Computerized genetic map of *Bacillus subtilis*

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Introduction

Bacillus subtilis is a Gram-positive soil organism endowed with an interesting developmental programme, which includes acquisition of competence for transformation with exogenous DNA, sporulation and germination, and is taxonomically closely related to various bacilli used for production of numerous industrial enzymes. It is well-characterized genetically and physiologically, due to a number of studies carried out in the past few decades [714], and is thus an excellent model organism for Gram-positive bacteria, in particular those that have relatively A + T-rich genomes, such as lactic acid bacteria, clostridia or mycoplasmas. Present and future work with *B. subtilis* includes systematic characterization of its genes, carried out within a consortium of European laboratories, in co-ordination with a number of laboratories from Japan [382, 540].

The accumulation of large quantities of data by the European and Japanese laboratories prompted us to develop a new software package to facilitate their organization and management. We therefore developed a database, on an Oracle relational system, dedicated to the analysis of bacterial genomes, which we called Micado (MICrobial Advanced Database Organization). It is designed to cross-reference or link heterogeneous information such as nucleotide sequences and the associated features, bibliographic references, genetic map data and properties of mutant strains. The sequence information comes from primary entries in EMBL and GenBank, and a non-redundant controlled set of *B. subtilis* sequences from *SubtiList* [488], a database cleaner than non-specialized databases.

Micado is endowed with a user-friendly query interface through a WorldWide Web networked hypermedia server on the Internet (its address is <http://locus.jouy.inra.fr>). It gives an international multiplatform and countless access to the database. Searching sequences and genes is based on annotations such as features, descriptions or bibliography. It makes use of selection menus and

clickable images to obtain information about genes by selecting gene names on genetic or physical map graphical representations. Interactive requests on the database allow users to scale a gene and its region at the sequence level, thus providing fine details on map contents. Printing-quality outputs exist for interactively displayed regions, and for documents in this paper and future updates.

A program has been written to draw the *B. subtilis* genetic map automatically (Fig. 1) and present the global organization of the loci and their order on the chromosome in a compact and readable form. It is independent of the variable number of genes in each degree, an indispensable feature considering the permanent increase of uncovered genes in the last few years, and its foreseeable continuation. We cross genetic map information and sequence data inside Micado for control and addition of new genes. Organization of sequences in large contigs, coming from the sequencing groups or *SubtiList* database, allowed us to check for wrongly located genes on the genetic map, and to modify orientation information for some contigs and loci. Also, aligning genes on sequences showed inaccuracies in position measurement, and gave us an opportunity to remedy them. The present version of the *B. subtilis* genetic map is the first in which a table and graphical representation were automatically generated by a computer program.

The genetic map and the information reported on Table 1 were derived, with revision and updating, from the sixth edition [23] of a series of revised versions of the *B. subtilis* 168 chromosome map, starting with that of Henner & Hoch in 1980 [287, 288, 580, 581, 582, 23]. The linear vertical form adopted in the last edition has also been used in this version. The map is, as usual, divided in degrees of a circle starting from the origin of chromosome replication. The size of the *B. subtilis* genome has been estimated as approximately 4.2 Mb from the data of the physical map of Amjad *et al.* [21] and 4.188 Mb from that of Itaya & Tanaka [330]. A degree, therefore, corresponds to about 11.6 kb. The number of genes placed on the present map is 1089; 410 more genes have therefore been

Fig. 1. *B. subtilis* genetic map

added since the last edition. The reader is referred to the introduction of the last edition [23] as regards accuracy of map position of a gene, distance between genes and nomenclature. Gene position and distances are of course now sufficiently accurate in the already-sequenced areas. In Table 1, besides the usual information (gene symbol, map position, function, references), we added the symbols

formerly or alternatively used by authors. For updates of the *B. subtilis* genetic map, we regularly search the literature and the network for novel information. The current map includes published data up to 1 May 1996. In the particular cases where no publication has been found, the bibliography reports references from the sequence databases (the annotation 'Direct submission to EMBL/

Fig. 1. *B. subtilis* genetic map (cont.)

Fig. 1. *B. subtilis* genetic map (cont.)

Fig. 1. *B. subtilis* genetic map (cont.)

Table 1. Genes of *B. subtilis*

Map positions are given in degrees: NM, not mapped; UC, map position not fully defined. References: *, locus sequenced; #, locus cloned.

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>aadK</i>	232	Aminoglycoside 6-adenylyltransferase	527*, 546
<i>abfA</i>	254	α -L-Arabinofuranosidase <i>Streptomyces lividans</i> homologue	825*
<i>abb</i>	124	Homologous to the <i>abrB</i> gene, gene <i>ylxT</i>	367*, 824
<i>abnA</i>	256	Gene involved in the utilization of arabinan and arabinose; <i>Aspergillus niger</i> arabinase homologue	825*
<i>abrA</i>		See <i>rev-4</i>	
<i>abrB</i>	4	Transition state regulatory protein controlling a variety of genes; <i>cpsX</i>	563*
<i>accB</i>	218	Biotin carboxyl carrier protein	437*
<i>accC</i>	218	Biotin carboxylase subunit of acetyl-CoA carboxylase	437*
<i>acdA</i>	323	Acyl-CoA dehydrogenase	228*
<i>aceA</i>		See <i>pdhA</i>	
<i>aceB</i>		See <i>pdhB</i>	
<i>aceC</i>		See <i>pdhC</i>	
<i>aceD</i>		See <i>pdhD</i>	
<i>acfA</i>	228	Resistance to acriflavin, ethidium bromide and distamycin; sensitivity to streptomycin	326
<i>acfB</i>	212	Same phenotype as <i>acfA</i>	688
<i>ackA</i>	261	Acetate kinase	245*
<i>acsA</i>	263	Acetyl-CoA synthetase	246*, 247
<i>acuA</i>	263	Acetoin dehydrogenase	246*, 247
<i>acuB</i>	263	Acetoin dehydrogenase	246*, 247
<i>acuC</i>	263	Acetoin dehydrogenase	246*, 247
<i>adaA</i>	23	Adaptive response to alkylating agents; methylphosphotriester-DNA methyltransferase	483*, 484*, 485
<i>adaB</i>	23	O ⁶ -Methylguanine-DNA methyltransferase	483*, 484*, 485
<i>addA</i>	98	Subunit of ATP-dependent deoxyribonuclease; equivalent to <i>E. coli</i> RecBCD enzyme; now considered an allele of this locus; helicase	253, 373#, 374*, 681*
<i>addB</i>	98	Subunit of ATP-dependent deoxyribonuclease; mutants show increased stability for some plasmids	253, 373#, 374*, 681*
<i>ade</i>		See <i>adeC</i>	
<i>adeC</i>	124	Adenine deaminase; <i>ade</i>	529, 530*, 824
<i>adk</i>	12	Adenylate kinase	505*
<i>aecA</i>		See <i>lysC</i>	
<i>aecB</i>	282	Aminoethylcysteine resistance	452
<i>ahpC</i>	352	Probable alkyl hydroperoxide reductase; <i>ndh</i>	541, 873*
<i>ahpF</i>	352	Probable alkyl hydroperoxide reductase	541
<i>ahrA</i>	342	Arginine hydroxamate resistance	489
<i>ahrB</i>	328	Arginine hydroxamate resistance	489
<i>ahrC</i>	217	Arginine hydroxamate resistance	707#
<i>ahrD</i>	99	Arginine hydroxamate resistance	41
<i>ala</i>	281	Alanine requirement	452
<i>ald</i>	281	L-Alanine dehydrogenase; <i>spoVN</i>	649, 691*, 769
<i>alkA</i>	23	3-Methyladenine DNA glycosylase	486*
<i>alsA</i>		See <i>ccpA</i>	
<i>alsC</i>	317	Regulator homologous to the <i>lysR</i> family	616*
<i>alsD</i>	317	Acetolactate decarboxylase	616*
<i>alsR</i>	317	Constitutive acetolactate synthase	616*, 866, 869
<i>alsS</i>	317	Structural gene for acetolactate synthase	616*
<i>alsT</i>	171	Alanine sodium symport protein T	630*
<i>ampS</i>	124	AmpS protein	824*
<i>amyA</i>		See <i>amyE</i>	

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>amyB</i>		See <i>degQ</i>	
<i>amyE</i>	26	Amylase structural gene; <i>amyA</i>	839*, 840*
<i>amyH</i>		See <i>amyR</i>	
<i>amyR</i>	26	Control of amylase synthesis; <i>gra</i> , <i>amyH</i>	521*, 839*, 865
<i>amyX</i>	264	Starch-degrading enzyme; pullulanase	393*
<i>ansA</i>	212	L-Asparaginase	745*
<i>ansB</i>	212	L-Aspartase	745*
<i>ansR</i>	212	Repressor of the <i>ans</i> operon	747*
<i>appA</i>	104	Oligopeptide permease system	368*
<i>appB</i>	104	Oligopeptide permease system	368*
<i>appC</i>	104	Oligopeptide permease system	368*
<i>appD</i>	104	Oligopeptide permease system; probable ATP-binding protein	368*
<i>appF</i>	104	Oligopeptide permease system; probable ATP-binding protein	368*
<i>apr</i>		See <i>aprE</i>	
<i>aprA</i>		See <i>aprE</i>	
<i>aprE</i>	78	Structural gene for subtilisin; <i>aprA</i> , <i>apr</i> , <i>sprE</i>	525, 721*
<i>apt</i>	235	Adenine phosphoribosyl transferase	659
<i>ara</i>	172	Arabinose utilization	558
<i>araA</i>	256	Arabinose utilization; L-arabinose isomerase	641#, 825*
<i>araB</i>	256	Arabinose utilization; L-ribulokinase	641#, 825*
<i>araC</i>	294	Arabinose utilization regulation	640
<i>araD</i>	256	Arabinose utilization; L-ribulose-5-phosphate 4-epimerase	641#, 825*
<i>argA</i>		See <i>argJ</i>	
<i>argB</i>	102	Arginine requirement; identified by complementation of corresponding locus in <i>E. coli</i>	490#, 531
<i>argC</i>	102	Arginine requirement; identified by complementation of corresponding locus in <i>E. coli</i>	531, 708*, 709*
<i>argD</i>	102	Arginine requirement; identified by complementation of corresponding locus in <i>E. coli</i>	490#, 531
<i>argE</i>		See <i>argJ</i>	
<i>argF</i>	102	Ornithine carbamoyltransferase; identified by complementation of corresponding locus in <i>E. coli</i> ; formerly <i>argC</i>	490, 491#, 531
<i>argG</i>	261	Arginine requirement; identified by complementation of corresponding locus in <i>E. coli</i>	39, 393*, 490
<i>argH</i>	261	Arginine requirement; identified by complementation of corresponding locus in <i>E. coli</i>	39, 393*, 490
<i>argJ</i>	102	The product of this gene combines both the activities of the <i>argA</i> (amino acid acetyl transferase) and <i>argE</i> (acetylornithine deacetylase) gene products of <i>E. coli</i> ; <i>argA</i> , <i>argE</i>	531
<i>argS</i>	324	Arginyl-tRNA synthetase	609*
<i>aroA</i>	263	3-Deoxy-D-arabinoheptulosonic-7-phosphate synthase; chorismate mutase isozyme 3	61*, 302
<i>aroB</i>	203	Dehydroquinate synthase	292, 429#
<i>aroC</i>	208	Dehydroquinate dehydratase	717*, 805#
<i>aroD</i>	226	Shikimate dehydrogenase	302, 715#
<i>aroE</i>	202	3-Enolpyruvylshikimate-5-phosphate synthase	290*
<i>aroF</i>	203	Chorismate synthase	292*, 302
<i>aroH</i>	203	Chorismate mutase isozymes 1 and 2	238, 292*
<i>aroI</i>	27	Shikimate kinase	506*, 552#
<i>aroJ</i>		See <i>hisH</i>	
<i>asaA</i>	228	Arsenate resistance	2
<i>asaB</i>	57	Arsenate resistance (derived from <i>B. subtilis</i> W23)	3
<i>asd</i>	149	Aspartate semialdehyde dehydrogenase; problem of gene symbol redundancy; see other <i>asd</i> at 253°	112*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>asd</i>	253	<i>Bacteroides ovatus</i> arabinosidase homologue; problem of gene symbol redundancy; see other <i>asd</i> at 149°	825*
<i>ask</i>	252	Aspartokinase II attenuator	825*
<i>asnS</i>	200	Asparaginyl-tRNA synthetase	80*
<i>aspB</i>	200	Aspartate aminotransferase	80*, 301
<i>aspH</i>	212	Aspartase, constitutive	320
<i>aspT</i>	92	Aspartate transport	817
<i>atb</i>		See <i>purM</i>	
<i>atpA</i>	321	ATP synthase subunit α	652*
<i>atpB</i>	321	ATP synthase subunit a	652*
<i>atpC</i>	321	ATP synthase subunit ϵ	652*
<i>atpD</i>	321	ATP synthase subunit β	652*
<i>atpE</i>	321	ATP synthase subunit c	652*
<i>atpF</i>	321	ATP synthase subunit b	652*
<i>atpG</i>	321	ATP synthase subunit γ	652*
<i>atpH</i>	321	ATP synthase subunit δ	652*
<i>atpI</i>	321	ATP synthase subunit i	652*
<i>attSPO2</i>	13	Integration site for phage SPO2	700
<i>attSPR</i>	218	Integration site for phage SPR	136
<i>attSPβ</i>	190	Integration site for phage SP β and related phages IG1, IG3, and IG4	867
<i>azc</i>	27	Resistance to azetidine-2-carboxylic acid; <i>azc</i> 90 % co-transformed with <i>aroI</i>	209
<i>azj</i>		See <i>secA</i>	
<i>azlA</i>	247	4-Azaleucine resistance; derepressed leucine biosynthetic enzymes	427#
<i>azlB</i>	234	4-Azaleucine resistance	806
<i>azp-12</i>		See <i>polC</i>	
<i>azpB</i>	329	Resistance to azopyrimidines	95
<i>bac</i>	327	Bacilysin biosynthesis	299
<i>bcsA</i>	198	Bacterial chalcone synthase A	97*
<i>betR</i>	128	Resistance to betacin produced by SP β lysogens	280
<i>bex</i>	224	<i>Bacillus</i> Era-complementing segment; an essential small G-protein in <i>E. coli</i>	343*
<i>bfmA</i>		See <i>pdbA</i>	
<i>bfmB</i>		See <i>bfmBB</i>	
<i>bfmB1a</i>		See <i>bfmB.A.A</i>	
<i>bfmB1b</i>		See <i>bfmB.AB</i>	
<i>bfmB2</i>		See <i>bfmBB</i>	
<i>bfmB.A.A</i>	215	Branched-chain α -ketoacid dehydrogenase E1- α ; <i>bfmB1a</i>	67, 800*
<i>bfmB.AB</i>	215	Branched-chain α -ketoacid dehydrogenase E1- β ; <i>bfmB1b</i>	67, 800*
<i>bfmBB</i>	215	Branched-chain 2-oxo-acid dehydrogenase E2 subunit; <i>bfmB</i> , <i>bfmB2</i>	5*, 67, 800*
<i>bgl</i>		See <i>bglS</i>	
<i>bglA</i>	352	Phospho- β -glucosidase	873*
<i>bglC</i>		See <i>eglS</i>	
<i>bglH</i>	336	β -Glucosidase	854*
<i>bglP</i>	336	β -Glucoside permease; similar to β -glucoside-specific phosphotransferase Enzymes II	398*
<i>bglS</i>	335	Endo-1,3-1,4- β -glucanase (lichenase); <i>bgl</i>	500*, 827
<i>bioA</i>	268	Biotin biosynthesis; DAPA aminotransferase	393*, 553
<i>bioB</i>	268	Biotin biosynthesis	393*, 553
<i>bioD</i>	268	Dethiobiotin synthetase	393*
<i>bioF</i>	268	Biotin biosynthesis; 7-XAP synthetase	393*
<i>bioI</i>	268	Biotin biosynthesis; cytochrome P450 protein	393*
<i>bioW</i>	268	Biotin biosynthesis; pimelyl-CoA synthetase	393*
<i>birA</i>	201	Bifunctional biotin operon repressor; biotin acetyl-CoA-carboxylase ligase; transcription regulator	68*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>blt</i>	231	Multidrug efflux transporter; resistance to acriflavin, ethidium bromide and distamycin; sensitivity to streptomycin	6*
<i>bltD</i>	231	Transacetylase co-transcribed with <i>blt</i>	6*
<i>bltR</i>	231	Transcriptional regulator of <i>blt</i>	6*
<i>bmr</i>	215	Bacterial multidrug resistance; homologous to <i>tet</i> gene of pBR322; also called <i>bmr1</i>	5*, 519*
<i>bmr-1R</i>		See <i>bmrR</i>	
<i>bmrR</i>	215	Multidrug-efflux transporter regulator; <i>bmr-1R</i>	5*
<i>bmrU</i>	215	Bacterial multidrug resistance protein BmrU, co-transcribed with <i>bmr</i>	5*
<i>bofA</i>	0	Activation of σ^K during sporulation	619*
<i>bofB</i>		See <i>spoIVFA</i> and <i>spoIVFB</i>	
<i>bpf</i>		See <i>bpr</i>	
<i>bpr</i>	135	Bacillopeptidase F; <i>bpf</i>	168*, 696*, 697*, 835*
<i>but</i>	NM	5-Bromouracil tolerance	56
<i>cad</i>	126	Cadaverine synthesis, lysine decarboxylase	279*, 824
<i>cafA</i>	46	Caffeine resistance	96
<i>cafB</i>		See <i>gyrA</i>	
<i>cab</i>	27	Cephalosporin C deacetylase	474*
<i>cal</i>	14	Chalcomycin resistance	683
<i>cam-2</i>	45	Chloramphenicol resistance	26
<i>carA</i>	102	Carbamoylphosphate synthetase subunit A, arginine-specific; <i>cpaA</i>	142*, 490
<i>carB</i>	102	Carbamoylphosphate synthetase subunit B, arginine-specific; <i>cpaB</i>	142*, 490
<i>catA</i>		See <i>bpr</i>	
<i>cccA</i>	223	Gene for cytochrome c_{550}	793*
<i>ccdA</i>	170	Required for cytochrome <i>c</i> synthesis	665*
<i>ccpA</i>	263	Catabolite control protein involved in glucose regulation of several genes; <i>alsA</i> is allelic to <i>ccpA</i> ; <i>graR</i> , <i>alsA</i>	247, 284*, 866, 869
<i>cdd</i>	224	Deoxycytidine-cytidine deaminase	716*
<i>cdr</i>	38	Cadmium resistance	871
<i>celA</i>	333	Putative cellobiose phosphotransferase Enzyme II	227*
<i>celB</i>	333	Putative cellobiose phosphotransferase Enzyme II	227*
<i>celC</i>	333	Putative cellobiose phosphotransferase Enzyme III	227*
<i>celD</i>	333	Putative 6-phospho- β -glucosidase	227*
<i>celR</i>	333	<i>cel</i> operon regulator	227*
<i>cgeA</i>	181	Operon <i>cgeAB</i> genes controlled by the sporulation regulatory protein GerE; <i>cgeAA</i>	625*
<i>cgeAA</i>		See <i>cgeA</i>	
<i>cgeAB</i>		See <i>cgeB</i>	
<i>cgeB</i>	181	Operon <i>cgeAB</i> genes controlled by the sporulation regulatory protein GerE; <i>cgeAB</i>	625*
<i>cgeBA</i>		See <i>cgeC</i>	
<i>cgeBB</i>		See <i>cgeD</i>	
<i>cgeBC</i>		See <i>cgeE</i>	
<i>cgeC</i>	181	Operon <i>cgeCDE</i> genes controlled by the sporulation regulatory protein GerE; <i>cgeBA</i>	625*
<i>cgeD</i>	181	Operon <i>cgeCDE</i> genes controlled by the sporulation regulatory protein GerE; <i>cgeBB</i>	625*
<i>cgeE</i>	181	Operon <i>cgeCDE</i> genes controlled by the sporulation regulatory protein GerE; <i>cgeBC</i>	625*
<i>cheA</i>	142	Chemotaxis, histidine kinase chemotactic signal modulator; previous <i>cheA</i> is now <i>fliZ</i> ; <i>cheN</i>	52*, 198, 360, 549, 869, 871
<i>cheB</i>	142	Chemotaxis; previous <i>cheB</i> is now <i>cheY</i> ; <i>cheL</i>	359*, 360, 549, 875, 876
<i>cheC</i>		See <i>fliP</i>	

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>cheD</i>		See <i>fliY</i>	
<i>cheF</i>		See <i>fliJ</i>	
<i>cheL</i>		See <i>cheB</i>	
<i>cheN</i>		See <i>cheA</i>	
<i>cheR</i>	204	Chemotactic methyltransferase	292*, 548#
<i>cheV</i>	120	Chemotaxis	195*
<i>cheW</i>	142	Chemotaxis	260*, 360, 549, 875, 876
<i>cheX</i>	118	Chemotaxis	875
<i>cheY</i>	142	Chemotaxis; formerly <i>cheB</i>	52*, 53, 54*, 360, 549, 875, 876
<i>cisA</i>		See <i>spoIVCA</i>	
<i>cisB</i>		See <i>spoIVCB</i>	
<i>citA</i>	73	Citrate synthase	340*, 525
<i>citB</i>	170	Aconitase	144*, 630*
<i>citC</i>	259	Isocitrate dehydrogenase	215, 340*, 341*, 573#
<i>citF</i>		See <i>sdhA</i>	
<i>citG</i>	289	Fumarate hydratase	464*
<i>citH</i>	259	Malate dehydrogenase; <i>mdh</i>	215, 341*
<i>citK</i>		See <i>odhA</i>	
<i>citL</i>		See <i>pdbD</i>	
<i>citM</i>		See <i>odhB</i>	
<i>citR</i>	73	Regulatory protein of the <i>lysR</i> family located upstream of <i>citA</i>	340*, 525
<i>citZ</i>	259	Citrate synthase II	340*, 341*
<i>clpC</i>		See <i>mecB</i>	
<i>clpX</i>	244	Possible ATP-dependent Clp protease; ATP-binding subunit	825*, 849
<i>cmk</i>	205	Cytidine monophosphate kinase; <i>cmp</i>	718*
<i>cmp</i>		See <i>cmk</i>	
<i>codV</i>	141	Similar to XerC and XerD of <i>E. coli</i>	307*, 692*
<i>codW</i>	141	Heat-shock protein; similar to <i>hslV</i> of <i>E. coli</i> ; <i>hslV</i>	307*, 692*
<i>codX</i>	141	Heat-shock protein; similar to <i>hslV</i> of <i>E. coli</i> and ClpX ATPase (a regulatory subunit of the <i>E. coli</i> ClpP protease); <i>hslU</i>	307*, 692*
<i>codY</i>	141	Regulatory gene of the <i>dpp</i> operon	307*, 692*
<i>comA1</i>		See <i>comAA</i>	
<i>comA2</i>		See <i>comAB</i>	
<i>comAA</i>	279	Competence; early block effector signal transduction; <i>com-9</i> may map in <i>comA</i> or <i>comB</i> ; <i>comA1</i>	152*, 811*
<i>comAB</i>	279	Competence; early block; <i>com-9</i> may map in <i>comA</i> or <i>comB</i> ; <i>comA2</i>	152*, 811*
<i>comC</i>	242	Competence	152*
<i>comE1</i>		See <i>comEA</i>	
<i>comE2</i>		See <i>comEB</i>	
<i>comE3</i>		See <i>comEC</i>	
<i>comE4</i>		See <i>comER</i>	
<i>comEA</i>	226	Competence protein; <i>comE1</i>	152*, 252*
<i>comEB</i>	226	Competence protein; <i>comE2</i>	152*, 252*
<i>comEC</i>	226	Competence protein; <i>comE3</i>	152*, 252*
<i>comER</i>	226	Competence protein; <i>comE4</i>	152*, 252*
<i>comF1</i>		See <i>comFA</i>	
<i>comF2</i>		See <i>comFB</i>	
<i>comF3</i>		See <i>comFC</i>	
<i>comFA</i>	306	Competence protein; <i>comF1</i>	152*, 417*
<i>comFB</i>	306	Competence protein; <i>comF2</i>	152*, 417*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>comFC</i>	306	Competence protein; <i>comF3</i>	152*, 417*
<i>comG1</i>		See <i>comGA</i>	
<i>comG2</i>		See <i>comGB</i>	
<i>comG3</i>		See <i>comGC</i>	
<i>comG4</i>		See <i>comGD</i>	
<i>comG5</i>		See <i>comGE</i>	
<i>comG6</i>		See <i>comGG</i>	
<i>comGA</i>	220	Competence; may include <i>com-71</i> ; <i>comG1</i>	10*, 152*
<i>comGB</i>	220	Competence; may include <i>com-71</i> ; <i>comG2</i>	10*, 152*
<i>comGC</i>	220	Competence; may include <i>com-71</i> ; <i>comG3</i>	10*, 152*
<i>comGD</i>	220	Competence; may include <i>com-71</i> ; <i>comG4</i>	10*, 152*
<i>comGE</i>	220	Competence; may include <i>com-71</i> ; <i>comG5</i>	10*, 152*
<i>comGG</i>	220	Competence; may include <i>com-71</i> ; <i>comG6</i>	10*, 152*
<i>comI</i>		See <i>nucA</i>	
<i>comJ</i>	31	Competence; encodes an 18 kDa protein that is isolated with the ComI protein; <i>nin</i>	199*, 794*
<i>comK</i>	80	Required for genetic competence; includes <i>com-30</i>	152, 777*, 779
<i>comL</i>		See <i>srfAA</i>	
<i>comM</i>	346	Competence; formerly <i>com-104</i>	152, 174
<i>comN</i>	152	Competence	445
<i>comO</i>	68	Competence; formerly <i>com-18</i>	445
<i>comP</i>	279	Competence; homologous to sensor class of signal-transduction proteins	812*
<i>comQ</i>	279	Competence; competence regulatory gene	492*
<i>comR</i>	80	Competence; previously <i>com-44</i>	40#, 445
<i>comS</i>	31	Required for competence; a small protein S	127*, 259
<i>cotA</i>	52	Spore-coat protein	65*, 146#
<i>cotB</i>	290	Spore-coat protein	146#, 874
<i>cotC</i>	168	Spore-coat protein	146*, 874
<i>cotD</i>	199	Spore-coat protein	146*, 874
<i>cotE</i>	150	Spore-coat protein; peroxidase	147, 620*, 810, 874
<i>cotF</i>	356	Spore-coat protein	125*
<i>cotG</i>	300	Spore-coat protein	642*, 711
<i>cotJ</i>	62	σ^E -controlled operon affecting the polypeptide composition of spore coats	294*
<i>cotS</i>	274	Spore-coat protein	807*
<i>cotT</i>	108	Spore-coat protein	30*
<i>cotV</i>	107	Spore-coat protein	872*
<i>cotW</i>	107	Spore-coat protein	872*
<i>cotX</i>	107	Spore-coat protein	872*
<i>cotY</i>	107	Spore-coat protein	872*
<i>cotZ</i>	107	Spore-coat protein	872*
<i>cpaA</i>		See <i>carA</i>	
<i>cpaB</i>		See <i>carB</i>	
<i>cpsX</i>		See <i>abrB</i>	
<i>crk</i>	NM	Cytidine kinase	621
<i>err</i>		See <i>ptsG</i>	
<i>crsA</i>		See <i>sigA</i>	
<i>crsB</i>	56	Requires high glucose for sporulation	742
<i>crsC</i>	217	Carbon-source-resistant sporulation; maps close to or in <i>spo0A</i>	742
<i>crsD</i>	10	Carbon-source-resistant sporulation	742
<i>crsE</i>		See <i>rpoB</i>	
<i>crsF</i>	119	Carbon-source-resistant sporulation	742
<i>csaA</i>	197	Homologous to <i>csaA</i> gene from plants	97*
<i>csbA</i>	303	Gene controlled by σ^B	70*, 711
<i>csb</i>	NM	Genes controlled by the sporulation regulatory gene <i>spo0H</i>	296, 334*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>cspB</i>	69	Cold-shock protein	525, 823*
<i>cspC</i>	42	Cold-shock protein	501*
<i>cspD</i>	197	Cold-shock protein, homologous to <i>cspB</i>	97*
<i>csrA</i>	306	Carbon storage regulator; homologous to <i>csrA</i> of <i>E. coli</i>	623, 711*
<i>cstA</i>	254	Induced in carbon starvation; homologous to <i>cstA</i> of <i>E. coli</i>	825*
<i>ctaA</i>	127	Required for expression of cytochrome <i>aa₃</i>	495*
<i>ctaB</i>	127	Cytochrome- <i>a</i> oxidase assembly factor	654*
<i>ctaC</i>	127	Cytochrome- <i>aa₃</i> oxidase subunit II	654*
<i>ctaD</i>	127	Cytochrome- <i>aa₃</i> oxidase subunit I	654*
<i>ctaE</i>	127	Cytochrome- <i>aa₃</i> oxidase subunit III	654*
<i>ctaF</i>	127	Cytochrome- <i>aa₃</i> oxidase subunit IVB	654*
<i>ctc</i>	7	Expressed at the end of exponential growth under conditions in which the enzymes of the tricarboxylic acid cycle are repressed	298, 318*, 523*
<i>ctrA</i>	323	CTP synthetase; requirement for cytidine in the absence of ammonium ion; <i>pyrG</i>	621, 762*
<i>cwbA</i>		See <i>lytB</i>	
<i>cwlA</i>	228	Autolytic amidase; minor autolysin	187*, 383*, 384
<i>cwlB</i>		See <i>lytC</i>	
<i>cwlC</i>	153	Cell wall hydrolase	208, 386*
<i>cwlD</i>	13	High similarity to a major autolysin of <i>B. subtilis</i> CwlB	679*
<i>cyc</i>	95	D-Cycloserine resistance	210
<i>cysA</i>	10	Cysteine requirement, serine trans-acetylase; original isolate contained four linked mutations; <i>cys</i> (cysteine sensitivity), <i>cym</i> (cysteine or methionine), <i>hts</i> (hydrogen sulfide excretion) and <i>cysA</i> ; <i>cysE</i>	205*, 346
<i>cysB</i>	292	Cysteine requirement	149
<i>cysC</i>	139	Cysteine, methionine, sulfite, or sulfide requirement	861
<i>cysE</i>		See <i>cysA</i>	
<i>cysK</i>	9	Cysteine synthase A	534*, 539*
<i>cysS</i>	10	Cysteinyl-tRNA synthetase	205, 680*
<i>cyt</i>	284	Requires cytidine	306
<i>dacA</i>	0	D-Alanine carboxypeptidase; vegetative penicillin-binding protein 5	83, 755*
<i>dacB</i>	208	DD-Carboxypeptidase penicillin-binding protein 5, operon with <i>spmAB</i>	84*, 595, 717*
<i>dacF</i>	211	Putative DD-carboxypeptidase; penicillin-binding protein	670, 833*, 834
<i>dae</i>		See <i>dltA</i>	
<i>dal</i>	38	D-Alanine requirement; alanine racemase	177*
<i>dapA</i>	149	Dihydrodipicolinate synthase	112*
<i>dapE</i>	135	N-Acetyl-L-diaminopimelic acid deacylase; <i>lssB</i>	76, 91, 193, 631
<i>dapG</i>	149	Aspartokinase I; <i>lssD</i>	112*, 631
<i>dat</i>	NM	Constitutive O ⁶ -methylguanine-DNA alkyltransferase	483*
<i>dbpA</i>		See <i>hbs</i>	
<i>dcd</i>	NM	Deoxycytidine 5'-monophosphate deaminase	479
<i>dciAA</i>		See <i>dppA</i>	
<i>dciAB</i>		See <i>dppB</i>	
<i>dciAC</i>		See <i>dppC</i>	
<i>dciAD</i>		See <i>dppD</i>	
<i>dciAE</i>		See <i>dppE</i>	
<i>dck</i>	NM	Deoxycytidine/deoxyadenosine kinase	480
<i>ddd</i>	NM	Deoxycytidine kinase	621
<i>ddlA</i>	37	D-Alanyl-D-alanine ligase	91
<i>dds</i>		See <i>divB</i>	
<i>degA</i>	99	Involved in the control of degradation of <i>B. subtilis</i> glutamine 5-phosphoribosyl-1-pyrophosphate amidotransferase	86, 681*
<i>degQ</i>	279	Degradative enzyme regulation; <i>sacQ</i> , <i>amyB</i>	404, 842*
<i>degR</i>	197	Degradative enzyme regulation; <i>prrR</i>	843*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>degS</i>	306	Degradative enzyme regulation; part of <i>sacU</i>	291*, 381*
<i>degU</i>	306	Degradative enzyme regulation; part of <i>sacU</i> ; <i>iep</i>	754*
<i>deoA</i>	NM	Thymidine phosphorylase	455
<i>deoR</i>	338	Repression of the <i>dra-nupC-pdp</i> operon	663*
<i>dfrA</i>	195	Dihydrofolate reductase; coordinately regulated with <i>thyB</i>	333*
<i>dgkA</i>	224	Diacylglycerol kinase	477
<i>dhbA</i>	291	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase; based on similarity to <i>E. coli</i> EntA	635*
<i>dhbB</i>	291	Isochorismatase; based on similarity to <i>E. coli</i> EntB	635*
<i>dhbC</i>	291	Isochorismate synthase; based on similarities to <i>E. coli</i> EntC	634*, 635*
<i>dhbE</i>	291	2,3-Dihydroxybenzoate-AMP ligase; based on similarity to <i>E. coli</i> EntE	635*
<i>dhbF</i>	291	Similar to <i>E. coli</i> EntF	635*
<i>din</i>	121	Deoxyribonuclease inhibitor	596
<i>dinA</i>		See <i>uvrB</i>	
<i>dinB</i>	45	DNA-damage-inducible	113*, 222
<i>dinC</i>		See <i>tagC</i>	
<i>dinR</i>		See <i>lexA</i>	
<i>div-341</i>		See <i>secA</i>	
<i>divA</i>		See <i>divIC</i>	
<i>divB</i>		See <i>divV</i>	
<i>divC</i>		See <i>divII</i>	
<i>divD</i>		See <i>divI</i>	
<i>divI</i>	138	Temperature-sensitive cell division; <i>divD</i>	92, 773
<i>divIB</i>	134	Deficient in division and sporulation; <i>dds</i>	45*, 168*, 269*, 270
<i>divIC</i>	8	Minicell production; <i>divA</i> , <i>divIVC</i>	410*, 773
<i>divII</i>	317	Temperature-sensitive cell division; <i>divC</i>	773
<i>divIVA</i>	138	Minicell production	92, 613
<i>divIVB</i>		See <i>minD</i>	
<i>divIVC</i>		See <i>divIC</i>	
<i>divV</i>	278	Temperature-sensitive cell division; <i>divB</i>	773
<i>dltA</i>	333	D-Alanine esterification of lipoteichoic acid and wall teichoic acid; carrier protein ligase; <i>dae</i>	225*, 567*
<i>dltB</i>	333	D-Alanine esterification of lipoteichoic acid and wall teichoic acid	225*, 567*
<i>dltC</i>	333	D-Alanine esterification of lipoteichoic acid and wall teichoic acid; carrier protein	225*, 567*
<i>dltD</i>	333	D-Alanine esterification of lipoteichoic acid and wall teichoic acid; precursor	225*, 567*
<i>dltE</i>	333	Similar to ketoacyl reductase	225*, 567*
<i>dnaA</i>	0	DNA synthesis, initiation of chromosome replication; homologous to <i>dnaA</i> of <i>E. coli</i> ; previous <i>dnaA</i> locus is now <i>nrdA</i>	535*
<i>dnaB</i>	256	DNA synthesis; initiation of chromosome replication	314, 537*
<i>dnaC</i>	355	DNA synthesis; homologous to <i>dnaB</i> of <i>E. coli</i> (replicative DNA helicase); <i>dnaTsA</i> , <i>dnaTsB</i>	266, 647*
<i>dnaD</i>	200	DNA synthesis, initiation of chromosome replication	80*, 350
<i>dnaE</i>		See <i>dnaG</i>	
<i>dnaF</i>		See <i>polC</i>	
<i>dnaG</i>	223	DNA synthesis; homologous to <i>dnaG</i> of <i>E. coli</i> (DNA primase); previous <i>dnaG</i> is now <i>dnaN</i> ; <i>dnaE</i>	16, 801*
<i>dnaH</i>		See <i>dnaX</i>	
<i>dnaI</i>	256	DNA synthesis	79, 350, 537*
<i>dnaJ</i>	225	Homologous to <i>dnaJ</i> of <i>E. coli</i> (heat-shock protein)	815*
<i>dnaK</i>	225	Homologous to <i>dnaK</i> of <i>E. coli</i> (heat-shock protein)	273*, 814*, 815#
<i>dnaN</i>	0	DNA synthesis, homologous to <i>dnaN</i> of <i>E. coli</i> (β subunit of DNA polymerase III); formerly <i>dnaG</i>	536*
<i>dnaP</i>		See <i>polC</i>	

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>dnaTsA</i>		See <i>dnaC</i>	
<i>dnaTsB</i>		See <i>dnaC</i>	
<i>dnaX</i>	0	DNA synthesis, homologous to <i>dnaZX</i> of <i>E. coli</i> (τ and γ subunits of DNA polymerase III); subunit of holoenzyme DNA polymerase III; formerly <i>dnaH</i> and <i>dna-8132</i>	18*, 735*, 738*
<i>dpaA</i>	148	DPA synthetase; the original <i>dpa-1</i> mutation is an allele of <i>dpaA</i> ; <i>spoVFA</i>	35, 112*, 133*, 578
<i>dpaB</i>	148	DPA synthetase; <i>spoVFB</i>	35, 112*, 133*, 578
<i>dppA</i>	113	Dipeptide permease; DNA sequence has five adjacent ORFs; <i>dciAA</i>	448, 449*, 692
<i>dppB</i>	113	Dipeptide permease; DNA sequence has five adjacent ORFs; <i>dciAB</i>	448, 449*, 692
<i>dppC</i>	113	Dipeptide permease; DNA sequence has five adjacent ORFs; <i>dciAC</i>	448, 449*, 692
<i>dppD</i>	113	Dipeptide permease; DNA sequence has five adjacent ORFs; <i>dciAD</i>	448, 449*, 692
<i>dppE</i>	113	Dipeptide permease; DNA sequence has five adjacent ORFs; <i>dciAE</i>	448, 449*, 692
<i>dra</i>	338	Deoxyriboaldolase	663*, 741
<i>drm</i>	211	Phosphodeoxyribomutase	671
<i>dst</i>	229	Resistance to distamycin and acriflavin	688
<i>durR</i>	20	Duramycin resistance	514
<i>ebr</i>	215	Ethidium bromide resistance; perhaps the same as <i>bmr</i>	56, 137*
<i>eglS</i>	171	Endo-1,4- β -glucanase (CM-cellulase); <i>bglC</i> , <i>gld</i>	426*, 630*, 827*
<i>eno</i>	NM	Enolase	143*, 411*
<i>entA</i>	41	EntA enterochelin synthesis	4*
<i>entE</i>	41	EntE enterochelin synthesis	4*
<i>epr</i>	332	Minor extracellular protease	694*
<i>estB</i>	296	Esterase B defect	179*, 297
<i>etfA</i>	253	α subunits of electron-transfer flavoprotein	825*
<i>etfB</i>	253	β subunits of electron-transfer flavoprotein	825*
<i>ethA</i>	NM	Ethionine resistance	795
<i>exoA</i>	358	3'-Exodeoxyribonuclease	539*
<i>exoI</i>	198	Homologous to polymerase N-terminal exonuclease	97*
<i>expZ</i>	45	Nucleotide-binding protein	140*
<i>fabE</i>	218	Fatty acid biosynthesis; homologous to <i>fabE</i> of <i>E. coli</i>	437, 732*
<i>fbaA</i>	323	Fructose-bisphosphate aldolase; <i>tsr</i>	472, 473, 762*
<i>fbaB</i>		See <i>iolJ</i>	
<i>fdpA</i>	344	Fructose-bisphosphatase	200
<i>feuA</i>	14	Periplasmic iron-binding protein	846
<i>feuB</i>	14	Component of iron-uptake system	846
<i>feuC</i>	14	Component of iron-uptake system	846
<i>ffh</i>	147	Signal-recognition particle; homologous to Ffh of <i>E. coli</i>	208, 310*
<i>fhuD</i>	286	Ferrichrome-binding protein	265*
<i>fibA</i>	307	Macrofibre formation; weak linkage to <i>hisA</i>	658
<i>fibB</i>	295	Macrofibre formation	658
<i>flaB</i>		See <i>sigD</i>	
<i>flaC</i>	311	Defect in flagellar synthesis	586
<i>flaD</i>		See <i>sinR</i>	
<i>flgB</i>	142	Part of <i>che-fla</i> operon; three loci B, C, G; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>Salmonella typhimurium</i>	876*
<i>flgC</i>	142	Part of <i>che-fla</i> operon; three loci B, C, G; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	876*
<i>flgG</i>	142	Part of <i>che-fla</i> operon; three loci B, C, G; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	14*, 876
<i>flgK</i>	306	Flagellar hook-filament junction protein, flagellin synthesis regulatory protein	468*
<i>flgM</i>	306	Flagellar hook-filament junction protein, flagellin synthesis regulatory protein	468*
<i>flhA</i>	142	Part of the <i>che-fla</i> operon; three loci A, B, F; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i> ; flagellar genes	103*, 360

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>flbB</i>	142	Part of the <i>che-fla</i> operon; three loci <i>A</i> , <i>B</i> , <i>F</i> ; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i> ; flagellar genes	102*, 360
<i>flbF</i>	142	Part of the <i>che-fla</i> operon; three loci <i>A</i> , <i>B</i> , <i>F</i> ; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i> ; flagellar genes	101*
<i>fliD</i>	305	Flagellar protein; homologous to <i>fliD</i> of <i>E. coli</i>	109*
<i>fliE</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	876*
<i>fliF</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	360, 876*
<i>fliG</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	14*, 876
<i>fliH</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	14*, 876
<i>fliI</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	14*, 876
<i>fliJ</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i> ; <i>cheF</i>	14*, 851, 876
<i>fliK</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	14*, 876
<i>fliL</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	14*, 876
<i>fliM</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	14*, 876, 877*
<i>fliP</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i> ; <i>cheC</i>	52*, 102, 876
<i>fliQ</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	52*, 102, 876
<i>fliR</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i>	52*, 102, 360, 876
<i>fliS</i>	305	Flagellar protein; homologous to <i>fliS</i> of <i>E. coli</i>	109*
<i>fliT</i>	305	Flagellar protein; homologous to <i>fliT</i> of <i>E. coli</i>	109*
<i>fliY</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i> ; <i>cheD</i>	55*, 876, 877*
<i>fliZ</i>	142	Part of <i>che-fla</i> operon; 13 loci <i>E-K</i> , <i>P-R</i> and <i>Z</i> ; flagellar genes; homologous to the corresponding genes of <i>E. coli</i> and <i>S. typhimurium</i> ; formerly <i>cheA</i>	52*, 876
<i>fnr</i>	324	Anaerobic regulatory protein	609*
<i>folC</i>	242	Folypolyglutamate synthetase	434*
<i>folK</i>	9	Dihydropteridine pyrophosphokinase	539*
<i>fruA</i>	123	Fructose transport	217
<i>fruB</i>	123	Fructose-1-phosphate kinase	217
<i>fruC</i>	51	Fructokinase	219
<i>ftr</i>	uc	Fluorotryptophan resistance; maps near <i>aroC</i>	43
<i>ftsA</i>	134	Homologous to <i>E. coli</i> cell division gene <i>ftsA</i> ; location of <i>spoIIN279</i>	44*, 168, 220, 235
<i>ftsH</i>	8	Cell division protein	139, 539*
<i>ftsL</i>	133	Cell division gene homologous to <i>E. coli</i>	134*, 844
<i>ftsZ</i>	134	Homologous to <i>E. coli</i> cell division gene <i>ftsZ</i> ; <i>ts-1</i>	44*, 168, 235, 269*
<i>fumR</i>	288	Regulation of fumarate hydratase	305
<i>fun</i>		See <i>rpsL</i>	
<i>furA</i>		See <i>pyrAA</i>	
<i>furB</i>	41	Fluorouracil resistance	868
<i>furC</i>	326	Resistance to 5-fluorouracil in the presence of uracil	870
<i>furE</i>	326	Resistance to 5-fluorouracil in the presence of uracil	870
<i>furF</i>	170	Resistance to 5-fluorouracil in the presence of uracil	138

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>fus</i>	11	Elongation factor G	846
<i>gabP</i>	52	γ -Aminobutyrate permease	65, 831*
<i>galK</i>	331	Galactokinase	225*
<i>galT</i>	331	Galactose-1-phosphate-uridylyltransferase	225*
<i>gap</i>		See <i>gapB</i>	
<i>gapB</i>	256	Glyceraldehyde-3-phosphate dehydrogenase; <i>gap</i>	393*, 790*
<i>gcaA</i>		See <i>glmS</i>	
<i>gcaD</i>	7	N-Acetylglucosamine-1-phosphate uridylyltransferase; <i>tms</i>	254#, 298*, 523*
<i>gdh</i>	34	Structural gene for glucose dehydrogenase	392*
<i>gerA1</i>		See <i>gerAA</i>	
<i>gerA2</i>		See <i>gerAB</i>	
<i>gerA3</i>		See <i>gerAC</i>	
<i>gerAA</i>	289	Germination defective; defective in germination response to alanine and related amino acids; <i>gerA1</i>	175*
<i>gerAB</i>	289	Germination defective; defective in germination response to alanine and related amino acids; <i>gerA2</i>	175*
<i>gerAC</i>	289	Germination defective; defective in germination response to alanine and related amino acids; <i>gerA3</i>	175*
<i>gerBA</i>	311	Germination defective; defective in germination response to the combinations of glucose, fructose, asparagine and KCl; comprises three genes	120, 121*, 478
<i>gerBB</i>	311	Germination defective; defective in germination response to the combinations of glucose, fructose, asparagine and KCl; comprises three genes	120, 121*, 478
<i>gerBC</i>	311	Germination defective; defective in germination response to the combinations of glucose, fructose, asparagine and KCl; comprises three genes	120, 121*, 478
<i>gerC1</i>		See <i>gerCA</i>	
<i>gerC2</i>		See <i>gerCB</i>	
<i>gerC3</i>		See <i>gerCC</i>	
<i>gerCA</i>	204	Germination defective; temperature-sensitive germination in alanine; comprises three genes; <i>gerCB</i> product containing S-adenosylmethionine-binding site; <i>gerCC</i> is homologue to <i>cotE</i> ; <i>gerC58</i> mutation is in <i>gerCC</i> ; <i>gerC1</i>	478, 847*
<i>gerCB</i>	204	Germination defective; temperature-sensitive germination in alanine; comprises three genes; <i>gerCB</i> product containing S-adenosylmethionine-binding site; <i>gerCC</i> is homologue to <i>cotE</i> ; <i>gerC58</i> mutation is in <i>gerCC</i> ; <i>gerC2</i>	478, 847*
<i>gerCC</i>	204	Germination defective; temperature-sensitive germination in alanine; comprises three genes; <i>gerCB</i> product containing S-adenosylmethionine-binding site; <i>gerCC</i> is homologue to <i>cotE</i> ; <i>gerC58</i> mutation is in <i>gerCC</i> ; <i>gerC3</i>	478, 847*
<i>gerD</i>	13	Defective germination in a range of germinants	478, 846, 852*
<i>gerE</i>	252	Germination defective; defective germination in a range of germinants; transcriptional regulator of spore-coat genes	124*
<i>gerF</i>	301	Germination defective; defective germination in a range of germinants	478, 711*
<i>gerG</i>	294	Germination defective; a mutant lacks phosphoglycerate kinase (<i>pgk</i> activity); germinates poorly in alanine; sporulates poorly	478
<i>gerH</i>	248	Defective germination in a range of germinants	578
<i>gerI</i>	296	Defective germination in a range of germinants	578
<i>gerJ</i>	206	Defective germination in a range of germinants; allele <i>gerJ51</i> is in many laboratory strains; <i>tzm</i>	429#, 804
<i>gerKA</i>	32	Defective germination response to glucose	328, 329*
<i>gerKB</i>	32	Defective germination response to glucose	328, 329*
<i>gerKC</i>	32	Defective germination response to glucose	328, 329*
<i>gerM</i>	251	Defective germination and sporulation	648#, 699*
<i>gga</i>		See <i>ggaA</i> and <i>ggaB</i>	
<i>ggaA</i>	309	Membrane-bound enzyme involved in the biosynthesis of galactosamine-containing minor teichoic acids; <i>gga</i> , <i>pha-3</i>	169, 170, 396*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>ggaB</i>	309	Membrane-bound enzyme involved in the biosynthesis of galactosamine-containing minor teichoic acids; <i>gga</i> , <i>pha-3</i>	169, 170, 396*
<i>gidA</i>	360	Two genes homologous to <i>gidA</i> and <i>B</i> of <i>E. coli</i>	538*
<i>gidB</i>	360	Two genes homologous to <i>gidA</i> and <i>B</i> of <i>E. coli</i>	538*
<i>gld</i>		See <i>eglS</i>	
<i>glgA</i>	275	Fourth gene in glycogen operon; synthesizes 1,4- α -glucan chains using ADP glucose; starch (bacterial glycogen synthase)	357*
<i>glgB</i>	275	First gene of glycogen operon; introduces 1,6- α -linkages in starch and glycogen; 1,4- α -glucan-branching enzyme	357*
<i>glgC</i>	275	Second gene in glycogen operon; activates glucose-1-phosphate using ATP; ADPglucose pyrophosphorylase	357*
<i>glgD</i>	275	Third gene in glycogen operon; protein with similarity to ADPglucose pyrophosphorylase	357*
<i>glgP</i>	275	Fifth and last gene of glycogen operon; degrades starch and glycogen by phosphorylation; glycogen phosphorylase	357*
<i>glmS</i>	23	L-Glutamine-D-fructose-6-phosphate aminotransferase; <i>gcaA</i>	196
<i>glnA</i>	167	Glutamine synthetase structural gene	512*, 734*
<i>glnR</i>	167	Negative regulator of glutamine synthetase	184#, 734*
<i>glnX</i>	178	Glutamine biosynthesis	7*
<i>glpD</i>	70	Glycerol-3-phosphate dehydrogenase	309*, 525
<i>glpF</i>	70	Shows identity to <i>E. coli</i> gene <i>glpF</i> which is a glycerol facilitator	48*, 525
<i>glpK</i>	70	Glycerol kinase	48*, 309*, 525
<i>glpP</i>	70	Pleiotropic glycerol mutant; positively acting regulator protein	48*, 413, 525
<i>glpQ</i>	18	Hydrolysis of deacylated phospholipids; glycerophosphoryl diester phosphodiesterase	524*
<i>glpT</i>	18	Fosfomycin resistance, glycerol phosphate transport defect	354
<i>glrS</i>	232	Glutamate racemase	62*
<i>gltA</i>		See <i>gltB</i>	
<i>gltB</i>	177	Glutamate synthase; <i>gltA</i>	57#, 58*
<i>gltC</i>	177	Positive regulator of <i>gltAB</i>	58*
<i>gltP</i>	NM	Proton/glutamate symport protein	757*
<i>gltX</i>	10	Glutamyl-tRNA synthetase	77*, 205*
<i>glyA</i>	321	Glycine requirement; <i>glyC</i>	95, 444*
<i>glyB</i>	76	Glycine requirement	268, 525
<i>glyC</i>		See <i>glyA</i>	
<i>gnaB</i>		See <i>guaB</i>	
<i>gneA</i>	332	UDP-N-acetylglucosamine 4-epimerase	170
<i>gntK</i>	344	Gluconate utilization; gluconate kinase	201*, 856*
<i>gntP</i>	344	Gluconate utilization; gluconate permease	201*, 856*
<i>gntR</i>	344	Gluconate utilization; repressor	202*, 856*
<i>gntZ</i>	344	Gluconate utilization; 6-phosphogluconate dehydrogenase	201*, 615, 856*
<i>gpr</i>	226	Spore protein; germination protease for small acid-soluble spore proteins	749*
<i>gpsA</i>	205	NADH-dependent glycerol-3-phosphate dehydrogenase	481, 717*
<i>gra</i>		See <i>amyR</i>	
<i>graR</i>		See <i>ccpA</i>	
<i>grlA</i>	171	Gyrase-like protein B	630*
<i>grlB</i>	171	Gyrase-like protein A	630*
<i>groEL</i>	45	Phage growth; heat-shock protein chaperonin	104, 412*, 541, 666*
<i>groES</i>	45	Phage growth; heat-shock protein chaperonin	104, 412*, 541, 666*
<i>grpE</i>	225	Homologous to <i>grpE</i> of <i>E. coli</i>	814*
<i>gsiAA</i>	115	Glucose-starvation-inducible genes; two cistrons	496*, 497*, 566

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>gsiAB</i>	115	Glucose-starvation-inducible genes; two cistrons	496*, 497*, 566
<i>gsiB</i>	36	Glucose-starvation-inducible protein B	497*
<i>gsiC</i>		See <i>kinA</i>	
<i>gsp10</i>	uc	Spore outgrowth; maps near the <i>che</i> cluster	208*
<i>gspA</i>	333	σ^B -dependent general stress protein	27*
<i>gtaA</i>		See <i>tagE</i>	
<i>gtaB</i>	308	Glucosylation of teichoic acid; UDPglucose pyrophosphorylase	78#, 587, 710*, 788
<i>gtaC</i>	71	Glucosylation of teichoic acid; lacks phosphoglucomutase	587
<i>gtaD</i>		See <i>tagE</i>	
<i>gtaE</i>	71	Glucosylation of teichoic acid	587
<i>guaA</i>	54	GMP synthetase; previous <i>guaA</i> is now <i>guaB</i>	65, 432*, 660
<i>guaB</i>	0	Inosine monophosphate dehydrogenase; previous <i>guaB</i> is now <i>guaA</i> ; <i>gnaB</i>	348*, 660
<i>guaC</i>	NM	Guanosine monophosphate reductase	160
<i>guaF</i>	NM	Hypoxanthine-guanine phosphoribosyltransferase	160
<i>guaP</i>	NM	Inosine-guanosine phosphorylase	160
<i>gutA</i>	50	D-Glucitol permease	219#
<i>gutB</i>	50	D-Glucitol hydrogenase	219#, 520*
<i>gutR</i>	50	Constitutive synthesis of D-glucitol permease and D-glucitol dehydrogenase; regulatory for glucitol catabolism; transcriptional regulation	219#, 848*
<i>gyrA</i>	0	DNA gyrase; <i>nalA</i> , <i>cafB</i>	96, 482*
<i>gyrB</i>	0	DNA gyrase; <i>novA</i>	267, 482*
<i>bag</i>	306	Flagellin	388*, 466
<i>bbs</i>	204	DNA-binding protein HBsu; immediately upstream of <i>mtrA</i> ; <i>bbsU</i> , <i>dbpA</i>	292*, 461*
<i>bbsU</i>		See <i>bbs</i>	
<i>bds</i>	5	Pleiotropic extragenic suppressors of mutations	689
<i>hemA</i>	244	Glutamyl-tRNA reductase of the C-5 pathway for δ -aminolevulinate synthetase	263*, 362, 572*, 668, 669
<i>hemB</i>	244	Porphobilinogen synthase	49, 263*, 722
<i>hemC</i>	244	Hydroxymethylbilane synthase	49, 263*, 572*, 722
<i>hemD</i>	244	Uroporphyrinogen III synthase	263*, 463, 722
<i>hemE</i>	77	Uroporphyrinogen decarboxylase	264*, 462
<i>hemF</i>		See <i>hemH</i>	
<i>hemG</i>		See <i>hemY</i>	
<i>hemH</i>	77	Ferrochelatase; <i>hemF</i>	264*, 462
<i>hemK</i>		See <i>hemL</i>	
<i>hemL</i>	244	Glutamate-1-semialdehyde 2,1-aminotransferase; <i>hemK</i>	263*
<i>hemX</i>	244	Membrane protein of unknown function required for <i>hemL</i> synthesis	263*, 669
<i>hemY</i>	77	Coproporphyrinogen III oxidase and protoporphyrinogen IX oxidase; <i>hemG</i>	264*
<i>hisA</i>	300	Histidine requirement; probable location of all histidine enzymes except <i>hisH</i>	711*, 799#
<i>hisH</i>	202	Histidinol-phosphate aminotransferase, tyrosine and phenylalanine aminotransferase; <i>aroJ</i>	290*, 516
<i>holB</i>	2	Probable DNA polymerase III, δ subunit	541
<i>hom</i>	284	Threonine and methionine requirement; homoserine dehydrogenase; a deletion in this area over this gene, the gene for homoserine dehydratase and <i>thrB</i> ; <i>tdm</i>	24, 557*, 785, 786
<i>hos</i>	14	Suppresses the temperature-sensitive phenotype of elongation factor G mutants	451
<i>hpr</i>	76	Overproduction of proteases; <i>catA</i> , <i>scoC</i>	525, 562*
<i>hprT</i>	8	Hypoxanthine-guanine phosphoribosyltransferase; <i>hpt</i>	539*
<i>hpt</i>		See <i>hprT</i>	
<i>hrcA</i>	225	Encodes a negative regulator of class I heat-shock genes	672*
<i>hsdBM</i>	344	DNA-methyltransferase <i>BsuB</i> ; modification methylase <i>BsuBI</i>	321, 767, 836*
<i>hsdBR</i>	344	Host-specificity-determinant B of <i>B. subtilis</i> IAM 1247; restriction endonuclease <i>BsuB</i> ; previously <i>hsrB</i> ; type II restriction enzyme <i>BsuBI</i>	321, 767, 836*
<i>hsdCM</i>	59	DNA-methyltransferase <i>BsuC</i>	321, 767

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>hsdCR</i>	59	Host-specificity-determinant C of <i>B. subtilis</i> IAM 1247; restriction endonuclease <i>BsuC</i> ; previously <i>hsrC</i>	321, 767
<i>hsdEM</i>	338	DNA-methyltransferase <i>BsuE</i>	206, 321, 767
<i>hsdER</i>	338	Host-specificity-determinant E of <i>B. subtilis</i> IAM 1231; restriction endonuclease <i>BsuE</i> ; previously <i>hsdE</i>	321, 767
<i>hsdFM</i>	59	DNA-methyltransferase <i>BsuF</i>	321, 767, 798*
<i>hsdFR</i>	59	Host-specificity-determinant F of <i>B. subtilis</i> IAM 1231; restriction endonuclease <i>BsuF</i> ; isoschizomer of <i>HpaII</i> ; previously <i>hsrF</i>	321, 349*, 767
<i>hsdMM</i>	47	DNA-methyltransferase <i>BsuM</i>	321, 645, 767
<i>hsdMR</i>	47	Host-specificity-determinant M of <i>B. subtilis</i> Marburg identical to <i>nonB</i> ; restriction endonuclease <i>BsuM</i> ; isoschizomer of <i>XhoI</i> ; previously <i>hsrM</i>	321, 645, 767
<i>hsdRM</i>	59	DNA-methyltransferase <i>BsuR</i>	321, 361*, 766, 767
<i>hsdRR</i>	59	Host-specificity-determinant R of <i>B. subtilis</i> ; restriction endonuclease <i>BsuR</i> ; isoschizomer of <i>HaeIII</i> ; previously <i>hsrR</i>	321, 361*, 766, 767
<i>hsIU</i>		See <i>codX</i>	
<i>hsIV</i>		See <i>codW</i>	
<i>hutG</i>	337	Histidine utilization; formiminoglutamate hydrolase	345, 829, 854*
<i>hutH</i>	337	Histidine utilization; histidase	532*, 829, 854*
<i>hutI</i>	337	Histidine utilization; imidazolone hydrolase	345, 829, 854*
<i>hutM</i>	337	Putative histidine permease	532*, 829, 854*
<i>hutP</i>	337	Histidine utilization; positive regulator of the <i>hut</i> operon	532*, 829, 854*
<i>hutU</i>	337	Histidine utilization; urocanase	532*, 829, 854*
<i>idb</i>		See <i>iolG</i>	
<i>iep</i>		See <i>degU</i>	
<i>ifm</i>	304	Hypermotility; suppresses <i>flaA</i> and <i>flaD</i> mutations	586
<i>ileS</i>	135	Isoleucine tRNA synthetase	193
<i>ilvA</i>	195	Threonine dehydratase	22, 29*, 39
<i>ilvB</i>	247	Condensing enzyme	237*, 427#
<i>ilvC</i>	247	α -Hydroxy- β -ketoacid reductoisomerase	237*, 427#
<i>ilvD</i>	196	Dihydroxyacid dehydratase	22, 39
<i>ilvN</i>	247	Subunit of the AhaS enzyme (<i>ilvB</i>)	237*, 427#
<i>infA</i>	12	Initiation factor I	69*
<i>infB</i>	147	Initiation factor II	685*
<i>infC</i>	256	<i>Bacillus stearothermophilus infC</i> homologue; initiation factor IF3	825*
<i>iol</i>		See <i>iolG</i>	
<i>iolA</i>	341	Probable methylmalonate-semialdehyde dehydrogenase; <i>mmsA</i>	853*
<i>iolB</i>	341	Involved in <i>iol</i> operon	853*
<i>iolC</i>	341	Involved in <i>iol</i> operon; probable kinase	853*
<i>iolD</i>	341	Involved in <i>iol</i> operon	853*
<i>iolE</i>	341	Involved in <i>iol</i> operon	853*
<i>iolF</i>	341	Probable inositol transport	853*
<i>iolG</i>	341	Inositol dehydrogenase; <i>idb</i> , <i>iol</i>	200, 203*, 853*
<i>iolH</i>	341	Involved in <i>iol</i> operon	853*
<i>iolI</i>	341	Involved in <i>iol</i> operon	853*
<i>iolJ</i>	341	Probable fructose-bisphosphate aldolase; <i>fbaB</i>	853*
<i>iolR</i>	341	Regulation of the <i>iol</i> operon	853*
<i>iolS</i>	341	Involved in <i>iol</i> operon	853*
<i>ipi</i>	101	Intracellular proteinase inhibitor <i>BsuPI</i>	681*, 686*
<i>ispA</i>	117	Intracellular serine protease	369*
<i>jag</i>	360	Jag <i>spoIIIJ</i> -associated gene	167*, 538*
<i>kan</i>	10	Kanamycin resistance; maps in the ribosomal protein cluster	231
<i>kapB</i>	280	Kinase-B-associated protein	764*
<i>kat</i>		See <i>katA</i>	

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>kat-19</i>	NM	Catalase; distinct from <i>katA</i>	60*
<i>katA</i>	69	Catalase; <i>kat</i>	60*, 416
<i>katB</i>		See <i>katE</i>	
<i>katE</i>	335	Catalase; σ^B -dependent; <i>katB</i>	162*
<i>kauA</i>	182	Branched-chain α -keto transport	229
<i>kdgA</i>	198	Genes involved in pectin catabolism, deoxyphosphogluconate aldolase	719*
<i>kdgK</i>	198	Genes involved in pectin catabolism, deoxygluconate kinase	719*
<i>kdgR</i>	198	Genes involved in pectin catabolism, regulation of transcription of <i>kdg</i> operon	719*
<i>kdgT</i>	198	Genes involved in pectin catabolism, deoxygluconate permease	719*
<i>kduD</i>	198	Genes involved in pectin catabolism, deoxygluconate oxidoreductase	719*
<i>kduI</i>	198	Genes involved in pectin catabolism, deoxyuronate isomerase	719*
<i>kinA</i>	118	Sporulation-specific protein kinase; <i>spoIIJ</i> , <i>spoIIF</i> , <i>scoD</i> , <i>gsiC</i>	28*, 564*
<i>kinB</i>	280	Sporulation-specific protein kinase	764*
<i>kinC</i>	124	Histidine protein kinase; phosphorylation of Spo0A	367, 399*, 824
<i>ksgA</i>	4	High-level kasugamycin resistance	759
<i>ksgB</i>	277	Low-level kasugamycin resistance	759
<i>ksgC</i>	287	Fumarate hydratase defective; kasugamycin resistance	305
<i>lacA</i>	290	Structural gene for β -galactosidase	166
<i>lacR</i>	290	Regulatory gene for β -galactosidase	166
<i>lcfA</i>	253	Homology with a coenzyme synthetase from <i>E. coli</i>	825*
<i>lctE</i>	26	L-Lactate dehydrogenase	274*, 839*
<i>leuA</i>	247	α -Isopropylmalate synthase	503#, 825*
<i>leuB</i>	247	β -Isopropylmalate dehydrogenase; previous name <i>leuC</i>	325*, 825*
<i>leuC</i>	247	Isopropylmalate isomerase; previous name <i>leuB</i>	503#, 825*
<i>leuD</i>	247	Subunit of isopropylmalate isomerase	427#, 825*
<i>leuS</i>	269	Leucyl-tRNA synthetase	783*
<i>levD</i>	233	Enzyme III for fructose (phosphotransferase-system transport system); <i>sacL</i>	443*
<i>levE</i>	233	Enzyme III for fructose (phosphotransferase-system transport system); <i>sacL</i>	443*
<i>levF</i>	233	Enzyme II for fructose (phosphotransferase-system transport system)	443*
<i>levG</i>	233	Enzyme II for fructose (phosphotransferase-system transport system)	443*
<i>levR</i>	233	Regulator of levanase	158*
<i>lexA</i>	170	SOS regulatory protein; <i>dinR</i>	612*, 630*
<i>licT</i>	335	Transcription antiterminator; positive regulation of utilization of β -glucans	398, 855*
<i>lin</i>	24	Lincomycin resistance	230
<i>lip</i>		See <i>lipA</i>	
<i>lipA</i>	22	Lipase; <i>lip</i>	135
<i>lon</i>		See <i>lonA</i>	
<i>lonA</i>	244	ATP-dependent protease; induced by various stresses including heat shock; homologous to <i>lon</i> of <i>E. coli</i> ; <i>lon</i>	620*, 849
<i>lonB</i>	244	Lon-like protein	620*, 849*
<i>lpm</i>		See <i>rpoC</i>	
<i>lpmB</i>	286	Lipiamycin resistance	713
<i>lppX</i>		See <i>lytA</i>	
<i>lssA</i>	35	Thermosensitive lysis; linked to <i>ddl</i> by transformation	76
<i>lssB</i>		See <i>dapE</i>	
<i>lssD</i>		See <i>dapG</i>	
<i>lssE</i>	353	Thermosensitive lysis	76
<i>lssF</i>		See <i>murA</i>	
<i>lssG</i>		See <i>secA</i>	
<i>lssH</i>	293	Thermosensitive lysis	76
<i>lysA</i>	210	Lysine requirement, diaminopimelate decarboxylase	39, 338#, 717*, 838*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>lysC</i>	252	Aspartokinase II; <i>aecA</i>	110*, 111, 423, 571, 825*
<i>lysS</i>	10	Lysyl-tRNA synthetase	608
<i>lytA</i>	308	Involved in the secretion of LytC (amidase); <i>lppX</i>	394*
<i>lytB</i>	308	Modifier of LytC (amidase); <i>cwbA</i>	394*
<i>lytC</i>	308	N-Acetylmuramoyl-L-alanine amidase in vegetative growth; major autolysin; <i>cwlB</i>	384*, 385*, 394, 435, 711*
<i>lytD</i>	310	N-Acetylglucosaminidase	436*, 610#
<i>lytR</i>	308	Regulator of LytC (amidase)	394*
<i>lytS</i>	256	<i>Staphylococcus aureus</i> <i>lytS</i> homologue; sensor-kinase involved in controlling the rate of autolysis	825*
<i>lytT</i>	256	<i>Staph. aureus</i> <i>lytR</i> homologue; response-regulator involved in controlling the rate of autolysis	825*
<i>maf</i>	242	Possible septation function	88*
<i>mal</i>	264	Malate dehydrogenase, decarboxylating	393*
<i>map</i>	12	Methionine amino peptidase	505*
<i>mbi</i>	317	MBL protein, homologous to <i>E. coli</i> <i>mreB</i> morphogene	1*
<i>mcpA</i>	281	Methyl-accepting chemotaxis protein; transmembrane receptor	261*
<i>mcpB</i>	281	Methyl-accepting chemotaxis protein; transmembrane receptor	261*
<i>mdh</i>		See <i>citH</i>	
<i>mecA</i>	103	Medium-independent expression of competence	151, 370*
<i>mecB</i>	10	Medium-independent expression of competence; <i>clpC</i>	151, 493*
<i>menB</i>	273	Menaquinone deficient; multiple aminoglycoside resistance; dihydroxynaphthoate synthase	148*, 633*
<i>menD</i>	273	Menaquinone deficient; multiple aminoglycoside resistance; blocked in formation of <i>o</i> -succinylbenzoic from chorismic acid	633*
<i>menE</i>	273	Menaquinone deficient; multiple aminoglycoside resistance; <i>o</i> -succinylbenzoyl coenzyme A synthetase	148*, 633*
<i>menF</i>	273	Menaquinone deficient; multiple aminoglycoside resistance; blocked in formation of <i>o</i> -succinylbenzoic from chorismic acid	633*, 634
<i>metA</i>	110	Responds to methionine, cystathionine or homocysteine	723
<i>metB</i>	197	Responds to methionine or homocysteine; homoserine succinyl transferase	22, 39
<i>metC</i>	115	Responds to methionine	149
<i>metD</i>	100	Responds to methionine	860
<i>metE</i>	272	S-Adenosylmethionine synthetase	393*, 795#
<i>metS</i>	4	Methionyl-tRNA synthetase	539*
<i>mfd</i>	7	Transcription-repair coupling factor	539*
<i>minC</i>	242	Cell division inhibitor; Minicell production	401*, 408*, 787*
<i>minD</i>	242	ATPase-activator of MinC; Minicell production; <i>divIVB</i>	401*, 408*, 613, 787*
<i>mmgA</i>	216	Similar to <i>Alcaligenes eutrophus</i> acetyl-CoA C-acetyltransferase	81*
<i>mmgB</i>	216	Similar to <i>Clostridium acetobutylicum</i> NAD-dependent β -hydroxybutyryl-CoA dehydrogenase	81*
<i>mmgC</i>	216	Similar to product encoded by <i>B. subtilis</i> short-chain acyl-CoA dehydrogenase gene	81*
<i>mmgD</i>	216	Citrate synthase III	81*
<i>mmgE</i>	216	Involved in <i>mmg</i> operon	81*
<i>mmr</i>	325	Methylenomycin-A-resistance protein	602*
<i>mmsA</i>		See <i>iolA</i>	
<i>motA</i>	118	Paralysed flagella; motility protein	467, 875
<i>motB</i>	118	Paralysed flagella; motility protein	467, 875
<i>mpo</i>	218	Membrane protein overproduction, temperature-sensitive sporulation	450
<i>mpr</i>	21	Metalloprotease, extracellular	695*
<i>mraY</i>	133	Cell wall synthesis; homologous to <i>mraY</i> of <i>E. coli</i>	168*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>mreB</i>	242	Cell shape determination	408*, 787*
<i>mreBH</i>	124	MreBH protein	824*
<i>mreC</i>	242	Cell shape determination	408*, 787*
<i>mreD</i>	242	Cell shape determination; <i>rodB</i>	351, 408*, 787*
<i>mrgA</i>	294	Metalloregulation	108*
<i>mrgC</i>	198	Metalloregulation	108*
<i>mtlA</i>	34	Lacks mannitol transport	8*, 365
<i>mtlB</i>		See <i>mtlD</i>	
<i>mtlD</i>	34	Mannitol-1-phosphate dehydrogenase; <i>mtlB</i>	8*, 107#
<i>mtrA</i>	204	Resistance to 5-methyl-tryptophan; GTP cyclohydrolase I, involved in folic acid biosynthesis	33, 232*
<i>mtrB</i>	204	Resistance to 5-methyl-tryptophan; RNA-binding transcription regulator	33, 232*
<i>murA</i>	316	Thermosensitive lysis; phosphoenolpyruvate; uridine- <i>N</i> -acetylglucosamine enolpyruvyltransferase; <i>lssF</i>	76, 632
<i>murB</i>	134	Cell division gene region with significant similarity to <i>murB</i> of <i>E. coli</i>	636*
<i>murD</i>	133	Cell wall synthesis; homologous to <i>murD</i> of <i>E. coli</i>	168*, 293*
<i>murE</i>	133	Cell wall synthesis; homologous to <i>murE</i> of <i>E. coli</i>	168*, 293*
<i>murG</i>	134	Cell wall synthesis; homologous to <i>murG</i> of <i>E. coli</i>	168*, 293*, 323*
<i>murZ</i>	323	UDP- <i>N</i> -acetylglucosamine 1-carboxyvinyltransferase	762*
<i>mut-1</i>		See <i>polC</i>	
<i>mutL</i>	150	Mismatch-repair recognition	223*
<i>mutS</i>	150	Mismatch-repair recognition	223*
<i>nadB</i>	240	Required for NAD biosynthesis; L-aspartate oxidase	746*
<i>nadC</i>	240	Required for NAD biosynthesis; probable nicotinate-nucleotide pyrophosphorylase	746*
<i>nadE</i>	27	A sporulation protein; <i>outB</i>	13*, 98, 515
<i>nalA</i>		See <i>gyrA</i>	
<i>nap</i>	42	Carboxylesterase	603*
<i>narA</i>	320	Inability to use nitrate as a nitrogen source; <i>narAB</i>	226*, 405
<i>narAA</i>		See <i>narQ</i>	
<i>narAB</i>		See <i>narA</i>	
<i>narB</i>		See <i>nasBB</i>	
<i>narG</i>	324	Nitrate reductase subunit α	308*, 609*
<i>narH</i>	324	Nitrate reductase subunit β	308*, 609*
<i>narI</i>	324	Nitrate reductase subunit γ	308*, 609*
<i>narJ</i>	324	Nitrate reductase subunit δ	308*, 609*
<i>narK</i>	324	Nitrite-extrusion protein	609*
<i>narQ</i>	320	Inability to use nitrate as a nitrogen source; <i>narAA</i>	226*, 405
<i>nasA</i>	28	Nitrate transporter	511, 540*, 543
<i>nasBA</i>	28	Nitrate reductase; electron-transfer subunit	511, 540*, 543
<i>nasBB</i>	28	Catalytic subunit of nitrate reductase; <i>nasC</i> , <i>narB</i>	540*, 543, 866
<i>nasBC</i>	28	Nitrate reductase; <i>nasD</i> , <i>nirB</i>	540*, 543
<i>nasBD</i>	28	Assimilatory nitrate reductase; <i>nasE</i> , <i>nirD</i>	540*, 543
<i>nasBE</i>	28	Uroporphyrinogen III; methyltransferase; <i>nasF</i>	540*, 543
<i>nasC</i>		See <i>nasBB</i>	
<i>nasD</i>		See <i>nasBC</i>	
<i>nasE</i>		See <i>nasBD</i>	
<i>nasF</i>		See <i>nasBE</i>	
<i>ndb</i>		See <i>ahpC</i>	
<i>ndbF</i>	23	NADH dehydrogenase subunit 5	487
<i>ndk</i>	204	Nucleotide diphosphate kinase	292*
<i>nea</i>	UC	Neamine resistance; see ribosomal protein cluster	230
<i>neo</i>	UC	Neomycin resistance; see ribosomal protein cluster	267
<i>nic</i>	240	Nicotinic acid requirement	180#

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>nidS</i>	232	2-Nitropropane dioxygenase	62*
<i>nifS</i>	240	Required for NAD biosynthesis; homologous to the <i>nifS</i> gene products of other bacteria	746*
<i>nin</i>		See <i>comJ</i>	
<i>nirB</i>		See <i>nasBC</i>	
<i>nirD</i>		See <i>nasBD</i>	
<i>nonA</i>	uc	Permissive for bacteriophage SP10 and ϕ NR2; closely linked to <i>rfm</i>	645
<i>novA</i>		See <i>gyrB</i>	
<i>nprB</i>	101	Neutral protease	681*, 765*
<i>nprE</i>	126	Neutral metalloprotease	824, 841*
<i>nprR</i>	126	Regulatory gene for neutral protease	758*
<i>nrdA</i>		See <i>nrdE</i>	
<i>nrdE</i>	153	Ribonucleoside-diphosphate reductase; major subunit; <i>nrdA</i>	561#, 674*
<i>nrdF</i>	153	Ribonucleoside-diphosphate reductase; minor subunit	674*
<i>nrgA</i>	318	Nitrogen-regulated membrane-associated protein	830*
<i>nrgB</i>	318	Nitrogen-regulated PII-like protein	830*
<i>ntb</i>	200	Probable endonuclease III	80*
<i>nucA</i>	31	Plays a role in the competence signal; DNase subunit; <i>comI</i>	199*, 780*, 794*
<i>nucB</i>	226	Extracellular DNase produced during sporulation	9, 777, 780
<i>nupC</i>	338	Pyrimidine nucleoside transport protein	663*
<i>nusA</i>	147	Transcription termination	685*
<i>nusG</i>	11	Transcription antitermination factor NusG	339*
<i>obg</i>	240	Essential GTP-binding protein of unknown function	763*
<i>odhA</i>	181	2-Oxoglutarate dehydrogenase, E1 subenzyme of the 2-oxoglutarate dehydrogenase complex; <i>citK</i>	99#, 100*, 617
<i>odhB</i>	181	Dihydrolipoamide transsuccinylase, E2 subenzyme of the 2-oxoglutarate dehydrogenase complex; <i>citM</i>	99#, 100*, 617
<i>ole</i>	uc	Oleandomycin resistance; see ribosomal protein cluster	230
<i>oppA</i>	104	Oligopeptide permease; comprises five genes also called <i>spo0K</i> ; <i>spo0KA</i>	565*, 576, 637*
<i>oppB</i>	104	Oligopeptide permease; comprises five genes also called <i>spo0K</i> ; <i>spo0KB</i>	565*, 576, 637*
<i>oppC</i>	104	Oligopeptide permease; comprises five genes also called <i>spo0K</i> ; <i>spo0KC</i>	565*, 576, 637*
<i>oppD</i>	104	Oligopeptide permease; comprises five genes also called <i>spo0K</i> ; <i>spo0KD</i>	565*, 576, 637*
<i>oppF</i>	104	Oligopeptide permease; comprises five genes also called <i>spo0K</i> ; <i>spo0KE</i>	565*, 576, 637*
<i>opuAA</i>	26	Glycine betaine transport; ATPase; osmotically regulated binding-protein-dependent transport system	356*
<i>opuAB</i>	26	Glycine betaine transport; transmembrane protein	356*
<i>opuAC</i>	26	Glycine betaine transport; glycine-betaine-binding protein	356*
<i>ordA</i>	NM	Ornithine:2-oxo-acid aminotransferase	817
<i>outA</i>	20	Blocked in outgrowth after RNA-, protein- and DNA syntheses have started; formerly <i>gspIV</i>	11
<i>outB</i>		See <i>nadE</i>	
<i>outC</i>	28	Blocked in outgrowth after RNA- and protein syntheses have started, but before DNA synthesis; formerly <i>gsp-25</i>	11
<i>outD</i>	158	Blocked in outgrowth; protein- and DNA syntheses reduced; formerly <i>gsp-1</i>	207
<i>outE</i>	300	Blocked in outgrowth; RNA synthesis normal; protein synthesis reduced; DNA synthesis prevented; formerly <i>gsp-42</i>	11
<i>outF</i>	316	Blocked in outgrowth; RNA- and protein syntheses reduced; DNA synthesis prevented; formerly <i>gsp-4</i>	11, 12
<i>outG</i>		See <i>pksL</i>	
<i>outH</i>		See <i>pksL</i>	
<i>oxr</i>	19	Oxolinic acid resistance	789

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>pab</i>	9	<i>p</i> -Aminobenzoic acid requirement; subunit A of <i>p</i> -aminobenzoate synthase; <i>pabB</i>	347, 693*
<i>pabA</i>		See <i>trpG</i>	
<i>pabB</i>		See <i>pab</i>	
<i>pabC</i>	9	Enzyme required for <i>p</i> -aminobenzoate synthesis	693*
<i>pac</i>	5	Resistance to pactamycin	771
<i>paiA</i>	283	Regulation of sporulation and degradative enzyme production	313*
<i>paiB</i>	283	Regulation of sporulation and degradative enzyme production	313*
<i>pal</i>		See <i>slp</i>	
<i>panB</i>	57	Ketopantoate hydroxymethyltransferase	34
<i>panE</i>	57	Ketopantoic acid reductase	34
<i>papQ</i>	72	Phosphatase-associated protein; muralytic when cloned in <i>E. coli</i> ; Iap60 homologue; inactivation leads to alkaline phosphatase over-expression	816*
<i>patA</i>	118	Putative aminotransferase; <i>nat</i>	28*, 564*, 764
<i>patB</i>	280	Putative aminotransferase	764*
<i>pbp</i>	175	Penicillin-binding protein; mutations affecting PBPs 2a, 2b, 3 and 4; probably four loci	82, 687
<i>pbpB</i>	133	Penicillin-binding protein; closely related to <i>pbpB</i> of <i>E. coli</i>	134*, 168*, 687, 844
<i>pbpD</i>	280	Penicillin-binding protein 4	593*
<i>pbpE</i>	296	Penicillin-binding protein 4	592*
<i>pbpF</i>	77	Penicillin-binding protein class A putative; formerly <i>ponA</i>	264, 591*
<i>pbuG</i>	55	Purine base uptake	659
<i>pbuX</i>	198	Xanthine permease	664*
<i>pcf</i>	110	Positive control factor; similar to regions 4,1 and 4,2 of sigma factors	459*
<i>pckA</i>	272	Phosphoenolpyruvate carboxykinase	393*
<i>pcp</i>	25	Pyroglutamate carboxyl peptidase; L-pyroglutamyl peptide hydrolase	31*
<i>pdbA</i>	125	Pyruvate dehydrogenase; E-1- α (pyruvate decarboxylase); <i>bfmA</i> , <i>aceA</i>	67, 277*, 824
<i>pdbB</i>	125	Pyruvate dehydrogenase component E-1- β ; <i>aceB</i>	277*, 824
<i>pdbC</i>	125	Pyruvate dehydrogenase component E2; <i>aceC</i>	277*, 824
<i>pdbD</i>	125	Pyruvate dehydrogenase; lipoamide dehydrogenase E-3 component of both pyruvate dehydrogenase and α -ketoglutarate dehydrogenase complexes; <i>aceD</i> , <i>citL</i>	277*, 303, 824
<i>pdp</i>	338	Pyrimidine nucleoside phosphorylase	639, 663*
<i>pfk</i>	260	Phosphofructokinase	219, 393*
<i>pgk</i>	NM	3'-Phosphoglycerolkinase	197, 411*
<i>pgm</i>	NM	Phosphoglycerate mutase, PGM	411*
<i>pha-1</i>	47	Resistance to phage SPO1	405
<i>pha-2</i>	280	Resistance to phage SPP1	653
<i>pha-3</i>		See <i>ggaA</i> and <i>ggaB</i>	
<i>pha-4</i>	295	Resistance to phage	136
<i>pheA</i>	240	Phenylalanine requirement; prephenate dehydratase	763*
<i>pheB</i>	240	Chorismate mutase	763*
<i>pheS</i>	254	Phenylalanyl-tRNA synthetase α subunit	72#, 73*
<i>pheT</i>	254	Phenylalanyl-tRNA synthetase β subunit	72#, 73*
<i>pbl</i>		See <i>rpsL</i>	
<i>pboA</i>	72	Alkaline phosphatase A; <i>pboAIV</i>	316*, 317*, 525
<i>pboAIII</i>	45	Alkaline phosphatase III; <i>pboB</i>	63*, 316, 317*
<i>pboAIV</i>		See <i>pboA</i>	
<i>pboB</i>		See <i>pboAIII</i>	
<i>pboP</i>	258	Regulation of alkaline phosphatase and phosphodiesterase; homologous to <i>pboB</i> of <i>E. coli</i>	676*
<i>pboR</i>	258	Regulation of alkaline phosphatase and phosphodiesterase; homologous to <i>pboR</i> of <i>E. coli</i>	677*
<i>pboS</i>	114	Constitutive alkaline phosphatase	577
<i>pboT</i>	248	Constitutive alkaline phosphatase	583

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>pksA</i>		See <i>pksL</i>	
<i>pksF</i>	152	Polyketide synthases	15*, 673*
<i>pksG</i>	152	Polyketide synthases	15*, 673*
<i>pksH</i>	152	Polyketide synthases	15*, 673*
<i>pksI</i>	152	Polyketide synthases	15*, 673*
<i>pksJ</i>	152	Polyketide synthases	15*, 673*
<i>pksK</i>	152	Polyketide synthases	15*, 673*
<i>pksL</i>	152	Polyketide synthase; <i>outG</i> , <i>outH</i> , <i>pksA</i> , <i>pksX</i>	15*, 221#, 673*
<i>pksM</i>	152	Polyketide synthases; <i>pksY</i>	15*, 673*
<i>pksX</i>		See <i>pksL</i>	
<i>pksY</i>		See <i>pksM</i>	
<i>pmi</i>	310	Probable mannose-6-phosphate isomerase	436*
<i>pnp</i>	211	Putative purine nucleoside phosphorylase	834*
<i>pnpA</i>	140	Polynucleotide phosphorylase	425*
<i>polA</i>	257	DNA polymerase I	393*, 561#
<i>polC</i>	147	DNA synthesis, mutator, azopyrimidique resistance; homologous to <i>polC</i> (<i>dnaE</i>) and <i>dnaQ</i> (<i>mutD</i>) of <i>E. coli</i> (α and ϵ subunits of DNA polymerase III, carrying respectively polymerase and 3' $\rightarrow$ 5' exonuclease activities); <i>dnaF</i> , <i>dnaP</i> , <i>mut-1</i> , <i>azp-12</i>	258*, 650
<i>ponA</i>	200	Penicillin-binding proteins 1A and 1B; cell wall synthesis; transglycosilase and transpeptidase	594*, 719*
<i>ppiB</i>	210	Peptide-prolyl-isomerase; 45 % homologous to <i>ppiB</i> of <i>E. coli</i>	295*, 717*
<i>pps-1</i>		See <i>ppsA</i>	
<i>pps-2</i>		See <i>ppsB</i>	
<i>pps-3</i>		See <i>ppsC</i>	
<i>ppsA</i>	175	Peptide synthetase; <i>pps-1</i>	756*
<i>ppsB</i>	175	Peptide synthetase; <i>pps-2</i>	756*
<i>ppsC</i>	175	Peptide synthetase; <i>pps-3</i>	756*
<i>prfB</i>	305	Peptide-chain-release factor 2	559*
<i>prkA</i>	69	Novel serine protein kinase	183*, 525
<i>proA</i>	115	Proline requirement; γ -glutamylphosphate reductase	90, 544*
<i>proB</i>	115	Proline requirement; γ -glutamyl kinase	90, 544*
<i>prs</i>	7	Phosphoribosyl diphosphate synthetase	298, 522#, 523*
<i>prs-11</i>	298	Protein secretion	371, 481
<i>prs-33</i>	149	Protein secretion	371, 481
<i>prsA</i>	76	Lipoprotein involved in protein secretion	371, 372*, 525
<i>priR</i>		See <i>degR</i>	
<i>pss</i>	NM	Phosphatidylserine synthase	547*
<i>ptg</i>	129	Peptidoglycan biosynthesis	91
<i>ptm</i>	107	Pyrithymine resistance	208
<i>ptsG</i>	118	An ORF with homology to the <i>E. coli ptsG</i> locus (glucose-specific Enzyme II of phosphotransferase system has been identified to <i>ptsH</i>); <i>err</i> , <i>ptsX</i>	141*, 233#, 234*, 750*
<i>ptsH</i>	118	Phosphoenolpyruvate:phosphotransferase, Hpr	233#, 234*
<i>ptsI</i>	118	Phosphoenolpyruvate:phosphotransferase, Enzyme I	233#, 234*
<i>ptsX</i>		See <i>ptsG</i>	
<i>pupA</i>	NM	Adenosine phosphorylase	257
<i>pupG</i>	NM	Inosine-guanosine phosphorylase	529#
<i>purA</i>	355	Adenylsuccinate synthetase	432*, 585#, 660#
<i>purB</i>	55	Purine requirement; adenylsuccinate lyase; formerly <i>purE</i>	65*, 159*
<i>purC</i>	55	Purine requirement; phosphoribosyl-aminoimidazole-succinocarboxamide synthetase	65*, 159*
<i>purD</i>	55	Purine requirement; phosphoribosylglycamide synthetase; previous <i>purD</i> is now <i>purK</i>	65*, 159*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>purE</i>	55	Purine requirement; phosphoribosylaminoimidazole carboxylase I; previous <i>purE</i> is now <i>purB</i>	65*, 159*
<i>purF</i>	55	Purine requirement; amido-phosphoribosyltransferase previously designated <i>purB</i>	65*, 430*
<i>purH</i>	55	Purine requirement; phosphoribosylaminoimidazole/carboxamide formyltransferase/IMP (inosinic acid) cyclohydrolase; <i>purHJ</i>	65*, 159*
<i>purHJ</i>		See <i>purH</i>	
<i>purK</i>	55	Purine requirement; phosphoribosylaminoimidazole carboxylase II; formerly <i>purD</i>	65*, 159*
<i>purL</i>	55	Purine requirement; 5'-phosphoribosyl- <i>N</i> -formylglycinamide synthetase II	65*, 159*
<i>purM</i>	55	Phosphoribosylaminoimidazole synthetase; <i>ath</i>	65*, 159*
<i>purN</i>	55	Purine requirement; phosphoribosylglycamide formyltransferase	65*, 159*
<i>purQ</i>	55	Purine requirement; 5'-phosphoribosyl- <i>N</i> -formylglycinamide synthetase II	65*, 159*
<i>purR</i>	6	Repressor of the <i>pur</i> operon	813*
<i>purT</i>	21	5'-Phosphoribosyl-1-glycinamide transformylase	661*, 662
<i>pycA</i>	127	Pyruvate carboxylase	494#
<i>pykA</i>	260	Pyruvate kinase	393*
<i>pyrAA</i>	139	Glutaminase of carbamyl phosphate synthetase; mutation confers fluoracyl resistance; <i>furA</i>	92, 149, 406#, 604*, 772*
<i>pyrAB</i>	139	Carbamyl-phosphate synthetase	406#, 604*, 772*
<i>pyrB</i>	139	Aspartate carbamoyltransferase	406#, 604*
<i>pyrC</i>	139	Dihydroorotase	406#, 604*
<i>pyrD</i>	139	Dihydroorotate dehydrogenase	406#, 604*
<i>pyrE</i>	139	Orotate phosphoribosyltransferase; <i>pyrX</i>	406#, 604*
<i>pyrF</i>	139	Orotidine-5'-phosphate decarboxylase	406#, 604*
<i>pyrG</i>		See <i>ctrA</i>	
<i>pyrP</i>	139	Putative membrane-bound uracil permease	772*
<i>pyrR</i>	139	Negative regulatory protein PyrR	444*, 772*
<i>pyrX</i>		See <i>pyrE</i>	
<i>qcrA</i>	202	Menaquinone oxidase; Rieske iron-sulfur protein	719*, 863*
<i>qcrB</i>	202	Cytochrome reductase; cytochrome <i>bc</i> complex <i>b</i> domain	719*, 863*
<i>qcrC</i>	202	Cytochrome <i>c</i> reductase complex; cytochrome <i>c</i> domain	719*, 863*
<i>qoxA</i>	331	Quinol oxidase	225*, 651*
<i>qoxB</i>	331	Quinol oxidase	225*, 651*
<i>qoxC</i>	331	Quinol oxidase	225*, 651*
<i>qoxD</i>	331	Quinol oxidase	225*, 651*
<i>racE</i>	251	Glutamate racemase	825*
<i>racX</i>	296	Apparent amino acid racemase	592*
<i>rapA</i>	115	Response regulator aspartate phosphatase; <i>spo0L</i>	566*
<i>recA</i>	149	Genetic recombination and radiation resistance; homologous to <i>recA</i> of <i>E. coli</i> ; the former <i>recE</i> mutations corresponds to alleles of <i>recA</i> ; <i>recE</i>	150, 208*, 300, 440#, 733*, 845
<i>recB</i>	240	Genetic recombination and radiation resistance	300
<i>recD</i>		See <i>recR</i>	
<i>recE</i>		See <i>recA</i>	
<i>recF</i>	0	Genetic recombination and radiation resistance	482*
<i>recG</i>	199	Genetic recombination and radiation resistance	456, 561#
<i>recH</i>	69	Genetic recombination and radiation resistance	457
<i>recI</i>	74	Genetic recombination and radiation resistance	457
<i>recL</i>	uc	Genetic recombination and radiation resistance; linked to <i>cysA</i>	150
<i>recM</i>		See <i>recR</i>	
<i>recN</i>	217	Genetic recombination, homologous to <i>E. coli recN</i>	775*
<i>recP</i>	11	Reduced recombination and high sensitivity to mitomycin C; prevents $\phi 105$ restriction in <i>BsuR</i> ⁺ hosts; formerly <i>rec-149</i>	17
<i>recR</i>	0	Genetic recombination and radiation resistance; homologous to <i>recR</i> of <i>E. coli</i> ; <i>recD</i> , <i>recM</i>	18*, 19, 456, 738

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>relA</i>	248	ATP:GTP 3'-phosphotransferase; resistance to aminotriazole	242, 703
<i>relC</i>		See <i>rplK</i>	
<i>relG</i>	13	Defect in glucose uptake	600
<i>resA</i>	208	Regulatory role in respiration, essential gene	717*, 748
<i>resB</i>	208	Regulatory role in respiration, essential gene	717*, 748
<i>resC</i>	208	Regulatory role in respiration, essential gene	717*, 748
<i>resD</i>	208	Regulatory role in respiration, signal transduction regulator	717*, 748
<i>resE</i>	208	Regulatory role in respiration, protein kinase	717*, 748
<i>rev-4</i>	323	Suppressor of some pleiotropic effects (but not asporogeny of <i>spo0</i> mutations); suppresses effect on sporulation of various drug-resistance mutations; <i>abrA</i>	762*, 770
<i>rfm</i>		See <i>rpoB</i>	
<i>rho</i>	323	Transcription termination factor Rho	605
<i>ribA</i>	209	Riboflavin requirement, GTP cyclohydrolase	358, 469*, 470*, 471, 606#
<i>ribB</i>	209	Riboflavin synthase	358, 469*, 471, 606#, 667
<i>ribC</i>	147	Provide constitutive expression of the riboflavin operon	376
<i>ribD</i>	209	Riboflavin requirement	358, 469*, 470*, 471, 606#
<i>ribG</i>	209	Riboflavin requirement, deaminase	358, 469*, 470*, 471, 607#
<i>ribH</i>	209	Riboflavin requirement, lumazine synthase (β subunit)	358, 424*, 469*, 470*, 471, 607#
<i>ribT</i>	209	Riboflavin requirement, reductase	358, 469*, 470*, 471, 607#
<i>ripX</i>	211	Similar to site-specific recombinases/integrases	671
<i>rna-53</i>	312	Temperature-sensitive, RNA-sensitive	622
<i>rnpA</i>	360	Homologous to <i>rnpA</i> of <i>E. coli</i>	535*
<i>rnpB</i>	199	The RNA component of RNase P	455*, 614*
<i>rocA</i>	327	Arginine utilization	225*
<i>rocB</i>	327	Arginine utilization	225*
<i>rocC</i>	327	Arginine utilization	225*
<i>rocD</i>	354	Arginine utilization; ornithine aminotransferase	93*, 211
<i>rocE</i>	354	Arginine utilization; amino acid permease	93*, 211
<i>rocF</i>	354	Arginine utilization; arginase	93*, 211
<i>rocR</i>	354	Positive regulatory protein	93*
<i>rodB</i>		See <i>mreD</i>	
<i>rodC</i>		See <i>tagF</i>	
<i>rodD</i>	198	Cell-wall-defective; previous <i>rodD</i> is now <i>tagE</i>	583
<i>rph</i>	251	RNase PH; suppression of cold-sensitive mutations in <i>E. coli</i>	123*
<i>rplA</i>	11	Ribosomal protein BL1, chloramphenicol resistance II	132, 339*
<i>rplB</i>	12	Ribosomal protein L2 (BL2)	704, 859*
<i>rplC</i>	12	Ribosomal protein L3 (BL3); probably micrococin resistance	129, 859*
<i>rplD</i>	12	Ribosomal protein L4	859*
<i>rplE</i>	12	Ribosomal protein L5 (BL6)	283*
<i>rplF</i>	12	Ribosomal protein L6 (BL8)	129, 599*
<i>rplI</i>	356	Ribosomal protein L9	539*
<i>rplJ</i>	11	Ribosomal protein L10 (BL5)	132, 858*
<i>rplK</i>	11	Ribosomal protein L11 (BL11); thiostrepton resistance; <i>relC</i>	132, 339*
<i>rplL</i>	11	Ribosomal protein L12 (BL9); chloramphenicol resistance VI	64*, 132
<i>rplM</i>	13	Ribosomal protein L13	846*
<i>rplN</i>	12	Ribosomal protein L14	283*
<i>rplO</i>	12	Ribosomal protein L15; chloramphenicol resistance III	505*, 551

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>rplP</i>	12	Ribosomal protein L16	283*
<i>rplQ</i>	12	Ribosomal protein L17 (BL15)	69*
<i>rplR</i>	12	Ribosomal protein L18	740*
<i>rplT</i>	256	<i>B. stearothermophilus rplT</i> homologue; L20	825*
<i>rplU</i>	241	Ribosomal protein L21 (BL20)	128
<i>rplV</i>	12	Ribosomal protein L22 (BL17); erythromycin resistance	704, 859*
<i>rplW</i>	12	Ribosomal protein L23	859*
<i>rplX</i>	12	Ribosomal protein L24 (BL23)	283*, 682*
<i>rpmA</i>	241	Ribosomal protein L27 (BL24)	181*
<i>rpmB</i>	140	Ribosomal protein L28	409*
<i>rpmC</i>	12	Ribosomal protein L29	283*
<i>rpmD</i>	12	Ribosomal protein L30 (BL27)	505*
<i>rpmE</i>	323	Ribosomal protein L31	605
<i>rpmG</i>	11	Ribosomal protein L33	339*
<i>rpmH</i>	0	Ribosomal protein L34	482*
<i>rpmI</i>	256	<i>B. stearothermophilus rpmI</i> homologue; L35	825*
<i>rpmJ</i>	12	Ribosomal protein B	599*
<i>rpoA</i>	12	RNA polymerase α subunit	739*
<i>rpoB</i>	11	β subunit of RNA polymerase; rifampin resistance; <i>crsE</i> , <i>rfm</i>	64*, 598#, 742
<i>rpoC</i>	11	β subunit of RNA polymerase; streptolydigin resistance; <i>lpm</i> , <i>std</i>	64*, 598#
<i>rpoD</i>		See <i>sigA</i>	
<i>rpoE</i>	323	δ subunit of RNA polymerase	391*
<i>rpoF</i>		See <i>sigB</i>	
<i>rpsC</i>	12	Ribosomal protein S3 (BS3)	704, 859*
<i>rpsD</i>	263	Ribosomal protein S4 (BS4)	244*
<i>rpsE</i>	12	Ribosomal protein S5; spectinomycin resistance; <i>spcA</i>	131, 857*
<i>rpsF</i>	358	Ribosomal protein S6 (BS9)	130, 539*
<i>rpsG</i>	11	Ribosomal protein S7 (BS7)	132
<i>rpsH</i>	12	Ribosomal protein S8 (BS8)	283*
<i>rpsI</i>	13	Ribosomal protein S9 (BS10)	131, 846*
<i>rpsJ</i>	11	Ribosomal protein S10 (BS13); <i>tetA</i>	704
<i>rpsK</i>	12	Ribosomal protein S11 (BS11)	739*
<i>rpsL</i>	11	Ribosomal protein S12 (BS12, <i>strA</i>); streptomycin resistance; <i>fun</i> , <i>pbl</i> , <i>strA</i>	129, 230, 282, 319
<i>rpsM</i>	12	Ribosomal protein S13	739*
<i>rpsN</i>	12	Ribosomal protein S14	283*
<i>rpsO</i>	140	Ribosomal protein S15 (BS18)	425*
<i>rpsP</i>	147	Ribosomal protein S16 (BS17)	130, 208, 310*
<i>rpsQ</i>	12	Ribosomal protein S17 (BS16)	283*
<i>rpsR</i>	358	Ribosomal protein S18	539*
<i>rpsS</i>	12	Ribosomal protein S19 (BS19)	551, 859*
<i>rpsT</i>	12	Ribosomal protein S20 (BS20)	551
<i>rrnA</i>	0	rRNA operon	533*
<i>rrnB</i>	275	rRNA operon	239*
<i>rrnD</i>	67	rRNA operon	387#
<i>rrnE</i>	45	rRNA operon	387#, 644*
<i>rrnF</i>	NM	rRNA operon known to exist but not cloned or mapped	66
<i>rrnG</i>	14	rRNA operon	66#
<i>rrnH</i>	14	rRNA operon	66#
<i>rrnI</i>	13	rRNA operon	66#
<i>rrnJ</i>	10	rRNA operon	818#
<i>rrnO</i>	0	rRNA operon	533*
<i>rrnW</i>	10	rRNA operon	818#

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>rsbU</i>	38	Predicted RsbU product has significant similarity to RsbX negative regulator of σ^B ; product involved in regulation of <i>sigB</i> activity	791*, 826*
<i>rsbV</i>	38	Positive regulator of σ^B -dependent gene expression	70, 826*
<i>rsbW</i>	38	Negative regulator of σ^B -dependent gene expression	70, 826*
<i>rsbX</i>	38	Negative effector of σ^B -dependent gene expression	70, 71, 826*
<i>ritp</i>	178	Replication terminator protein	7*
<i>rvtA</i>		See <i>spo0A</i>	
<i>sacA</i>	330	β -Fructofuranosidase (sucrase)	190*
<i>sacB</i>	296	Levansucrase	726*
<i>sacC</i>	233	Levanase	442*
<i>sacL</i>		See <i>levD</i> and <i>levE</i>	
<i>sacP</i>	330	Sucrose transport; Enzyme II of sucrose phosphotransferase system	189*
<i>sacQ</i>		See <i>degQ</i>	
<i>sacR</i>	296	Constitutive for levansucrase	725*
<i>sacS</i>		See <i>sacX</i> and <i>sacY</i>	
<i>sacT</i>	330	Constitutive β -fructofuranosidase production	156*, 404
<i>sacU</i>		See <i>degS</i>	
<i>sacV</i>	40	Regulatory gene for levansucrase	441*
<i>sacX</i>	332	Levansucrase regulation; <i>sacS</i>	32#, 726*
<i>sacY</i>	332	Levansucrase regulation; antiterminator; <i>sacS</i>	32#, 878*
<i>sapA</i>	114	Mutations overcome the sporulation-phosphatase-negative phenotype of early-blocked <i>spo</i> mutants	579
<i>sapB</i>	56	Mutations overcome sporulation-phosphatase-negative phenotype of early blocked <i>spo</i> mutations	577
<i>sas</i>		See <i>spoIIA.A</i>	
<i>sbcD</i>	98	Homologous to exonuclease SbcD of <i>E. coli</i>	374
<i>sbp</i>	134	Small basic protein	168*, 636*
<i>scoA</i>	109	Sporulation control; protease and phosphatase overproduction; delayed spore formation	465
<i>scoC</i>		See <i>hpr</i>	
<i>scoD</i>		See <i>kinA</i>	
<i>scr</i>	0	Small cytoplasmic RNA; homologous to <i>ffs</i> of <i>E. coli</i>	18*, 736, 738*
<i>sdhA</i>	252	Flavoprotein subunit of succinate dehydrogenase; note that the <i>sdh</i> loci have been reorganized; <i>citF</i>	574*
<i>sdhB</i>	252	Iron protein subunit of succinate dehydrogenase	574*
<i>sdhC</i>	252	Cytochrome <i>b₅₅₈</i> ; subunit of succinate dehydrogenase complex	428*
<i>secA</i>	305	Secretion of proteins; homologous to <i>secA</i> of <i>E. coli</i> ; mutation confers resistance to sodium azide; <i>lssG</i> , <i>ts-341</i> , <i>div-341</i> , <i>azj</i>	76, 305, 364*, 475, 643*
<i>secE</i>	11	Pre-protein translocase SecE subunit	339*
<i>secY</i>	12	Secretion of proteins; homologous to <i>secY</i> of <i>E. coli</i>	505*, 740*
<i>senS</i>	69	Enhances expression of genes for several extracellular proteins	803*
<i>serA</i>	207	Requirement for serine; glycerophosphate dehydrogenase	429, 717*
<i>serC</i>	257	Requirement for serine; defined by Tn917 insertion	784
<i>serR</i>	26	Serine resistance	839*
<i>serS</i>	0	Seryl-tRNA synthetase	539*
<i>sfp</i>	31	Surfactin production; highly homologous to the <i>E. coli entD</i> gene	243*, 510
<i>sigA</i>	223	Major RNA polymerase sigma factor, σ^A or σ^{43} ; <i>rpoD</i> , <i>crsA</i>	597, 742, 802*
<i>sigB</i>	38	RNA polymerase sigma factor, σ^B or σ^{37} ; <i>rpoF</i>	50, 70, 71, 155*, 826
<i>sigC</i>	NM	RNA polymerase sigma factor, σ^C or σ^{32}	342
<i>sigD</i>	142	RNA polymerase sigma factor, σ^D or σ^{28} ; autolytic enzymes, allelic to <i>flaB</i>	276*, 438, 439, 586
<i>sigE</i>	135	RNA polymerase sigma factor, σ^E or σ^{29} ; <i>spoIIIGB</i>	168*, 447*, 569, 629, 730*, 768*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>sigF</i>	211	RNA polymerase sigma factor, σ^F ; <i>spoIIAC</i>	163*, 185*, 670, 744*, 832, 834*
<i>sigG</i>	135	RNA polymerase sigma factor, σ^G ; <i>spoIIIG</i>	168*, 352*, 446*, 744*
<i>sigH</i>	11	RNA polymerase sigma factor, σ^H or σ^{30} ; <i>spo0H</i>	154*
<i>sigK</i>		See <i>spoIIIC</i>	
<i>sigL</i>	295	RNA polymerase sigma factor, σ^{54} , σ^L	157*
<i>sigZ</i>	232	RNA polymerase subunit sigma factor	62*
<i>sin</i>		See <i>sinR</i>	
<i>sinI</i>	219	Sporulation inhibition at high-copy-number	216*
<i>sinR</i>	219	Sporulation inhibition at high-copy-number; <i>sin</i> , <i>flaD</i>	216*, 586, 678*
<i>sipS</i>	209	Signal peptidase I	717*, 774*
<i>skin</i>	227	226–230°; genetic element of 48 kb (most probably is defective prophage) inserted between <i>spoIVCB</i> and <i>spoIIIC</i> ; inside <i>sigK</i> gene	751*
<i>slp</i>	125	Small lipoprotein; <i>pal</i>	278*, 824
<i>smo</i>	295	Smooth/rough colony morphology	218#
<i>sms</i>	10	Homologous to ATP-dependent protease	541
<i>soj</i>		See <i>spo0JA</i>	
<i>spcA</i>		See <i>rpsE</i>	
<i>spcB</i>	146	Spectinomycin resistance	421
<i>spcD</i>	2	Spectinomycin dependence	281
<i>spdA</i>	288	Sporulation derepressed; low pyruvate carboxylase activity	161
<i>spe</i>	NM	Endonuclease-excising spore photoproducts; formerly <i>ssp-1</i>	499
<i>spl</i>	118	Spore photoproduct lyase	171*, 172*
<i>spmA</i>	208	Spore-maturation operon	595, 717*
<i>spmB</i>	208	Spore-maturation operon	595, 717*
<i>spo0A</i>	217	Sporulation; mutants blocked at stage 0; <i>rvtA</i> , <i>spo0C</i> , <i>spo0G</i>	182*, 304*, 684
<i>spo0B</i>	240	Sporulation; mutants blocked at stage 0; part of phosphorelay; <i>spo0D</i>	181*
<i>spo0C</i>		See <i>spo0A</i>	
<i>spo0D</i>		See <i>spo0B</i>	
<i>spo0E</i>	115	Stage 0 sporulation; oligosporogenous mutations giving stage 0 block; less pleiotropic than <i>spo0A</i> , <i>spo0B</i> or <i>spo0F</i> mutations	560*
<i>spo0F</i>	323	Stage 0 sporulation; part of phosphorelay	761*
<i>spo0G</i>		See <i>spo0A</i>	
<i>spo0H</i>		See <i>sigH</i>	
<i>spo0JA</i>	359	Allele 87; originally placed in this locus was found to be in a distinct locus; named <i>spoIIIJ</i> ; <i>soj</i> , <i>spoCM</i>	74, 164#, 167*, 327, 502*, 538*, 629
<i>spo0JB</i>	359	Stage 0 sporulation; production of Spo0A–P	305, 327, 502*
<i>spo0KA</i>		See <i>oppA</i>	
<i>spo0KB</i>		See <i>oppB</i>	
<i>spo0KC</i>		See <i>oppC</i>	
<i>spo0KD</i>		See <i>oppD</i>	
<i>spo0KE</i>		See <i>oppF</i>	
<i>spo0L</i>		See <i>rapA</i>	
<i>spoIIAA</i>	211	Stage II sporulation; encoding an anti-anti-sigma-factor antagonist of <i>spoIIAB</i> ; <i>sas</i>	163*, 185*, 670, 832, 834*, 864
<i>spoIIAB</i>	211	Stage II sporulation; encoding an anti-sigma-factor for SigF and possibly SigG	163*, 185*, 670, 832, 834*
<i>spoIIAC</i>		See <i>sigF</i>	
<i>spoIIB</i>	242	Stage II sporulation	434*, 576
<i>spoIIC</i>		See <i>spoIID</i>	
<i>spoIID</i>	316	Stage II sporulation; <i>spoIIC</i>	419*, 576
<i>spoIIE</i>	8	Stage II sporulation; <i>spoIIE</i> is an allele of <i>spoIIE</i> ; <i>spoIIH</i>	250*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>spoIIF</i>		See <i>kinA</i>	
<i>spoIIGA</i>	135	Stage II sporulation <i>spoIIG</i> operon	168*, 447*, 569, 629, 730*
<i>spoIIGB</i>		See <i>sigE</i>	
<i>spoIIH</i>		See <i>spoIIE</i>	
<i>spoIIJ</i>		See <i>kinA</i>	
<i>spoIIM</i>	212	Defined by Tn917 insertion; distinct from <i>spoIIA</i>	649, 705*, 706
<i>spoIIP</i>	226	Stage II sporulation	194*
<i>spoIIR</i>	321	Stage II sporulation protein R	353*
<i>spoIIIAA</i>	218	Stage III sporulation	164#, 248#, 324*
<i>spoIIIAB</i>	218	Stage III sporulation	164#, 248#, 324*
<i>spoIIIAC</i>	218	Stage III sporulation	249*, 477
<i>spoIIIAD</i>	218	Stage III sporulation	249*, 477
<i>spoIIIAE</i>	218	Stage III sporulation	249*, 477
<i>spoIIIAF</i>	218	Stage III sporulation	249*, 477
<i>spoIIIAG</i>	218	Stage III sporulation	249*, 477
<i>spoIIIAH</i>	218	Stage III sporulation	249*, 477
<i>spoIIIC</i>	230	Initially designated as stage III sporulation, but very similar phenotype to <i>spoIVC</i> ; 3' end of <i>sigK</i> ; <i>sigK</i>	165*, 380, 731*
<i>spoIIID</i>	317	Stage III sporulation	379*, 576, 728*
<i>spoIIIE</i>	149	Stage III sporulation; gene required for post-septational chromosome partitioning	87*, 191*, 193, 587#
<i>spoIIIF</i>		See <i>spoVB</i>	
<i>spoIIIG</i>		See <i>sigG</i>	
<i>spoIIIJ</i>	360	Stage III sporulation; vegetatively expressed gene essential for σ^G activity at stage III; previously <i>spo0J87</i>	167*, 538*
<i>spoIVA</i>	205	Stage IV sporulation, spore-coat assembly protein; <i>spoVP</i>	147, 429#, 624*, 649, 729*
<i>spoIVB</i>	217	Stage IV sporulation; maps immediately upstream of <i>spo0A</i>	576, 775*
<i>spoIVCA</i>	226	Stage IV sporulation; <i>spoIVCA</i> encodes a recombinase; <i>cisA</i>	378*, 656*, 657, 731*
<i>spoIVCB</i>	226	Stage IV sporulation; <i>spoIVCB</i> encodes the N-terminal half of SigK; <i>cisB</i>	378*, 656*
<i>spoIVFA</i>	241	Stage IV sporulation; <i>bofB</i>	126*, 164#
<i>spoIVFB</i>	241	Stage IV sporulation; <i>bofB</i>	126*, 164#
<i>spoIVG</i>	97	Stage IV sporulation	576
<i>spoVAA</i>	211	Stage V sporulation	186*, 717*, 838*
<i>spoVAB</i>	211	Stage V sporulation	186*, 717*, 838*
<i>spoVAC</i>	211	Stage V sporulation	186*, 717*, 838*
<i>spoVAD</i>	211	Stage V sporulation	186*, 717*, 838*
<i>spoVAE</i>	211	Stage V sporulation	186*, 717*, 838*
<i>spoVAF</i>	211	Stage V sporulation	186*, 717*, 838*
<i>spoVB</i>	236	Stage V sporulation; the previous <i>spoIIIF</i> is part of <i>spoVB</i> ; membrane protein involved in cortex; <i>spoIIIF</i>	186*, 717*, 838*
<i>spoVC</i>	7	Stage V sporulation; the two mutations placed in this locus may be in separate loci	318*
<i>spoVD</i>	133	Stage V sporulation; closely related to <i>pbpB</i> of <i>E. coli</i>	168*, 576
<i>spoVE</i>	134	Stage V sporulation; homologous to <i>ftsW</i> of <i>E. coli</i>	85*, 168*, 293, 322*, 344*, 476
<i>spoVFA</i>		See <i>dpaA</i>	
<i>spoVFB</i>		See <i>dpaB</i>	
<i>spoVG</i>	6	Stage V sporulation; previously called 0.4 kb gene	315*, 675#
<i>spoVJ</i>		See <i>spoVK</i>	
<i>spoVK</i>	153	Defined by Tn917 insertion; <i>spoVJ</i>	173*, 192, 208, 649
<i>spoVM</i>	140	Defined by Tn917 insertion	193, 409*, 649

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>spoVN</i>		See <i>ald</i>	
<i>spoVP</i>		See <i>spoIVA</i>	
<i>spoVQ</i>	213	Defined by Tn917 insertion; less closely linked to <i>lys</i> than <i>spoVA</i>	649
<i>spoVR</i>	72	Stage V sporulation	47*, 525
<i>spoVS</i>	150	Stage V sporulation protein S	208*, 618*
<i>spoVIA</i>	255	Stage VI sporulation	336
<i>spoVIB</i>	248	Stage VI sporulation	337
<i>spoVIC</i>	293	Stage VI sporulation	335
<i>spoVID</i>	244	Stage VI sporulation	46*
<i>spoCM</i>		See <i>spo0JA</i>	
<i>spoL</i>	226	'Decadent' sporulation	36
<i>sprA</i>	NM	Derepression of homoserine kinase, homoserine dehydrogenase and of the weak threonine activity (<i>tdm</i>); see <i>hom</i>	786
<i>sprE</i>		See <i>aprE</i>	
<i>spsA</i>	328	Spore-coat polysaccharide	225*
<i>spsB</i>	328	Spore-coat polysaccharide	225*
<i>spsC</i>	328	Spore-coat polysaccharide	225*
<i>spsD</i>	328	Spore-coat polysaccharide	225*
<i>spsE</i>	328	Spore-coat polysaccharide	225*
<i>spsF</i>	328	Spore-coat polysaccharide	225*
<i>spsG</i>	328	Spore-coat polysaccharide	225*
<i>spsH</i>	328	Spore-coat polysaccharide	225*
<i>spsI</i>	328	Spore-coat polysaccharide	225*
<i>spsJ</i>	328	Spore-coat polysaccharide	225*
<i>spsK</i>	328	Spore-coat polysaccharide	225*
<i>srfA</i>		See <i>srfAA</i>	
<i>srfA1</i>		See <i>srfAA</i>	
<i>srfA2</i>		See <i>srfAB</i>	
<i>srfA3</i>		See <i>srfAC</i>	
<i>srfA4</i>		See <i>srfAD</i>	
<i>srfAA</i>	31	Surfactin production; <i>srfA1</i> , <i>srfA</i> , <i>comL</i>	122*, 204*, 507#, 509*, 776, 781#
<i>srfAB</i>	31	Surfactin production; <i>srfA2</i>	122*, 204*, 507#, 509*, 776
<i>srfAC</i>	31	Surfactin production; <i>srfA3</i>	122*, 507#, 509*, 776
<i>srfAD</i>	31	Surfactin production; <i>srfA4</i>	122*, 507#, 509*, 776
<i>srn</i>	14	Modifies resistance of <i>spcA</i> strains	94
<i>ssa</i>	217	Alcohol-resistant sporulation; maps close to or in <i>spo0A</i> ; <i>rvt</i> mutations have same phenotype	59
<i>ssb</i>	358	Single-stranded DNA-binding protein	539*
<i>sspA</i>	261	One member of multigene family encoding small acid-soluble spore proteins	118*, 393*
<i>sspB</i>	75	Small acid-soluble spore protein; similar product to <i>sspA</i>	21, 117, 118*, 525
<i>sspC</i>	182	Small acid-soluble spore protein; similar product to <i>sspA</i>	116*, 117
<i>sspD</i>	121	Similar product to <i>sspA</i>	117, 118*
<i>sspE</i>	62	Small acid-soluble spore protein; similar product to <i>sspA</i>	21, 251*
<i>sspF</i>	6	Similar product to <i>sspA</i> ; same as '0.3 kb gene'	420, 727*
<i>std</i>		See <i>rpoC</i>	
<i>strA</i>		See <i>rpsL</i>	
<i>strB</i>	124	Streptomycin resistance	720
<i>strC</i>	218	Streptomycin-uptake-deficient, possible cytochrome oxidase regulator	460
<i>suA20</i>	147	Suppressor of <i>recH</i> mutations with increased ATP-dependent deoxyribonuclease	208, 389

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>sub</i>	NM	Structural gene for peptide antibiotic subtilin; also called <i>spaS</i>	38*, 363*
<i>sul</i>	9	Sulfonilamide resistance; probably dihydropteroate synthase	458#, 693*
<i>sup-3</i>	39	Suppressor, lysyl-tRNA	286, 415, 498
<i>sup-44</i>	39	Suppressor, leucyl-tRNA	415, 422
<i>tag-3</i>		See <i>tagF</i>	
<i>tagA</i>	310	Polyglycerol phosphate assembly and export	453*, 454
<i>tagB</i>	310	Polyglycerol phosphate assembly and export	453*, 454
<i>tagC</i>	310	Polyglycerol phosphate assembly and export; probably identical to <i>dinC</i> ; <i>dinC</i>	113*, 222, 453*, 454, 651
<i>tagD</i>	310	Glycerol-3-phosphate cytidyltransferase	453*, 454, 588
<i>tagE</i>	310	UDPglucose-teichoic acid glycosyltransferase; cell-wall-defective; formerly <i>rodD</i> ; <i>gtaA</i> , <i>gtaD</i>	454*
<i>tagF</i>	309	CDPglycerol:poly(glycerol phosphate) glycerophosphotransferase; <i>rodC</i> , <i>tag-3</i>	311, 312*, 454, 589*
<i>tagG</i>	309	Teichoic acid biosynthesis; essential gene	395, 396*
<i>tagH</i>	309	Teichoic acid biosynthesis; essential gene	395, 396*
<i>tal</i>	240	Resistance to β -thienylalanine	115
<i>tdhF</i>	360	Thiophen and furan oxidation	539*
<i>tdk</i>	323	Thymidine kinase	605
<i>tdm</i>		See <i>hom</i>	
<i>ten</i>	248	Constitutive transfection enhancement of phage SP82 DNA; transformation defective	241
<i>tenA</i>	61	Transcription enhancement of <i>aprE</i>	555*
<i>tenE</i>	61	Reduction of <i>aprE</i> transcription	555*
<i>tenI</i>	61	Regulatory protein TenI	555*
<i>terC</i>	179	Terminus of replication	105*
<i>tet</i>		See <i>tetB</i>	
<i>tetA</i>		See <i>rpsJ</i>	
<i>tetB</i>	357	Resistance to tetracycline; <i>tet</i>	20*, 539*, 646*, 821
<i>tetL</i>	357	Tetracycline resistance leader peptide	539*, 646*
<i>tetR</i>	357	Tetracycline resistance	539*
<i>thfS</i>	304	Tetrahydrofolate synthetase	403#
<i>thiA</i>	69	Thiamine requirement	355
<i>thiB</i>	105	Thiamine requirement	301
<i>thiC</i>	335	Thiamine requirement	870
<i>thrA</i>		See <i>thrB</i>	
<i>thrB</i>	284	Threonine requirement; homoserine kinase; previous <i>thrB</i> is now <i>thrC</i> ; <i>thrA</i>	556*
<i>thrC</i>	284	Threonine requirement; threonine synthase; formerly <i>thrB</i>	556*
<i>thrS</i>	256	Major threonyl-tRNA synthetase	601*
<i>thrZ</i>	325	Minor threonyl-tRNA synthetase; maps near <i>sacA</i>	601*, 602*
<i>thyA</i>	168	Thymidylate synthetase A	517, 752*
<i>thyB</i>	195	Thymidylate synthetase B	22, 333*
<i>tig</i>	244	Possible trigger factor	825*
<i>tkt</i>	170	Transketolase	655, 665*
<i>tlpA</i>	170	Thioredoxin-like protein A; problem of gene symbol redundancy see other <i>tlpA</i> at 281°	630*
<i>tlpA</i>	281	Transmembrane receptor with strong homology to chemotaxis proteins; problem of gene symbol redundancy see other <i>tlpA</i> at 170°	261*
<i>tlpB</i>	281	Transmembrane receptor with strong homology to chemotaxis proteins	261*
<i>tlpC</i>	31	Methylation enzyme; methyl-accepting chemotaxis protein	199*, 262*
<i>tmrA</i>	24	Tunicamycin resistance; hyperproductivity of extracellular α -amylase	528
<i>tmrB</i>	27	Tunicamycin resistance; ATP-binding membrane protein	526, 552#, 839*
<i>tms</i>		See <i>gcaD</i>	

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>tolB</i>	NM	Tolerance to bacteriophage	331
<i>topB</i>	34	Topoisomerase III	644
<i>tpi</i>	NM	Triose-phosphate isomerase	411*
<i>treA</i>	62	Trehalose-6-phosphate hydrolase; phospho- α (1-1-glucosidase); <i>treC</i>	236*, 275*, 405
<i>treB</i>		See <i>treP</i>	
<i>treC</i>		See <i>treA</i>	
<i>treP</i>	62	Permease Enzyme II trehalose; <i>treB</i>	236*, 275*, 405
<i>treR</i>	62	Repressor of the trehalose operon	275*
<i>trnA</i>	0	Genes for Ile and Ala tRNAs located between 16S and 23S RNAs in the <i>rrnA</i> operon	533*
<i>trnB</i>	275	Linked set of tRNA genes distal to <i>rrnB</i> that contains tRNAs for Val, Thr, Lys, Leu, Gly, Leu, Arg, Pro, Ala, Met, Ile, Ser, fMet, Asp, Phe, His, Gly, Ile, Met, Asn, Ser and Glu; previous <i>trnB</i> is now <i>trnI</i> ; formerly <i>trnE</i>	239*
<i>trnD</i>	67	Linked set of tRNA genes thought to be distal to <i>rrnR</i> that contains tRNAs for Asn, Ser, Glu, Val, Met, Asp, Phe, Thr, Tyr, Trp, His, Gln, Gly, Cys, Leu1 and Leu2; <i>trnR</i>	809*
<i>trnE</i>	45	tRNA Met and Asp; previous <i>trnE</i> is now <i>trnB</i>	644*
<i>trnH</i>		See <i>trnI</i>	
<i>trnI</i>	13	Linked set of six tRNA genes including tRNAs for Ala, Pro, Arg, Gly, Thr and Asn located between <i>rrnH</i> and <i>rrnI</i> ; formerly <i>trnB</i> ; <i>trnH</i>	808*
<i>trnJ</i>	10	Linked set of nine tRNA genes, Val, Thr, Lys, Leu1, Gly, Arg, Pro, Ala located between <i>rrnJ</i> and <i>rrnW</i>	240*
<i>trnO</i>	0	Same tRNA genes as <i>trnA</i> but located in <i>rrnO</i>	792
<i>trnR</i>		See <i>trnD</i>	
<i>trnS</i>	39	tRNA Asn, Ser, Glu, Gln, Lys, Leu1 and Leu2	212*
<i>trnY</i>	355	Linked set of tRNA genes for Lys, Glu, Asp and Phe	539*, 837*
<i>trpA</i>	203	Tryptophan synthase α	289*
<i>trpB</i>	203	Tryptophan synthase β	289*
<i>trpC</i>	203	Indol-3-glycerol-phosphate synthase	289*
<i>trpD</i>	203	Anthranilate phosphoribosyl-transferase	37*, 289
<i>trpE</i>	203	Anthranilate synthase	37*, 289
<i>trpF</i>	203	Phosphoribosylanthranilate isomerase	289*
<i>trpG</i>	9	<i>p</i> -Aminobenzoic acid synthase, component II; glutamine amidotransferase; <i>pabA</i> , <i>trpX</i>	347, 693*
<i>trpS</i>	104	Tryptophanyl-tRNA synthase	114*, 723
<i>trpX</i>		See <i>trpG</i>	
<i>trx</i>		See <i>trxA</i>	
<i>trxA</i>	252	Thioredoxin; <i>trx</i>	111*
<i>trxC</i>	264	Thioredoxin	393*
<i>ts-1</i>		See <i>ftsZ</i>	
<i>ts-31</i>	131	Temperature-sensitive division	475
<i>ts-341</i>		See <i>secA</i>	
<i>ts-39</i>	226	Temperature-sensitive synthesis of phosphatidylethanolamine	414
<i>ts-526</i>	2	Temperature-sensitive division	475
<i>tsi</i>	48	Temperature-sensitive induction of all known SOS functions	690
<i>tsr</i>		See <i>fbaA</i>	
<i>tuaA</i>	307	Biosynthesis of teichuronic acid, operon of eight genes	397*
<i>tuaB</i>	307	Biosynthesis of teichuronic acid, operon of eight genes	397*
<i>tuaC</i>	307	Biosynthesis of teichuronic acid, operon of eight genes	397*
<i>tuaD</i>	307	Biosynthesis of teichuronic acid, operon of eight genes	397*
<i>tuaE</i>	307	Biosynthesis of teichuronic acid, operon of eight genes	397*
<i>tuaF</i>	307	Biosynthesis of teichuronic acid, operon of eight genes	397*
<i>tuaG</i>	307	Biosynthesis of teichuronic acid, operon of eight genes	397*

Table 1 (cont.)

Gene symbol	Map position	Functions, products, phenotypes, other characteristics, former or alternative symbols	Reference
<i>tnaH</i>	307	Biosynthesis of teichuronic acid, operon of eight genes	397*
<i>tufA</i>	11	Elongation factor Tu	153
<i>tyrA</i>	202	Tyrosine requirement; prephenate dehydrogenase	290*
<i>tyrR</i>		See <i>tyrZ</i>	
<i>tyrS</i>	263	Tyrosyl-tRNA synthetase	244, 285*
<i>tyrT</i>		See <i>tyrZ</i>	
<i>tyrZ</i>	332	Tyrosyl-tRNA synthetase, minor, expresses when <i>tyrS</i> is inactivated; <i>tyrT</i> , <i>tyrR</i>	224*
<i>tzm</i>		See <i>gerJ</i>	
<i>uat</i>		See <i>patA</i>	
<i>udk</i>	NM	Uridine kinase; also lacks cytidine kinase; mutant resistant to fluorouridine	518
<i>udp</i>	NM	Uridine phosphorylase	455#
<i>unc</i>	NM	Uncoupler resistance	377
<i>ung</i>	330	Putative uracyl-DNA glycosylase	225*
<i>upp</i>	321	Uracil phosphoribosyl transferase	444*, 518
<i>urg</i>	NM	N-Glucosidase	431
<i>uvr</i>		See <i>uvrB</i>	
<i>uvrA</i>	303	Excision of UV-induced pyrimidine dimers in DNA	113*, 300, 711
<i>uvrB</i>	303	Excision of UV-induced pyrimidine dimers in DNA; cytoplasmic protein; previous <i>uvrB</i> is now <i>uvrC</i> ; <i>uvr</i> , <i>dinA</i>	70*, 113*, 711
<i>uvrC</i>	252	Excision of UV-induced pyrimidine dimers in DNA; homologous to <i>uvrC</i> of <i>E. coli</i> ; formerly <i>uvrB</i>	111*, 499
<i>valS</i>	242	Valyl-tRNA synthetase	433*
<i>veg</i>	4	Veg protein	539*
<i>vpr</i>	330	Minor extracellular serine protease	698*
<i>VS</i>	14	Virginiamycin (VS component) resistance	627
<i>wapA</i>	336	Wall-associated protein	188*
<i>xepA</i>	112	XepA protein; homologues of <i>xepA</i> are associated with cell lysis genes	418*
<i>xhi</i>	112	Heat-inducible PBSX	89
<i>xhlA</i>	112	Protein associated with cell lysis upon induction of PBSX; role of a holin	418*
<i>xhlB</i>	112	Gene product involved in cell lysis upon induction of PBSX; role of a holin; <i>xpaB</i>	400#, 418*
<i>xlt</i>	112	Induced PBSX lacks tails	213
<i>xlyA</i>	112	N-Acetylmuramoyl-L-alanine amidase	418*
<i>xpaA</i>	277	Hydrolysis of 5-bromo-4-chloroindolyl phosphate (X-phos)	400#
<i>xpaB</i>		See <i>xhlB</i>	
<i>xpaC</i>	2	Hydrolysis of 5-bromo-4-chloroindolyl phosphate (X-phos)	400#
<i>xpt</i>	198	Xanthine phosphoribosyltransferase	97, 659, 664*
<i>xre</i>	110	PBSX repressors	828*
<i>xylA</i>	168	Xylose isomerase	375, 820*
<i>xylB</i>	168	Xylulose kinase	375, 819#
<i>xylR</i>	168	Regulation of xylose regulon	271#, 375
<i>xynA</i>	175	Extracellular β -xylanase	554*, 628, 760, 827*
<i>xynB</i>	168	Cell-associated β -xylooxidase	271#, 628, 760
<i>xynC</i>	168	Probably xyloside permease	271#, 760
<i>xynD</i>	171	Endo-1,4- β -xylanase D	630*

GenBank/DDBJ – Accession Number’ replaces the bibliographic reference).

As stated above, the method adopted to automatically build the *B. subtilis* genetic map can be applied to other bacterial species, and can help in the follow-up of genome sequencing and gene function analysis projects. We have organized the genetic map data for *Escherichia coli* from the ECD database [796] on the same model.

To assist in the preparation of *B. subtilis* genetic map updates, we would appreciate information regarding the position and function of new genes or corrections (bsmap@biotec.jouy.inra.fr).

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