional regulator (LysR family)	<i>ydh36</i>	738	transcriptional regulator (MerR family)	<i>rpmM</i>	3035	ribosomal protein S4 (BS4)
<i>ycxD</i>	406	transcriptional regulator (GntR family) / amino-transferase (MocR-like)	<i>ydh37</i>	740	transcriptional regulator (MerR family)	<i>rpmN</i>	143	ribosomal protein S5
<i>ycaZ</i>	439	transcriptional regulator (ArsR family)	<i>ydh38</i>	742	transcriptional regulator (MerR family)	<i>rpmO</i>	4199	ribosomal protein S6 (BS9)
<i>ycaA</i>	467	transcriptional antiterminator (BglG family)	<i>ydh39</i>	744	transcriptional regulator (MerR family)	<i>rpmP</i>	130	ribosomal protein S7 (BS7)
<i>ydcG</i>	499	two-component response regulator [YdcF]	<i>ydh40</i>	746	transcriptional regulator (MerR family)	<i>rpmQ</i>	142	ribosomal protein S8 (BS8)
<i>ydcN</i>	531	transcriptional regulator (phage-related) (Xre family)	<i>ydh41</i>	748	transcriptional regulator (MerR family)	<i>rpmR</i>	154	ribosomal protein S9
			<i>ydh42</i>	750	transcriptional regulator (MerR family)	<i>rpmS</i>	135	ribosomal protein S10 (BS13)
			<i>ydh43</i>	752	transcriptional regulator (MerR family)	<i>rpmT</i>	148	ribosomal protein S11 (BS11)
			<i>ydh44</i>	754	transcriptional regulator (MerR family)	<i>rpmU</i>	130	ribosomal protein S12 (BS12)
			<i>ydh45</i>	756	transcriptional regulator (MerR family)	<i>rpmV</i>	148	ribosomal protein S13
			<i>ydh46</i>	758	transcriptional regulator (MerR family)	<i>rpmW</i>	142	ribosomal protein S14
			<i>ydh47</i>	760	transcriptional regulator (MerR family)	<i>rpmX</i>	173	ribosomal protein S15 (BS18)
			<i>ydh48</i>	762	transcriptional regulator (MerR family)	<i>rpmY</i>	1638	ribosomal protein S16 (BS17)
			<i>ydh49</i>	764	transcriptional regulator (MerR family)	<i>rpmZ</i>	140	ribosomal protein S17 (BS16)
			<i>ydh50</i>	766	transcriptional regulator (MerR family)	<i>rplA</i>	4198	ribosomal protein S18
			<i>ydh51</i>	768	transcriptional regulator (MerR family)	<i>rplB</i>	138	ribosomal protein S19 (BS19)
			<i>ydh52</i>	770	transcriptional regulator (MerR family)	<i>rplC</i>	2635	ribosomal protein S20 (BS20)
			<i>ydh53</i>	772	transcriptional regulator (MerR family)	<i>rplD</i>	2620	ribosomal protein S21
			<i>ydh54</i>	774	transcriptional regulator (MerR family)	<i>rplE</i>	129	ribosomal protein LTAE family
			<i>ydh55</i>	776	transcriptional regulator (MerR family)	<i>rplF</i>	965	ribosomal protein L7AE family
			<i>ydh56</i>	778	transcriptional regulator (MerR family)	<i>rplG</i>	1733	ribosomal protein L7AE family
			<i>ydh57</i>	780	transcriptional regulator (MerR family)	<i>rplH</i>	3631	ribosomal protein S30AE family
			<i>ydh58</i>	782	transcriptional regulator (MerR family)			
			<i>ydh59</i>	784	transcriptional regulator (MerR family)	III.7.2	AMINOACYL-TRNA SYNTHETASES.....25	
			<i>ydh60</i>	786	transcriptional regulator (MerR family)	<i>alaS</i>	2800	alanyl-tRNA synthetase
			<i>ydh61</i>	788	transcriptional regulator (MerR family)	<i>argS</i>	3834	arginyl-tRNA synthetase
			<i>ydh62</i>	790	transcriptional regulator (MerR family)	<i>asnS</i>	2347	asparaginyl-tRNA synthetase
			<i>ydh63</i>	792	transcriptional regulator (MerR family)	<i>aspS</i>	2815	aspartyl-tRNA synthetase
			<i>ydh64</i>	794	transcriptional regulator (MerR family)	<i>cysS</i>	113	cysteinyl-tRNA synthetase
			<i>ydh65</i>	796	transcriptional regulator (MerR family)	<i>glxX</i>	111	glutamyl-tRNA synthetase
			<i>ydh66</i>	798	transcriptional regulator (MerR family)	<i>glyQ</i>	2608	glycyl-tRNA synthetase (α subunit)
			<i>ydh67</i>	800	transcriptional regulator (MerR family)	<i>glyS</i>	2607	glycyl-tRNA synthetase (β subunit)
			<i>ydh68</i>	802	transcriptional regulator (MerR family)	<i>hisS</i>	2817	histidyl-tRNA synthetase
			<i>ydh69</i>	804	transcriptional regulator (MerR family)	<i>hisZ</i>	3588	histidyl-tRNA synthetase
			<i>ydh70</i>	806	transcriptional regulator (MerR family)	<i>ileS</i>	1613	isoleucyl-tRNA synthetase
			<i>ydh71</i>	808	transcriptional regulator (MerR family)	<i>leuS</i>	3104	leucyl-tRNA synthetase
			<i>ydh72</i>	810	transcriptional regulator (MerR family)	<i>lysS</i>	89	lysyl-tRNA synthetase
			<i>ydh73</i>	812	transcriptional regulator (MerR family)	<i>metS</i>	46	methionyl-tRNA synthetase
			<i>ydh74</i>	814	transcriptional regulator (MerR family)	<i>pheS</i>	2930	phenylalanyl-tRNA synthetase (α subunit)
			<i>ydh75</i>	816	transcriptional regulator (MerR family)	<i>pheT</i>	2929	phenylalanyl-tRNA synthetase (β subunit)
			<i>ydh76</i>	818	transcriptional regulator (MerR family)	<i>proS</i>	1725	prolyl-tRNA synthetase
			<i>ydh77</i>	820	transcriptional regulator (MerR family)	<i>serS</i>	21	seryl-tRNA synthetase
			<i>ydh78</i>	822	transcriptional regulator (MerR family)	<i>thrS</i>	296	

<i>lepA</i>	2632	GTP-binding protein	<i>yvE</i>	3515	spore coat polysaccharide biosynthesis	<i>xxdC</i>	1322	PBSX prophage
<i>tsf</i>	1718	elongation factor Ts	<i>yvB</i>	3384	serine protease Do	<i>xxdD</i>	1323	PBSX prophage
<i>tufA</i>	133	elongation factor Tu	<i>ywqC</i>	3732	capsular polysaccharide biosynthesis	<i>xxdE</i>	1327	PBSX prophage
<i>yiaG</i>	1546	GTP-binding elongation factor	<i>ywqD</i>	3732	capsular polysaccharide biosynthesis	<i>xxdF</i>	1328	PBSX prophage
			<i>ywqE</i>	3731	capsular polysaccharide biosynthesis	<i>xxdG</i>	1329	PBSX prophage
III.75	TERMINATION	3	<i>ywsC</i>	3700	capsular polyglutamate biosynthesis	<i>xxdH</i>	1330	PBSX prophage
<i>frr</i>	1720	ribosome recycling factor	<i>ywtA</i>	3698	capsular polyglutamate biosynthesis	<i>xxdI</i>	1331	PBSX prophage
<i>prfA</i>	3797	peptide chain release factor 1	<i>ywtB</i>	3698	capsular polyglutamate biosynthesis	<i>xxdJ</i>	1331	PBSX prophage
<i>prfB</i>	3627	peptide chain release factor 2	<i>yxxA</i>	4148	serine protease Do	<i>xxdK</i>	1332	PBSX prophage
						<i>xxdM</i>	1333	PBSX prophage
III.8	PROTEIN MODIFICATION	27	IV.2	DETOXIFICATION	68	<i>xxdN</i>	1334	PBSX prophage
<i>amhX</i>	325	amidohydrolase	<i>aadK</i>	2736	aminoglycoside 6-adenyltransferase	<i>xxdO</i>	1334	PBSX prophage
<i>igt</i>	3593	prolipoprotein diacylglycerol transferase (lipoprotein biosynthesis)	<i>ahpC</i>	4118	alkyl hydroperoxide reductase (small subunit)	<i>xxdP</i>	1338	PBSX prophage
			<i>ahpF</i>	4119	alkyl hydroperoxide reductase (large subunit) / NADH dehydrogenase	<i>xxdQ</i>	1339	PBSX prophage
<i>map</i>	147	methionine aminopeptidase	<i>bmrU</i>	2493	multidrug resistance protein cotranscribed with <i>bmr</i>	<i>xxdR</i>	1340	PBSX prophage
<i>pcp</i>	287	pyroglutamate-carboxylate peptidase	<i>cah</i>	342	cephalosporin C deacetylase	<i>xxdS</i>	1340	PBSX prophage
<i>ppbB</i>	2435	peptidyl-prolyl isomerase	<i>cypA</i>	2732	cytochrome P450-like enzyme	<i>xxdT</i>	1341	PBSX prophage
<i>prkA</i>	973	serine protein kinase	<i>cypX</i>	3603	cytochrome P450-like enzyme	<i>xxdU</i>	1342	PBSX prophage
<i>igl</i>	3212	transglutaminase	<i>katA</i>	960	vegetative catalase 1	<i>xxdV</i>	1343	PBSX prophage
<i>ybdM</i>	224	protein kinase	<i>katB</i>	4009	catalase 2	<i>xxdW</i>	1345	PBSX prophage
<i>ydiC</i>	642	glycoprotein endopeptidase	<i>katX</i>	3964	catalase	<i>xxdX</i>	1345	PBSX prophage
<i>ydiD</i>	643	ribosomal-protein-alanine N-acetyltransferase	<i>ksgA</i>	51	dimethyladenosine transferase (kasugamycin resistance)	<i>xxdY</i>	1345	PBSX prophage lytic exoenzyme
<i>ydiE</i>	643	glycoprotein endopeptidase	<i>mmr</i>	3857	methylerythromycin A resistance protein	<i>xrmA</i>	1325	PBSX terminase (small subunit)
<i>yfkJ</i>	862	protein-tyrosine phosphatase	<i>padC</i>	3532	methylenetetrahydrofolate reductase	<i>xrmB</i>	1325	PBSX terminase (large subunit)
<i>yfjG</i>	840	methionine aminopeptidase	<i>penP</i>	2048	β -lactamase	<i>xtrA</i>	1324	PBSX prophage
<i>yjck</i>	1261	ribosomal-protein-alanine N-acetyltransferase	<i>pksS</i>	1859	hydroxylase of the polyketide produced by the <i>pks</i> cluster	<i>ycaD</i>	304	3'-alanoyl-D-glutamate peptidase
<i>ykbB</i>	1528	formylmethionine deformylase	<i>sodA</i>	2585	superoxide dismutase	<i>yhcE</i>	530	integrase
<i>ykyY</i>	1453	Xaa-Pro dipeptidase	<i>sodF</i>	2103	superoxide dismutase	<i>ydcM</i>	531	immunity region protein in prophage
<i>yloP</i>	1651	protein kinase	<i>tetL</i>	4188	tetracycline resistance leader peptide	<i>yhgE</i>	1090	phage infection protein
<i>yppP</i>	2287	peptide methionine sulfoxide reductase	<i>thdF</i>	4212	thiophen and furan oxidation	<i>yjbJ</i>	1235	lytic transglycosylase
<i>yqeT</i>	2624	ribosomal protein L11 methyltransferase	<i>tmrB</i>	339	tunicamycin resistance	<i>yjqB</i>	1318	phage-related replication protein
<i>yqhT</i>	2539	Xaa-Pro dipeptidase	<i>yaaN</i>	36	toxic cation resistance	<i>ymaC</i>	1863	phage-related protein
<i>ytel</i>	3020	protease IV	<i>ydbE</i>	190	β -lactamase	<i>ymaH</i>	1867	host factor-1 protein
<i>ytpJ</i>	3068	Xaa-His dipeptidase	<i>ydiO</i>	581	antibiotic resistance protein	<i>ymlD</i>	1755	phage-related protein
<i>yvtA</i>	3105	protein kinase	<i>ydiE</i>	618	macrolide glycosyltransferase	<i>ymlE</i>	1756	phage-related protein
<i>yxtM</i>	3150	prolyl aminopeptidase	<i>yerP</i>	732	acriflavine resistance protein	<i>ymlL</i>	1914	phage-related replication protein
<i>yylE</i>	3297	leucyl aminopeptidase	<i>yeyM</i>	790	salicylate 1-monoxygenase	<i>yobO</i>	2075	phage-related pre-neck appendage protein
<i>yylE</i>	3791	protein-tyrosine phosphatase	<i>yfnC</i>	804	fosmidycin resistance protein	<i>yokA</i>	2284	DNA recombinase
<i>yxaL</i>	4102	serine/threonine protein kinase	<i>yfnD</i>	836	nitric-oxide synthase	<i>yokL</i>	2274	phage-related protein
			<i>yfnE</i>	804	fosmidycin resistance protein	<i>yolB</i>	2272	phage-related protein
III.9	PROTEIN FOLDING	8	<i>yfnF</i>	836	nitric-oxide synthase	<i>yomA</i>	2264	holin
<i>dnaK</i>	2627	class I heat-shock protein (chaperonin)	<i>yfnG</i>	804	fosmidycin resistance protein	<i>yomJ</i>	2248	phage-related immunity protein
<i>groEL</i>	650	class I heat-shock protein (chaperonin)	<i>ygaF</i>	943	thiol-specific antioxidant protein	<i>yomP</i>	2243	phage-related protein
<i>groES</i>	650	class I heat-shock protein (chaperonin)	<i>yhiG</i>	1122	monooxygenase	<i>yomR</i>	2242	phage-related protein
<i>tig</i>	2887	trigger factor (prolyl isomerase)	<i>yisY</i>	1169	chlorine peroxidase	<i>yomS</i>	2241	phage-related lytic exoenzyme
<i>ykkC</i>	1376	chaperonin	<i>yjgB</i>	1291	monooxygenase	<i>yqaD</i>	2200	phage-related DNA-binding protein anti-repressor
<i>ykkD</i>	1376	chaperonin	<i>yjgC</i>	1292	macrolide glycosyltransferase	<i>yqz</i>	2190	phage-related protein
<i>ykdR</i>	3541	chaperonin	<i>yjgA</i>	1366	immunity to bacteriotoxins	<i>yqzB</i>	2160	phage-related endodeoxyribonuclease
<i>yksD</i>	3541	chaperonin	<i>ykkB</i>	1375	N-acetyltransferase	<i>yqzC</i>	2160	phage-related protein
IV	OTHER FUNCTIONS 289		<i>ykoY</i>	1410	toxic anion resistance protein	<i>yqal</i>	2696	phage-related protein
IV.1	ADAPTATION TO ATYPICAL CONDITIONS	72	<i>yndN</i>	1916	fosfomycin resistance protein	<i>yqak</i>	2695	phage-related protein
<i>bbsA</i>	2304	glutathione peroxidase	<i>yocD</i>	2088	immunity to bacteriotoxins	<i>yqam</i>	2694	phage-related protein
<i>clpC</i>	104	class III stress response-related ATPase (repressor of competence)	<i>yocE</i>	2117	macrolide glycosyltransferase	<i>yqaO</i>	2692	phage-related protein
<i>clpE</i>	1437	ATP-dependent Clp protease-like	<i>yokJ</i>	2115	superoxide dismutase	<i>yqaS</i>	2690	phage-related terminase large subunit
<i>clpP</i>	3645	ATP-dependent Clp protease proteolytic subunit (class III heat-shock protein)	<i>yokM</i>	2281	aminoglycoside N ³ -acetyltransferase	<i>yqaT</i>	2689	phage-related terminase small subunit
<i>clpQ</i>	1688	B-type subunit of the 20S proteasome	<i>yokN</i>	2281	arsenate reductase	<i>yqbA</i>	2688	phage-related protein
<i>clpX</i>	2885	ATP-dependent Clp protease ATP-binding subunit (class III heat-shock protein)	<i>yokO</i>	2595	penicillin tolerance	<i>yqbD</i>	2684	phage-related protein
<i>clpY</i>	1688	ATP-dependent Clp protease-like	<i>yokP</i>	2595	penicillin tolerance	<i>yqbE</i>	2683	phage-related protein
<i>csbB</i>	930	stress response protein	<i>yokQ</i>	2595	penicillin tolerance	<i>yqbl</i>	2681	phage-related protein
<i>csbB</i>	994	major cold-shock protein	<i>yokR</i>	2595	penicillin tolerance	<i>yqbl</i>	2681	phage-related protein
<i>csbC</i>	559	cold-shock protein	<i>yokS</i>	2595	penicillin tolerance	<i>yqbk</i>	2680	phage-related protein
<i>csbD</i>	2307	cold-shock protein	<i>yokT</i>	2595	penicillin tolerance	<i>yqbl</i>	2680	phage-related protein
<i>cstA</i>	2937	carbon starvation-induced protein	<i>yokU</i>	2595	penicillin tolerance	<i>yqbl</i>	2679	phage-related protein
<i>ctc</i>	59	general stress protein	<i>yokV</i>	2595	penicillin tolerance	<i>yqbM</i>	2679	phage-related protein
<i>degQ</i>	3256	degradative enzyme production	<i>yokW</i>	2595	penicillin tolerance	<i>yqbN</i>	2677	phage-related protein
<i>degR</i>	2308	degradative enzyme production	<i>yokX</i>	2595	penicillin tolerance	<i>yqbO</i>	2677	phage-related protein
<i>dnaL</i>	2625	heat-shock protein (activation of DnaK)	<i>yokY</i>	2595	penicillin tolerance	<i>yqbP</i>	2672	phage-related protein
<i>dps</i>	3136	stress- and starvation-induced gene controlled by	<i>yokZ</i>	2595	penicillin tolerance	<i>yqbQ</i>	2671	phage-related protein
			<i>yokAA</i>	2595	penicillin tolerance	<i>yqbR</i>	2670	phage-related protein
<i>gbsA</i>	3186	glycine betaine aldehyde dehydrogenase (osmoprotection)	<i>yokAB</i>	2595	penicillin tolerance	<i>yqbS</i>	2670	phage-related protein
<i>gbsB</i>	3184	alcohol dehydrogenase (osmoprotection)	<i>yokAC</i>	2595	penicillin tolerance	<i>yqbT</i>	2670	phage-related protein
<i>gpeE</i>	2628	heat-shock protein (activation of DnaK)	<i>yokAD</i>	2595	penicillin tolerance	<i>yqcA</i>	2669	phage-related protein
<i>gsiB</i>	494	general stress protein	<i>yokAE</i>	2595	penicillin tolerance	<i>yqcC</i>	2668	phage-related protein
<i>gspA</i>	3944	general stress protein	<i>yokAF</i>	2595	penicillin tolerance	<i>yqcD</i>	2667	phage-related protein
<i>hit</i>	1076	Hit-like protein involved in cell-cycle regulation	<i>yokAG</i>	2595	penicillin tolerance	<i>yqcE</i>	2666	phage-related protein
<i>htpG</i>	4090	class III heat-shock protein (chaperonin)	<i>yokAH</i>	2595	penicillin tolerance	<i>yqxG</i>	2666	phage-related lytic exoenzyme
<i>htrA</i>	1359	serine protease Do (heat-shock protein)	<i>yokAI</i>	2595	penicillin tolerance	<i>yqxH</i>	2665	holin
<i>ispU</i>	1387	activation of σ^H	<i>yokAJ</i>	2595	penicillin tolerance			
<i>lonA</i>	2882	class III heat-shock ATP-dependent protease	<i>yokAK</i>	2595	penicillin tolerance	IV.5	TRANSPOSON AND IS	10
<i>lonB</i>	2884	Lon-like ATP-dependent protease	<i>yokAL</i>	2595	penicillin tolerance	<i>ydcP</i>	533	transposon protein
<i>mrpA</i>	3383	metalloregulation DNA-binding stress protein	<i>yokAM</i>	2595	penicillin tolerance	<i>ydcQ</i>	533	transposon protein
<i>rsbR</i>	519	positive regulator of σ^E activity (interaction with RsbS)	<i>yokAN</i>	2595	penicillin tolerance	<i>ydcR</i>	535	transposon protein
			<i>yokAO</i>	2595	penicillin tolerance	<i>ydcB</i>	537	transposon protein
<i>rsbS</i>	520	negative regulator of σ^E activity (antagonist of RsbT)	<i>yokAP</i>	2595	penicillin tolerance	<i>ydcE</i>	538	transposon protein
<i>rsbT</i>	520	positive regulator of σ^E activity (switch protein/serine kinase [RsbS])	<i>yokAQ</i>	2595	penicillin tolerance	<i>ydcH</i>	544	transposon protein
<i>rsbU</i>	521	indirect positive regulator of σ^E activity (serine phosphatase [RsbV-P])	<i>yokAR</i>	2595	penicillin tolerance	<i>yefB</i>	739	site-specific recombinase
<i>rsbV</i>	522	positive regulator of σ^E activity (anti-anti-sigma factor [RsbW])	<i>yokAS</i>	2595	penicillin tolerance	<i>yefC</i>	739	resolvase
<i>rsbW</i>	522	negative regulator of σ^E activity (switch protein/serine kinase [RsbV], anti-sigma factor [σ^E])	<i>yokAT</i>	2595	penicillin tolerance	<i>yneB</i>	1918	resolvase
<i>rsbX</i>	523	indirect negative regulator of σ^E activity (serine phosphatase [RsbS-P])	<i>yokAU</i>	2595	penicillin tolerance	<i>yocA</i>	2085	transposon-related protein
<i>ycdH</i>	308	adhesion protein	IV.3	ANTIBIOTIC PRODUCTION	30			
<i>ydaG</i>	473	general stress protein	<i>pksB</i>	1782	involved in polyketide synthesis	IV.6	MISCELLANEOUS	26
<i>yfiK</i>	910	surface adhesion	<i>pksC</i>	1783	involved in polyketide synthesis	<i>bex</i>	2610	GTP-binding protein
<i>yjRL</i>	1414	heat-shock protein	<i>pksD</i>	1785	involved in polyketide synthesis	<i>csbA</i>	3614	putative membrane protein
<i>yjKA</i>	1381	general stress protein	<i>pksE</i>	1785	involved in polyketide synthesis	<i>csbB</i>	36	σ^E -transcribed gene
<i>yjBA</i>	1637	fibrinectin-binding protein	<i>pksF</i>	1788	involved in polyketide synthesis	<i>ctaG</i>	1564	function unknown
<i>yloU</i>	1655	alkaline-shock protein	<i>pksG</i>	1789	involved in polyketide synthesis	<i>eag</i>	1430	small membrane protein
<i>ynbA</i>	1875	GTP-binding protein protease modulator	<i>pksH</i>	1790	involved in polyketide synthesis	<i>ecsC</i>	1079	function unknown
<i>ynzF</i>	1880	δ -endotoxin	<i>pksI</i>	1791	involved in polyketide synthesis	<i>mmgE</i>	2509	function unknown
<i>yocK</i>	2097	general stress protein	<i>pksJ</i>	1792	involved in polyketide synthesis	<i>niZ</i>	3027	NiF protein homologue
<i>yocM</i>	2098	small heat-shock protein	<i>pksK</i>	1794	polyketide synthase	<i>sapB</i>	726	mutant activates alkaline phosphatase during sporulation independently of σ^E and σ^H
<i>yodU</i>	2151	capsular polysaccharide biosynthesis	<i>pksL</i>	1808	polyketide synthase	<i>sbp</i>	1595	small basic protein
<i>yokG</i>	2279	δ -endotoxin	<i>pksM</i>	1821	polyketide synthase	<i>veg</i>	53	function unknown
<i>yopP</i>	2286	capsular polysaccharide biosynthesis	<i>pksN</i>	1834	polyketide synthase	<i>yacI</i>	102	creatine kinase
<i>yxG</i>	3047	general stress protein	<i>pksO</i>	1835	polyketide synthase	<i>ybaL</i>	257	ATP-binding Mrp-like protein
<i>yxD</i>	3047	general stress protein	<i>pksP</i>	1850	polyketide synthase	<i>ybcU</i>	257	NiF protein homologue
<i>yxD</i>	3046	general stress protein	<i>pksQ</i>	1850	polyketide synthase	<i>yefN</i>	730	pet112-like protein
<i>yxEK</i>	3529	capsular polysaccharide biosynthesis	<i>pksR</i>	1850	polyketide synthase	<i>yhdP</i>	1033	hemolysin
<i>yxEK</i>	3528	capsular polysaccharide biosynthesis	<i>pksS</i>	1850	polyketide synthase	<i>yhdT</i>	1035	hemolysin
<i>yxEK</i>	3527	capsular polysaccharide biosynthesis	<i>pksT</i>	1850	polyketide synthase	<i>yheG</i>	1049	calcium-binding protein
<i>yxEK</i>	3527	capsular polysaccharide biosynthesis	<i>pksU</i>	1850	polyketide synthase	<i>yplQ</i>	2295	hemolysin III homologue
<i>yxEK</i>	3527	capsular polysaccharide biosynthesis	<i>pksV</i>	1850	polyketide synthase	<i>yqxC</i>	2523	hemolysin-like
<i>yxEK</i>	3527	capsular polysaccharide biosynthesis	<i>pksW</i>	1850	polyketide synthase	<i>yrkA</i>	2720	hemolysin-like
<i>yxEK</i>	3527	capsular polysaccharide biosynthesis	<i>pksX</i>	1850	polyketide synthase	<i>yrvO</i>	2811	NiF protein homologue
<i>yxEK</i>	3527	capsular polysaccharide biosynthesis	<i>pksY</i>	1850	polyketide synthase	<i>yuaG</i>	3181	epidermal surface antigen