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. Bessires⁵, A. Bolotin⁵, S. Borchert⁶, R. Borris⁷, L. Boursier³, A. Brans⁸, M. Braun⁹, S. C. Brignell¹⁰, 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. Dsterhft⁹, 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. Hnaut²⁹, 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. Lardinois⁸, J. Lauber⁹, V. Lazarevic³³, S.-M. Lee³⁵, A. Levine³⁶, H. Liu²⁸, S. Masuda³⁰, C. Maul³³, C. Mdigue^{3,12}, N. Medina³⁶, R. P. Mellado³⁷, M. Mizuno³⁰, D. Moesti⁵, 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. Vandenbol⁴⁰, F. Vannier⁴⁵, 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. Zmstein⁵, H. Yoshikawa² & A. Danchin³

- ¹ Institut Pasteur, Unit 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, Unit de Rgulation de l'Expression Gntique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France
- ⁴ Dipartimento di Genetica e Microbiologia, Universita di Pavia, Via Abbiategrasso 207, 27100 Pavia, Italy
- ⁵ INRA, Gntique Microbienne, Domaine de Vilvert, 78352 Jouy-en-Josas Cedex, France
- ⁶ Institut fr Mikrobiologie, J. W. Goethe-Universitt, Marie Curie Strasse 9, 60439 Frankfurt/Maine, Germany
- ⁷ Institut fr Genetik und Mikrobiologie, Humboldt Universitt, Chausseestrasse 17, D-10115 Berlin, Germany
- ⁸ Centre d'Ingnierie des Protines, Universit de Lige, Institut de Chimie B6, Sart Tilman, B-4000 Lige, 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, Universit Paris VI, 12 rue Cuvier, 75005 Paris, France
- ¹³ ICGBE, 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 Bactrienne, 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 Facult des Sciences Agronomiques, Unit de Biochimie Physiologique, Universit 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 Eniricerche, 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 Gnome et Informatique, Universit de Versailles, Btiment Buffon, 45 Avenue des tats-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 Minamioyoo, 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 Gntique et Biologie Microbiennes, Universit de Lausanne, 19 rue Csar 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 Gntique et Microbiologie, Universit Paris Sud, URA CNRS 2225, Universit Paris XI-Btiment 409, 91405 Orsay Cedex, France
- ³⁷ Centro Nacional de Biotecnologia (CSIC), Campus Universidad Autnoma, Cantoblanco, 28049 Madrid, Spain
- ³⁸ National Institute of Basic Biology, 38 Nishigounaka, Myodaiji-chou, Okazaki 444, Japan
- ³⁹ Gesellschaft fr Analyse-Technik und Consulting mbH, Fritz-Arnold Strae 23, D-78467 Konstanz, Germany
- ⁴⁰ Department of Microbiology, Faculty of Agronomy, 6 Avenue du Marchal 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, SPB 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 *yxaL* and *yxaO* 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 SP β) 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 SP β) 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 (SP β , 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), *ypfD*, 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-ts*, *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'-AAGGAGGTG-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.

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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), Genecor (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 F.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/DBJ with accession numbers from Z99104 to Z99124.

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90 Tottenham Court Road, London W1P 0LP
Telephone: 0171 436 5931 Fax: 0171 436 3986

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<i>flgA</i>	1700	flagellar hook protein	<i>coiX</i>	1251	spore coat protein (insoluble fraction)			SASP)
<i>flgB</i>	3639	flagellar hook-associated protein 1 (HAP1)	<i>coiY</i>	1250	spore coat protein (insoluble fraction)	<i>sspE</i>	937	small acid-soluble spore protein (major γ -type SASP)
<i>flgC</i>	3637	flagellar hook-associated protein 3 (HAP3)	<i>coiZ</i>	1249	spore coat protein (insoluble fraction)			
<i>flgM</i>	3640	flagellin synthesis regulatory protein (anti-sigma factor [σ^H])	<i>csqA</i>	228	sporulation-specific SASP protein	<i>sspF</i>	53	small acid-soluble spore protein (minor α/β -type SASP)
<i>flhA</i>	1707	flagella-associated protein	<i>jaq</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>spoIIID</i>
<i>flhF</i>	1709	flagella-associated protein	<i>kapD</i>	3232	inhibitor of the KinA pathway to sporulation	<i>ynkT</i>	1495	sporulation protein σ^E -controlled
<i>flhO</i>	3746	flagellar basal-body rod protein	<i>kbaA</i>	159	activation of the KinB signaling pathway to sporulation	<i>ynkU</i>	1449	spore cortex membrane protein
<i>flhP</i>	3745	flagellar hook-basal body protein	<i>obg</i>	2853	GTP-binding protein involved in initiation of sporulation (SpoOA activation)	<i>ynzH</i>	1901	spore coat protein
<i>flhD</i>	3633	flagellar hook-associated protein 2 (HAP2)				<i>yobW</i>	2083	membrane protein σ^E -controlled
<i>flhE</i>	1652	flagellar hook-basal body protein	<i>phrA</i>	1316	phosphatase (RapA) inhibitor (imported by Opp)	<i>yagT</i>	2568	l- γ -glutamyl-L-diamino acid endopeptidase I
<i>flhG</i>	1652	flagellar basal-body M-ring protein	<i>phrC</i>	430	phosphatase (RapC) regulator / competence and sporulation stimulating factor (CSF)	<i>yagU</i>	2430	pyrospolignone SpoIII-like
<i>flhH</i>	1694	flagellar motor switch protein				<i>yraE</i>	2754	spore coat protein
<i>flhI</i>	1695	flagellar assembly protein	<i>phrE</i>	2660	phosphatase (RapE) regulator	<i>yraF</i>	2752	spore coat protein
<i>flhJ</i>	1695	flagellar-specific ATP synthase	<i>phrF</i>	3846	phosphatase (RapF) regulator	<i>yraG</i>	2752	spore coat protein
<i>flhK</i>	1697	flagellar protein required for formation of basal body	<i>phrG</i>	4141	phosphatase (RapG) regulator	<i>yraB</i>	2845	spore coat protein
<i>flhL</i>	1698	flagellar hook-length control	<i>phrI</i>	548	phosphatase (RapI) regulator	<i>yraC</i>	2844	spore coat protein
<i>flhM</i>	1701	flagellar motor required for flagellar formation	<i>phrK</i>	2063	phosphatase (RapK) regulator	<i>yraD</i>	2843	spore coat protein
<i>flhN</i>	1701	flagellar motor switch protein	<i>rapA</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>rapB</i>	3771	response regulator aspartate phosphatase [SpoOF-P]	<i>ytaP</i>	3074	spore cortex protein
<i>flhQ</i>	1705	flagellar protein required for flagellar formation	<i>rapC</i>	428	response regulator aspartate phosphatase	<i>ytaT</i>	3051	DNA translocase stage III sporulation protein
<i>flhR</i>	1705	flagellar protein required for flagellar formation	<i>rapD</i>	423	response regulator aspartate phosphatase	<i>ytaA</i>	4208	DNA-binding protein SpoII-like
<i>flhS</i>	1702	flagellar motor switch protein	<i>rapE</i>	2658	response regulator aspartate phosphatase			
<i>flhT</i>	1704	flagellar protein required for flagellar formation	<i>rapF</i>	3845	response regulator aspartate phosphatase	<i>gerAA</i>	3330	germination response to L-alanine
<i>flhU</i>	1702	flagellar motor switch protein	<i>rapG</i>	4139	response regulator aspartate phosphatase	<i>gerAB</i>	3331	germination response to L-alanine
<i>flhV</i>	1702	flagellar motor switch protein	<i>rapH</i>	750	response regulator aspartate phosphatase	<i>gerAC</i>	3332	germination response to L-alanine
<i>flhW</i>	1702	flagellar motor switch protein	<i>rapI</i>	547	response regulator aspartate phosphatase	<i>gerBA</i>	3688	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhX</i>	1702	flagellar motor switch protein	<i>rapJ</i>	304	response regulator aspartate phosphatase	<i>gerBB</i>	3689	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>flhY</i>	1702	flagellar motor switch protein	<i>rapK</i>	2061	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>sinI</i>	2552	antagonist of SinR	<i>gerCB</i>	2384	heptaprenyl diphosphate synthase component I (menaquinone biosynthesis)
<i>hag</i>	3635	flagellin protein	<i>soj</i>	4206	centromere-like function involved in forespore chromosome partitioning / inhibition of SpoOA activation	<i>gerCB</i>	2383	heptaprenyl diphosphate synthase component II (menaquinone biosynthesis)
<i>mcpA</i>	3207	methyl-accepting chemotaxis protein (glucose and α -methyl-glucoside)	<i>spB</i>	1461	spore maturation protein (spore core dehydratation)	<i>gerCC</i>	2382	heptaprenyl diphosphate synthase component II (menaquinone biosynthesis)
<i>mcpB</i>	3212	methyl-accepting chemotaxis protein (asparagine, glutamine and histidine)	<i>spmA</i>	2423	spore maturation protein (spore core dehydratation)	<i>gerD</i>	159	germination response to L-alanine and to the combination of glucose, fructose, L-asparagine, and KCl
<i>mcpC</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spmB</i>	2422	spore maturation protein (spore core dehydratation)	<i>gerE</i>	420	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>mcpD</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spo0B</i>	2854	sporulation initiation phosphoprotein (part of phosphorelay: Spo0F-P $\rightarrow$ Spo0B-P $\rightarrow$ Spo0A-P)	<i>gerF</i>	421	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>mcpE</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spo0C</i>	1430	negative sporulation regulatory phosphatase [SpoOA-P]	<i>gerG</i>	2902	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>mcpF</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spo0D</i>	4	chromosome positioning near the pole and transport through the polar septum / antagonist of <i>Soj</i> anti-anti-sigma factor [SpoIAB]	<i>gerM</i>	2902	germination response to the combination of glucose, fructose, L-asparagine, and KCl
<i>mcpG</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAA</i>	2406	antagonist of SpoIIAB			
<i>mcpH</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAB</i>	2444	antagonist of SpoIIAA and serine kinase [SpoIIAC]			
<i>mcpI</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIA</i>	2444	antagonist of SpoIIAB and serine kinase [SpoIIAC]			
<i>mcpJ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIB</i>	2864	endospore development (oligosporogenous mutation)	<i>gpr</i>	2635	spore protease (degradation of SASPs)
<i>mcpK</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIID</i>	3777	required for complete dissolution of the asymmetric septum	<i>sleB</i>	2399	spore cortex-lytic enzyme
<i>mcpL</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIE</i>	71	serine phosphatase [SpoIIAA-P] (σ^E activation) / asymmetric septum formation	<i>yfkQ</i>	850	spore germination response
<i>mcpM</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIA</i>	1603	protease (processing of pro- σ^E to active σ^E)	<i>yfkR</i>	848	spore germination protein
<i>mcpN</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAG</i>	2537	mutants block sporulation after engulfment	<i>yfkT</i>	847	spore germination protein
<i>mcpO</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAH</i>	2538	mutants block sporulation after engulfment	<i>ykvT</i>	1448	spore cortex-lytic enzyme
<i>mcpP</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAI</i>	2539	mutants block sporulation after engulfment	<i>yndD</i>	1907	spore germination protein
<i>mcpQ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAJ</i>	2540	mutants block sporulation after engulfment	<i>yndF</i>	1908	spore germination protein
<i>mcpR</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAK</i>	2541	mutants block sporulation after engulfment			
<i>mcpS</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAL</i>	2542	mutants block sporulation after engulfment			
<i>mcpT</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAM</i>	2543	mutants block sporulation after engulfment			
<i>mcpU</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAN</i>	2544	mutants block sporulation after engulfment			
<i>mcpV</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAO</i>	2545	mutants block sporulation after engulfment			
<i>mcpW</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAP</i>	2546	mutants block sporulation after engulfment			
<i>mcpX</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAQ</i>	2547	mutants block sporulation after engulfment			
<i>mcpY</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAR</i>	2548	mutants block sporulation after engulfment			
<i>mcpZ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAS</i>	2549	mutants block sporulation after engulfment			
<i>mcpAA</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAT</i>	2550	mutants block sporulation after engulfment			
<i>mcpAB</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAU</i>	2551	mutants block sporulation after engulfment			
<i>mcpAC</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAV</i>	2552	mutants block sporulation after engulfment			
<i>mcpAD</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAW</i>	2553	mutants block sporulation after engulfment			
<i>mcpAE</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAX</i>	2554	mutants block sporulation after engulfment			
<i>mcpAF</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAY</i>	2555	mutants block sporulation after engulfment			
<i>mcpAG</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAZ</i>	2556	mutants block sporulation after engulfment			
<i>mcpAH</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIBA</i>	1348	disruption blocks sporulation after septum formation			
<i>mcpAI</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAB</i>	1349	disruption blocks sporulation after septum formation			
<i>mcpAJ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAC</i>	1350	disruption blocks sporulation after septum formation			
<i>mcpAK</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAD</i>	1351	disruption blocks sporulation after septum formation			
<i>mcpAL</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAE</i>	1352	disruption blocks sporulation after septum formation			
<i>mcpAM</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAF</i>	1353	disruption blocks sporulation after septum formation			
<i>mcpAN</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAG</i>	1354	disruption blocks sporulation after septum formation			
<i>mcpAO</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAH</i>	1355	disruption blocks sporulation after septum formation			
<i>mcpAP</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAI</i>	1356	disruption blocks sporulation after septum formation			
<i>mcpAQ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAJ</i>	1357	disruption blocks sporulation after septum formation			
<i>mcpAR</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAK</i>	1358	disruption blocks sporulation after septum formation			
<i>mcpAS</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAL</i>	1359	disruption blocks sporulation after septum formation			
<i>mcpAT</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAM</i>	1360	disruption blocks sporulation after septum formation			
<i>mcpAU</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAN</i>	1361	disruption blocks sporulation after septum formation			
<i>mcpAV</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAO</i>	1362	disruption blocks sporulation after septum formation			
<i>mcpAW</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAP</i>	1363	disruption blocks sporulation after septum formation			
<i>mcpAX</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAQ</i>	1364	disruption blocks sporulation after septum formation			
<i>mcpAY</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAR</i>	1365	disruption blocks sporulation after septum formation			
<i>mcpAZ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAS</i>	1366	disruption blocks sporulation after septum formation			
<i>mcpBA</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAT</i>	1367	disruption blocks sporulation after septum formation			
<i>mcpBB</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAU</i>	1368	disruption blocks sporulation after septum formation			
<i>mcpBC</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAV</i>	1369	disruption blocks sporulation after septum formation			
<i>mcpBD</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAW</i>	1370	disruption blocks sporulation after septum formation			
<i>mcpBE</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAX</i>	1371	disruption blocks sporulation after septum formation			
<i>mcpBF</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAY</i>	1372	disruption blocks sporulation after septum formation			
<i>mcpBG</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAZ</i>	1373	disruption blocks sporulation after septum formation			
<i>mcpBH</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIBA</i>	1374	disruption blocks sporulation after septum formation			
<i>mcpBI</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAB</i>	1375	disruption blocks sporulation after septum formation			
<i>mcpBJ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAC</i>	1376	disruption blocks sporulation after septum formation			
<i>mcpBK</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAD</i>	1377	disruption blocks sporulation after septum formation			
<i>mcpBL</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAE</i>	1378	disruption blocks sporulation after septum formation			
<i>mcpBM</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAF</i>	1379	disruption blocks sporulation after septum formation			
<i>mcpBN</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAG</i>	1380	disruption blocks sporulation after septum formation			
<i>mcpBO</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAH</i>	1381	disruption blocks sporulation after septum formation			
<i>mcpBP</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAI</i>	1382	disruption blocks sporulation after septum formation			
<i>mcpBQ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAJ</i>	1383	disruption blocks sporulation after septum formation			
<i>mcpBR</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAK</i>	1384	disruption blocks sporulation after septum formation			
<i>mcpBS</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAL</i>	1385	disruption blocks sporulation after septum formation			
<i>mcpBT</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAM</i>	1386	disruption blocks sporulation after septum formation			
<i>mcpBU</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAN</i>	1387	disruption blocks sporulation after septum formation			
<i>mcpBV</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAO</i>	1388	disruption blocks sporulation after septum formation			
<i>mcpBW</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAP</i>	1389	disruption blocks sporulation after septum formation			
<i>mcpBX</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAQ</i>	1390	disruption blocks sporulation after septum formation			
<i>mcpBY</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAR</i>	1391	disruption blocks sporulation after septum formation			
<i>mcpBZ</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAS</i>	1392	disruption blocks sporulation after septum formation			
<i>mcpCA</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAT</i>	1393	disruption blocks sporulation after septum formation			
<i>mcpCB</i>	1463	methyl-accepting chemotaxis protein (cysteine, proline, threonine, glycine, serine, lysine, valine and arginine)	<i>spoIIAU</i>	1394	disruption blocks sporulation after septum formation			

gldH	4033	β-glucosidase (cellulose degradation)	yjmA	1300	glucuronate isomerase	mngD	2510	citrate synthase III
gls1	4031	endo-1-3-1,4 glucanase (lichenan degradation)	yjmD	1304	sorbitol dehydrogenase	odhA	2111	2-oxoglutarate dehydrogenase (E1 subunit)
glt	3569	catabolite repression HPr-like protein	yjme	1305	o-mannanot hydrolase	odhB	2108	2-oxoglutarate dehydrogenase (dihydrolipoamide transsuccinylase, E2 subunit)
csn	2748	chitinase	yjmf	1306	2-deoxy-D-glucanate 3-dehydrogenase			
csrA	3635	carbon storage regulator	yjml	1309	tagaturonate reductase	sdhA	2907	succinate dehydrogenase (flavoprotein subunit)
frbB	1508	fructose 1-phosphate kinase	yjml	1311	altronate hydrolase	sdhB	2905	succinate dehydrogenase (iron-sulphur protein)
galE	3990	UDP-glucose 4-epimerase (galactose metabolism)	yk6C	1356	dolichol phosphate mannose synthase	sdhC	2908	succinate dehydrogenase (cytochrome b ₅₅₈ subunit)
galK	3921	galactokinase (galactose metabolism)	yk6T	1367	polysugar degrading enzyme	sucC	1680	succinyl-CoA synthetase (β subunit)
galT	3919	galactokinase 1-phosphate uridylyltransferase (galactose metabolism)	yk6T	1403	dolichol phosphate mannose synthase	sucD	1681	succinyl-CoA synthetase (α subunit)
			ykrW	1427	ribulose-bisphosphate carboxylase	yjmc	1303	malate dehydrogenase
gdh	445	glucose 1-dehydrogenase	yk6K	1537	myo-inositol-1 or 4-α-monophosphatase	yqJ	2452	malate dehydrogenase
glcK	2571	glucose kinase	ykrU	1477	glucose 1-dehydrogenase	ytl	2930	malate dehydrogenase
glgA	3167	start (bacterial glycogen) synthase (glycogen biosynthesis)	yk6O	1442	glucose 1-dehydrogenase	ywkA	3801	malate dehydrogenase
			ykoV	1445	chitinase			
glgB	3171	1,4- glucan branching enzyme (glycogen biosynthesis)	yloR	1653	ribulose-5-phosphate 3-epimerase			
			ykyX	1741	deacetylase	II.2		METABOLISM OF AMINO ACIDS AND RELATED MOLECULES 205
glgC	3169	glucose-1-phosphate adenylyltransferase (glycogen biosynthesis)	ynfF	1943	endo-xylanase	ald	3277	L-alanine dehydrogenase
			yngE	1951	propionyl-CoA carboxylase	ampS	1516	aminopeptidase
glgD	3168	required for glycogen biosynthesis	yoaC	2023	xylulokinase	ansA	2456	L-asparaginase
glp5	3165	glycogen phosphorylase (glycogen metabolism)	yoaD	2024	phosphoglycerate dehydrogenase	ansB	2455	L-aspartase
glpD	1004	glycerol-3-phosphate dehydrogenase (glycerol utilization)	yoeA	2025	formate dehydrogenase	aprE	1105	extracellular alkaline serine protease (subtilisin E)
			yocA	2031	4-hydroxyphenylacetate-3-hydroxylase	aprX	1862	intracellular alkaline serine protease
glpK	1003	glycerol kinase (glycerol utilization)	yogA	2007	alcohol dehydrogenase	argB	1197	N-acetylglutamate 5-phosphotransferase (arginine biosynthesis)
glvA	6-phospho-β-glucosidase (arbutin fermentation)		yogP	2507	phosphoenolpyruvate mutase	argC	1195	N-acetylglutamate γ-semialdehyde dehydrogenase (arginine biosynthesis)
gntK	4113	glutamate kinase (glutamate utilization)	yqjD	2488	apocyclic-CoA carboxylase	argD	1198	N-acetylornithine aminotransferase (arginine biosynthesis)
gntZ	4116	6-phosphogluconate dehydrogenase (gluconate utilization)	yrfE	2780	formate dehydrogenase			
			yrfG	2780	formate dehydrogenase			
gpsA	2389	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	yrfH	2778	methyltransferase	argE	2142	N-acetylornithine deacetylase (arginine biosynthesis)
			yrfH	2768	cycloextrin metabolism			
gutB	667	sorbitol dehydrogenase	yrgP	2742	sugar-phosphate dehydrogenase	argF	1203	ornithine carbamoyltransferase (arginine biosynthesis)
iolB	4082	myo-inositol catabolism	yrdC	2950	endo-1,4- glucanase			
iolC	4081	myo-inositol catabolism	ysfC	2932	glycolate oxidase subunit	argG	3013	argininosuccinate synthase (arginine biosynthesis)
iolD	4080	myo-inositol catabolism	ytdD	2934	glycolate oxidase subunit			
iolE	4078	myo-inositol catabolism	ytdE	2969	plant metabolite dehydrogenase	argH	3012	argininosuccinate lyase (arginine biosynthesis)
iolG	4076	myo-inositol 2-dehydrogenase (inositol catabolism)	ytdA	3155	NDP-sugar dehydrogenase	argI	1196	ornithine acetyltransferase (arginine biosynthesis)
			ytdB	3155	NDP-sugar epimerase			
iolH	4075	myo-inositol catabolism	ytdC	3024	shikimate-CoA ligase	aroA	3046	3-deoxy-α-arabino-heptulosonate 7-phosphate synthase / chorismate mutase-isozyme 3 (shikimate pathway)
iolI	4074	myo-inositol catabolism	ytdD	3155	UTP-glucose 1-phosphate uridylyltransferase			
iolJ	4084	myo-inositol catabolism	ytdB	3138	carbonic anhydrase			
kdgA	2323	deoxyphosphogluconate aldolase (pectin utilization)	ytdP	3055	endo-1,4- glucanase	aroB	2378	3-dehydroquininate synthase (shikimate pathway)
			ytdI	2989	acetyl-CoA carboxylase	aroC	2413	3-dehydroquininate dehydratase (shikimate pathway)
kdgK	2324	2-keto-3-deoxygluconate kinase (pectin utilization)	yugF	3227	dihydrolipoamide S-acetyltransferase			
			yugI	3224	NADH-dependent butanol dehydrogenase	aroD	2645	shikimate 5-dehydrogenase (shikimate pathway)
kduD	2326	2-keto-3-deoxygluconate oxidoreductase (pectin utilization)	yugK	3222	NADH-dependent butanol dehydrogenase	aroE	2368	5-enolpyruvylshikimate-3-phosphate synthase (shikimate pathway)
			yugT	3215	exo-1,4-glucosidase			
kduI	2325	5-keto-4-deoxyuronate isomerase (pectin utilization)	yulC	3200	rhamnulokinase	aroF	2380	chorismate synthase (shikimate pathway)
			yulE	3198	L-rhamnose isomerase	aroH	2377	chorismate mutase (isozymes 1 and 2) (aromatic amino acids biosynthesis)
lacA	3504	β-galactosidase	yusZ	3382	retinol dehydrogenase			
lctE	329	lactate dehydrogenase	yulF	3318	N-acetylglucosamine catabolism	arol	340	shikimate kinase (shikimate pathway)
lctH	3959	6-phospho-β-glucosidase	yuxG	3203	sorbitol-6-phosphate 2-dehydrogenase	asd	1745	aspartate-semialdehyde dehydrogenase
lplD	782	hydrolytic enzyme	yvaM	3455	hydrolase	ask	2910	aspartokinase II attenuator
melA	3100	α-D-galactoside galactohydrolase	yvcN	3568	N-hydroxyarylamino O-acetyltransferase	asnB	3127	asparagine synthetase
mtiD	4051	mannitol-1-phosphate dehydrogenase	yvcT	3562	glycerate dehydrogenase	asnH	4098	asparagine synthetase
nagA	3594	N-acetylglucosamine-6-phosphate deacetylase (N-acetyl glucosamine utilization)	yvdA	3561	carbonic anhydrase	aspB	2348	aspartate aminotransferase
			yvdF	3557	glucan 1,4-maltohydrolase	bcsA	2317	naringenin-chalcone synthase (phenylalanine metabolism)
nagB	3596	N-acetylglucosamine-6-phosphate isomerase (N-acetyl glucosamine utilization)	yvdL	3548	oligo-1,6-glucosidase			
			yvdM	3547	β-phosphoglucosmutase	bfbBAA	2499	branched-chain α-keto acid dehydrogenase E1 (2-oxoisovalerate dehydrogenase α subunit)
narQ	3773	required for formate dehydrogenase activity	yveB	3537	levanase	bfbBAB	2498	branched-chain α-keto acid dehydrogenase E1 (2-oxoisovalerate dehydrogenase β subunit)
pel	828	pectate lyase	yvfo	3502	arabinogalactan endo-1,4-galactosidase	bfbMB	2497	branched-chain α-keto acid dehydrogenase E2 subunit (lipamide acyltransferase)
pelB	2034	pectate lyase	yvfo	3499	hydrolase	bitD	2718	spermine / spermidine acetyltransferase
pmi	3698	mannose-6-phosphate isomerase	yvvF	3495	acolate oxidase	bpr	1599	bacillopeptidase F
pps	2053	phosphoenolpyruvate synthase	yvqN	3427	plant-metabolite dehydrogenase	cad	1535	lysine decarboxylase
pta	3865	phosphotransacetylase	ywkC	3615	pyruvate, water kinase	carA	1199	carbamoyl-phosphate transferase-arginine (sub-unit A) (arginine biosynthesis)
pttH	1459	histidine-containing phosphocarrier protein of the phosphotransferase system (PTS) (HPr protein)	ywkE	3592	phosphoglycolate phosphatase	carB	1200	carbamoyl-phosphate transferase-arginine (sub-unit B) (arginine biosynthesis)
ptsK	3701	ribokinase (ribose metabolism)	yvoF	3591	O-acetyltransferase	ctpA	2133	carboxy-terminal processing protease
sacA	3902	sucrase-6-phosphate hydrolase	yvpA	3590	pectate lyase	cysE	113	serine acetyltransferase (cysteine biosynthesis)
sacB	3535	levansucrase	yvyH	3664	UDP-N-acetylglucosamine 2-epimerase	cysH	1630	phosphoadenosine phosphosulfate reductase (cysteine biosynthesis)
sacC	2759	levanase	ywdH	3895	aldehyde dehydrogenase	cysK	82	cysteine synthetase A (cysteine biosynthesis)
sacX	3941	negative regulatory protein of SacY	ywdI	3872	glucose 1-dehydrogenase	dal	517	D-alanine racemase
treA	891	trehalose-6-phosphate hydrolase	ywyF	3805	glycerol-inducible protein	dapA	1748	dihydrodipicolinate synthase (diaminopimelate / lysine biosynthesis)
xxa	251	β-xylosidase / α-L-arabinosidase (xylan degradation)	ywyQ	3730	NDP-sugar dehydrogenase	dapB	2359	dihydrodipicolinate reductase (diaminopimelate / lysine biosynthesis)
			yxdD	4091	glucose 1-dehydrogenase	dapG	1747	aspartokinase I (α and β subunits)
			yxA	4040	endo-1,5- L-arabinosidase	def	1646	polypeptide deformylase
xyIA	1891	xyllose isomerase (xyllose metabolism)	xyfA	4000	gluconate 5-dehydrogenase	epo	3939	minor extracellular serine protease
xyIB	1893	xylulose kinase (xyllose metabolism)	xyfF	4107	glucose 1-dehydrogenase	gms	200	L-glutamine-D-fructose-6-phosphate amidotransferase
xynA	2054	endo-1,4-xylanase (xylan degradation)	xyjA	4202	formate dehydrogenase	glnA	1878	glutamine synthetase
xynB	1888	xylan β-1,4-xylosidase (xylan degradation)	yyaE	4196	galactoside acetyltransferase	gltA	2014	glutamate synthase (large subunit) (glutamate biosynthesis)
xynD	1945	endo-1,4-xylanase (xylan degradation)	yyeR	4136	formaldehyde dehydrogenase	gltB	2009	glutamate synthase (small subunit) (glutamate biosynthesis)
ybnA	161	polysaccharide deacetylase				glyA	3789	serine hydroxymethyltransferase (glycine / serine / threonine metabolism)
ybbD	188	β-hexosaminidase				hisA	3584	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (histidine biosynthesis)
ybcM	213	glucosamine-fructose-6-phosphate aminotransferase	II.2		MAIN GLYCOLYTIC PATHWAYS 28	hisB	3585	imidazoleglycerol-phosphate dehydratase (histidine biosynthesis)
			eno	3477	enolase (glycolysis)	hisC	2371	phosphoribosyl-phosphate aminotransferase (histidine biosynthesis) / tyrosine and phenylalanine aminotransferase
ybtT	258	glucosamine-6-phosphate isomerase	fbpA	3808	fructose-1,6-bisphosphate aldolase (glycolysis)	hisD	3587	histidinol dehydrogenase (histidine biosynthesis)
ybtC	258	5-dehydro-D-deoxyglucarate dehydratase	tba2	4127	fructose-1,6-bisphosphatase (gluconogenesis)	hisF	3583	HisF cyclase-like protein (synthesis of D-erythroimidazole glycerol) phosphate)
ybtD	269	acetylaldehyde dehydrogenase	gap	3482	glyceraldehyde 3-phosphate dehydrogenase (glycolysis)	hisG	3587	ATP phosphoribosyltransferase (histidine biosynthesis)
ycbF	272	glutamate dehydratase	gapB	2967	fructose-1,6-phosphate dehydrogenase (glycolysis)	hisH	3585	amidotransferase (histidine biosynthesis)
ycdF	305	glucose 1-dehydrogenase				hisI	3583	phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphohydrolase (histidine biosynthesis)
ycdG	306	oligo-1,6-glucosidase	iolI	4073	fructose-1,6-bisphosphate aldolase (glycolysis)	hom	3315	homoserine dehydrogenase (threonine / methionine biosynthesis)
ycgS	352	aromatic hydrocarbon catabolism	pckA	3129	phosphoenolpyruvate carboxykinase	hutG	4045	formiminoglutamate hydrolase (histidine utilization)
yckE	370	β-glucosidase	pdhA	1528	pyruvate dehydrogenase (E1 α subunit)	hutH	4041	histidase (histidine utilization)
yckG	375	D-arabino-3-hexulose 6-phosphate formaldehyde lyase	pdhB	1529	pyruvate dehydrogenase (E1 β subunit)	hutU	4042	urocanase (histidine utilization)
			pdhC	1530	pyruvate dehydrogenase (dihydrolipoamide acyltransferase E2 subunit)	ilvA	2896	threonine dehydratase (isoleucine biosynthesis)
ycsN	466	aryl-alcohol dehydrogenase	pdhD	1531	pyruvate dehydrogenase / 2-oxoglutarate dehydrogenase (dihydrolipoamide dehydrogenase E3 subunit)	ilvB		acetoalactate synthase (large subunit) (valine / isoleucine biosynthesis)
ydaD	471	alcohol dehydrogenase				ilvC	2894	ketolactone reductoisomerase (valine / isoleucine biosynthesis)
ydaF	473	acetyltransferase	pkf	2987	6-phosphofructokinase (glycolysis)	ilvD	2302	dihydroxy-acid dehydratase (valine / isoleucine biosynthesis)
ydaM	482	cellulose synthase	pgi	3221	glucose-6-phosphate isomerase (glycolysis)	ilvN	2894	acetoalactate synthase (small subunit)
ydaP	488	reticuline oxidase	pgk	3480	phosphoglycerate kinase (glycolysis)			
ydhP	628	β-glucosidase	pkm	3478	phosphoglycerate mutase (glycolysis)			
ydhR	631	fructokinase	pvcA	1554	pyruvate carboxylase			
ydhS	632	mannose-6-phosphate isomerase	pykA	2986	pyruvate kinase (glycolysis)			
ydhT	632	mannan endo-1,4-mannosidase	tkf	1919	transketolase (pentose phosphate)			
ydjE	670	fructokinase	tpi	3479	triose phosphate isomerase (glycolysis)			
ydlJ	679	L-iditol 2-dehydrogenase	ybtT	198	phosphoglucosmutase (glycolysis)			
ydlP	682	arylesterase	ydeA	558	glyceraldehyde 3-phosphate dehydrogenase (glycolysis)			
yeaC	688	methanethiolase glucose regulation						
yesY	774	rhannogalacturonan acetyltransferase						
yexZ	774	β-galactosidase						
yfhM	829	epoxide hydrolase	yfhR	1109	phosphoglycerate mutase (glycolysis)			
yfhR	937	glucose 1-dehydrogenase	yqrC	2651	6-phosphogluconate dehydrogenase (pentose phosphate)			
yfS	969	polysaccharide deacetylase						
yfmT	807	benzaldehyde dehydrogenase	yqjV	2501	dihydrolipoamide dehydrogenase			
yfhH	798	glucose 1-phosphate cytidylyltransferase	yqjL	2481	6-phosphogluconate dehydrogenase (pentose phosphate)			
ygaK	958	reticuline oxidase						
yhcW	997	phosphoglycolate phosphatase	yqjL	2478	glucose-6-phosphate 1-dehydrogenase (pentose phosphate)			
yhdF	1022	glucose 1-dehydrogenase	ywhH	3807	transaldolase (pentose phosphate)			
yhdN	1030	aldo / keto reductase	ywhF	3791	ribose 5-phosphate epimerase (pentose phosphate)			
yheN	1041	endo-1,4-xylanase						
yhiE	1095	glucanase						
yhx0	1006	phosphomannomutase	II.13		TCA CYCLE 19			
yhxC	1115	alcohol dehydrogenase	citA	1021	citrate synthase I			
yhxD	1116	alcohol dehydrogenase	citB	1926	aconitate hydratase			
yisS	1164	myo-inositol 2-dehydrogenase	citC	2980	isocitrate dehydrogenase			
yitF	1175	mandelate racemase	citG	3389	fumarate hydratase			
yitY	1192	L-gulonolactone oxydase	citH	2979	malate dehydrogenase			
yidE	1274	mannose-6-phosphate isomerase	citZ	2981	citrate synthase II			
yieA	1281	endo-1,4-xylanase	malS	3058	malate dehydrogenase			
yigC	1285	formate dehydrogenase

ioiA	4083	(valine/isoleucine biosynthesis) methylmalonate-semialdehyde dehydrogenase (valine metabolism)	yqjE	2486	tripeptidase	xpt	2319	xanthine phosphoribosyltransferase (purine biosynthesis)
ipr	1189	intracellular proteinase inhibitor	yqjN	2475	amino acid degradation	yaaF	23	deoxyuridine kinase subunit
ispA	1386	major intracellular serine protease	yqjO	2472	pyruvate-5-carboxylate reductase	yaaG	24	deoxyuridine kinase subunit
kbl	1771	2-amino-3-ketobutyrate CoA ligase	yqjR	2470	D-serine dehydratase	yabR	70	polynucleotide nucleotidyltransferase
leuA	2893	2-isopropylmalate synthase (leucine biosynthe- sis)	yrbA	2839	opine catabolism	yerA	713	adenine deaminase
leuB	2891	3-isopropylmalate dehydrogenase (leucine biosynthesis)	yrbB	2786	cysteine synthase	yfkN	859	2',3'-cyclic-nucleotide 2'-phosphodiesterase
leuC	2890	3-isopropylmalate dehydratase (large subunit) (leucine biosynthesis)	yrbP	2785	cystathionine γ -synthase	yhaM	1069	GMP-binding factor
leuD	2889	3-isopropylmalate dehydratase (small subunit) (leucine biosynthesis)	yrbY	2768	dihydrodipicolinate reductase	yhcR	991	5'-nucleotidase
lysA	2437	diaminopimelate decarboxylase (lysine biosynthe- sis)	yrcP	2738	glutamate racemase	yirY	1144	DNA exonuclease
lysC	2910	aspartokinase II (α and β subunits) (diaminopimelate/lysine biosynthesis)	yrrN	2794	protease	yjblM	1236	GTP pyrophosphokinase
metB	2305	homoserine O-succinyltransferase (methionine biosynthesis)	yrrO	2793	protease	yjblP	1240	diadenosine tetraphosphatase
metC	1385	cobalamin-independent methionine synthase (methionine biosynthesis)	ysrE	2897	acetyltransferase	ykkE	137	IMP dehydrogenase
metK	3128	S-adenosylmethionine synthetase	ytd	3146	N-acetylmuramic acid racemase	yjlb	1565	IMP dehydrogenase
npi	245	extracellular metalloprotease	ytkP	3066	cysteine synthase	yldD	1641	guanylate kinase
nasB	362	assimilatory nitrate reductase (electron transfer subunit)	yubC	3183	cysteine dioxygenase	ymaA	1868	ribonucleoprotein
nasC	360	assimilatory nitrate reductase (catalytic subunit)	yugH	3226	aspartate aminotransferase	yncB	1895	micrococcal nuclease
nasD	358	assimilatory nitrite reductase (subunit)	yurG	3341	aspartate aminotransferase	yncF	1899	deoxyuridine 5'-triphosphate pyrophosphatase
nasE	355	assimilatory nitrite reductase (subunit)	yurH	3343	N-carbamyl-L-amino acid amidohydrolase	yosN	2165	ribonucleoside-diphosphate reductase (α sub- unit)
nprB	1186	extracellular neutral protease B	yurL	3347	opine catabolism	yosO	2164	ribonucleoside-diphosphate reductase (α sub- unit)
nprE	1541	extracellular neutral metalloprotease	yurP	3351	opine catabolism	yosP	2161	ribonucleoside-diphosphate reductase (β sub- unit)
nrgB	3757	nitrogen-regulated Pil-like protein	yurR	3353	opine catabolism	yosS	2159	deoxyuridine 5'-triphosphate nucleotidohydro- lase
patA	1472	aminotransferase	yurT	3354	methylyglyoxalase	yprD	2395	ribosomal protein S1 homologue
patB	3228	aminotransferase	yusH	3356	glycine cleavage system protein H	yqjB	2528	exodeoxyribonuclease VII (large subunit)
pepT	3394	peptidase	yusM	3373	purine dehydrogenase	yqjC	2526	exodeoxyribonuclease VII (small subunit)
pheA	2851	prephenate dehydratase (phenylalanine biosyn- thesis)	yusX	3381	oligodeoxyribose	yrdF	2730	ribonuclease inhibitor
pheB	2852	chorismate mutase (phenylalanine biosynthe- sis)	yutL	3306	diaminopimelate epimerase	yrrU	2707	purine nucleoside phosphorylase
proA	1379	γ -glutamyl phosphate reductase (proline biosyn- thesis)	yuxL	3312	acylaminoacyl-peptidase	yumD	3282	GMP reductase
proB	1378	γ -glutamyl kinase (proline biosynthesis)	yuxK	3454	carboxylesterase	yunH	3328	allantoinease
proH	2017	involved in proline biosynthesis (salt-inducible)	yvdD	3516	serine O-acetyltransferase	yurL	3323	uracase
rac	2016	glutamate 5-kinase (proline biosynthesis)	yvjB	3623	carboxy-terminal processing protease	yurP	3343	uracase
rocA	3879	pyrroline-5-carboxylate dehydrogenase (argi- nine and ornithine utilization)	ywaA	3956	branched-chain amino acid aminotransferase	ywcD	3287	GTP-pyrophosphokinase
rocB	3878	involved in arginine and ornithine utilization	ywaD	3947	aminopeptidase	il4	77	METABOLISM OF LIPIDS
rocD	4145	ornithine aminotransferase (arginine and ornithine utilization)	yweB	3881	glutamate dehydrogenase	accA	2988	acetyl-CoA carboxylase (α subunit) (long-chain fatty acid biosynthesis)
rocF	4142	arginase (arginine and ornithine utilization)	ywgG	3968	aspartate aminotransferase	accB	2531	acetyl-CoA carboxylase (biotin carboxyl carrier subunit) (long-chain fatty acid biosynthesis)
serA	2410	phosphoglycerate dehydrogenase (serine biosynthesis)	ywhF	3849	permidine synthase	accC	2531	acetyl-CoA carboxylase (biotin carboxylase subunit) (long-chain fatty acid biosynthesis)
serC	1076	phosphoserine aminotransferase (serine biosynthesis)	ywhD	3848	agmatinase	acdA	3813	acetyl-CoA dehydrogenase
tdh	1770	threonine 3-dehydrogenase (threonine catabo- lism)	yxeP	4057	aminoacylase	acdA	1665	acyl carrier protein (fatty acid biosynthesis)
thrB	3313	homoserine kinase (threonine biosynthesis)	il3	77	METABOLISM OF NUCLEOTIDES AND NUCLEIC ACIDS	acdA	1721	phosphatidate cytidyltransferase (phospho- lipid biosynthesis)
thrC	3314	threonine synthase (threonine biosynthesis)	adeC	1521	adenine deaminase	dkgA	2611	diacylglycerol kinase (phospholipid biosynthe- sis)
trpA	2372	tryptophan synthase (α subunit) (tryptophan biosynthesis)	adeK	146	adenylate kinase	fabD	1663	malonyl-CoA-acyl carrier protein transacylase (fatty acid biosynthesis)
trpB	2373	tryptophan synthase (β subunit) (tryptophan biosynthesis)	adp	2823	adenine phosphoribosyltransferase	fabG</		

<i>ywpB</i>	3743	hydroxymyristoyl-(acyl carrier protein) dehydrogenase	<i>yjbT</i>	1245	thiamin biosynthesis	<i>recR</i>	29	DNA repair and genetic recombination
<i>yxD</i>	4001	3-oxoadipate CoA-transferase	<i>yjbU</i>	1246	thiamin biosynthesis	<i>ruvA</i>	2636	Holliday junction DNA helicase
<i>yxE</i>	4001	3-oxoadipate CoA-transferase	<i>yjbV</i>	1246	phosphomethylpyrimidine kinase	<i>ruvB</i>	2636	Holliday junction DNA helicase
			<i>ykpB</i>	1513	thiamin biosynthesis	<i>sbcD</i>	1143	endonuclease SbcD homologue
			<i>ykvK</i>	1440	6-pyruvoyl tetrahydrobiopterin synthase	<i>yfpB</i>	1659	ATP-dependent DNA helicase
II.5		METABOLISM OF COENZYMES AND PROSTHETIC GROUPS	<i>ykvL</i>	1440	coenzyme PQQ synthetase	<i>yocI</i>	2095	ATP-dependent DNA helicase
<i>bioA</i>	3094	adenosylmethionine-8-amino-7-oxononanoate aminotransferase (biotin biosynthesis)	<i>ykbQ</i>	1577	pyrimidine-thiamine biosynthesis	<i>yorkK</i>	2180	single-strand DNA-specific exonuclease
<i>bioB</i>	3091	biotin synthetase (biotin biosynthesis)	<i>ylnD</i>	1633	uroporphyrin-III C-methyltransferase	<i>yqhH</i>	2549	SNF2 helicase
<i>bioD</i>	3091	dethiobiotin synthetase (biotin biosynthesis)	<i>ylnF</i>	1635	uroporphyrin-III C-methyltransferase	<i>yrrC</i>	2808	conjugation transfer protein
<i>bioF</i>	3092	8-amino-7-oxononanoate synthase (biotin biosynthesis)	<i>yiol</i>	1642	pantothenate metabolism flavoprotein	<i>yrvE</i>	2825	single-strand DNA-specific exonuclease
<i>bioI</i>	3089	cytochrome P450-like enzyme (biotin biosynthesis)	<i>yngH</i>	1954	biotin carboxylase	<i>yvwA</i>	3735	SNF2 helicase
<i>bioW</i>	3094	6-carboxyhexanoate-CoA ligase (biotin biosynthesis)	<i>yodC</i>	2127	nitroreductase			
<i>dtfA</i>	2296	dihydrofolate reductase (glycine/purine/DNA precursor synthesis, conversion of dUMP to dTMP)	<i>yqgV</i>	2574	5-formyltetrahydrofolate cyclo-ligase	III.4		DNA PACKAGING AND SEGREGATION
<i>dhaS</i>	2100	aldehyde dehydrogenase	<i>yqS</i>	2469	pantothenate kinase	<i>grlA</i>	1935	DNA gyrase-like protein (subunit A)
<i>dhaB</i>	3291	2,3-dihydroxy-2,3-dihydroxybenzoate dehydrogenase (2,3-dihydroxybenzoate biosynthesis)	<i>yrrL</i>	2795	folate metabolism	<i>grlB</i>	1933	DNA gyrase-like protein (subunit B)
<i>dhaB</i>	3288	isochorismatase (2,3-dihydroxybenzoate biosynthesis)	<i>yrrM</i>	2795	caffeoyl-CoA C-methyltransferase	<i>gyrA</i>	7	DNA gyrase (subunit A)
<i>dhaC</i>	3291	isochorismatase synthase (2,3-dihydroxybenzoate biosynthesis)	<i>yueD</i>	3265	sepiapterin reductase	<i>gyrB</i>	5	DNA gyrase (subunit B)
<i>dhaE</i>	3289	2,3-dihydroxybenzoate-AMP ligase (enterobactin synthetase component E) (2,3-dihydroxybenzoate biosynthesis)	<i>yueI</i>	3261	pyrazinamidase/nicotinamidase	<i>hbs</i>	2385	non-specific DNA-binding protein HBSu
<i>dhaF</i>	3287	involved in 2,3-dihydroxybenzoate biosynthesis	<i>yueK</i>	3260	nicotinate phosphoribosyltransferase	<i>smc</i>	1666	chromosome segregation SMC protein homologue
<i>folA</i>	87	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase (dihydrofolate biosynthesis)	<i>yulG</i>	3293	biotin metabolism			
<i>folC</i>	2866	folyl-polyglutamate synthetase (folate biosynthesis)	<i>yurB</i>	3335	4-hydroxybenzoyl-CoA reductase	<i>smf</i>	1682	DNA processing Sml protein homologue
<i>folD</i>	2529	methylene tetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase (purines and amino acids biosynthesis)	<i>yurC</i>	3338	4-hydroxybenzoyl-CoA reductase	<i>topA</i>	1683	DNA topoisomerase I
<i>folK</i>	87	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase (dihydrofolate biosynthesis)	<i>yurD</i>	3338	4-hydroxybenzoyl-CoA reductase	<i>topB</i>	476	DNA topoisomerase III
<i>ggt</i>	2004	γ -glutamyltranspeptidase (glutathione metabolism)	<i>yutB</i>	3320	lipic acid synthetase	<i>yonN</i>	2225	HU-related DNA-binding protein
<i>gsaB</i>	943	glutamate-1-semialdehyde aminotransferase	<i>ywaB</i>	3950	quinone biosynthesis			
<i>hemA</i>	2878	glutamyl-tRNA reductase (porphyrin biosynthesis)	<i>ywkE</i>	3796	porphyrinogen oxidase	III.5		RNA SYNTHESIS
<i>hemB</i>	2874	8-aminolevulinic acid dehydratase (porphyrin biosynthesis)	<i>ywoC</i>	3755	isochorismatase			
<i>hemC</i>	2876	porphobilinogen deaminase (porphyrin biosynthesis)				III.5.1		INITIATION
<i>hemD</i>	2875	uroporphyrinogen III cosynthase (porphyrin biosynthesis)	II.6		METABOLISM OF PHOSPHATE	<i>sigA</i>	2601	RNA polymerase major sigma factor (σ^70)
<i>hemE</i>	1086	uroporphyrinogen III decarboxylase (porphyrin biosynthesis)	<i>phoA</i>	1018	alkaline phosphatase A	<i>sigB</i>	522	RNA polymerase general stress sigma factor (σ^32)
<i>hemH</i>	1087	ferrochelatase (porphyrin biosynthesis)	<i>phoB</i>	621	alkaline phosphatase III	<i>sigD</i>	1716	RNA polymerase flagella, motility, chemotaxis and autolysis sigma factor (σ^24)
<i>hemL</i>	2873	glutamate-1-semialdehyde 2,1-aminotransferase (porphyrin biosynthesis)	<i>phoD</i>	284	phosphodiesterase/alkaline phosphatase	<i>sigE</i>	1604	RNA polymerase sporulation mother cell-specific (early) sigma factor (σ^54) (SpoIIIG)
<i>hemN</i>	2630	coproporphyrinogen III oxidase (porphyrin biosynthesis)	<i>phoH</i>	2615	phosphate starvation-induced protein	<i>sigF</i>	2443	RNA polymerase sporulation forespore-specific (early) sigma factor (σ^70) (SpoIIAC)
<i>hemX</i>	2877	negative effector of the concentration of HemA	<i>xpaC</i>	36	hydrolysis of 5-bromo-4-chloroindolyl phosphate	<i>sigG</i>	1605	RNA polymerase sporulation forespore-specific (late) sigma factor (σ^70) (SpoIIIG)
<i>hemY</i>	1088	protoporphyrinogen IX oxidase (porphyrin biosynthesis)	<i>yblM</i>	248	alkaline phosphatase	<i>sigH</i>	117	RNA polymerase vegetative and early stationary-phase sigma factor (σ^70) (SpoIIH)
<i>menB</i>	3149	dihydroxynaphthoic acid synthetase (menaquinone biosynthesis)	<i>ykoX</i>	1409	alkaline phosphatase	<i>sigL</i>	3513	RNA polymerase sigma factor (σ^70)
<i>menD</i>	3151	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase / 2-oxoglutarate decarboxylase (menaquinone biosynthesis)	<i>yiaK</i>	1549	phosphate starvation inducible protein	<i>sigV</i>	2769	RNA polymerase ECF-type sigma factor (σ^54)
<i>menE</i>	3148	O-succinylbenzoic acid-CoA ligase (menaquinone biosynthesis)	<i>yngC</i>	1947	alkaline phosphatase	<i>sigW</i>	195	RNA polymerase ECF-type sigma factor (σ^54)
<i>menF</i>	3153	menaquinone-specific isochorismatase synthase (menaquinone biosynthesis)	II.7		METABOLISM OF SULPHUR	<i>sigX</i>	2414	RNA polymerase ECF-type sigma factor (σ^54)
<i>moaB</i>	3014	molybdopterin precursor biosynthesis	<i>yisZ</i>	1170	adenylsulfate kinase	<i>sigY</i>	3970	RNA polymerase ECF-type sigma factor (σ^54)
<i>moaD</i>	1499	molybdopterin converting factor (subunit 1)	<i>yitA</i>	1171	sulfate adenyltransferase	<i>sigZ</i>	2742	RNA polymerase ECF-type sigma factor (σ^54)
<i>moaE</i>	1498	molybdopterin converting factor (subunit 2)	<i>yitB</i>	1172	phospho-adenylsulfate sulfotransferase	<i>spolIC</i>	2701	RNA polymerase sporulation mother cell-specific (late) sigma factor (σ^70) (C-terminal half)
<i>moaB</i>	1498	molybdopterin-guanine dinucleotide biosynthesis	<i>yitC</i>	1632	sulfate adenyltransferase			
<i>moaC</i>	1497	molybdopterin-guanine dinucleotide biosynthesis	<i>ylnC</i>	1633	adenylsulfate kinase	<i>xpf</i>	1324	RNA polymerase PBX sigma factor-like
<i>moaB</i>	1496	molybdopterin biosynthesis protein	<i>yuiH</i>	3293	sulfite oxidase	<i>yhdM</i>	1030	RNA polymerase ECF-type sigma factor
<i>mtA</i>	2385	GTP cyclohydrolase I (tetrahydrofolate biosynthesis)	<i>yvgQ</i>	3431	sulfite reductase	<i>ykoZ</i>	1411	RNA polymerase sigma factor
<i>nadA</i>	2846	quinolinate synthetase (quinolinate biosynthesis)	<i>yvgR</i>	3433	sulfite reductase	<i>yiaC</i>	1543	RNA polymerase ECF-type sigma factor
<i>nadB</i>	2849	L-aspartate oxidase (quinolinate biosynthesis)	III		INFORMATION PATHWAYS 482	III.5.2		REGULATION
<i>nadC</i>	2847	nicotinate-nucleotide pyrophosphorylase (NAD/NADP biosynthesis)	III.1		DNA REPLICATION	<i>abf</i>	1517	transcriptional regulator of transition state genes (AbrB-like)
<i>nadE</i>	338	NH ₄ -dependent NAD ⁺ synthetase (NAD biosynthesis)	<i>dnaA</i>	0	initiation of chromosome replication	<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>spo0H</i> , <i>spoVG</i> , <i>spoVE</i> , <i>tycA</i>)
<i>narA</i>	3772	molybdopterin precursor biosynthesis	<i>dnaB</i>	2965	initiation of chromosome replication / membrane attachment protein	<i>ahrC</i>	2522	transcriptional activator of the acetoin dehydrogenase operon (<i>acoABCD</i>)
<i>narS</i>	355	uroporphyrin-III C-methyltransferase (porphyrin biosynthesis)	<i>dnaC</i>	4158	replicative DNA helicase	<i>alsR</i>	3711	transcriptional regulator of the α -acetolactate operon (<i>alsSD</i>)
<i>nifS</i>	2849	required for NAD biosynthesis	<i>dnaD</i>	2345	initiation of chromosome replication	<i>ansR</i>	2456	transcriptional repressor of the <i>ansAB</i> operon (Xre family)
<i>pabA</i>	84	p-aminobenzoate synthase glutamine amidotransferase (subunit B) / anthranilate synthase (subunit II) (folate and tryptophan biosynthesis)	<i>dnaE</i>	2994	DNA polymerase III (α subunit)	<i>araR</i>	3485	transcriptional repressor of the arabinose operon (<i>araBADLMNPO</i>)
<i>pabB</i>	83	p-aminobenzoate synthase (subunit A) (folate biosynthesis)	<i>dnaG</i>	2603	DNA primase	<i>azlB</i>	2729	transcriptional repressor of the <i>azlBCD</i> operon
<i>pabC</i>	85	aminodeoxychorismate lyase (folate biosynthesis)	<i>dnaI</i>	2963	primosome component (helicase loader)	<i>birA</i>	2355	transcriptional repressor of the biotin operon (<i>bioWAFDBI</i>) / biotin acetyl-CoA-carboxylase synthetase
<i>panB</i>	2354	ketopantoate hydroxymethyltransferase (pantothenate biosynthesis)	<i>dnaJ</i>	2	DNA polymerase III (β subunit)	<i>bltR</i>	2716	transcriptional regulator of the <i>bltD</i> operon
<i>panC</i>	2353	pantothenate synthetase (pantothenate biosynthesis)	<i>dnaK</i>	27	DNA polymerase III (γ and δ subunits)	<i>bmrR</i>	2495	transcriptional activator of the <i>bmrUR</i> operon
<i>panD</i>	2352	aspartate 1-decarboxylase (pantothenate biosynthesis)	<i>hoiB</i>	41	DNA polymerase III (δ subunit)	<i>ccpA</i>	3044	transcriptional regulator involved in carbon catabolite control
<i>ribA</i>	2429	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase (riboflavin biosynthesis)	<i>polA</i>	2975	DNA polymerase I	<i>cheB</i>	1711	two-component response regulator-like [CheA] / methyl-accepting chemotaxis proteins-glutamate methyltransferase
<i>ribB</i>	2429	riboflavin synthase (α subunit) (riboflavin biosynthesis)	<i>polC</i>	1727	DNA polymerase III (α subunit)	<i>cheY</i>	1703	two-component response regulator [CheA] involved in modulation of flagellar switch bias (chemotaxis)
<i>ribC</i>	1737	riboflavin kinase / FAD synthase (riboflavin biosynthesis)	<i>priA</i>	1643	primosomal replication factor Y	<i>citR</i>	1020	transcriptional repressor of the citrate synthase I gene (<i>citA</i>)
<i>ribG</i>	2431	riboflavin-specific deaminase (riboflavin biosynthesis)	<i>mh</i>	1677	ribonuclease H	<i>citT</i>	832	two-component response regulator [CitS]
<i>ribH</i>	2428	riboflavin synthase (β subunit) (riboflavin biosynthesis)	<i>rtp</i>	2018	replication terminator protein	<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>ureAB</i>)
<i>ribT</i>	2427	reductase (riboflavin biosynthesis)	<i>ssb</i>	4199	single-strand DNA-binding protein	<i>comA</i>	3253	two-component response regulator [ComP] of late competence genes / surfactin production
<i>sul</i>	86	dihydropterate synthase (dihydrofolate biosynthesis)	<i>yerF</i>	719	ATP-dependent DNA helicase	<i>comK</i>	1117	competence transcription factor (CTF), final autoregulatory control switch prior to competence development
<i>thiA</i>	955	synthesis of the pyrimidine moiety of thiamin (thiamin biosynthesis)	<i>yerG</i>	721	DNA ligase	<i>comQ</i>	3256	transcriptional regulator of late competence operon (<i>comG</i>) and surface expression (<i>srfA</i>)
<i>thiC</i>	3930	thiamine-phosphate pyrophosphorylase (thiamin biosynthesis)	<i>yocV</i>	2192	DNA ligase	<i>ctsR</i>	101	transcriptional repressor of class III stress genes (<i>clpC</i> , <i>clpP</i>)
<i>thiD</i>	3930	phosphomethylpyrimidine kinase (thiamin biosynthesis)	<i>yolC</i>	2179	DNA polymerase III (α subunit)	<i>degA</i>	1163	transcriptional activator involved in the degradation of glutamine phosphoribosylpyrophosphate amidotransferase
<i>thiK</i>	3931	hydroxyethylthiazole kinase (thiamin biosynthesis)	<i>yopC</i>	2311	5'-3' exonuclease	<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>yaal</i>	26	isochorismatase	<i>yphH</i>	3740	single-strand DNA-binding protein	<i>deoR</i>	4052	transcriptional repressor of the <i>draI</i> / <i>nupC</i> / <i>pdp</i> operon (deoxynucleoside)
<i>ydiA</i>	640	thiamin-monophosphate kinase	III.2		DNA RESTRICTION/MODIFICATION AND REPAIR	<i>fnr</i>	3831	transcriptional regulator of anaerobic genes (<i>narK</i> , <i>narGHI</i>)
<i>ydiG</i>	646	molybdopterin precursor biosynthesis	III.3		DNA RECOMBINATION	<i>fruR</i>	1507	transcriptional repressor of the fructose operon (<i>fruRBA</i>)
<i>yhaV</i>	1058	coproporphyrinogen III oxidase	<i>addA</i>	1139	ATP-dependent deoxyribonuclease (subunit A)	<i>gerE</i>	2904	transcriptional regulator required for expression of late spore coat genes
<i>yhcB</i>	979	flavodoxin	<i>addB</i>	1136	ATP-dependent deoxyribonuclease (subunit B)	<i>glcR</i>	3739	transcriptional repressor involved in the expression of the phosphotransferase system
<i>yhfU</i>	1112	biotin biosynthesis	<i>recA</i>	1764	multifunctional protein involved in homologous recombination and DNA repair (LexA-autocleavage)	<i>glcT</i>	1456	transcriptional antiterminator essential for the expression of the <i>ptsGHI</i> operon
<i>yhxA</i>	1000	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	<i>recF</i>	3	DNA repair and genetic recombination	<i>glrR</i>	1877	transcriptional repressor of the glutamine synthetase gene (<i>glrA</i>)
			<i>recN</i>	2522	DNA repair and genetic recombination	<i>glpP</i>	1001	transcriptional antiterminator and control of mRNA stability of <i>glpD</i>
			<i>recQ</i>	2408	ATP-dependent DNA helicase	<i>glpC</i>	2014	transcriptional activator of the glutamate synthase operon (<i>gluAB</i>)
						<i>glrR</i>	2725	transcriptional repressor of the glutamate synthase operon (<i>gluAB</i>)
						<i>gntR</i>	4113	transcriptional repressor of the gluconate operon (<i>gntRKFPZ</i>)

<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>	1331	elongation factor Tu	<i>ywqC</i>	3732	capsular polysaccharide biosynthesis	<i>xxdE</i>	1327	PBSX prophage
<i>ylaG</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.7.5	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>yyxA</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>lgt</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) /	<i>xxdQ</i>	1339	PBSX prophage
<i>map</i>	147	methionine aminopeptidase	<i>bmrU</i>	2493	NADH dehydrogenase	<i>xxdR</i>	1340	PBSX prophage
<i>pcp</i>	287	pyrrolidone-carboxylate peptidase				<i>xxdS</i>	1340	PBSX prophage
<i>ppbB</i>	2435	serine protein kinase	<i>bmr</i>	2493	multidrug resistance protein cotranscribed with	<i>xxdT</i>	1341	PBSX prophage
<i>prkA</i>	973	protein kinase	<i>cah</i>	342	cephalosporin C deacetylase	<i>xxdU</i>	1342	PBSX prophage
<i>tgl</i>	3212	transglutaminase	<i>cypA</i>	2732	cytochrome P450-like enzyme	<i>xxdV</i>	1343	PBSX prophage
<i>ybdM</i>	224	protein kinase	<i>cypX</i>	3603	cytochrome P450-like enzyme	<i>xxdW</i>	1345	PBSX prophage
<i>ydiC</i>	642	glycoprotein endopeptidase	<i>katA</i>	960	vegetative catalase 1	<i>xxdX</i>	1345	PBSX prophage
<i>ydiD</i>	643	ribosomal-protein-alanine N-acetyltransferase	<i>katB</i>	4009	catalase 2	<i>xxdY</i>	1345	PBSX prophage lytic exoenzyme
<i>ydiE</i>	643	glycoprotein endopeptidase	<i>katX</i>	3964	catalase	<i>xmxA</i>	1325	PBSX terminase (small subunit)
<i>ytkJ</i>	862	protein-tyrosine phosphatase	<i>ksgA</i>	51	dimethyladenosine transferase (kasugamycin resistance)	<i>xmB</i>	1325	PBSX terminase (large subunit)
<i>ytlG</i>	840	methionine aminopeptidase				<i>xmC</i>	1324	PBSX prophage
<i>yvCk</i>	1261	ribosomal-protein-alanine N-acetyltransferase	<i>mmr</i>	3657	methylerythromycin A resistance protein	<i>ycdD</i>	304	-alaninol-D-glutamate peptidase
<i>yvKb</i>	1528	formylmethionine deformylase	<i>padC</i>	3532	ferulate decarboxylase	<i>ydcL</i>	530	integrase
<i>yvY</i>	1453	Xaa-Pro dipeptidase	<i>penP</i>	2048	β -lactamase	<i>ydcM</i>	531	immunity region protein in prophage
<i>yvP</i>	1651	protein kinase	<i>pksS</i>	1859	hydrolyase of the polyketide produced by the	<i>yhgE</i>	1090	phage infection protein
<i>yvpP</i>	2287	peptide methionine sulfoxide reductase				<i>yjbl</i>	1235	lytic transglycosylase
<i>yqeT</i>	2624	ribosomal protein L11 methyltransferase	<i>sodA</i>	2585	superoxide dismutase	<i>yjgB</i>	1318	phage-related replication protein
<i>yqhT</i>	2539	Xaa-Pro dipeptidase	<i>sodF</i>	2103	superoxide dismutase	<i>ymaC</i>	1863	phage-related protein
<i>ytl</i>	3020	protease IV	<i>tetL</i>	4188	tetracycline resistance leader peptide	<i>ymaH</i>	1867	host factor-1 protein
<i>ytlP</i>	3068	Xaa-His dipeptidase	<i>thdF</i>	4212	thiophen and furan oxidation	<i>ymlD</i>	1755	phage-related protein
<i>yvA</i>	3105	protein kinase	<i>tmmB</i>	339	unicarmycin resistance	<i>ymlE</i>	1756	phage-related protein
<i>yvM</i>	3150	prolyl aminopeptidase	<i>yaaN</i>	36	toxic cation resistance	<i>ymlL</i>	1914	phage-related replication protein
<i>yvU</i>	3297	leucyl aminopeptidase	<i>yvDE</i>	190	β -lactamase	<i>yobO</i>	2075	phage-related pre-neck appendage protein
<i>yvE</i>	3791	protein-tyrosine phosphatase	<i>yvFO</i>	250	erythromycin esterase	<i>yokA</i>	2284	DNA recombinase
<i>yyaL</i>	4102	serine/threonine protein kinase	<i>yvKl</i>	229	β -lactamase	<i>yokL</i>	2274	phage-related protein
			<i>yvbl</i>	276	viomycin phosphotransferase	<i>yolB</i>	2272	phage-related protein
III.9	PROTEIN FOLDING	8	<i>yvB</i>	283	toxic cation resistance protein	<i>yomA</i>	2264	holin
<i>dnaK</i>	2627	class I heat-shock protein (chaperonin)	<i>yceC</i>	312	tellurium resistance protein	<i>yomJ</i>	2248	phage-related immunity protein
<i>groEL</i>	650	class I heat-shock protein (chaperonin)	<i>yceD</i>	312	tellurium resistance protein	<i>yomP</i>	2243	phage-related protein
<i>groES</i>	650	class I heat-shock protein (chaperonin)	<i>yceE</i>	313	tellurium resistance protein	<i>yomR</i>	2242	phage-related protein
<i>tig</i>	2887	trigger factor (prolyl isomerase)	<i>yceF</i>	314	tellurium resistance protein	<i>yomS</i>	2241	phage-related lytic exoenzyme
<i>ykkC</i>	1376	chaperonin	<i>yceH</i>	316	toxic anion resistance protein	<i>yqaD</i>	2200	phage-related DNA-binding protein anti-repressor
<i>ykkD</i>	1376	chaperonin	<i>yceF</i>	457	lactam utilization protein	<i>yqz</i>	2190	phage-related protein
<i>yvKd</i>	3541	chaperonin	<i>yvD</i>	496	manganese-containing catalase	<i>yvC</i>	2160	phage-related endonuclease
<i>yvS</i>	3541	chaperonin	<i>yvB</i>	581	antibiotic resistance protein	<i>yvB</i>	2700	phage-related protein
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IV.1	ADAPTATION TO ATYPICAL CONDITIONS	72	<i>yerP</i>	732	acriflavine resistance protein	<i>yqak</i>	2695	phage-related protein
<i>bssA</i>	2304	glutathione peroxidase	<i>yetM</i>	790	salicylate 1-monooxygenase	<i>yqam</i>	2694	phage-related protein
<i>clpC</i>	104	class III stress response-related ATPase (repressor of competence)	<i>yetO</i>	792	cytochrome P450 / NADPH-cytochrome P450 reductase	<i>yqaO</i>	2692	phage-related protein
<i>clpE</i>	1437	ATP-dependent Clp protease-like	<i>yilM</i>	836	nitric-oxide synthase	<i>yqaS</i>	2690	phage-related terminase large subunit
<i>clpP</i>	3545	ATP-dependent Clp protease proteolytic subunit (class III heat-shock protein)	<i>yilN</i>	804	fosmidmycin resistance protein	<i>yqaT</i>	2689	phage-related terminase small subunit
<i>clpQ</i>	1688	B-type subunit of the 20S proteasome	<i>ygaF</i>	943	thiol-specific antioxidant protein	<i>yqbA</i>	2688	phage-related protein
<i>clpX</i>	2885	ATP-dependent Clp protease ATP-binding subunit (class III heat-shock protein)	<i>yhgG</i>	1122	monooxygenase	<i>yqbD</i>	2684	phage-related protein
<i>clpY</i>	1688	ATP-dependent Clp protease-like	<i>yibY</i>	1169	chloride peroxidase	<i>yqde</i>	2683	phage-related protein
<i>csbB</i>	930	stress response protein	<i>yijB</i>	1291	monooxygenase	<i>yqdeH</i>	2682	phage-related protein
<i>csbP</i>	984	major cold-shock protein	<i>yijC</i>	1292	macrolide glycosyltransferase	<i>yqbl</i>	2681	phage-related protein
<i>csbC</i>	559	cold-shock protein	<i>yikA</i>	1366	immunity to bacteriotoxins	<i>yqbl</i>	2681	phage-related protein
<i>csbD</i>	2307	cold-shock protein	<i>ykkB</i>	1375	N-acetyltransferase	<i>yqk</i>	2680	phage-related protein
<i>cstA</i>	2937	carbon starvation-induced protein	<i>yyoY</i>	1410	toxic anion resistance protein	<i>yqbl</i>	2679	phage-related protein
<i>ctc</i>	59	general stress protein	<i>yndN</i>	1916	fosfomycin resistance protein	<i>yqbM</i>	2679	phage-related protein
<i>degQ</i>	3256	degradative enzyme production	<i>yocD</i>	2088	immunity to bacteriotoxins	<i>yqbN</i>	2677	phage-related protein
<i>degR</i>	3206	degradative enzyme production	<i>yoiK</i>	2117	macrolide glycosyltransferase	<i>yqbO</i>	2677	phage-related protein
<i>dnaL</i>	2625	heat-shock protein (activation of DnaK)	<i>yoiM</i>	2115	superoxide dismutase	<i>yqbP</i>	2672	phage-related protein
<i>dps</i>	3136	stress- and starvation-induced gene controlled by	<i>yokD</i>	2281	aminoglycoside N ³ -acetyltransferase	<i>yqbQ</i>	2671	phage-related protein
			<i>yqcm</i>	2655	arsenate reductase	<i>yqR</i>	2670	phage-related protein
<i>gbsA</i>	3186	glycine betaine aldehyde dehydrogenase (osmoprotection)	<i>yqP</i>	2596	penicillin tolerance	<i>yqBT</i>	2670	phage-related protein
<i>gbsB</i>	3184	alcohol dehydrogenase (osmoprotection)	<i>yrlJ</i>	2776	cytochrome P450 / NADPH-cytochrome P450 reductase	<i>yqC</i>	2669	phage-related protein
<i>griP</i>	2628	heat-shock protein (activation of DnaK)	<i>ytrB</i>	2736	2-nitropropane dioxygenase	<i>yqC</i>	2668	phage-related protein
<i>gsiB</i>	494	general stress protein	<i>ytlG</i>	3017	thiol peroxidase	<i>yqC</i>	2666	phage-related protein
<i>gspA</i>	3944	general stress protein	<i>ytnJ</i>	3002	nitrotriacetate monooxygenase	<i>yqXG</i>	2666	phage-related lytic exoenzyme
<i>hit</i>	1076	Hit-like protein involved in cell-cycle regulation	<i>yubB</i>	3195	bactitracin resistance protein (undecaprenol kinase)	<i>yqxH</i>	2665	holin
<i>htpG</i>	4090	class III heat-shock protein (chaperonin)	<i>yusi</i>	3366	arsenate reductase	IV.5	TRANSPOSON AND IS	10
<i>htrA</i>	1359	serine protease Do (heat-shock protein)	<i>yvT</i>	3487	alkanol monooxygenase	<i>ydcP</i>	533	transposon protein
<i>ispU</i>	1387	activation of σ^E	<i>yvD</i>	3543	reticulone oxidase	<i>ydcQ</i>	533	transposon protein
<i>lonA</i>	2882	class III heat-shock ATP-dependent protease	<i>yvH</i>	3810	monooxygenase	<i>ydcR</i>	535	transposon protein
<i>lonB</i>	2884	Lon-like ATP-dependent protease	<i>ywnH</i>	3760	phosphatidylcholine acetyltransferase	<i>ydcB</i>	537	transposon protein
<i>mrqA</i>	3983	metallorepression DNA-binding stress protein	<i>yxel</i>	4062	penicillin amidase	<i>ydeE</i>	538	transposon protein
<i>rsbR</i>	519	positive regulator of σ^E activity (interaction with RsbS)	<i>yxkC</i>	4061	monooxygenase	<i>yddH</i>	544	transposon protein
<i>rsbS</i>	520	negative regulator of σ^E activity (antagonist of RsbT)	<i>yvYR</i>	4185	streptothricin acetyl-transferase	<i>yefB</i>	739	site-specific recombinase
<i>rsbT</i>	520	positive regulator of σ^E activity (switch protein/serine kinase [RsbS])	IV.3	ANTIBIOTIC PRODUCTION	30	<i>yefC</i>	739	resolvase
<i>rsbU</i>	521	indirect positive regulator of σ^E activity (serine phosphatase [RsbV-P])	<i>pksB</i>	1782	involved in polyketide synthesis	<i>yneB</i>	1918	resolvase
<i>rsbV</i>	522	positive regulator of σ^E activity (anti-anti-sigma factor [RsbV])	<i>pksC</i>	1783	involved in polyketide synthesis	<i>yocA</i>	2085	transposon-related protein
<i>rsbW</i>	522	negative regulator of σ^E activity (switch protein/serine kinase [RsbV], anti-sigma factor [σ^E])	<i>pksD</i>	1785	involved in polyketide synthesis	IV.6	MISCELLANEOUS	26
<i>rsbX</i>	523	indirect negative regulator of σ^E activity (serine phosphatase [RsbS-P])	<i>pksE</i>	1785	involved in polyketide synthesis	<i>bex</i>	2610	GTP-binding protein
<i>ydcH</i>	308	adhesion protein	<i>pksF</i>	1788	involved in polyketide synthesis	<i>csbA</i>	3614	putative membrane protein
<i>ydaG</i>	473	general stress protein	<i>pksG</i>	1789	involved in polyketide synthesis	<i>csbB</i>	36	σ^E -transcribed gene
<i>ytlR</i>	910	surface adhesion	<i>pksH</i>	1790	involved in polyketide synthesis	<i>ctaG</i>	1564	function unknown
<i>yvKl</i>	1414	heat-shock protein	<i>pksI</i>	1791	involved in polyketide synthesis	<i>eag</i>	1430	small membrane protein
<i>yvZA</i>	1381	general stress protein	<i>pksJ</i>	1792	involved in polyketide synthesis	<i>ecsC</i>	1079	function unknown
<i>yvA</i>	1637	fibrinectin-binding protein	<i>pksK</i>	1794	polyketide synthase	<i>mmgE</i>	2509	function unknown
<i>yvU</i>	1655	alkaline-shock protein	<i>pksL</i>	1808	polyketide synthase	<i>nifZ</i>	3027	NiF protein homologue
<i>yvB</i>	1875	GTP-binding protein protease modulator	<i>pksM</i>	1821	polyketide synthase	<i>sapB</i>	726	mutant activates alkaline phosphatase during sporulation independently of σ^E and σ^F
<i>ynzF</i>	1880	δ -endotoxin	<i>pksN</i>	1834	polyketide synthase	<i>sbp</i>	1595	small basic protein
<i>yocK</i>	2097	general stress protein	<i>pksP</i>	1835	polyketide synthase	<i>veg</i>	53	function unknown
<i>yocM</i>	2098	small heat-shock protein	<i>pksR</i>	1850	polyketide synthase	<i>yael</i>	102	creatine kinase
<i>yodU</i>	2151	capsular polysaccharide biosynthesis	<i>ppsA</i>	1997	peptide synthetase	<i>ybaL</i>	157	ATP-binding Mip-like protein
<i>yokG</i>	2279	δ -endotoxin	<i>ppsB</i>	1990	peptide synthetase	<i>ybcU</i>	287	NiF protein homologue
<i>yvpP</i>	2286	capsular polysaccharide biosynthesis	<i>ppsC</i>	1992	peptide synthetase	<i>yerN</i>	730	pet112-like protein
<i>yvX</i>	3047	general stress protein	<i>ppsD</i>	1974	peptide synthetase	<i>yhdP</i>	1033	hemolysin
<i>yvJ</i>	3046	general stress protein	<i>ppsE</i>	1963	peptide synthetase	<i>yhdT</i>	1035	hemolysin
<i>yvK</i>	3529	capsular polysaccharide biosynthesis	<i>sbo</i>	3835	subtilisin A	<i>yheG</i>	1049	calcium-binding protein
<i>yvE</i>	3528	capsular polysaccharide biosynthesis	<i>sfp</i>	408	surface production	<i>yplQ</i>	2295	hemolysin III homologue
<i>yvM</i>	3527	capsular polysaccharide biosynthesis	<i>srfAA</i>	377	surface synthesis / competence	<i>yqxG</i>	2523	hemolysin-like
<i>yvN</i>	3525	capsular polysaccharide biosynthesis	<i>srfAB</i>	387	surface synthesis / competence	<i>yvA</i>	2720	hemolysin-like
<i>yvO</i>	3524	exopolysaccharide biosynthesis	<i>srfAC</i>	398	surface synthesis / competence	<i>yvO</i>	2811	NiF protein homologue
<i>yvP</i>	3523	capsular polysaccharide biosynthesis	<i>srfAD</i>	402	surface synthesis / competence	<i>yuaG</i>	3187	epidermal surface antigen
<i>yvQ</i>	3522	capsular polysaccharide biosynthesis	<i>sunA</i>	2269	sublancin 168 lantibiotic antimicrobial precursor	<i>yurV</i>	3357	NiF protein homologue
<i>yvR</i>	3521	spore coat polysaccharide biosynthesis				<i>yurW</i>	3358	NiF protein homologue
<i>yvT</i>	3519	capsular polysaccharide biosynthesis	<i>yomB</i>	2264	bacteriocin	<i>yutI</i>	3309	NiF protein homologue
<i>yvX</i>	3517	capsular polysaccharide biosynthesis	<i>yukL</i>	3282	antibiotic synthetase			
			<i>yukM</i>	3283	antibiotic synthetase			
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