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Genetic Map of *Salmonella typhimurium*, Edition VIII

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INTRODUCTION

We present edition VIII of the genetic map of *Salmonella typhimurium* LT2. We list a total of 1,159 genes; 1,080 of these have been located on the circular chromosome and 29 are on pSLT, the 90-kb plasmid which is almost invariably found in LT2 lines; the remaining 50 genes are not yet mapped. The first edition of the map in 1965 contained 133 genes; later editions were published in 1967, 1970, 1972, 1978, and 1983; and edition VII, the most recent, was published in 1988 (581).

Strain LT2 is one of 25 different *S. typhimurium* isolates established by Lilleengen (392) and designated LT1 to LT25; these strains represent 25 different phage sensitivity phenotypes. Many of these LT strains were used by Zinder and Lederberg for a study of genetic exchange, which led to the discovery of phage-mediated transduction (773). Demerec obtained the LT strains from Zinder and began an exhaustive series of studies in the mid-1950s. The most important materials used were mutant strains derived from strain LT2, although a few were derived from strain LT7. Since the 1950s, strain LT2 has been the major focus of genetic and biochemical analysis, and thus the map we present here is derived primarily from work with LT2. However, more recently other strains have been used for specific reasons; e.g., some strains of *S. typhimurium* have been studied because they have higher levels of virulence than strain LT2; strain LT2 does not utilize histidine as the sole carbon source, so other wild-type strains which do so have been used to study the *hut* operon.

All genes presently known to us are listed in Table 1, with formerly used or alternative symbols in Table 2. However, the references which describe these genes are not normally presented if they have been given in an earlier edition, except when they refer to DNA sequence listed in Table 3. Generally, to find all relevant references to a gene, it may be necessary to consult earlier map editions. Most of the relevant references published up to and including edition VI have been assembled in a summary of the map presented earlier (579), and there are some additional references in edition VII (581).

GENETIC MAP

The coordinate system used in the first four editions of the linkage map of *S. typhimurium* was determined by F-mediated conjugation; Hfr strains were used in interrupted conjugation experiments to place individual genes and P22 transduction linkage groups on a 138-min time-of-entry linkage map. In edition V, the map was changed to 100 units to correspond to the 100-min linkage map of *Escherichia coli* K-12. This was done to emphasize the similarity of the two genera and to facilitate comparisons. This 100-unit system was also used in editions VI and VII. In those editions, the 100 units of the map were based on "phage lengths" of the transducing phage P22 (581). P22 can normally encapsulate about 45 kb of DNA; this is approximately 1% of the *Salmonella* chromosome. The map described here is the first edition in which we present a physical map of the chromosome with the interval between genes based directly on the length of the DNA. We report these gene intervals as centisomes (Cs), each of which represents 1% of the length of DNA in the chromosome, and we also present the DNA segments in kilobase pairs.

This physical map of the chromosome is based on a low-resolution genomic cleavage map determined by digestion with rare-cutting endonucleases and separation of the resulting fragments by pulsed-field gel electrophoresis (PFGE). Preliminary cleavage maps used the enzymes *Xba*I (406), *Bln*I (585, 745), and I-*Ceu*I (hereafter called *Ceu*I) (405). The overall structure of the chromosome shown in Fig. 1 is based on a summary of work with these three enzymes (404), plus some additional unpublished work.

The genomic cleavage map shows the positions of 24 *Xba*I fragments, 12 *Bln*I fragments, and 7 *Ceu*I fragments on a circular molecule of 4,808 kb of DNA (404). The positions of genes on this cleavage map were determined by three methods. (i) Strains with insertions of the transposon Tn*10* into known genes were analyzed. The presence of *Xba*I and *Bln*I sites in Tn*10* permitted the location of these insertions, and thus of the gene into which Tn*10* is inserted, through digestion of the DNA of the strain by the enzyme followed by separation of the fragments by PFGE. A total of 109 independent strains with Tn*10* insertions were reported, but some of these were not in genes of known function (404); this work, together with unpublished work done recently, has led to a total of 75 genes being located on the physical map solely through analysis of Tn*10*-containing strains. (ii) A total of 12 genes could be placed on the map because their DNA sequence included a site

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for the endonucleases *Xba*I, *Bln*I, or *Ceu*I. (iii) In some situations, restriction mapping data or data from nucleotide sequences were used to correct or refine the locations of genes on the map. For example, a high-resolution restriction map for a 240-kb region spanning the 91- to 96-Cs region of the map located the positions of several genes (749); these data were used to modify the locations of some genes in this interval.

The physically mapped Tn*10* insertions and genes (discussed above) were used to align genes whose positions were known only by linkage data and also as "anchors" for DNA sequence (described in detail below).

The chromosome is a closed circle of DNA, and early editions of the linkage map were shown in this way. In editions V to VII, the linkage map was displayed not as a circle but as 10 linear 10-min intervals. The present edition is similar, but because the number of known genes has increased, it is shown as 20 linear 5-Cs intervals (Fig. 1). This figure integrates gene location information discovered by genetic linkage and by physical analyses. The position of any gene shown was determined by using the data available in the following preference order: first, by the order of genes found in sequenced DNA segments; second, by Tn*10* or other physical anchors; third, by genetic linkage data; and, last, by extrapolation based on data from *E. coli* K-12 (see below).

Most of the elements shown on the map are structural genes for proteins or, in smaller number of cases, for rRNA or tRNA. We have not shown control elements for operons such as promoters, mRNA leaders, and terminators, nor have we shown the position of unnamed or poorly characterized chromosomal genes. We have not shown chromosomal elements such as repetitive extragenic palindromic sequences (259, 474), but an exception is that we have indicated the positions of the six IS*200* sequences which are mapped on the chromosome of LT2 (365, 367, 582).

NOMENCLATURE

We use the system of nomenclature for genes which was established by Demerec et al. (120). This system uses a three-letter designation for the gene or operon, e.g., *his* for mutations in the genes for histidine synthesis, followed by a capital letter, also in italics, designating the specific gene in that operon, e.g., *hisD* for a mutation in the gene for histidinol dehydrogenase. This system has become the de facto standard for bacterial genetics. Authors considering a three-letter designation for a new gene in *S. typhimurium* should check the published maps of *S. typhimurium* and *E. coli* to see whether the proposed name has been used previously; they are also encouraged to contact the *Salmonella* Genetic Stock Center (SGSC) to see whether a proposed name has been used previously but not published. Allele number assignments should also be obtained from the SGSC. It is important to clear such numbers with the SGSC so that each mutation is identified by a unique allele number. A mutation is defined by its three-letter designation plus the allele number; i.e., the mutation *his-1* might be initially thought to be *hisD1*, on the basis of its perceived enzyme defect, but later changed to *hisE1*. Thus, there should be only one *his-1* mutation. Using assigned numbers is especially important for transposon insertions named by the "z--" system proposed by Hong and Ames (277). In this case, the allele number may be the only identifier for a mutation, since all mutations mapped with "z--" have a single series of allele numbers. As mapping is refined, the "z--" designation of a mutation may change but the original allele number is retained. It is therefore important that assigned allele numbers be used to avoid confusion of different laboratories using the same number for different insertions. It is also vital that strains be identified by a unique strain designation, which includes two or three capital letters (assigned for *Salmonella* strains by the SGSC to the laboratory or by the *E. coli* Genetic Stock Center [CGSC] for *E. coli* strains) plus a number. The expanding use of the computer to keep records demands the use of correct strain designations; suffixes and phenotype designations after the strain designation to refer to derivatives of a parent strain are often not accepted by programs used for cataloging strains.

When possible, the same name should be used for homologous genes in related species such as *E. coli* and *Salmonella* spp. Many changes have been made in naming genes in these organisms to bring them into correspondence, and each edition of the maps has seen such changes. For example, a system of naming the genes for flagellar synthesis and function was proposed which recognizes the homology of these genera (298), and this system, now widely accepted, is used here. We encourage the trend to the use of the names for *E. coli* and *S. typhimurium* genes in other bacterial species, when functional data and amino acid sequence data indicate that the genes are homologous.

PLASMID pSLT IN *S. TYPHIMURIUM* LT2

Because the plasmid content of strains of a species of bacteria is often extremely variable, the plasmids are not normally considered part of the genome; therefore, neither the F factor in some lines of *E. coli* K-12 nor several types of plasmids frequently found in some wild-type *Salmonella* strains are treated as components of the normal genome. However, the original line of *S. typhimurium* LT2 contains a specific plasmid which we consider part of the genome. This plasmid has been called the virulence plasmid, the 90-kb plasmid, the 60-MDa plasmid, the cryptic plasmid, and pSLT (standing for *Salmonella* LT); we use the last designation.

For two reasons, we consider this plasmid to be part of the normal genome of *S. typhimurium* LT2. The first is that the plasmid is an almost invariable part of the genome of LT2 lines. It is carried by all the lines of LT2 which we have tested, except for those few from which it has been intentionally eliminated. This is true even though LT2 has been in culture for many years and has been subjected to innumerable single-colony isolations. Genes on the plasmid which regulate replication, incompatibility, and partitioning (37, 54, 69) enable the plasmid to be maintained stably at low copy number. In addition, pSLT or a closely related plasmid is commonly found in independent *S. typhimurium* isolates from nature.

The second reason for considering pSLT to be part of the genome is that genes on the plasmid influence the phenotype in several ways, and thus mutations of genes on the plasmid may be mistaken for mutations of chromosomal genes. This influence of pSLT on the phenotype was first seen by Smith et al. (624), who noted that it encoded Fin$^+$ (fertility inhibition) properties, reducing the fertility of Hfr strains of *S. typhimurium*; special measures have been developed which restore fertility up to the level found in *E. coli* K-12 (580). Many other genes have been detected because of their effect on phenotype. For example, mutations in the *traT* gene of pSLT cause an increase in outer membrane permeability, leading to an antibiotic supersensitivity phenotype; this gene is listed in Table 1. Other genes on pSLT, many of which influence the virulence of the strain, are also listed in Table 1 and are shown on a restriction map of pSLT in Fig. 1.

SEQUENCED GENES OF *S. TYPHIMURIUM*

Gene identification can be based largely on open reading frames, codon usage distributions, and sequence-based evidence of homology (47, 561). A significant amount of genomic DNA sequence has become available for *S. typhimurium*. By the end of 1994, we could assemble StySeq1, a nonredundant DNA sequence database modeled after the EcoSeq collection of *E. coli* genomic DNA sequences (573). In fact, the extensive genomic sequence data available for *E. coli* (see, e.g., references 43 and 635) are close to two-thirds of the genome. Therefore, many *S. typhimurium* genes were identified at the sequence level as partial but convincing matches to one of the *E. coli* protein sequences in the EcoGene subset of SWISS-PROT (24).

StySeq1 has 197 contiguous sequence blocks (contigs) that do not overlap. Together, the nonredundant chromosomal genomic *S. typhimurium* StySeq1 DNA sequence collection is 548,508 bp in length. This represents 11.4% of the *Salmonella* chromosome, estimated to be 4,808 kb in length (404). Eight contigs are greater than 10,000 bp in length. The longest contig, hisGstyM (Table 3), is 33,958 bp in length.

Of the 197 DNA sequences in this collection (Table 3), 191 are ordered and oriented as they might be on the *S. typhimurium* chromosome. This was accomplished in several ways: physical anchor, genetic pin, and extrapolation.

(i) In the physical anchor method, if a Tn*10* insertion, rare restriction site, or other direct physical link could be associated with one of the genes from StySeq, it was anchored and the positions of the other nearby genes were calculated on the basis of a single-base-pair anchor point per contig. Gene positions thus have high local precision (1-bp resolution) and coarse genomic map position accuracy, based on analysis by PFGE (ranging from 1,000 bp in some situations to over 10,000 bp depending on the locations of restriction sites for the enzymes used). Unsequenced genes could also be anchored, and this information was taken into account in mapping the unsequenced genes depicted in Fig. 1. Sixty-two StySeq1 contigs were positioned in this way. (ii) In the genetic pin method, gene positions were assigned to a number of sequenced and unsequenced genes on the basis of linkage data. The positions of the anchors were used to realign conjugation and transduction mapping distances, allowing the integration of physical and genetic maps presented in Fig. 1. In turn, those genetic map positions were used to pin more sequences to the integrated genomic map. An additional 93 contigs in Table 3 were positioned by this approach. (iii) The extrapolation method was used to position a final 36 contigs by using map position information from *E. coli-Salmonella* gene pairs to extrapolate a position.

The aligned DNA sequences are ordered to coincide with the orientations of homologous sequences in the EcoSeq7 collection of aligned and oriented *E. coli* genes. Although some local inversions are likely to have occurred, most comparisons indicate a close correlation of the orientations and map positions of genes between *E. coli* and *S. typhimurium*, with one major exception. There is a large inversion of a chromosomal segment relative to the corresponding *E. coli* region with endpoints near 26 and 36 min on the genetic map (581). We could localize this region on the physical map (Fig. 1), and this allowed us to set the orientation of genes in this region of *S. typhimurium* as opposite to that of the *E. coli* homologs in this inverted segment.

Alignment of all but six of the StySeq1 contigs, at least as a best approximation subject to constant refinement, allowed the genes encoded in the DNA sequences to also be aligned. In this way, 523 protein-coding genes and 15 structural RNA genes were given genomic map positions based locally on DNA sequence information and globally on a combination of physical anchor points, genetic-cross data, and extrapolation from the *E. coli* map. Fifty-one unnamed genes (described as *orf* or similar in GenBank entries) were given provisional names beginning with the letter y (573); these genes are excluded from Table 1 but are listed in Table 3.

Until a larger proportion of the *S. typhimurium* genome is sequenced, the genetic linkage data will remain useful as the basis for the map. *E. coli* has a high-resolution genomic restriction map for the entire chromosome, whereas the high-resolution map of *S. typhimurium* is being assembled as parts (749). Nonetheless, several genes were physically positioned by DNA sequence and high-resolution restriction map data in the 91- to 96-Cs region of the *S. typhimurium* LT2 chromosome (749) by using a single anchor.

Having access to both *E. coli* and *S. typhimurium* DNA sequence over the same region provides an opportunity to predict frameshift corrections and helps ensure the highest level of accuracy. Other organisms help identify probable new genes in *S. typhimurium* with homologs as well, but the comparison with *E. coli* involves enough preference for third-position changes to establish the correct frame for most protein-coding genes.

MAP REFINEMENT

If errors are detected in this work, we hope that this information will be transmitted to us to allow corrections. To assist in the preparation of future map editions or updates, we would appreciate receiving any information regarding the position and function of new genes or refinements to the positions or roles of the genes described here. Electronic mail should be addressed to kesander@acs.ucalgary.ca and to rudd@ncbi.nlm.nih.gov. StySeq1 and associated files can be retrieved in electronic form from the anonymous ftp site ncbi.nlm.nih.gov in the /repository/Eco/Sty directory. Diskettes will be mailed on request to those without Internet access. A list of strains with transposon insertions (Tn*10*, Tn*5*, and others) was given in edition VII (581); an updated and greatly extended list will be available shortly (13).

Several database files (maintained as binhexed Stuffit Self Extracting Archives) are available from the University of Calgary via Internet using the Gopher menu system. These include updated versions of Tables 1 and 3, the list of strains in the SGSC, and the list of strains with transposon insertions. Interested parties should navigate to the University of Calgary Gopher and then select, in order, "Faculty and Departments Information," "Department of Biological Sciences," and "Salmonella Genetic Stock Centre." These databases are also available via World Wide Web (http://www.ucalgary.ca/~kesander).

TABLE 1. Genes of *S. typhimurium*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
accA		Acetyl-CoA carboxylase	6.0	369
aceA	Acetate	Growth on acetate or fatty acids; isocitrate lyase (EC 4.1.3.1)	91.3	579, 581
aceB	Acetate	Growth on acetate or fatty acids; malate synthase (EC 4.1.3.2)	91.3	579, 581
aceE	Acetate	Acetate requirement; pyruvate dehydrogenase (pyruvate:cytochrome b_1 oxidoreductase) (EC 1.2.2.2)	3.7	579, 581
aceF	Acetate	Acetate requirement; pyruvate dehydrogenase (pyruvate lipoate oxidoreductase) (EC 1.2.4.1)	3.7	579, 581
aceK	Acetate	Isocitrate dehydrogenase kinase/phosphatase	91.3	433
aciA	Acid inducible	pH-regulated gene; acid inducible	99.5	168
aciB	Acid inducible	pH-regulated gene; acid inducible	92.4	168
ack	Acetate kinase	Acetate kinase (ATP:acetate phosphotransferase) (EC 2.7.2.1)	50.9	579, 581
ada		Inducible DNA repair system protecting against methylating and alkylating agents; O^6-methylguanine DNA methyltransferase	50.1	237, 723, 759
adhE		Reduced survival in macrophages; CoA-linked acetaldehyde dehydrogenase and alcohol dehydrogenase	38.4	29
adk		Adenylate kinase; sensitivity to glycine betaine in high-osmolality media (EC 2.7.4.3)	11.6	230
ahpC	Alkyl hydroperoxide	Alkyl hydroperoxide reductase, C_{22} subunit	14.1	148, 410, 581, 665, 666
ahpF	Alkyl hydroperoxide	Alkyl hydroperoxide reductase, F52a subunit	14.1	148, 581, 665, 666
alaS	Alanine	Alanine-tRNA synthetase	62.0	194
alkB	Alkylation	DNA repair system specific for alkylated DNA	50.1	237
alr	Alanine racemase	Biosynthetic alanine racemase (EC 5.1.1.1)	92.2	581
amiA		*N*-Acetylmuramyl-L-alanine amidase activity; putative	53.2	757
amiB		*N*-Acetylmuramyl-L-alanine amidase (EC 3.5.1.28)	95.0	434
amk		AMP kinase	9.1	581
ampC	Ampicillin	β-Lactamase; penicillin resistance (EC 3.5.2.6)	94.5	15
ampD	Ampicillin	β-Lactamase regulation; putative signalling protein	3.6	291
amtA		Resistance to 40 mM 3-amino-1,2,4-triazole in the presence of histidine	37.6	579, 581
amyA	Amylase	Cytoplasmic α-amylase (EC 3.2.1.1)	42.6	337, 547
ana		Anaerobic gas production	38.7	581
aniB	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	93.9	581
aniC	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	93.9	581
aniD	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	92.4	581
aniF	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	68.0	581
aniG	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	67.8	581
aniH	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	82.6	581
aniI	Anaerobically inducible	Induced by anaerobiosis; does not reduce benzyl viologen	40.1	581
ansB		L-Asparaginase II; regulated by CRP and anaerobiosis	67.1	309
apbA		Alternative pyrimidine biosynthetic pathway; synthesis of thiamine in presence of exogenous purines	10.0	128
apeB	Acyl peptide esterase	Acyl amino acid esterase; hydrolyzes *N*-acetyl-L-phenylalanine-β-naphthyl ester	11.0	579, 581
apeE	Acyl peptide esterase	Membrane-bound acyl amino acid esterase; hydrolyzes *N*-acetyl-L-phenylalanine-β-naphthyl ester	13.5	96, 579, 581
apeR	Acyl peptide esterase	*apeD*; regulatory gene for *apeE*	85.0	579, 581
aphA		Nonspecific acid phosphatase II	NM	579, 581
apt		Adenine phosphoribosyltransferase	11.5	579, 581
araA	Arabinose	L-Arabinose isomerase (EC 5.3.1.4)	2.4	579, 581
araB	Arabinose	Ribulokinase (EC 2.7.1.16)	2.5	579, 581
araC	Arabinose	Regulatory gene for arabinose catabolic enzymes	2.5	92, 579, 581
araD	Arabinose	L-Ribulose-phosphate 4-epimerase (EC 5.1.3.4)	2.4	579, 581
arcA		Cytoplasmic DNA-binding component system for repression of genes during anaerobiosis	100.0	5, 17
arcB		Membrane-bound sensor of two-component system for repression of genes during anaerobiosis	72.4	5, 17
argA	Arginine	*argB*; amino acid acetyltransferase (EC 2.3.1.1)	65.1	579, 581
argB	Arginine	*argC*; *N*-acetyl-γ-glutamate kinase (EC 2.7.2.8)	89.6	579, 581
argC	Arginine	*argH*; *N*-acetyl-γ-glutamyl phosphate reductase (EC 1.2.1.38)	89.6	579, 581
argD	Arginine	*argG*; acetylornithine aminotransferase (EC 2.6.1.11)	75.1	579, 581
argE	Arginine	*argA*; acetylornithine deacetylase (EC 3.5.1.16)	89.6	579, 581
argG	Arginine	*argE*; argininosuccinate synthetase (EC 6.3.4.5)	72.0	579, 581
argH	Arginine	*argF*; argininosuccinate lyase (EC 4.3.2.1)	89.6	579, 581
argL	Arginine	Ornithine carbamoyltransferase (EC 2.1.3.3)	97.2	579, 581
argP	Arginine	Arginine transport	NM	579, 581
argQ	Arginine	Arginine tRNA 2	62.0	42

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
argR	Arginine	L-Arginine regulation	73.4	417, 419, 579, 581
argS	Arginine	Arginyl-tRNA synthetase (EC 6.1.1.19)	41.6	579, 581
argT	Arginine	Lysine-arginine-ornithine-binding protein	51.3	579, 581, 592
argU	Arginine	*fimU*; arginine tRNA 1 for rare codons (AGA and AGG); essential for fimbriae expression	15.2	679
argV	Arginine	Arginine tRNA 2	62.0	42
argX	Arginine	*argT*, *argU*, *use*; arginine tRNA 1	85.6	418, 581
argY	Arginine	Arginine tRNA 2	62.0	42
argZ	Arginine	Arginine tRNA 2	62.0	42
aroA	Aromatic	3-Enolpyruvylshikimate 5-phosphate synthetase	19.9	75, 85, 579, 581, 586
aroB	Aromatic	5-Dehydroquinate synthetase	75.7	579, 581
aroC	Aromatic	*aroD*; chorismate synthetase	52.0	579, 581, 668, 669
aroD	Aromatic	*aroE*; 5′-dehydroquinate dehydratase (EC 4.2.1.10)	30.5	579, 581, 601, 629
aroE	Aromatic	*aroC*; 5-dehydroshikimate reductase	74.4	579, 581
aroF	Aromatic	Tyrosine-repressible DAHP synthetase	58.6	461, 579, 581
aroG	Aromatic	Phenylalanine-repressible DAHP synthetase	17.3	579, 581
aroH	Aromatic	Tryptophan-repressible DAHP synthetase	30.4	579, 581
aroP	Aromatic	Aromatic amino acid transport	3.6	292, 579, 581
aroT	Aromatic	Transport of tryptophan, phenylalanine, and tyrosine	39.3	579, 581
asd		Aspartic semialdehyde dehydrogenase (EC 1.2.1.11)	77.4	101, 186, 579, 581
asm		Unable to assimilate low levels of ammonia; deficient in glutamate synthase and glutamine synthase	70.5	579, 581
asn	Asparagine	Asparagine synthesis	82.4	579, 581
asnU	Asparagine	Asparagine tRNA	44.1	78
aspA	Aspartate	L-Aspartate ammonia-lyase (EC 4.3.1.1)	94.2	15
aspC	Aspartate	Aspartate aminotransferase (EC 2.6.1.1)	22.7	581
asrA		Anaerobic sulfite reductase	57.1	286, 287
asrB		Anaerobic sulfite reductase	57.1	286, 287
asrC		Anaerobic sulfite reductase	57.1	286, 287
ataA	Attachment	*attP22 I*; attachment site for prophage P22	7.8	579, 581
atbA	Attachment	*attP27 I*; attachment site for prophage P27	12.7	579, 581
atbB	Attachment	*attP27 II*; second attachment site for prophage P27	8.1	579, 581
atcA	Attachment	*attP221*; attachment site for prophage P221	25.9	579, 581
atdA	Attachment	*attP14*; attachment site for prophage P14 in group C *Salmonella* spp.	61.1	579, 581
atp		*unc*, *uncA*; membrane-bound (Mg^{2+}, Ca^{2+}) ATPase	84.6	165, 166, 192, 579, 581
atrB	Acid tolerance response	Defective in pre- but not post-acid shock-induced acid tolerance	32.2	162, 164, 165
atrD	Acid tolerance response	Defective in both pre- and post-acid shock-induced acid tolerance	68.1	162, 164
atrF	Acid tolerance response	Defective in both pre- and post-acid shock-induced acid tolerance	13.7	162, 164
atrG	Acid tolerance response	Defective in both pre- and post-acid shock-induced acid tolerance	NM	164
atrR	Acid tolerance response	*atbR*; constitutive acid tolerance; *trans*-acting regulator of *atrB*	89.5	164
ats		Arylsulfatase	NM	579, 581
att15	Attachment	Attachment site for phage e15 in group E *Salmonella* spp.	46.3	579, 581
att34	Attachment	Attachment site for phage e34 in group E *Salmonella* spp.	5.7	579, 581
attN	Attachment	Attachment site for prophage N in *S. montevideo*	52.0	579, 581
avtA		Alanine-valine transaminase, transaminase C (EC 2.6.1.66)	80.2	581
aziA	Azide	Resistant to 3 mM sodium azide on L-methionine	3.4	579, 581
bfp	Bundle-forming pili	Interbacterial linkage, adhesion to epithelial cells	NM	636
bioA	Biotin	*bio*; 7,8-diaminopelargonic acid synthetase	18.1	579, 581, 611
bioB	Biotin	Biotin synthetase	18.1	611
bioC	Biotin	Block prior to pimeloyl-CoA	18.2	611
bioD	Biotin	Dethiobiotin synthetase	18.2	611
bioF	Biotin	7-Keto-8-aminopelargonic acid synthetase	18.1	611
birA	Biotin repressor	Biotin-(acetyl-CoA carboxylase) holoenzyme synthetase	90.0	125
brnQ		*ilvT*; branched-chain amino acid transport	8.9	579, 581
btuB	B_{12} utilization	*bfe*; transport of cobalamins	89.7	123, 558, 559, 579, 581, 738
btuC	B_{12} utilization	Transport of cobalamins	30.4	123, 629
btuD	B_{12} utilization	Transport of cobalamins	30.4	123
btuE	B_{12} utilization	Transport of cobalamins	30.4	123, 373
cadA	Cadaverine	Lysine decarboxylase (EC 4.1.1.18)	56.2	168, 193

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
cadC	Cadaverine	Regulation of *cadA*	56.2	168
capS	Capsule	Capsular polysaccharide synthesis	31.1	579, 581
carA		*argD*, *ars*, *cap*, *pyrA*; carbamyl phosphate synthase, glutamine (light) subunit (EC 2.7.2.9)	1.6	72, 241, 310, 343, 419, 420
carB		*pyrA*; carbamyl phosphate synthase, ammonia (heavy) subunit (EC 2.7.2.9)	1.7	72, 241, 310, 343, 419, 420
cbiA		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.7	571
cbiB		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.7	571
cbiC		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.7	571
cbiD		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.7	571
cbiE		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.7	571
cbiF		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.7	571
cbiG		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.6	571
cbiH		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.6	571
cbiJ		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.6	571
cbiK		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.6	571
cbiL		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.6	571
cbiM		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.6	571
cbiN		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.5	571
cbiO		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.5	571
cbiP		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.5	571
cbiQ		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.5	571
cbiT		*cobI*; synthesis of vitamin B_{12} adenosyl cobinamide precursor	43.7	571
cdd		Cytidine deaminase (EC 3.5.4.5)	47.5	579, 581
cheA	Chemotaxis	*cheP*; chemotaxis; ATP-dependent kinase; phosphorylates CheB and CheY	42.0	131, 370, 423, 579, 581, 663, 664
cheB	Chemotaxis	*cheX*; chemotaxis; bifunctional monomeric protein; C-terminal γ-carboxyl methylesterase and N-terminal transferase	41.9	423, 579, 581, 663, 664
cheR	Chemotaxis	Chemotaxis; *S*-adenosylmethionine-dependent methyltransferase	41.9	423, 579, 581, 664, 670
cheS	Chemotaxis	Chemotaxis	NM	579, 581
cheW	Chemotaxis	Chemotaxis	42.0	579, 581, 664
cheY	Chemotaxis	*cheQ*; chemotaxis; cytoplasmic protein; interacts at flagellar motor to reverse flagellar rotation	41.8	21, 77, 131, 421–423, 429, 581, 634, 663, 664
cheZ	Chemotaxis	*cheT*; chemotaxis; stimulates phospho-CheY dephosphorylation	41.8	131, 421, 423, 579, 581, 634, 664
chlF	Chlorate	Resistance; may be part of *moe* operon	19.1	579, 581, 604, 653
chlG	Chlorate	Resistance; affects nitrate reductase, tetrathionate reductase, chlorate reductase, and hydrogen lyase	56.8	579, 581, 653
cil	Citrate lyase	Mutants unable to utilize citrate in anaerobic conditions without additional carbon sources	66.9	581
citA	Citrate	Citrate carrier, different from TctI, TctII, TctIII transport systems	17.0	610
citB	Citrate	Citrate carrier, different from TctI, TctII, TctIII transport systems	17.0	610
cld	Chain length determinant	*rol*; regulation of chain length in the O units of the LPS	44.9	26, 27
clmA	Conditional-lethal mutation	Heat- or cold-sensitive mutation	86.4	581, 589
clmB	Conditional-lethal mutation	Heat- or cold-sensitive mutation	8.8	581, 589
clmC	Conditional-lethal mutation	Heat- or cold-sensitive mutation	72.1	581, 589
clmD	Conditional-lethal mutation	Heat- or cold-sensitive mutation	85.5	581, 589
clmE	Conditional-lethal mutation	Heat- or cold-sensitive mutation	74.5	581, 589
clmG	Conditional-lethal mutation	Heat- or cold-sensitive mutation	12.3	581, 589
clmI	Conditional-lethal mutation	Heat- or cold-sensitive mutation	6.5	589
clmJ	Conditional-lethal mutation	Heat- or cold-sensitive mutation	32.4	589
clmK	Conditional-lethal mutation	Heat- or cold-sensitive mutation	62.4	589

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
clmM	Conditional-lethal mutation	Heat- or cold-sensitive mutation	99.1	589
clmN	Conditional-lethal mutation	Heat- or cold-sensitive mutation	46.9	589
clmP	Conditional-lethal mutation	Heat- or cold-sensitive mutation	81.1	589
clmQ	Conditional-lethal mutation	Heat- or cold-sensitive mutation	58.1	589
clmR	Conditional-lethal mutation	Heat- or cold-sensitive mutation	26.3	589
clmS	Conditional-lethal mutation	Heat- or cold-sensitive mutation	95.8	589
clmT	Conditional-lethal mutation	Heat- or cold-sensitive mutation	51.0	589
cmk		Cytidylate kinase (EC 2.7.4.14)	20.0	579, 581
coaA	Coenzyme A	CoA synthesis; pantothenate kinase	90.3	5, 579, 581
cobA	Cobalamin	*cobIV*; ATP:corrinoid adenosyltransferase	38.0	144, 318, 513, 581, 672, 673
cobB	Cobalamin	DMB ribose phosphate phosphatase	20.6	701
cobC	Cobalamin	DMB ribose phosphate phosphatase	15.6	213, 505, 515
cobD	Cobalamin	Synthesis of 1-amino-2-propanol moiety of vitamin B_{12}	15.6	213, 505
cobF	Cobalamin	Recessive regulator of *cbi* operon	26.9	18
cobI	Cobalamin	Operon encoding genes for synthesis of cobinamide intermediate of vitamin B_{12}	43.6	581
cobII	Cobalamin	Operon encoding genes for synthesis of DMB intermediate of vitamin B_{12}	43.3	581
cobIII	Cobalamin	Operon encoding genes for joining cobinamide and DMB intermediates of vitamin B_{12}	43.4	581
cobJ	Cobalamin	*cobII*; synthesis of 5,6-DMB	43.3	143
cobK	Cobalamin	*cobII*; synthesis of 5,6-DMB	43.3	143
cobL	Cobalamin	*cobII*; synthesis of 5,6-DMB	43.3	143
cobM	Cobalamin	*cobII*; synthesis of 5,6-DMB	43.3	143
cobR	Cobalamin	*cis*-acting, dominant regulator for the *cbi* operon	44.0	18
cobS	Cobalamin	*cobIII*; synthesis of the nucleotide loop that joins DMB to the corrin ring	43.5	143, 514, 571
cobT	Cobalamin	*cobIII*; synthesis of DMB and transfer of ribose phosphate from NMN to DMB	43.4	143, 514, 701
cobU	Cobalamin	*cobIII*; synthesis of the nucleotide loop that joins DMB to the corrin ring	43.5	143, 513, 514, 571
cod		Cytosine deaminase (EC 3.5.4.1)	72.8	579, 581
corA	Cobalt resistance	Magnesium transport; cobalt resistance (high level)	85.8	202, 270, 581, 627, 630–632
corB	Cobalt resistance	Magnesium transport; cobalt resistance (low level)	58.7	202
corC	Cobalt resistance	Magnesium transport; cobalt resistance (low level)	16.1	202, 228
corD	Cobalt resistance	*apaG*; magnesium transport; cobalt resistance (low level)	2.1	202
cpdB		*cpd*; 2′,3′-cyclic phosphodiesterase (EC 3.1.4.16)	69.5	403
cpsB	Capsule	M antigen capsular polysaccharide synthesis; homologous to *rfbM*	45.5	652
cpsG	Capsule	*rfbL*; M antigen capsular polysaccharide synthesis; homologous to *rfbK*	45.4	652
crp		cAMP receptor protein	75.0	5, 579, 581
crr		Factor III for sugar transport by phosphotransferase IIB′ (*ptsG*) system	52.9	569, 579, 581
cspA	Cold shock protein	Transcriptional activation of cold shock promoters	80.0	372
cspG	Cold shock protein	Transcriptional activation of cold shock promoters; putative	42.9	561
cutE		*lnt*; apolipoprotein *N*-acyltransferase	16.1	228
cwd	Cell wall defect	Sensitive to bile salts; mucoid	38.5	581
cyaA	cAMP	*cya*; adenylate cyclase (EC 4.6.1.1)	85.7	146, 579, 581, 696
cysA	Cysteine	Sulfate-thiosulfate transport; chromate resistance	53.0	284, 579, 581
cysB	Cysteine	Regulation of L-cysteine transport and biosynthesis	37.7	284, 285, 458, 508, 509, 579, 581
cysC	Cysteine	Adenylylsulfate kinase (EC 2.7.1.25)	64.3	579, 581
cysD	Cysteine	Sulfate adenylyltransferases (EC 2.7.7.4)	64.3	579, 581
cysE	Cysteine	Serine acetyltransferase (EC 2.3.1.30)	81.0	121, 579, 581
cysG	Cysteine	Bifunctional protein: siroheme synthetase; uroporphyrinogen III methylase	75.5	209, 579, 581, 643, 751
cysH	Cysteine	Adenylylsulfate reductase (EC 1.8.99.2)	64.2	458, 507, 508, 510, 579, 581

Continued on following page

TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
cysI	Cysteine	Heme protein component of sulfite reductase	64.2	239, 458, 507, 508, 510, 579, 581
cysJ	Cysteine	Flavoprotein component of sulfite reductase	64.2	239, 458, 507, 508, 510, 579, 581
cysK	Cysteine	*trz*; resistance to 1,2,4-triazole; *O*-acetylserine sulfhydrylase A (EC 4.2.99.8)	52.8	458, 579, 581
cysL	Cysteine	Resistance to selenate	53.1	579, 581
cysM	Cysteine	*O*-Acetylserine sulfhydrylase B (EC 4.2.99.8)	53.0	579, 581
cysP	Cysteine	Periplasmic thiosulfate binding protein	53.1	283, 284
cysQ	Cysteine	Regulation of 3′-phosphoadenoside 5′-phosphosulfate pools; putative	69.5	403
cysU	Cysteine	*cysAa*, *cysT*; sulfate-thiosulfate transport	53.1	283, 284
cysW	Cysteine	*cysAb*; sulfate-thiosulfate transport	53.1	284
cysZ	Cysteine	Sulfate transport; putative	52.8	61
cytR		Regulatory gene for *deo* operon and *udp* and *cdd* genes	88.6	579, 581
dadA		*dad*; D-histidine, D-methionine utilization; D-alanine dehydrogenase (EC 1.4.99.1)	41.1	579, 581
dadB		Catabolic alanine racemase (EC 5.1.1.1)	41.1	579, 581
dadR		Insensitivity of *dadA* to catabolite repression	41.1	579, 581
dam		DNA adenine methylase	75.6	235, 579, 581
dapA	Diaminopimelate	Dihydropicolinate synthetase (EC 4.2.1.52)	54.0	579, 581
dapB	Diaminopimelate	Dihydropicolinate reductase	0.5	579, 581
dapC	Diaminopimelate	Tetrahydropicolinate succinylase	5.2	579, 581
dapD	Diaminopimelate	Succinyl-diaminopimelate aminotransferase	5.2	579, 581
dapF	Diaminopimelate	Diaminopimelate epimerase (EC 5.1.1.7)	5.4	579, 581
dcd		dCTP deaminase (EC 3.5.4.13)	45.9	579, 581
dcm		DNA cytosine methylation	43.1	579, 581
dcp		Dipeptidyl carboxypeptidase	32.5	240, 579, 581
dctA		Transport of dicarboxylic acids	79.9	579, 581
ddlA	D-Alanine	D-Alanine:D-alanine ligase (EC 3.6.2.4)	8.7	115, 347
deoA	Deoxyribose	*tpp*; thymidine phosphorylase (EC 2.4.2.4)	99.0	579, 581
deoB	Deoxyribose	*drm*; phosphopentomutase (EC 2.7.5.6)	99.0	579, 581
deoC	Deoxyribose	*dra*; phosphodeoxyriboaldolase (EC 4.1.2.4)	99.0	579, 581
deoD	Deoxyribose	*pnu*, *pup*; purine nucleoside phosphorylase (EC 2.4.2.1)	99.0	579, 581
deoK	Deoxyribose	Deoxyribokinase	20.2	579, 581
deoP	Deoxyribose	Deoxyribose transport	20.3	579, 581
deoR	Deoxyribose	Constitutive for enzymes of *deoA*, *deoB*, *deoC*, and *deoD*	19.4	579, 581
dgo		D-Galactonate utilization	83.2	188
dgt		dGTP triphosphohydrolase (EC 3.1.5.1)	5.1	317
dhb		2,3-Dihydroxybenzoic acid requirement	19.3	579, 581
dhuA	D-Histidine	Utilization; increased activity of histidine-binding protein J	51.2	579, 581
divA	Division	*wrkA*; septum initiation defect	88.4	579, 581
divC	Division	*smoA*; septum initiation defect	3.1	579, 581
divD	Division	Round cell morphology	55.6	104, 579, 581
dml	D-Malate	Utilization	82.2	579, 581
dnaA	DNA	DNA initiation	83.6	243, 579, 581
dnaB	DNA	DNA synthesis	92.1	579, 581
dnaC	DNA	DNA synthesis initiation and cell division uncoupling	98.8	579, 581
dnaE	DNA	DNA synthesis	5.9	369, 579, 581
dnaG	DNA	DNA biosynthesis; DNA primase	70.0	579, 581
dnaJ	DNA	DNA biosynthesis	0.3	581
dnaK	DNA	DNA biosynthesis	0.3	148, 581
dnaL	DNA	DNA biosynthesis	NM	581
dnaN	DNA	DNA biosynthesis; DNA polymerase III, β subunit	83.6	581
dnaQ	DNA	DNA biosynthesis	6.9	368, 390, 581, 621
dnaX	DNA	DNA biosynthesis	11.5	581
dnaY	DNA	DNA biosynthesis	NM	581
dnaZ	DNA	DNA biosynthesis	NM	581
dor		Deletion of r-determinants from plasmids	55.7	581
dpp		Dipeptide permease	75.9	2, 138, 581
dsd		D-Serine sensitivity; D-serine dehydratase (EC 4.2.1.14)	52.7	579, 581
dum		dUMP synthesis	NM	579, 581
earA		Regulates expression of *aniG*	88.2	581
earC		*trans*-acting regulatory protein for *aciA*	46.8	168
eca		Enterobacterial common-antigen synthesis	NM	579, 581
endA		Endonuclease I	67.1	579, 581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
eno	Enolase	Enolase (EC 4.2.1.11)	64.3	579, 581
ent	Enterochelin	*asc*, *enb*; enterochelin (dihydroxybenzoylserine trimer)	13.6	73, 87, 541, 542, 581
envA	Envelope	Cell division defect, chain formation	3.2	579, 581
envD	Envelope	Autolysis; drug sensitivity; alterations in cell morphology	17.1	579, 581
envZ	Envelope	*ompB*, *tppB*, *tppA*; positive regulation of tripeptide permease and outer membrane protein	76.0	391, 581
eutA	Ethanolamine utilization	Vitamin B_{12} adenosyl transferase; required for use of ethanolamine as sole carbon or nitrogen source	53.3	567, 568, 581, 609
eutB	Ethanolamine utilization	Ethanolamine ammonia lyase, subunit I	53.3	151, 152, 567, 568, 581, 609
eutC	Ethanolamine utilization	Ethanolamine ammonia lyase, subunit II	53.2	151, 152, 567, 568, 581, 609
eutD	Ethanolamine utilization	CoA-dependent acetaldehyde dehydrogenase	53.3	567, 568, 581
eutE	Ethanolamine utilization	Acetaldehyde CoA-reductase	53.3	567, 568, 581
eutF	Ethanolamine utilization	Ethanolamine permease or transcription factor for expression of *eut* operon	38.2	512
eutG	Ethanolamine utilization	Function unknown	53.3	608
eutH	Ethanolamine utilization	Function unknown	53.2	329
eutR	Ethanolamine utilization	Positive regulatory gene for *eut* operon	53.2	567, 568, 581, 609
exbB		Biopolymer uptake; outer membrane protein	69.1	524
fabB	Fatty acid biosynthesis	β-Ketoacyl acyl carrier protein synthetase I (EC 2.3.1.41)	51.9	579, 581
fabI	Fatty acid biosynthesis	*envM*; enoyl-(acyl-carrier-protein) reductase (EC 1.3.1.9)	37.6	708
fabZ	Fatty acid biosynthesis	Fatty acid biosynthesis; putative	4.1	267
fdhB	Formate dehydrogenase H	Required for formate dehydrogenase H and N	18.0	579, 581, 653
fdhF	Formate dehydrogenase H	*fhl*; formate dehydrogenase H	92.8	581, 653
fdhR	Formate dehydrogenase H	Positive regulator of *fdhF* expression	75.0	149
fdhS	Formate dehydrogenase H	Positive regulator of *fdhF* expression	75.0	149
fdnA	Formate dehydrogenase N	Mutants lack formate dehydrogenase N and nitrate reductase	87.6	579, 581
fdnB	Formate dehydrogenase N	Synthesis or activation of the cytochrome associated with formate dehydrogenase N	87.7	579, 581, 654
fdnC	Formate dehydrogenase N	Synthesis or activation of the cytochrome associated with formate dehydrogenase N	87.7	581, 654
fdp		Fructose-1,6-diphosphatase (EC 3.1.3.11)	99.2	579, 581
fhlA	Formate hydrogenlyase	Formate hydrogenlyase; putative	62.8	454
fhlD	Formate hydrogenlyase	Mutants lack formate dehydrogenase H activity	81.8	579, 581
fhuA	Ferric hydroxamate uptake	Outer membrane receptor for ferrichrome	4.9	52, 349
fhuB	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	4.9	52, 349
fhuC	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	4.9	52, 349
fhuD	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component	5.0	52, 349
fic		Filamentation in presence of cAMP in mutant	75.1	700
fimA	Fimbriae	*pil*, *fim*; major subunit protein of the fimbriae	15.0	409, 410, 579, 581, 678
fimC	Fimbriae	Fimbriae	15.0	271, 679
fimD	Fimbriae	Fimbriae	15.1	678, 679
fimF	Fimbriae	Fimbriae	15.1	271, 679
fimH	Fimbriae	Adhesin component of the fimbriae	15.1	410, 678, 679
fimI	Fimbriae	Fimbriae	15.0	271, 679
fimW	Fimbriae	Fimbriae	15.2	271, 679
fimY	Fimbriae	Fimbriae	15.2	271, 679
fimZ	Fimbriae	Fimbriae	15.1	271, 679
fis	Factor for inversion stimulation	DNA-binding protein involved in site-specific inversion and recombination, gene regulation, and DNA replication	74.0	159, 511

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
flgA	Flagella	*flaFI*; flagellar synthesis; P-ring formation of the flagellar basal body	26.4	203, 362–364, 408, 579, 581
flgB	Flagella	*flaFII*; flagellar synthesis; function unknown	26.4	203, 265, 276, 322, 357, 362, 579, 581
flgC	Flagella	*flaFIII*; flagellar synthesis; basal-body protein	26.4	203, 276, 322, 357, 579, 581
flgD	Flagella	*flaFIV*; flagellar synthesis; hook-capping protein to enable assembly of hook protein subunits	26.4	203, 274, 359, 494, 579, 581
flgE	Flagella	*flaFV*; flagellar synthesis; hook protein	26.4	274, 459, 579, 581
flgF	Flagella	*flaFVI*; flagellar synthesis; basal-body rod protein	26.5	276, 321, 322, 357, 579, 581
flgG	Flagella	*flaFVII*; flagellar synthesis; basal-body rod protein	26.5	276, 322, 357, 579, 581
flgH	Flagella	*flaFVIII*; flagellar synthesis; basal-body L-ring protein	26.5	321, 579, 581
flgI	Flagella	*flaFIX*; flagellar synthesis; basal-body P-ring protein	26.5	321, 579, 581
flgJ	Flagella	*flaFX*; flagellar synthesis; function unknown	26.5	321, 579, 581
flgK	Flagella	*flaW*; flagellar synthesis; hook-associated protein 1	26.6	274, 299, 579, 581
flgL	Flagella	*flaU*; flagellar synthesis; hook-associated protein 3	26.6	274, 299, 579, 581
flgM	Flagella	*flgR*, *mviS*, *rflB*; negative regulator of σ^F	26.4	203–205, 360, 492, 591
flgN	Flagella	Initiation of flagellar filament assembly	26.4	364
flhA	Flagella	*flaC*; flagellar synthesis; function unknown	41.7	363, 454, 456, 579, 581, 725
flhB	Flagella	*flaM*; flagellar synthesis; assists *fliK* in hook length control	41.7	131, 265, 361, 362, 456, 579, 581
flhC	Flagella	*flaE*; flagellar synthesis; regulation of gene expression	42.1	205, 579, 581
flhD	Flagella	*flaK*; flagellar synthesis; regulation of gene expression; putative flagellum-specific σ factor	42.1	205, 362, 581
flhE	Flagella	Function unknown; not essential for flagellar synthesis or function	41.7	456
fliA	Flagella	*flaL*; flagellar synthesis; alternative σ factor, σ^F, for flagellar expression	42.4	205, 326, 360, 362, 363, 491, 492, 579, 581
fliB	Flagella	*nml*; flagellar synthesis; *N*-methylation of lysine residues in flagellin	42.5	579, 581
fliC	Flagella	*H1*; flagellar synthesis; phase 1 flagellin (filament structural protein)	42.5	204, 246, 297, 300, 302, 332, 492, 495, 625, 626, 699, 764
fliD	Flagella	*flaV*; flagellar synthesis; hook-associated protein 2	42.5	29, 299, 362, 579, 581
fliE	Flagella	*flaAI*; flagellar synthesis; function unknown	42.7	357, 362, 462, 547, 579, 581
fliF	Flagella	*flaAII.1*; flagellar synthesis; basal-body M-ring protein	42.7	171, 322, 362, 496, 547, 579, 581, 709, 710
fliG	Flagella	*flaAII.2*, *motC*, *cheV*; flagellar synthesis; motor switching and energizing	42.7	131, 134, 171, 301, 341, 342, 429, 500, 579, 581
fliH	Flagella	*flaAII.3*; flagellar synthesis; function unknown	42.8	579, 581, 725
fliI	Flagella	*flaAIII*; flagellar assembly; may be ATPase in protein export pathway	42.8	130, 131, 579, 581, 725
fliJ	Flagella	*flaS*; flagellar synthesis; function unknown	42.8	579, 581, 725
fliK	Flagella	*flaR*; flagellar synthesis; hook length control and replacement of *flgD* by *flgK*	42.8	265, 361, 579, 581
fliL	Flagella	*flaQJ*; flagellar synthesis; function unknown	42.8	342, 362, 548, 579, 581
fliM	Flagella	*flaQII*, *cheC*, *cheU*; flagellar synthesis; motor switching and energizing	42.8	134, 341, 342, 429, 500, 579, 581, 634
fliN	Flagella	*flaN*; flagellar synthesis; motor switching and energizing	42.8	131, 301, 341, 342, 429, 500, 579, 581, 725
fliO	Flagella	*flaP*; flagellar synthesis; function unknown	42.9	579, 581
fliP	Flagella	*flaB*; flagellar synthesis; function unknown	42.9	579, 581
fliQ	Flagella	*flaD*; flagellar synthesis; function unknown	42.9	579, 581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
fliR	Flagella	*flaX*; flagellar synthesis; function unknown	42.9	579, 581
fliS	Flagella	Member of axial family of structural proteins	42.6	337
fliT	Flagella	Member of the axial family of structural proteins	42.6	337
fliU	Flagella	Flagellar function; part of basal body, or required for flagellin processing or export	42.5	124
fliV	Flagella	Flagellar function; part of basal body, or required for flagellin processing or export	42.5	124
fljA	Flagella	*rhl*; flagellar synthesis; repressor of *fliC*	60.0	363, 581
fljB	Flagella	*H2*; flagellar synthesis; phase 2 flagellin (filament structural protein)	60.1	134, 204, 495, 579, 581
flrB	Fluoroleucine resistance	Leucine or isoleucine regulation or both	16.4	579, 581
fnr		*oxrA*; anaerobic induction of genes for anaerobic metabolism, such as *pepT*	36.6	209, 309, 412, 581, 653, 748
fol	Folate	Trimethoprim resistance; tetrahydrofolate dehydrogenase	1.9	579, 581
fpk	Fructose	Fructose phosphate kinase	48.3	581
frd	Fumarate reductase	Fumarate reductase (EC 1.3.99.1)	NM	581
fruA	Fructose	Enzyme II^{Fru} of the phosphotransferase system	48.2	154, 197
fruB	Fructose	*fruF*; enzyme III^{Fru}-modulator FPr tridomain fusion protein of the phosphotransferase system	48.1	154, 197, 581
fruK	Fructose	Fructose-1-phosphate kinase	48.1	154, 197
fruR	Fructose	Regulation of the fructose regulon; regulation of gluconeogenesis; may be the same as *ppsB*	3.0	154, 197, 581, 722
ftsZ		*sulB*; essential for cell division	3.1	581
fucA	Fucose	*fuc*; L-fucose utilization	65.1	463, 581
fucI	Fucose	L-Fucose utilization	65.1	463
fucK	Fucose	L-Fucose utilization	65.1	463
fucP	Fucose	L-Fucose utilization	65.1	463
fucR	Fucose	L-Fucose utilization	65.1	463
fumA	Fumarate	Regulatory gene; putative	31.3	560
furA	Ferrichrome	*fur*; ferrichrome uptake, regulation of iron uptake; constitutive synthesis of iron-enterochelin	16.9	163, 166–168, 192, 193, 581
fusA	Fusidic acid	Protein chain elongation factor EF-G	74.7	315
galE	Galactose	UDP glucose 4-epimerase (EC 5.1.3.2)	17.8	280, 579, 581
galF	Galactose	Modifier of UDP-glucose pyrophosphorylase	45.3	314, 579, 581
galK	Galactose	Galactokinase (EC 2.7.1.6)	17.8	280, 579, 581
galP	Galactose	Specific galactose permease	67.0	579, 581
galR	Galactose	Regulation	65.3	579, 581
galS	Galactose	*mglD*; *mgl* repressor and galactose ultrainduction factor	48.0	34, 581
galT	Galactose	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	17.8	280, 581
galU	Galactose	Glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	38.4	579, 581
gapA		Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	41.1	374
garA	Gamma resistant	Resistant to γ and UV radiation; large cells; high RNA and protein content; may be equivalent to *rodA*	0.4	579, 581
garB	Gamma resistant	Resistant to γ and UV radiation; large cells; high RNA and protein content	0.4	579, 581
gcv	Glycine cleavage	*invD*; defective in the glycine cleavage enzyme system	65.7	581, 650
gdhA		*gdh*; glutamate dehydrogenase (EC 1.4.1.4)	29.1	25, 234, 579, 581
gleR		Glycyl-leucyl-resistant regulatory gene for transport of branched-chain amino acids	8.1	579, 581
glgA	Glycogen	Glycogen synthase (EC 2.4.1.21)	77.2	579, 581
glgC	Glycogen	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)	77.2	565, 579, 581
glnA	Glutamine	Glutamine synthetase (EC 6.3.1.2)	87.5	538, 579, 581
glnD	Glutamine	PIIA uridyl transferase	4.3	579, 581
glnE	Glutamine	Covalent modification of glutamine synthetase; glutamine synthetase adenylyl transferase (EC 2.7.2.42)	69.5	579, 581
glnH	Glutamine	Periplasmic glutamine-binding protein	19.1	579, 581
glnP	Glutamine	High-affinity glutamine transport	19.1	579, 581
glpA	Glycerol phosphate	*sn*-Glycerol-3-phosphate dehydrogenase (anaerobic) (EC 1.1.99.5)	49.6	579, 581
glpD	Glycerol phosphate	*sn*-Glycerol-3-phosphate dehydrogenase (aerobic) (EC 1.1.1.8)	77.1	579, 581
glpK	Glycerol phosphate	Glycerol kinase (EC 2.7.1.30)	88.5	579, 581
glpQ	Glycerol phosphate	Glycerol-3-phosphate diesterase	49.4	581
glpR	Glycerol phosphate	Regulatory gene for *glpD*, *glpK*, and *glpT*	77.1	579, 581
glpT	Glycerol phosphate	*sn*-Glycerol-3-phosphate transport	49.5	579, 581
gltA	Glutamate	Requirement	17.1	579, 581
gltB	Glutamate	Glutamate synthetase (EC 2.6.1.53)	72.5	111, 579, 581
gltC	Glutamate	Growth on glutamate as sole source of carbon	81.7	579, 581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
gltD	Glutamate	Glutamate synthase, small subunit	72.7	111, 581
gltF	Glutamate	Glutamate-specific transport system	0.1	581
gltH	Glutamate	Requirement	28.0	579, 581
gltS	Glutamate	Glutamate permease	81.7	581
glyA	Glycine	Serine hydroxymethyltransferase (EC 2.1.2.1)	56.0	579, 581
glyS	Glycine	Glycyl-tRNA synthetase (EC 6.1.1.14)	80.1	579, 581
glyT	Glycine	*sufS*; glycine tRNA 2	90.0	498
gnd		Phosphogluconate dehydrogenase (EC 1.1.1.43)	44.9	314, 324, 551, 579, 581
gpd		Glucosamine-6-phosphate deaminase	NM	579, 581
gpsA		*sn*-Glycerol-3-phosphate dehydrogenase [NAD(P)$^+$] (EC 1.1.1.94)	81.0	579, 581
gpt		*gxu*; guanine-hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	7.4	502, 579, 581
gsk		Guanosine kinase	11.9	579, 581
guaA	Guanine	GMP synthetase (EC 6.3.4.1)	54.4	579, 581
guaB	Guanine	IMP dehydrogenase (EC 1.1.1.205)	54.4	579, 581
guaC	Guanine	GMP reductase (EC 1.6.6.8)	3.5	579, 581
guaP	Guanine	Guanine uptake	3.5	579, 581
gyrA	Gyrase	*hisW*, *nalA*; resistance or sensitivity to nalidixic acid; DNA gyrase	49.3	3, 488, 579, 581, 590
gyrB	Gyrase	*hisU*, *parA*; DNA gyrase	83.3	116, 424, 486, 488, 579, 581, 590
hemA	Heme	Glutamyl-tRNA dehydrogenase	38.8	32, 136, 137, 140, 539, 579, 581, 756
hemB	Heme	Heme deficient	8.7	579, 581, 756
hemC	Heme	Heme deficient; urogen I synthase	85.7	579, 581, 756
hemD	Heme	Heme deficient; uroporphyrinogen III cosynthase	85.7	579, 581, 756
hemE	Heme	Accumulation of uroporphyrin III	90.6	579, 581, 756
hemF	Heme	Coproporphyrinogen III oxidase	53.2	756, 757
hemG	Heme	Defective in heme synthesis	86.5	581, 756
hemH	Heme	*visA*; defective in heme synthesis	11.6	581, 756
hemK	Heme	Protoporphyrinogen oxidase; putative (EC 1.3.3.-)	38.8	136
hemL	Heme	Glutamate-1-semialdehyde aminotransferase	5.0	139, 140, 581, 756
hemM	Heme	Glutamyl-tRNA dehydrogenase or subunit; putative	38.8	136, 539
hemN	Heme	Oxygen-independent coproporphyrinogen III oxidase	86.7	756, 758
hil	Hyperinvasion locus	Hyperinvasion; essential for bacterial entry into epithelial cells	62.8	377, 454
himA		Integration host factor (IHF), α subunit; site-specific recombination	30.3	385
himD		Integration host factor (IHF), β subunit; site-specific recombination	20.1	486
hin	H inversion	*vh2*; flagellar synthesis; regulation of flagellin gene expression by site-specific inversion of DNA	60.1	208, 293, 426, 579, 581, 622
hisA	Histidine	*N*-(5′-Phospho-L-ribosylformimino)-5-amino-1-(5′-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	44.8	10, 65, 580, 582
hisB	Histidine	Imidazoleglycerol-phosphate dehydratase and histidinol phosphatase (EC 4.2.1.19, EC 3.1.3.15)	44.8	9, 65, 84, 579, 581
hisC	Histidine	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	44.8	8–10, 65, 579, 581
hisD	Histidine	Histidinol dehydrogenase (EC 1.1.1.23)	44.7	8, 10, 31, 223, 579, 581
hisF	Histidine	Cyclase	44.8	65, 579, 581
hisG	Histidine	ATP phosphoribosyltransferase (EC 2.4.2.17)	44.7	10, 44, 65, 71, 91, 488, 543, 579, 581, 602
hisH	Histidine	Amidotransferase (EC 2.4.2.-)	44.8	65, 579, 581
hisI	Histidine	*hisE*, *hisIE*; phosphoribosyl-AMP cyclohydrolase, phosphoribosyl-ATP pyrophosphatase (EC 3.5.4.19, EC 3.6.1.31)	44.8	65, 579, 581
hisJ	Histidine	Periplasmic histidine-binding protein J for high-affinity histidine transport system	51.2	544, 579, 581
hisM	Histidine	Histidine transport; inner membrane protein	51.2	579, 581
hisP	Histidine	High-affinity histidine transport; inner membrane protein	51.2	544, 579, 581, 596
hisQ	Histidine	Histidine transport; membrane protein	51.2	579, 581
hisR	Histidine	tRNA structural gene	85.6	157, 418, 488, 489, 579, 581
hisS	Histidine	Histidyl-tRNA synthetase (EC 6.1.1.21)	55.4	579, 581
hisT	Histidine	Pseudouridine modification of tRNA	51.8	324, 468, 579, 581
hmpA	Hemoprotein	Dihydropteridine reductase activity (EC 1.6.99.7)	56.0	651
hns		*osmZ*, *bglY*, *pilG*; histone-like protein; DNA-binding nucleoid-associated protein	38.4	145, 258, 264, 294, 437, 518, 707
hpt		Hypoxanthine phosphoribosyltransferase (not EC 2.4.2.8) (see *gpt*)	3.8	579, 581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype^a	Map position (Cs)^b	Reference(s)^c
hsdL	Host specificity	*hspLT*; restriction modification system	8.4	114, 117–119, 579, 581, 702
hsdM	Host specificity	*hsdSB*; restriction modification system; modification component	98.5	179, 579, 581, 605, 702
hsdS	Host specificity	*hsdSB*; restriction modification system; specificity component	98.4	179, 579, 581, 702
hsdSA	Host specificity	Restriction modification system (operon)	97.6	579, 581, 702
htrA	High-temperature requirement	*degP*; heat shock (stress) regulated periplasmic protease; essential for survival in macrophages	5.1	29, 75, 317
hupA		Histonelike protein HU-2	90.7	260, 263
hupB		Histonelike protein HU-1	11.4	263, 436
hutC	Histidine utilization	Repressor	17.9	36, 579, 581
hutG	Histidine utilization	Formiminoglutamase (EC 3.5.3.8)	17.9	579, 581
hutH	Histidine utilization	Histidine ammonia-lyase (EC 4.3.1.3)	17.9	579, 581
hutI	Histidine utilization	Imidazolonepropionase (EC 3.5.2.7)	17.9	579, 581
hutM	Histidine utilization	Promoter for *hutIGC*	17.9	579, 581
hutP	Histidine utilization	Promoter for *hutUH*	17.9	579, 581
hutQ	Histidine utilization	Promoter for *hutUH*	17.9	579, 581
hutR	Histidine utilization	Catabolite insensitivity of *hutUH*	17.9	579, 581
hutU	Histidine utilization	Urocanate hydratase (EC 4.2.1.49)	17.9	579, 581
hydA	Hydrogenase	*aniA*, *fhlB*, *hyd*; hydrogenase	62.5	579, 581
hydG	Hydrogenase	Hydrogenase regulation	90.8	88
hydH	Hydrogenase	Hydrogenase regulation	90.7	88
hyp	Hydrophobic peptide auxotrophy	Hydrophobic polypeptide requirement	52.0	579, 581
icd		Isocitrate dehydrogenase	27.6	166, 167
iclR		Constitutive expression of *aceBA* operon	91.2	187, 469
ilvA	Isoleucine-valine	*ile*; threonine deaminase (EC 4.2.1.16)	85.3	414, 579, 581
ilvB	Isoleucine-valine	Acetohydroxy acid synthase I, valine sensitive, large subunit (EC 4.1.3.18)	82.3	116, 579, 581
ilvC	Isoleucine-valine	*ilvA*; ketol-acid reductoisomerase (EC 1.1.1.86)	85.3	579, 581
ilvD	Isoleucine-valine	*ilvB*; dihydroxyacid dehydratase (EC 4.2.1.19)	85.3	414, 579, 581
ilvE	Isoleucine-valine	*ilvC*; branched-chain amino acid aminotransferase (EC 2.6.1.42)	85.2	153, 413, 414, 579, 581
ilvG	Isoleucine-valine	Acetohydroxy acid synthase II, valine insensitive, large subunit (EC 4.1.3.18)	85.2	413, 414, 579, 581
ilvH	Isoleucine-valine	Acetohydroxy acid synthase III, valine sensitive, small subunit (EC 4.1.3.18)	3.0	554, 579, 581, 733
ilvI	Isoleucine-valine	Acetohydroxy acid synthase III, valine sensitive, large subunit (EC 4.1.3.18)	3.0	554, 579, 581, 733
ilvL	Isoleucine-valine	*ilvGMEDA* operon leader peptide	85.2	375, 682
ilvM	Isoleucine-valine	Acetohydroxy acid synthase II, valine insensitive, small subunit (EC 4.1.3.18)	85.2	413, 414, 581
ilvN	Isoleucine-valine	Acetohydroxy acid synthase II, valine sensitive, small subunit (EC 4.1.3.18)	82.3	116, 581
ilvS	Isoleucine-valine	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	1.0	579, 581
ilvY	Isoleucine	Regulation of *ilvC*	85.3	579, 581
incR	Incompatibility	Required in *trans* with *parS*	pSLT	68, 69
infC		Protein chain initiation factor 3 (IF3)	30.2	407
inlA	Inositol	Fermentation	92.7	579, 581
inlB	Inositol	Fermentation	56.5	579, 581
inm		Sensitivity to mutagenesis by nitrosoguanidine	80.6	581
invA	Invasion	Affects invasion but not attachment to cultured epithelial cells; sequence similarity to proteins for protein translocation	63.1	170, 182–185, 218, 320, 454, 519
invD	Invasion	Invasion-related function	NM	182, 184
invE	Invasion	Triggering of the endocytic uptake of *Salmonella* spp. by epithelial cells; homologous to Mxic of *Shigella* spp.	63.1	206, 207, 218, 454
invF	Invasion	Defective in invasion but not in attachment to epithelial cells; similar to *araC*	63.2	331, 454
invG	Invasion	Defective in invasion of epithelial cells; member of PulA family of proteins for export of proteins lacking typical signal sequences	63.2	207, 331, 454
invH	Invasion	Defective in invasion of and attachment to epithelial cells	63.4	14, 454
iroA	Iron-regulated locus	Induced by alkaline pH; undefined role in iron transport	60.6	167, 168
IS*200*I		Insertion sequence	65.8	40, 199, 365–367, 582
IS*200*II		Insertion sequence	75.6	40, 199, 365–367, 582

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
*IS200*III		Insertion sequence	94.2	40, 199, 365–367, 582
IS*200*IV		Insertion sequence	42.4	40, 199, 365–367, 582
IS*200*V		Insertion sequence	53.6	40, 199, 365–367, 582
IS*200*VI		Insertion sequence	22.3	40, 199, 365–367, 582
katG	Catalase	*cls*; hydroperoxidase I (HPI) (EC 1.11.1.6)	89.4	148, 411, 521, 579, 581, 680, 687
kbl		2-Amino-3-ketobutyrate CoA ligase (glycine acetyltransferase) (EC 2.3.1.29)	81.2	617
kdsA		Ketodeoxyoctonate synthesis	38.7	579, 581
kdsB		CMP ketodeoxyoctonate synthetase	20.2	579, 581
lamB	Lambda	Encodes a protein resembling the λ receptor	91.7	172, 579, 581
lepA		GTP-binding protein	57.6	720
lepB		*lep*; signal peptidase I	57.6	719, 720
leuA	Leucine	α-Isopropylmalate synthase (EC 4.1.3.12)	2.9	553, 579, 581
leuB	Leucine	β-Isopropylmalate dehydrogenase	2.9	19, 579, 581
leuC	Leucine	α-Isopropylmalate isomerase subunit	2.9	570, 579, 581
leuD	Leucine	α-Isopropylmalate isomerase subunit	2.9	579, 581
leuS	Leucine	Leucyl-tRNA synthetase (EC 6.1.1.4)	15.8	579, 581
leuT	Leucine	Leucine transport	39.4	579, 581
leuU	Leucine	*leuT*; leucine tRNA	85.6	581
lev	Levomycetin	Levomycetin resistance	NM	579, 581
lexA		Regulatory gene for SOS functions	91.9	63, 196, 464
lgt		*umpA*; prolipoprotein diacylglyceryl transferase	64.9	190
lig	Ligase	DNA ligase	52.7	522, 581
lip	Lipoic acid	Requirement	15.3	410, 580, 581, 628
livF	Leucine, isoleucine, valine	*livG*; high-affinity branched-chain amino acid transport; membrane component	77.5	440
livG	Leucine, isoleucine, valine	*livF*; high-affinity branched-chain amino acid transport	77.5	440
livH	Leucine, isoleucine, valine	*livA*; high-affinity branched-chain amino acid transport; membrane component	77.5	440, 581
livJ	Leucine, isoleucine, valine	*livB*; high-affinity branched-chain amino acid transport; membrane component	77.6	440, 493
livK	Leucine, isoleucine, valine	*livC*; high-affinity branched-chain amino acid transport; membrane component	77.5	440, 493
livM	Leucine, isoleucine, valine	*livEF*; high-affinity branched-chain amino acid transport; membrane component	77.5	440
livS	Leucine, isoleucine, valine	*liv*; regulatory gene; high-affinity branched-chain amino acid transport	19.2	579, 581
lkyA	Leaky	Leakage of periplasmic proteins	59.8	579, 581
lkyB	Leaky	Leakage of periplasmic proteins	59.8	579, 581
lkyC	Leaky	Leakage of periplasmic proteins	22.9	579, 581
lkyD	Leaky	Leakage of periplasmic proteins; morphology defect	22.9	579, 581, 675
lon	Long form	*capR*; ATP-dependent protease	11.1	579, 581
lpd		Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	3.8	579, 581
lpp	Lipoprotein	Murein lipoprotein structural gene	30.6	579, 581
lpxA		UDP-*N*-acetylglucosamine acyltransferase	4.2	593, 727
lpxD		*ssc*, *omsA*, *firA*; UDP-3-*O*-(*R*-3-hydroxymyristoyl)-glucosamine *N*-acyltransferase; antibiotic supersensitivity (EC 2.3.1.-)	4.0	250, 267, 269, 572, 593, 726,–728
lrp		Leucine-responsive regulatory protein	19.1	733
lysA	Lysine	*lys*; requirement	65.4	579, 581
lysS	Lysine	Lysyl-tRNA synthetase (EC 6.1.1.6)	66.2	338
malE	Maltose	*malB*; maltose uptake; periplasmic maltose-binding protein	91.7	113, 579, 581
malF	Maltose	Maltose uptake; inner membrane protein	91.6	113, 581, 595
malG	Maltose	Maltose uptake; inner membrane protein	91.6	113, 173, 581
malK	Maltose	Maltose uptake; inner membrane protein	91.7	113, 581, 596, 729, 730
malM	Maltose	Possible periplasmic protein; function unknown	91.7	595
malQ	Maltose	Amylomaltase (EC 1.2.1.25)	77.0	579, 581
malT	Maltose	Regulation of maltose genes	76.8	579, 581
manA	Mannose	*pmi*; mannose-6-phosphate isomerase (EC 5.3.1.8)	31.3	97, 99, 560, 579, 581
mdh		Malate dehydrogenase (EC 1.1.1.37)	73.4	417

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
melA	Melibiose	α-Galactosidase (EC 3.2.1.22)	93.8	579, 581
melB	Melibiose	Melibiose carrier protein	93.8	358, 457, 579, 581
mem	Membrane	Sugar transport and membrane protein defective	80.8	579, 581
menA	Menaquinone	Menaquinone deficient; defective in trimethylamine oxide reduction; grows on vitamin K_1	88.5	579, 581
menB	Menaquinone	Biosynthesis; grows on vitamins K_1 and K_5	50.1	562, 579, 581
menC	Menaquinone	Biosynthesis	50.1	579, 581
menD	Menaquinone	Biosynthesis	50.1	579, 581
menE	Menaquinone	*O*-Succinyl benzoic acid-CoA synthase	50.1	562
metA	Methionine	*metI*; homoserine transsuccinylase (EC 2.3.1.46)	91.1	435, 579, 581
metB	Methionine	Cystathionine γ-synthase (EC 4.2.99.9)	89.3	579, 581
metC	Methionine	Cystathionine γ-lyase (EC 4.4.1.1)	69.1	523, 524, 579, 581
metD	Methionine	*metP*; high-affinity methionine transport	5.5	105, 224, 579, 581, 607
metE	Methionine	Tetrahydropteroyltriglutamate methyltransferase (EC 2.1.1.14)	86.1	536, 579, 581, 714, 715, 753, 754
metF	Methionine	5,10-Methylenetetrahydrofolate reductase (EC 1.1.99.15)	89.4	106, 579, 581, 648, 649
metG	Methionine	Methionyl-tRNA synthetase	47.1	579, 581
metH	Methionine	Vitamin B_{12}-dependent homocysteine-N^5-methylenetetrahydrofolate transmethylase	91.3	60, 497, 536, 579, 581, 649, 713, 714, 753, 754
metJ	Methionine	Methionine analog resistant; transcriptional repressor of *metE* and *metR*	89.3	106, 579, 581, 649, 754
metK	Methionine	Methionine analog resistant; *S*-adenosylmethionine synthetase	67.0	579, 581
metL	Methionine	Aspartokinase II-homoserine dehydrogenase II	89.4	581
metR	Methionine	Transcriptional activator of *metE* and *metH*	86.1	50, 60, 106, 252, 435, 579, 581, 714, 715, 754
mglA	Methyl galactoside	Membrane-bound protein for methygalactoside transport	48.0	34, 556, 581
mglB	Methyl galactoside	Galactose-binding protein	48.0	34, 556, 579, 581
mglC	Methyl galactoside	Membrane-bound transport protein	48.0	34, 557, 581
mglE	Methyl galactoside	Transport	NM	34, 556, 581
mgtA	Magnesium transport	Magnesium transport	96.7	270, 581, 630–632
mgtB	Magnesium transport	Magnesium transport	82.1	193, 270, 581, 630–633
mgtC	Magnesium transport	Magnesium transport	82.1	633
miaA		Deficient in the nucleotide ms^2io^6AA, a modified base present in some tRNAs	95.0	45, 324, 581
miaE		Lack of tRNA (ms^2io^6A37) hydroxylase	97.2	531
min	Minicells	Cell division	NM	581
moaA	Molybdenum	*chlA*; molybdenum-containing factor; biosynthesis of molybdopterin	19.0	579, 581, 604, 653
mob	Molybdenum	*chlB*; molybdenum-containing factor; biosynthesis of molybdopterin guanine dinucleotide	86.4	579, 581, 604, 653
modC	Molybdenum	*chlD*; molybdenum uptake	18.3	579, 581, 604, 653
moeA	Molybdenum	*chlE*; molybdenum-containing factor; biosynthesis of molybdopterin	19.1	579, 581, 604, 653
motA	Motility	Nonmotile but flagellate	42.1	131, 579, 581
motB	Motility	Nonmotile but flagellate	42.0	131, 579, 581
mre	Mecillinam resistance	*bac*, *envB*; round cell morphology; mecillinam resistance	73.6	104, 501, 579, 581
mscL	Mechanosensitive channel	Large-conductance mechanosensitive channel	74.5	526
mta	*meso*-Tartaric acid	Utilization of and resistance to *meso*-tartaric acid	NM	579, 581
mtlA	Mannitol	D-Mannitol phosphotransferase enzyme IIA	80.4	50, 579, 581
mtlD	Mannitol	Mannitol-1-phosphate dehydrogenase (EC 1.1.1.17)	80.4	579, 581
murB		UDP-*N*-acetylenolpyruvoylglucosamine reductase	90.0	125
murI		Glutamate synthase	89.7	738
mutG	Mutator	Increased frequency of mutation in host chromosome, not in P22	NM	579, 581
mutH	Mutator	Mutations inactivate methyl-directed mismatch repair	65.5	235, 415, 550, 581
mutL	Mutator	Mutations inactivate methyl-directed mismatch repair	95.0	434, 550, 579, 581, 766
mutS	Mutator	Mutations inactivate methyl-directed mismatch repair	63.9	232, 550, 579, 581, 766
mutU	Mutator	Increased frequency of mutation	NM	550
mutY	Mutator	*mutB*; increased frequency of mutation with alkylating agents	67.2	122, 235, 416, 579, 581
mviA	Mouse virulence	Mutants have increased virulence in Ity^s, not in Ity^r, mice	38.9	33, 581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
mviM	Mouse virulence	*mviB*; affects virulence of cells in mice	26.3	721
mviN	Mouse virulence	Affects virulence of cells in mice	26.3	721
mviS	Mouse virulence	Affects virulence of cells in mice	26.3	66
nadA	Nicotinamide	*nicA*; requirement; quinolinic acid synthetase	17.2	169, 579, 581, 641, 767
nadB	Nicotinamide	*nic*; L-aspartate oxidase	57.8	169, 579, 581, 768
nadC	Nicotinamide	Quinolinic acid PRPP phosphoribosyl transferase	3.6	291, 292, 579, 581
nadD	Nicotinamide	NAMN:ATP-ADP transferase	15.5	80, 579, 581
nadE	Nicotinamide	Essential biosynthetic gene, unsupplementable; NAD synthetase	29.5	581
nadF	Nicotinamide	NAD kinase I	14.7	80
nadG	Nicotinamide	NAD kinase II; quinolinate sensitive	74.9	80
nadR	Nicotinamide	*nadI*, *pnuA*; NMN transport and repression of transcription of *nadA*, *nadB*; bifunctional enzyme	99.9	169, 579, 581, 768, 769
nagA	*N*-Acetylglucosamine	*nag*; nonutilization	16.5	29, 579, 581
nalB	Nalidixic acid	Resistance or sensitivity	61.6	579, 581
nanH	Neurarminidase	Sialidase (EC 3.2.2.18)	23.7	281, 282, 690, 734
nap	Nonspecific acid phosphatase	Deficiency for nonspecific acid phosphatase I	NM	579, 581
nar	Nitrate reductase	*chlC*; nitrate reductase (operon) (EC 1.7.99.4)	38.6	579, 581, 604, 653
narK	Nitrate reductase	Regulatory gene for *nar* operon	38.6	278
ndk		Nucleosidediphosphate kinase (EC 2.7.4.6)	55.5	579, 581
neaA	Neamine	Neamine resistance	74.1	160
newD		Substitute gene for *leuD*	8.0	579, 581
nfnB		*nfsI*; sensitivity to nitrofurantoin	13.6	736
nhoA		*N*-Hydroxyarylamine *O*-acetyltransferase (EC 2.3.1.118)	104.0	737
nirB	Nitrite reductase	NADH-nitrite oxidoreductase apoprotein, subunit I (EC 1.6.6.4)	75.2	209, 751
nirC	Nitrite reductase	Nitrite transport; putative (EC 1.6.6.4)	75.5	751
nirD	Nitrite reductase	NADH-nitrite oxidoreductase apoprotein, subunit II	75.5	751
nirP	Nitrite reductase	Nitrite permease	7.5	209
nit	Nitrogen	Nitrogen metabolism	30.1	579, 581
nlpD		Lipoprotein precursor	63.7	354
nmpC	New membrane protein	Outer membrane porin protein	38.7	278
nol	Norleucine	Norleucine resistance; possible defect in valine uptake or regulation	64.5	579, 581
nrdA		Ribonucleoside diphosphate reductase, α subunit (R1) (EC 1.17.4.1)	49.3	326, 581, 653
nrdB		Ribonucleoside diphosphate reductase, β subunit (R2) (EC 1.17.4.1)	49.4	326, 653
nrdE		Ribonucleoside-diphosphate reductase subunit (EC 1.17.4.1)	61.3	326
nrdF		Ribonucleoside-diphosphate reductase subunit (EC 1.17.4.1)	61.4	326
nsiA	Nicotinamide starvation inducible	NAD metabolism regulation	77.8	579, 581
ntrB	Nitrogen regulation	*glnR*; regulation of *glnA* expression and other nitrogen-controlled genes	87.3	579, 581
ntrC	Nitrogen regulation	*glnR*; regulation of *glnA* expression and other nitrogen-controlled genes	87.2	538, 579, 581, 592
nuoD		NADH ubiquinone oxidoreductase	51.0	20
nuoE		NADH ubiquinone oxidoreductase	51.0	20
nuoF		NADH ubiquinone oxidoreductase	51.0	20
nuoG		NADH ubiquinone oxidoreductase	51.0	20
nusA	N utilization	Transcription termination; does not support transcription antitermination of N protein of λ	72.0	108
nuvA		Uridine thiolation factor A activity	9.5	581
oadA		Oxalacetate decarboxylase, α subunit (EC 4.1.1.3)	NM	743
oadB		Oxalacetate decarboxylase, β subunit (EC 4.1.1.3)	NM	743
oadG		Oxalacetate decarboxylase, γ subunit (EC 4.1.1.3)	NM	743
oafA	O-antigen factor	*O-5*, *ofi*; LPS O-factor 5, acetyl group	50.7	579, 581
oafC	O-antigen factor	Determines factor 1 in LPS of group E *Salmonella* spp.	15.2	579, 581
oafR	O-antigen factor	Synthesis of LPS O antigen 122	12.7	579, 581
ogt		*O*-6-Alkylguanine-DNA-alkyltransferase	36.6	376
ompA	Outer membrane protein	Outer membrane protein 33K	24.3	579, 581
ompC	Outer membrane protein	Outer membrane protein 36K	49.1	39, 74, 126, 214, 327, 579, 581
ompD	Outer membrane protein	Outer membrane protein 34K	33.7	126, 520, 579, 581
ompF	Outer membrane protein	Outer membrane protein 35K	22.8	74, 126, 214, 327, 579, 581
ompH	Outer membrane protein	Outer membrane protein 16K, cationic	4.0	266, 267, 350, 351

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
ompR	Outer membrane protein	*ompB*, *tppA*; positive regulation of tripeptide permease and of outer membrane protein	76.0	74, 126, 183, 391, 579, 581
opdA	Oligopeptidase	*optA*; endoprotease which hydrolyzes *N*-acetyl-L-Ala$_4$; required for normal phage P22 growth	79.7	101–103, 579, 581
oppA	Oligopeptide permease	Oligopeptide-binding protein	38.4	579, 581, 685
oppB	Oligopeptide permease	Oligopeptide transport system	38.3	529, 579, 581
oppC	Oligopeptide permease	Oligopeptide transport system	38.3	529, 579, 581
oppD	Oligopeptide permease	Oligopeptide transport system	38.3	579, 581
oppF	Oligopeptide permease	Oligopeptide transport system	38.3	189, 581
orf11		Putative role in fimbria production	pSLT	178
orf7		Putative role in fimbria production	pSLT	178
orf9		Putative role in fimbria production	pSLT	178
orfE		Function unknown; locates downstream of *spv* operon of pSLT	pSLT	227
orgA	Oxygen-regulated gene	Noninvasive mutant in low oxygen	62.9	319
oriC	Origin	*poh*; origin of replication of chromosome	84.9	579, 581, 606
osmB		Osmotically inducible lipoprotein; resistance to osmotic stress	37.6	691
oxdA	Oxygen dependent	Gene activity controlled by *fnr*	67.8	579, 581
oxdB	Oxygen dependent	Gene activity controlled by *fnr*	93.2	581
oxiA	Oxygen inducible	Induced by anaerobiosis	9.2	581
oxiB	Oxygen inducible	Induced by anaerobiosis	25.8	581
oxiC	Oxygen inducible	Induced by anaerobiosis	35.3	581
oxiE	Oxygen inducible	Induced by anaerobiosis	89.4	581
oxrF	Oxygen regulation	Regulates expression of *aniH*	NM	581
oxrG	Oxygen regulation	Regulates expression of *aniC*, *aniI*	89.4	168, 581
oxyR	Oxidative stress resistant	Transcriptional activator of oxidative stress response genes	89.6	90, 148, 521, 581, 666, 667, 687, 747
pabA	*p*-Aminobenzoate	Requirement; *p*-aminobenzoate synthase	75.1	581
pabB	*p*-Aminobenzoate	*p*-Aminobenzoate synthetase, component I (EC 4.1.3.-)	41.6	212
pagC	*phoP*-activated gene	*ail*, *lom*; *phoP*-activated gene for virulence	NM	450, 453, 545
panB	Pantothenic acid	Ketopantohydroxymethyl transferase (EC 4.1.2.12)	4.6	579, 581
panC	Pantothenic acid	Pantothenate synthetase (EC 6.3.2.1)	4.5	579, 581
panD	Pantothenic acid	Ketopantoic acid reductase	4.6	371, 579, 581
panE	Pantothenic acid	Ketopantoic acid reductase	NM	579, 581
panR	Pantothenic acid	Pantothenate excretion; suppression of the thiamine requirement of the *purF* mutation	4.6	129
panT	Pantothenic acid	Pantothenate transport	NM	579, 581
parA	Partition	Partitioning; homologous to *parA* of phage P1	pSLT	68, 69
parB	Partition	Partitioning; homologous to *parB* in phage P1	pSLT	68, 69
parC	Partition	*clmF*; defect in nucleoid segregation; topoisomerase IV subunit; similar to *gyrA*	69.3	4, 424, 581, 588–590
parE	Partition	*clmF*; defect in nucleoid segregation; topoisomerase IV subunit; similar to *gyrB*	69.4	424, 581, 588, 590, 645
parF	Partition	*clmF*; partitioning of nucleoid; topoisomerase	69.3	424, 581, 588, 645
parS	Partition	*incL*; partitioning of pSLT	pSLT	68, 69
pasA		6-Aminonicotinic acid sensitive	92.9	580, 582
pasB		6-Aminonicotinic acid sensitive	70.1	579, 581
pasC		6-Aminonicotinic acid sensitive	23.4	579, 581
pasD		6-Aminonicotinic acid sensitive	17.9	581
pasE		6-Aminonicotinic acid sensitive	56.8	581
pbpA	Penicillin-binding protein	Round cell morphology; mecillinam resistance; penicillin-binding protein 2	15.4	104
pckA		Phosphoenolpyruvate carboxykinase (ATP) activity (EC 4.1.1.49)	76.0	391
pckB		*pck*; phosphoenolpyruvate carboxykinase (ATP) activity (EC 4.1.1.49)	14.5	579, 581
pclA	Permissive for *cly*	Permissive for lytic growth of P22 *cly*	NM	579, 581
pclB	Permissive for *cly*	Permissive for lytic growth of P22 *cly*	NM	579, 581
pclC	Permissive for *cly*	Permissive for lytic growth of P22 *cly*	NM	579, 581
pde	Phosphodiesterase	2′,3′-Cyclic nucleotide 2′-phosphodiesterase	95.5	579, 581
pduA	Propanediol utilization	Propanediol utilization	43.8	5, 46, 79, 312
pduB	Propanediol utilization	Propanediol utilization	43.8	5, 46, 79, 312
pduC	Propanediol utilization	Propanediol dehydratase	43.9	5, 46, 312
pduD	Propanediol utilization	Propanediol dehydratase	44.0	5, 46, 312
pduE	Propanediol utilization	Vitamin B$_{12}$ adenosyl transferase	44.0	5, 46, 312
pduF	Propanediol utilization	Facilitated diffusion of propanediol	43.8	5, 46, 79, 312
pduG	Propanediol utilization	Propanediol utilization	44.0	5, 46, 312
pduH	Propanediol utilization	Propanediol utilization	44.0	5, 46, 312
pdxB	Pyridoxine	Requirement	51.8	579, 581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
pefA	Plasmid-encoded fimbriae	Fimbrial biosynthesis; fimbrial/pilin shaft subunits	pSLT	178, 558
pefB	Plasmid-encoded fimbriae	Fimbrial biosynthesis; fimbrial regulatory protein	pSLT	178, 558
pefC	Plasmid-encoded fimbriae	Fimbrial biosynthesis; outer membrane protein	pSLT	178, 558
pefD	Plasmid-encoded fimbriae	Fimbrial biosynthesis; sequence related to periplasmic chaperones	pSLT	178, 558
pefI	Plasmid-encoded fimbriae	Short polypeptide related in sequence to *papI* and *sfaC* of *E. coli*	pSLT	178, 558
pefK	Plasmid-encoded fimbriae	*orf5*; fimbrial biosynthesis	pSLT	178, 558
pefL	Plasmid-encoded fimbriae	*orf6*; fimbrial biosynthesis	pSLT	178, 558
pefS	Plasmid-encoded fimbriae	*orf8*; homologous to *dsbA* of *E. coli*	pSLT	178, 558
pepA	Peptidase	Peptidase A; similar to aminopeptidase A of *E. coli*	97.4	579, 581
pepB	Peptidase	Peptidase B; aminopeptidase	55.8	579, 581
pepD	Peptidase	*ptdD*; peptidase D; a dipeptidase, carnosinase	7.3	579, 581
pepE	Peptidase	α-Aspartyl dipeptidase; peptidase E; splits Asp-X peptide bonds	91.4	100, 579, 581
pepM	Peptidase	Peptidase M; aminopeptidase that removes N-terminal methionine from proteins	4.3	446, 460, 581, 742
pepN	Peptidase	*ptdN*; peptidase N; an aminopeptidase, naphthylamidase	24.4	579, 581
pepP	Peptidase	*ptdP*; peptidase P; splits X-Pro peptide bonds	66.6	579, 581
pepQ	Peptidase	Peptidase Q; splits X-Pro dipeptides	86.2	579, 581
pepT	Peptidase	Peptidase T; a tripeptidase	27.3	447, 579, 581
pfkA		6-Phosphofructokinase (EC 2.7.1.11)	88.2	579, 581
pfl		Pyruvate formate lyase	19.5	579, 581, 748
pgi	Phosphoglucose isomerase	*oxrC*, *pasA*; regulation of fermentative or biosynthetic enzymes; glucosephosphate isomerase (EC 5.3.1.9)	91.4	39, 579, 581
pgn		Poor growth on nutrient plates	3.6	292
pgtA	Phosphoglycerate	Activator of phosphoglycerate transport	52.1	581, 697
pgtB	Phosphoglycerate	Protein for signal transmission for phosphoglycerate transport	52.1	581
pgtC	Phosphoglycerate	Protein for signal transmission for phosphoglycerate transport	52.1	581
pgtE	Phosphoglycerate	Outer membrane protease E (E protein) precursor (EC 3.4.21.-)	52.0	216
pgtP	Phosphoglycerate	Transporter for phosphoglycerate transport	52.2	581
pheA	Phenylalanine	Chorismate mutase (EC 5.4.99.5)	58.3	579, 581
pheR	Phenylalanine	Regulation of *pheA*	67.7	579, 581
pheT	Phenylalanine	Phenylalanyl-tRNA synthetase, β subunit	30.3	385
phoE	Phosphate	Phosphate limitation-inducible outer membrane pore protein	7.6	644
phoN	Phosphate	Nonspecific acid phosphatase	94.2	336, 450, 579, 581
phoP	Phosphate	Phosphorylated transcriptional activator; regulator of expression of *phoN* and virulence genes	27.4	12, 30, 156, 165, 181, 219, 449–452, 579, 581
phoQ		Membrane sensor kinase; environmental response regulator in conjunction with PhoP	27.4	12, 219, 449–452
phoS	Phosphatase	Periplasmic phosphate-binding protein	NM	579, 581
phrB	Photoreactivation	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	16.9	384
phsA		*aniE*, *phs*; hydrogen sulfide production	44.3	6, 161, 579, 581
phsB		Iron sulfur subunit; electron transfer	44.2	7
phsC		Membrane-anchoring protein	44.2	7
phsD		Cytochrome *c*-containing subunit; electron transfer	44.2	7
phsE		Function unknown	44.2	7
phsF		Function unknown	NM	7
pig	Pigment	Brownish colonies	56.5	579, 581
pldA		Outer membrane phospholipase A	86.0	53
ply	Phage lysogeny	*pox*; control of P22 lysogeny	94.6	579, 581
pmrA		Polymyxin B resistance; regulation of transcription	93.5	563, 581
pmrB		Polymyxin B resistance; sensor protein (EC 2.7.3.-)	93.5	563
pmrD		Polymyxin B resistance	50.1	562
pncA	Pyridine nucleotide cycle	Nicotinamide deamidase (EC 3.5.1.19)	28.9	579, 581
pncB	Pyridine nucleotide cycle	Nicotinic acid phosphoribosyltransferase (EC 2.4.2.11)	23.2	579, 581, 724
pncC	Pyridine nucleotide cycle	NMN deamidase; mutations fail to use NMN as a pyridine source	88.8	81

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
pncH	Pyridine nucleotide cycle	Nicotinamide used as sole nitrogen source	29.0	581
pncX	Pyridine nucleotide cycle	6-Aminonicotinamide resistant	29.0	581
pnuA	Pyridine nucleotide uptake	NMN uptake deficient	99.7	579, 581
pnuB	Pyridine nucleotide uptake	Growth on lower than normal levels of NMN	99.7	579, 581
pnuC	Pyridine nucleotide uptake	NMN uptake deficient	17.2	169, 581, 767, 768
pnuD	Pyridine nucleotide uptake	Restores ability to use NMN to a *pnuC* mutant	64.0	581, 770
pnuE	Pyridine nucleotide uptake	Failure to use exogenous NAD; periplasmic NAD pyrophosphatase	88.3	581
pnuF	Pyridine nucleotide uptake	Mutations allow use of quinolinate as pyridine source	2.7	311
pnuG	Pyridine nucleotide uptake	Mutations allow use of quinolinate as pyridine source	38.9	311
pnuH	Pyridine nucleotide uptake	Mutations allow use of quinolinate as pyridine source	56.1	311
pocR		Positive regulator for *cob* and *pdu* genes	43.8	5, 46, 79, 566
polA	Polymerase	*atrC*; DNA nucleotidyltransferase (EC 2.7.7.7)	86.5	164, 235, 415, 579, 581
potA	Polyamine transport	Spermidine and putrescine transport; membrane-associated protein	27.3	447
poxA	Pyruvate oxidase	Hypersensitivity to antimicrobial agents; lower levels of pyruvate oxidase and acetolactate synthase deficiency in α-ketobutyrate metabolism	94.6	581
ppc		Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	89.6	579, 581
ppiA		Peptidyl-prolyl *cis-trans* isomerase A precursor (EC 5.2.1.8)	75.1	700
ppsA		Phosphoenolpyruvate synthase	30.5	85, 581, 629
ppsB		Deficiency in phosphoenolpyruvate synthase; may be identical to *fruR*	3.3	579, 581
praA		Phage P221 receptor function	93.8	579, 581
praB		Phage P221 receptor function	64.7	579, 581
prbA		Phage ES18 receptor function	93.8	579, 581
prbB		Phage ES18 receptor function	35.5	579, 581
prc		Reduced survival in macrophages; similar to *prc* protease of *E. coli*	41.6	29
prdB		Phage PH51 receptor function	35.6	579, 581
prfA		Protein release factor 1 (RF1)	38.8	136, 137, 141
prfB		*supT*, *supK*; protein release factor 2 (RF2)	66.2	338, 579, 581
prgH	*phoP*-repressed gene	Influences mouse virulence; defective in macrophage invasion	62.9	30
prh		Phage HK009 receptor function	94.0	579, 581
prk		Phage HK068 receptor function	35.4	579, 581
proA	Proline	Glutamate to glutamic-γ-semialdehyde	7.8	579, 581
proB	Proline	Glutamate to glutamic-γ-semialdehyde	7.8	579, 581
proC	Proline	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	8.9	579, 581
proL	Proline	*sufB*, *proW*; frameshift suppressor affecting proline tRNA and correcting +1 frameshifts at runs of C in mRNA	49.1	646
proM	Proline	*proT*; proline tRNA	85.6	581
proP	Proline	Proline permease II; glycine betaine and proline; low affinity	93.5	327, 579, 581
proV	Proline	*proU*; high affinity transport system for glycine betaine and proline; binding protein	61.4	39, 111, 327, 516, 517, 579, 581, 656
proW	Proline	*proU*; high-affinity transport system for glycine betaine and proline; hydrophobic membrane component	61.4	39, 111, 327, 516, 517, 656
proX	Proline	*proU*; high-affinity transport system for glycine betaine and proline; glycine betaine-binding protein	61.4	39, 111, 327, 516, 517, 656
proY	Proline	Proline transport system	9.0	386
proZ	Proline	Proline transport system	77.7	135
prpA	Propionate	*prp*; propionate metabolism	95.7	581
prpB	Propionate	Propionate metabolism	8.2	698
prsA		*prsB*; phosphoribosylpyrophosphate synthetase	38.9	136, 244, 245, 539, 579, 581
psiA		Phosphate starvation inducible	75.8	581
psiB		Phosphate starvation inducible	88.9	581
psiC		Phosphate starvation inducible	10.1	581
psiD		Phosphate starvation inducible	93.8	581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
psiR		Regulates *psiC* activity	84.8	581
pss		Outer membrane proteins which protect against oxidative intraleukocyte killing	94.3	655
psuA		Suppressor of polarity	NM	579, 581
pta	Phosphotransacetylase	Acetyl-CoA:orthophosphate acetyltransferase (EC 2.3.1.8)	50.8	579, 581
ptsF	Phosphotransferase system	*fruA*; fructose phosphotransferase enzyme IIa	48.8	579, 581
ptsG	Phosphotransferase system	*glu*, *gpt*; glucose phosphotransferase enzyme IIB′-factor III (*crr*) system (methyl-β-D-glucoside)	26.9	575, 576, 579, 581, 718
ptsH	Phosphotransferase system	*carB*; phosphohistidine protein-hexose phosphotransferase (EC 2.7.1.69)	52.9	581, 598
ptsI	Phosphotransferase system	*carA*; enzyme I of the phosphotransferase system	52.9	389, 579, 581, 598
ptsJ	Phosphotransferase system	Enzyme I* of the phosphotransferase system, not expressed in wild type	52.9	581
ptsM	Phosphotransferase system	*manA*; mannose-glucose phosphotransferase enzyme IIA (2-deoxyglucose)	NM	579, 581
purA	Purine	Adenylosuccinate synthetase (EC 6.3.4.4)	95.1	579, 581
purB	Purine	Adenylosuccinate lyase (EC 4.3.2.2)	27.5	579, 581
purC	Purine	Phosphoribosylaminoimidazole-succinocarboxamide synthetase (EC 6.3.2.6)	54.0	579, 581
purD	Purine	Phosphoribosylglycinamide synthetase (EC 6.3.1.13)	90.8	29, 89, 579, 581
purE	Purine	Phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21)	12.6	579, 581
purF	Purine	Amidophosphoribosyltransferase (EC 2.4.2.14)	51.7	127, 129, 579, 581
purG	Purine	Phosphoribosylglycinamidine synthetase (EC 6.3.5.3)	56.3	579, 581
purH	Purine	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	90.8	89, 579, 581
purI	Purine	Phosphoribosylaminoimidazole synthetase (EC 6.3.3.1)	54.5	579, 581
purJ	Purine	IMP cyclohydrolase (EC 3.5.4.10)	90.8	579, 581
purN	Purine	Cryptic *purF* analog; synthesis of phosphoribosylamine	4.7	581
purR	Purine	Constitutive high expression of *pur* genes	30.7	581
putA	Proline utilization	*putB*; bifunctional enzyme; proline oxidase and pyrroline-5-carboxylate dehydrogenase	25.6	11, 236, 503, 504, 579, 581, 587
putP	Proline utilization	Major L-proline permease	25.7	236, 448, 465, 486, 504, 579, 581
pyrB	Pyrimidine	Aspartate carbamoyltransferase (EC 2.1.3.2)	96.9	310, 579, 581
pyrC	Pyrimidine	Dihydroorotase (EC 3.5.2.3)	26.2	310, 340, 581, 638–640
pyrD	Pyrimidine	Dihydroorotate oxidase (EC 1.3.3.1)	24.1	176, 310, 579, 581, 638, 639
pyrE	Pyrimidine	Orotate phosphoribosyltransferase (EC 2.4.2.10)	81.4	38, 310, 471, 579, 581
pyrF	Pyrimidine	Orotidine-5′-phosphate decarboxylase (EC 4.1.1.23)	37.6	579, 581, 692
pyrG	Pyrimidine	CTP synthetase	64.4	579, 581
pyrH	Pyrimidine	UMP kinase	4.4	579, 581
pyrI	Pyrimidine	Regulatory polypeptide for aspartate transcarbamoylase, regulatory subunit (EC 2.1.3.2)	96.9	310, 581
pyrL	Pyrimidine	Aspartate transcarbamoylase leader peptide	96.9	444
qor		Quinoline reductase	92.1	466
rbsB	Ribose	*rbsP*; ribose-binding protein	85.0	579, 581
rck	Resistance to complement killing	17-kDa outer membrane protein; sequence similarity to *pagC*	pSLT	178, 233, 247, 248
recA	Recombination	Recombination deficient; degrades DNA	62.2	56, 381, 415, 549, 579, 581, 621, 637
recB	Recombination	Recombination deficient; exonuclease V (EC 3.1.11.15)	65.2	56, 430, 432, 549, 579, 581, 637
recC	Recombination	Recombination deficient; exonuclease V (EC 3.1.11.15)	65.3	56, 430, 432, 549, 579, 581
recD	Recombination	Endonuclease component of RecBCD enzyme	65.2	430, 445, 549
recF	Recombination	UV sensitive; recombination defective in *recB sbcBC* background	83.5	188, 583
recJ	Recombination	UV sensitive; recombination defective in *recB sbcBC* background	66.2	430, 431
recN	Recombination	Recombination defective in *recB sbcBC* background	58.2	188
recQ	Recombination	Recombination deficient; DNA helicase activity	86.0	53
relA	RNA relaxed	*RC*; regulation of RNA synthesis	64.6	468, 581, 603
repB	Replication	Plasmid partitioning	pSLT	178

Continued on following page

TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
repC	Replication	Plasmid partitioning	pSLT	178
rfaB	Rough	UDP-D-galactose:LPS α-1,6-D-galactosyltransferase (EC 2.1.4.-)	81.4	51, 346, 579, 581
rfaC	Rough	LPS core defect; LPS heptosyltransferase I	81.3	579, 581, 594, 675
rfaD	Rough	D-Glycero-D-manno-heptose epimerase (EC 5.1.3.-)	81.2	579, 581, 594, 617
rfaE	Rough	LPS core defect; proximal heptose deficient	78.5	201, 425, 579, 581, 675
rfaF	Rough	LPS core defect; ADP-heptose-LPS heptosyltransferase II	81.2	579, 581, 594, 617
rfaG	Rough	LPS core defect; glucose I transferase	81.4	51, 579, 581
rfaH	Rough	Deficient in LPS core synthesis and in F-factor expression; transcription control factor	86.1	51, 579, 581
rfaI	Rough	LPS core defect; LPS 1,3-galactosyltransferase (EC 2.4.1.44)	81.4	51, 67, 579, 581, 617
rfaJ	Rough	LPS core defect; LPS 1,2-glucosyltransferase	81.4	51, 67, 579, 581, 617
rfaK	Rough	LPS core defect; LPS 1,2-*N*-acetylglucosaminetransferase (EC 2.4.1.56)	81.3	345, 427, 580, 582, 595
rfaL	Rough	LPS core defect; O-antigen ligase	81.3	345, 427, 579, 581
rfaP	Rough	LPS core defect; heptose phosphorylation	81.4	251, 346, 579, 581
rfaY	Rough	LPS core defect	81.3	345, 427, 594, 617
rfaZ	Rough	LPS core defect	81.3	345, 427, 594
rfbA	Rough	*musA*, *musB*; LPS side chain defect; glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	45.2	49, 314, 316, 397, 579, 581
rfbB	Rough	LPS side chain defect; dTDP-D-glucose-4,6-dehydratase (EC 4.2.1.46)	45.3	49, 314, 439, 564, 579, 581, 732
rfbC	Rough	LPS side chain defect; dTDP-4-dehydroxyrhamnose-3,5-epimerase (EC 5.1.3.13)	45.2	314, 401, 439
rfbD	Rough	LPS side chain defect; NADPH:dTDP-4-dehydroxyrhamnose reductase (EC 1.1.1.133)	45.3	314, 401, 439, 579, 581
rfbF	Rough	LPS side chain defect; glucose-1-phosphate cytidylyltransferase (EC 2.7.7.33)	45.2	49, 314, 398, 399, 579, 581
rfbG	Rough	LPS side chain defect; CDP-glucose-4,6-dehydratase (EC 4.2.1.45)	45.2	49, 314, 399, 401, 579, 581
rfbH	Rough	LPS side chain defect; CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	45.1	49, 314, 399, 401, 579, 581
rfbI	Rough	LPS side chain defect; CDP-6-deoxy-Δ3,4-glucoseen reductase	45.2	314, 399
rfbJ	Rough	LPS side chain defect; CDP-abequose synthase (EC 4.2.1.-)	45.1	314, 399, 401, 402, 581
rfbK	Rough	LPS side chain defect; phosphomannomutase (EC 5.4.2.8)	45.0	49, 314, 401, 579, 581
rfbM	Rough	LPS side chain defect; mannose-1-phosphate guanylyltransferase (EC 2.7.7.22)	45.0	49, 314, 401, 579, 581
rfbN	Rough	LPS side chain defect; rhamnosyl transferase	45.0	314, 401, 579, 581
rfbP	Rough	*rfbT*; bifunctional enzyme; undecaprenyl-phosphate galactosephosphotransferase; may also relocate O-antigen from cytoplasmic to periplasmic face of cytoplasmic membrane	44.9	314, 401, 579, 581, 731
rfbU	Rough	LPS side chain defect; mannosyl transferase	45.0	49, 314, 401
rfbV	Rough	LPS side chain defect; abequosyltransferase; putative	45.1	314
rfbX	Rough	LPS side chain defect; rhanosyltransferase; putative (EC 2.4.1.-)	45.1	314
rfc	Rough	*rouC*; O-antigen polymerase	35.7	97, 98, 210, 467, 579, 581, 671
rfe	Rough	Defect in synthesis of enterobacterial common antigen, T1 antigen, and O side chains of *Salmonella* groups L and C1	85.4	579, 581
rffM	Rough	*rff*; synthesis of enterobacterial common antigen; UDP-*N*-acetyl-D-mannosaminuronic acid transferase (EC 2.4.1.-)	85.6	418
rffT	Rough	*rff*; synthesis of enterobacterial common antigen; 4-α-L-fucosyl transferase (EC 2.4.1.-)	85.5	418
rft	Rough	"Transient" T1 forms	16.2	579, 581
rfu	Rough	"Transient" T1 forms	NM	579, 581
rhaA	Rhamnose	L-Rhamnose isomerase (EC 5.3.1.14)	88.1	479, 579, 581
rhaB	Rhamnose	L-Rhamnulokinase (EC 2.7.1.5)	88.1	479, 579, 581
rhaD	Rhamnose	L-Rhamnulose-1-phosphate aldolase (EC 4.1.2.19)	88.1	479, 579, 581
rhaR	Rhamnose	*rhaC1*; regulation	88.1	479, 581
rhaS	Rhamnose	*rhaC2*; regulation	88.1	479, 581
rhaT	Rhamnose	L-Rhamnose transport	88.1	479, 581, 689
rhlB		RNA helicase; putative	85.4	455
rho		*psu*; polarity suppressor; transcription terminator factor rho	85.3	377, 579, 581
rna	RNase	*rnsA*; RNase I	15.2	579, 581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
rnc	RNase	RNase III	57.6	441, 579, 581
rnhA	RNase H	RNase H (EC 3.1.26.4)	6.9	305
rnhB	RNase H	RNase HII (EC 3.1.26.4)	5.9	369
rnpA	RNase P	RNase P, protein component (EC 3.1.26.5)	83.8	574
rnpB	RNase P	RNase P, RNA subunit, M1 RNA	71.1	581
rodA	Rod	Round cell morphology; mecillinam resistance	15.4	104, 579, 581
rph	RNase PH	tRNA nucleotidyltransferase; RNase PH (EC 2.7.7.56)	81.5	473
rplA	Ribosomal protein, large	50S ribosomal subunit protein L1	90.1	771
rplE	Ribosomal protein, large	50S ribosomal subunit protein L5	74.6	70
rplJ	Ribosomal protein, large	50S ribosomal subunit protein L10	90.2	528, 581, 771
rplK	Ribosomal protein, large	50S ribosomal subunit protein L11	90.1	771
rplL	Ribosomal protein, large	50S ribosomal subunit protein L7/L12	90.2	581, 771
rplS	Ribosomal protein, large	50S ribosomal subunit protein L19	57.9	530
rplX	Ribosomal protein, large	50S ribosomal subunit protein L24	74.6	70
rpoA	RNA polymerase	*oxrB*; RNA polymerase, α subunit (EC 2.7.7.6)	74.5	149, 412
rpoB	RNA polymerase	*rif*; RNA polymerase, β subunit (EC 2.7.7.6)	90.2	579, 581
rpoC	RNA polymerase	RNA polymerase, β' subunit (EC 2.7.7.6)	90.2	579, 581
rpoD	RNA polymerase	RNA polymerase, σ^{70} subunit	70.0	579, 581
rpoE	RNA polymerase	RNA polymerase, σ^{E} subunit	57.7	438
rpoN	RNA polymerase	*glnF*, *ntrA*; RNA polymerase, σ^{54} subunit (EC 2.7.7.6)	72.2	150, 537, 538, 579, 581
rpoS	RNA polymerase	*katF*; RNA polymerase, σ^{S} subunit	63.6	147, 148, 354, 485, 499, 667
rpsD	Ribosomal protein, small	30S ribosomal subunit protein S4	74.5	412
rpsE	Ribosomal protein, small	*spcA*; 30S ribosomal subunit protein S5	74.6	579, 581
rpsG	Ribosomal protein, small	30S ribosomal subunit protein S7	74.7	315
rpsL	Ribosomal protein, small	*strA*; 30S ribosomal subunit protein S12	74.7	290, 315, 579, 581, 703, 704
rpsP	Ribosomal protein small	30S ribosomal subunit protein S16	57.9	530
rpsU	Ribosomal protein, small	30S ribosomal subunit protein S21	70.0	581
rrfB		5S ribosomal RNA gene of *rrnB* operon	90.0	125
rrnA	rRNA	rRNA operon	87.0	58, 579, 581, 620
rrnB	rRNA	rRNA operon	90.0	58, 579, 581, 620
rrnC	rRNA	rRNA operon	85.0	58, 579, 581, 620
rrnD	rRNA	rRNA operon	74.3	58, 579, 581, 620
rrnE	rRNA	rRNA operon	90.9	58, 579, 581, 620
rrnG	rRNA	rRNA operon	58.1	58, 581, 620
rrnH	rRNA	rRNA operon	6.2	58, 579, 581, 620
rsk		Binding site for a regulatory element for virulence traits	pSLT	716, 717
samA	*Salmonella* mutagenesis	Mutagenesis by UV and mutagens; related to *umuDC* operon	pSLT	348, 480, 481
samB	*Salmonella* mutagenesis	Mutagenesis by UV and mutagens; related to *umuDC* operon	pSLT	348, 480, 481
sapA	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.1	525
sapB	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.2	525
sapC	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.2	219, 525
sapD	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.2	219, 525
sapE	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	3.4	219
sapF	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	37.2	525
sapI	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	38.7	219
sapJ	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	87.7	219
sapL	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	44.1	219
sapM	Sensitive to antimicrobial peptides	Resistance to antimicrobial peptides melittin and protamine	6.6	219
sbcB	Suppressor of *recBC*	Suppressor of *recBC* mutations	41.6	35

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
sbcC	Suppressor of *recBC*	Suppressor of *recBC* mutations	9.2	35
sbcD	Suppressor of *recBC*	Suppressor of *recBC* mutations	9.2	35
sbcE	Suppressor of *recBC*	Unstable suppressor of *recBC* mutations	57.0	158
sbp	Sulfate binding protein	Periplasmic sulfate binding protein	88.3	195, 303, 532, 533
selA	Selenium	*fdhA*; selenium metabolism; biosynthesis of selenoproteins	80.3	579, 581, 654
selB	Selenium	*fdhA*; selenium metabolism; translation factor necessary for biosynthesis of selenoproteins	80.3	579, 581, 654
selC	Selenium	*fdhC*; selenium metabolism; selenocysteine tRNA	81.5	579, 581, 654
selD	Selenium	*selA*; selenium metabolism; biosynthesis of selenoproteins and selenocysteine tRNA	29.0	581, 654
serA	Serine	Phosphoglycerate dehydrogenase (EC 1.1.1.95)	66.8	579, 581
serB	Serine	Phosphoserine phosphatase (EC 3.1.3.3)	99.5	579, 581
serC	Serine	Requirement	19.6	215, 579, 581
serD	Serine	Requirement for pyridoxine plus L-serine or glycine	47.2	579, 581
serV	Serine	Serine tRNA 3	62.0	42
sgdA	Suppressor of gyrase	Restores his attenuation in *gyrA* mutants and suppresses other *gyrA* phenotypes	62.0	42
sidC	Siderochrome	Siderochrome utilization; ferrichrome transport; albomycin resistance	3.8	579, 581
sidF	Siderochrome	Siderochrome utilization; ferrichrome transport; albomycin resistance	3.8	579, 581
sidK	Siderochrome	Siderochrome utilization; albomycin resistance; receptor of phage ES18 in *S. typhimurium* and of T5 in *S. paratyphi* B	5.0	579, 581
sinR	*Salmonella* insert regulator	Protein in the LysR family of transcription regulators; gene is unique to *Salmonella* spp.	NM	221
slt		Soluble lytic transglycosylase	99.9	619
slyA	Salmolysin	*cyx*; hemolysin, required for survival in macrophages and for virulence	30.8	387, 388
smoB	Smooth	Smooth colony morphology in histidine-constitutive mutants	98.6	579, 581
smpB	Small protein	Reduced survival in macrophages	59.5	29
sms		Repair of endogenous alkylation damage; putative; similarity with ATP-dependent proteases Lon and RecA	99.9	169
smvA		Methyl viologen-resistant	38.6	278
sodB		Iron superoxide dismutase; putative (EC 1.15.1.1)	30.7	82
spaK	Surface presentation of antigens	*invB*; reduced invasion; secretory pathway	63.1	133, 182, 184, 218, 320, 454
spaL	Surface presentation of antigens	*invC*; reduced invasion; secretory pathway, homologous to *spa* in *Shigella* spp.	63.1	133, 182, 184, 207, 218, 454
spaM	Surface presentation of antigens	*invI*; reduced invasion; secretory pathway	63.1	95, 218, 442, 454
spaN	Surface presentation of antigens	*invJ*; reduced invasion; secretory pathway	63.0	95, 218, 442, 454
spaO	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	218, 454
spaP	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	218, 454
spaQ	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	218, 454
spaR	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	218, 454
spaS	Surface presentation of antigens	Reduced invasion; secretory pathway	63.0	218, 454
spaT	Surface presentation of antigens	Reduced invasion; secretory pathway	62.9	218, 454
spcB	Spectinomycin	Nonribosomal resistance	74.5	579, 581
spoT	Spot	Guanosine 5′-diphosphate, 3′-diphosphate pyrophosphatase	81.6	579, 581
spvA	*Salmonella* plasmid virulence	*mkaB*, *vsdB*; hydrophilic protein, 28 kDa, outer membrane protein	pSLT	107, 226, 227, 354, 684
spvB	*Salmonella* plasmid virulence	*vsdC*, *mkaA*, *mkfB*; hydrophilic protein, 66 kDa, cytoplasmic protein	pSLT	107, 226, 227, 354, 483, 485, 487, 683, 684
spvC	*Salmonella* plasmid virulence	*virA*, *mkaD*, *mkfA*, *vsdD*; hydrophilic protein, 28 kDa	pSLT	107, 225–227, 354, 482, 484, 684
spvD	*Salmonella* plasmid virulence	*virB*, *vsdE*; hydrophilic protein, 25 kDa	pSLT	226, 227, 354, 482
spvR	*Salmonella* plasmid virulence	*mkaC*, *vsdA*; regulation of the *spv* operon; member of LysR family of positive regulatory proteins	pSLT	62, 107, 227, 354, 355, 684
srlA	Sorbitol	D-Glucitol-specific enzyme II of the phosphotransferase system	62.5	581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
srlB	Sorbitol	D-Glucitol-specific enzyme III of the phosphotransferase system	62.5	581
srlC	Sorbitol	*gut*; regulatory gene	62.4	579, 581
srlD	Sorbitol	Sorbitol-6-phosphate dehydrogenase (EC 1.1.1.140)	62.5	581
srlM	Sorbitol	DNA-binding protein which activates transcription of the *srl* operon	62.5	581
srlR	Sorbitol	Regulatory gene	62.5	581
ssb	Single-strand binding	Single-stranded DNA-binding protein	92.3	581
stiA	Starvation inducible	*sinA*; induced by starvation for carbon source or other requirements	35.8	581, 642
stiB	Starvation inducible	Induced by starvation for carbon source or other requirements	NM	581, 642
stiC	Starvation inducible	Induced by starvation for carbon source or other requirements	78.2	581, 642
stiD	Starvation inducible	Induced by starvation for carbon source or other requirements	35.9	581, 642
stiE	Starvation inducible	Induced by starvation for carbon source or other requirements	44.0	581, 642
stiF	Starvation inducible	Induced by starvation for carbon source or other requirements	NM	581, 642
stiG	Starvation inducible	Induced by starvation for carbon source or other requirements	88.2	581, 642
stiH	Starvation inducible	Induced by starvation for carbon source or other requirements	57.4	581, 642
stn	*Salmonella* toxin	*stx*; enterotoxin	NM	87, 541, 581
strB	Streptomycin	Low-level resistance plus auxotrophy; nonribosomal	55.7	579, 581
strC	Streptomycin	Streptomycin resistance; nonribosomal	NM	579, 581
sucA	Succinate	*lys*, *suc*; succinate requirement; α-ketoglutarate dehydrogenase, decarboxylase component	17.1	579, 581
sufA	Suppressor of frameshifts	Suppressor affecting proline tRNA and correcting +1 frameshifts at runs of C in the mRNA	79.9	579, 581
sufB	Suppressor of frameshifts	*sufC*; recessive suppressor of +1 frameshifts at runs of C in the mRNA	16.8	579, 581, 646
sufD	Suppressor of frameshifts	Frameshift suppressor affecting glycine tRNA and correcting +1 frameshifts at runs of G in the mRNA	65.8	579, 581
sufE	Suppressor of frameshifts	Frameshift suppressor correcting +1 frameshifts at runs of G in the mRNA	90.7	579, 581
sufF	Suppressor of frameshifts	Recessive frameshift suppressor correcting +1 frameshifts at runs of G in the mRNA	12.4	579, 581
sufG	Suppressor of frameshifts	*supI*; frameshift suppressor correcting +1 frameshifts at runs of A in the mRNA	16.6	579, 581
sufH	Suppressor of frameshifts	Suppressor	53.2	579, 581
sufI	Suppressor of frameshifts	Suppressor	12.5	579, 581
sulA	Suppressor of *lon*	Lacks SOS-induced filamentation	24.4	174, 188, 200
sumA	Suppressor of missense	Suppressor	95.2	443, 579, 581
supC	Suppressor	Ochre suppressor	38.6	579, 581
supD	Suppressor	Amber suppressor; serine insertion	42.9	579, 581
supE	Suppressor	*supY*; amber suppressor; glutamine insertion	16.7	579, 581
supG	Suppressor	Ochre suppressor; lysine insertion	NM	579, 581
supJ	Suppressor	*supH*; amber suppressor; leucine insertion	85.1	579, 581
supQ	Suppressor	Suppressor of nonsense and deletion mutations of *leuD*	7.9	579, 581
supR	Suppressor	Amber suppressor; haploid lethal	85.1	579, 581
supS	Suppressor	UGA suppressor; haploid lethal	85.1	579, 581
supU	Suppressor	Suppressor of UGA mutations; may be due to alteration of ribosome structure	74.8	579, 581
tar	Taxis-associated receptor	Chemotaxis transduction polypeptide; aspartate receptor	41.9	112, 579, 581
tcp		Transmembrane receptor for citrate (attractant) and phenol (repellent)	NM	760
tctA	Tricarboxylate transport	Membrane protein	60.9	579, 581, 741
tctB	Tricarboxylate transport	Membrane protein	60.8	581, 741
tctC	Tricarboxylate transport	Tricarboxylate-binding protein	60.8	579, 581, 741
tctD	Tricarboxylate transport	Regulatory protein	60.8	581, 741
tctII	Tricarboxylate transport	Transport	17.6	581
tctIII	Tricarboxylate transport	*triM*, *triR*; transport	1.3	579, 581
tdcB		Catabolic threonine dehydratase	70.9	344
tdk		Thymidine kinase (EC 2.7.1.21)	38.4	579, 581
tesA		*apeA*; thioesterase I (EC 3.1.2.-)	12.3	86, 579, 581
thiA	Thiamine	*thiG*; thiamine or thiazole moiety	90.5	371, 579, 581

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TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
thiC	Thiamine	*thiA*; thiamine or pyrimidine moiety	90.5	579, 581
thiD	Thiamine	Thiamine requirement	50.5	579, 581
thiE	Thiamine	Thiazole type	55.2	579, 581
thiF	Thiamine	Thiazole type	55.3	579, 581
thiH	Thiamine	*thiB*; thiamine requirement	56.6	579, 581
thiI	Thiamine	*thiC*; thiazole type	10.5	579, 581
thrA	Threonine	*thrC*, *thrD*; aspartokinase I and homoserine dehydrogenase I (EC 2.7.2.4, EC 1.1.1.3)	0.0	579, 581
thrB	Threonine	*thrA*; homoserine kinase (EC 2.7.1.39)	0.0	579, 581
thrC	Threonine	*thrB*; threonine synthase (EC 4.2.99.2)	0.1	579, 581
thrT	Threonine	*sufJ*; threonine tRNA	90.0	579, 581
thrW	Threonine	Threonine tRNA 2; sequence contains attachment site for prophage P22; see *ataA*	7.8	
thyA	Thymine	Requirement	65.3	579, 581
tip	Taxis-involved protein	Methyl-accepting chemotaxis protein, aspartate receptor	NM	578, 581
tkt		Transketolase (EC 2.2.1.1)	NM	579, 581
tlpA		Prokaryotic coiled-coil protein	pSLT	295, 352
tlpB		*tlp*; loss of protease II	40.4	579, 581
tlr		Thiolutin resistance; P22 development at high temperature	NM	579, 581
tonB	T-one	*chr*; regulates levels of some outer membrane proteins; resistance to ES18; determines a salmonellocin; affects iron transport	38.2	52, 242, 579, 581
topA	Topoisomerase	*supX*, *top*; DNA topoisomerase I	37.7	76, 183, 393, 555, 579, 581, 590
topB	Topoisomerase	DNA topoisomerase III (EC 5.99.1.2)	29.1	25
tor		Trimethylamine oxide reductase	82.5	579, 581
tppB	Tripeptide permease	Resistance to alafosfalin; tripeptide permease	32.1	39, 74
tppR	Tripeptide permease	Regulator of tripeptide permease	4.7	581
traT	Transfer	Membrane protein cross-reacts immunologically with TraT protein of F plasmid; restores permeability mutants to normal	pSLT	552, 581, 674, 676
treA	Trehalose	*tre*; utilization	40.2	579, 581
treR	Trehalose	Trehalose regulation	96.6	686
trkA	Transport of Potassium	*sapG*; potassium uptake protein	74.4	219, 526
trmA		tRNA (m^5U54) methyltransferase (EC 2.1.1.35)	89.7	229
trmD		tRNA (m^1G37) methyltransferase (EC 2.1.1.31)	57.9	41, 530, 581
trpA	Tryptophan	*trpC*; tryptophan synthetase, α subunit (EC 4.2.1.20)	38.1	16, 238, 296, 333, 579, 581
trpB	Tryptophan	*trpD*; tryptophan synthetase, β subunit (EC 4.2.1.20)	38.1	16, 55, 238, 296, 339, 579, 581
trpC	Tryptophan	*trpE*; *N*-(5-phosphoribosyl)anthranilate isomerase and indole-3-glycerol phosphate synthase (EC 5.1.3.24, EC 4.1.1.48)	38.1	579, 581
trpD	Tryptophan	*trpB*; anthranilate phosphoribosyltransferase (EC 2.4.2.18)	38.0	28, 579, 581
trpE	Tryptophan	*trpA*; anthranilate synthase (EC 4.1.3.27)	38.0	28, 64, 579, 581
trpR	Tryptophan	Resistance to 5-methyltryptophan; derepression of tryptophan enzymes	99.9	579, 581
trxA	Thioredoxin	Thioredoxin	85.3	353
tsr		Chemotaxis receptor; serine specificity	98.5	581
tsx	T-six	Nucleoside uptake; receptor for phage T6 (in *E. coli*)	9.1	477
ttr		Tetrathionate reductase	40.0	579, 581
tufA		Protein chain elongation factor EF-Tu	74.7	1, 22, 288, 289, 315, 579, 581, 703–706
tufB		Protein chain elongation factor EF-Tu	90.1	22, 288, 289, 579, 581, 703, 704, 706
tyn		Tyramine oxidase	NM	579, 581
tyrA	Tyrosine	Requirement	58.3	579, 581
tyrR	Tyrosine	Regulator gene for *aroF* and *tyrA*	37.1	579, 581
tyrS	Tyrosine	Tyrosyl-tRNA synthetase	30.9	387, 388
tyrT	Tyrosine	*supC*, *supF*; ochre suppressor; tyrosine tRNA 1	38.4	579, 581
tyrU	Tyrosine	*supM*; ochre suppressor; tyrosine tRNA 2	90.0	579, 581
ubiF	Ubiquinone	*cad*; deficient in ubiquinone synthesis; accumulates 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	16.3	579, 581
ubiG	Ubiquinone	Ubiquinone synthesis	49.3	325
ubiX	Ubiquinone	Growth stimulation by *p*-hydroxybenzoic acid; 3-octaprenyl-4-hydroxybenzoate decarboxylase	51.3	579, 581
udk		Uridine kinase (EC 2.7.1.48)	45.7	579, 581
udp		Uridine phosphorylase (EC 2.4.2.3)	86.3	579, 581

Continued on following page

TABLE 1—*Continued*

Gene symbol	Mnemonic	Former or alternative symbol; enzyme deficiency or other phenotype[a]	Map position (Cs)[b]	Reference(s)[c]
uhpA		Utilization of hexose phosphate	82.1	304, 579, 581
uhpB		Utilization of hexose phosphate	82.0	304
uhpC		Utilization of hexose phosphate	82.0	304
uhpT		Hexosephosphate transport	82.0	304, 579, 581
umuC		Induction of mutations by UV; error-prone repair	42.9	348, 480, 481, 579, 581, 600, 621, 623, 693–695
umuD		Induction of mutations by UV; error-prone repair	42.9	348, 480, 481, 600, 621, 623, 693–695, 750
upp		Uracil phosphoribosyltransferase (EC 2.4.2.9)	54.2	579, 581
urs	Uracil	Uracil catabolism defect	35.2	581
ushA	UDP sugar hydrolase	UDP-sugar hydrolase (5′-nucleotidase); silent gene in *Salmonella* spp. of subgenus I	12.2	132, 579, 581
ushB	UDP sugar hydrolase	Inner membrane-associated UDP-sugar hydrolase	88.3	132, 195, 579, 581
usp	Ureidosuccinate	Permeability to ureidosuccinate	NM	579, 581
uvrA	UV	Repair of UV damage to DNA; exinuclease ABC, subunit A	92.3	579, 581, 697
uvrB	UV	Repair of UV damage to DNA; exinuclease ABC, subunit B	18.4	415, 579, 581
uvrC	UV	Repair of UV damage to DNA; exinuclease ABC, subunit C	42.2	579, 581
uvrD	UV	Repair of UV damage to DNA; helicase II (EC 3.6.1.-)	85.8	415, 579, 581
valS	Valine	Valyl-tRNA synthetase (EC 6.1.1.9)	97.3	579, 581
viaA		ViA; Vi antigen (in *S. typhi*)	50.3	579, 581
xylA	D-Xylose	Xylose isomerase (EC 5.3.1.5)	80.0	579, 581
xylB	D-Xylose	Xylulokinase (EC 2.7.1.17)	80.0	579, 581
xylR	D-Xylose	Regulation	80.0	579, 581
xylT	D-Xylose	Transport	80.0	579, 581

[a] Abbreviations: CoA, coenzyme A; cyclic AMP; CRP, cAMP receptor protein; DAHP, 3-deoxy-D-arabinoheptulsonic acid 7-phosphate; DMB, dimethylbenzimidazole; HP, hydrogen peroxide; LPS, lipopolysaccharide; NAMN, nicotinic acid, mononucleotide; NMN, nicotinamide mononucleotide; PRPP, phosphoribosyl pyrophosphate.

[b] Map positions in centisomes (Cs) indicate the location of the gene on the map in Fig. 1, from 0 to 100 Cs. NM indicates that gene is on the chromosome but the map position is not known. The symbol pSLT indicates that the gene is on pSLT, the 90-kb plasmid of LT2; a map of pSLT is shown in Fig. 1.

[c] Reference 581 refers to edition VII of the linkage map, in which other references to the indicated gene are given. Also, there are many papers cited in reference 579, which have important information on the genes of *S. typhimurium*.

TABLE 2. Alternative gene symbols[a]

Former or alternative symbol	Current symbol	Former or alternative symbol	Current symbol
ail	*pagC*	*aroC*	*aroE*
aniA	*hydA*	*aroD*	*aroC*
aniE	*phsA*	*aroE*	*aroD*
apaG	*corD*	*ars*	*carA*
apeA	*tesA*	*asc*	*ent*
apeD	*apeR*	*atbR*	*atrR*
argA	*argE*	*atrC*	*polA*
argB	*argA*	*attP14*	*atdA*
argC	*argB*	*attP22 I*	*ataA*
argD	*carA*	*attP221*	*atcA*
argE	*argG*	*attP27 I*	*atbA*
argF	*argH*	*attP27 II*	*atbB*
argG	*argD*	*bac*	*mre*
argH	*argC*	*bfe*	*btuB*
argT	*argX*	*bglY*	*hns*
argU	*argX*	*bio*	*bioA*

Continued

TABLE 2—*Continued*

Former or alternative symbol	Current symbol	Former or alternative symbol	Current symbol
cad	*ubiF*	*chlE*	*moeA*
cap	*carA*	*chr*	*tonB*
capR	*lon*	*clmF*	*parC*
carA	*ptsI*	*clmF*	*parE*
carB	*ptsH*	*clmF*	*parF*
cheC	*fliM*	*cls*	*katG*
cheP	*cheA*	*cobI*	*cbiA*
cheQ	*cheY*	*cobI*	*cbiB*
cheT	*cheZ*	*cobI*	*cbiC*
cheU	*fliM*	*cobI*	*cbiD*
cheV	*fliG*	*cobI*	*cbiE*
cheX	*cheB*	*cobI*	*cbiF*
chlA	*moaA*	*cobI*	*cbiG*
chlB	*mob*	*cobI*	*cbiH*
chlC	*nar*	*cobI*	*cbiJ*
chlD	*modC*	*cobI*	*cbiK*

Continued on following page

TABLE 2—*Continued*

Former or alternative symbol	Current symbol	Former or alternative symbol	Current symbol
cobI	*cbiL*	*flaX*	*fliR*
cobI	*cbiM*	*flgR*	*flgM*
cobI	*cbiN*	*fruA*	*ptsF*
cobI	*cbiO*	*fruF*	*fruB*
cobI	*cbiP*	*fuc*	*fucA*
cobI	*cbiQ*	*fur*	*furA*
cobI	*cbiT*	*gdh*	*gdhA*
cobII	*cobJ*	*glnF*	*rpoN*
cobII	*cobK*	*glnR*	*ntrB*
cobII	*cobL*	*glnR*	*ntrC*
cobII	*cobM*	*glu*	*ptsG*
cobIII	*cobS*	*gpt*	*ptsG*
cobIII	*cobT*	*gut*	*srlC*
cobIII	*cobU*	*gxu*	*gpt*
cobIV	*cobA*	*H1*	*fliC*
cpd	*cpdB*	*H2*	*fljB*
cya	*cyaA*	*hisE*	*hisI*
cysAa	*cysU*	*hisIE*	*hisI*
cysAb	*cysW*	*hisU*	*gyrB*
cysT	*cysU*	*hisW*	*gyrA*
cyx	*slyA*	*hsdSB*	*hsdM*
dad	*dadA*	*hsdSB*	*hsdS*
degP	*htrA*	*hspLT*	*hsdL*
dra	*deoC*	*hyd*	*hydA*
drm	*deoB*	*ile*	*ilvA*
enb	*ent*	*ilvA*	*ilvC*
envB	*mre*	*ilvB*	*ilvD*
envM	*fabI*	*ilvC*	*ilvE*
fdhA	*selA*	*ilvT*	*brnQ*
fdhA	*selB*	*incL*	*parS*
fdhC	*selC*	*invB*	*spaK*
fhl	*fdhF*	*invC*	*spaL*
fhlB	*hydA*	*invD*	*gcv*
fim	*fimA*	*invI*	*spaM*
fimU	*argU*	*invJ*	*spaN*
firA	*lpxD*	*katF*	*rpoS*
flaAI	*fliE*	*lep*	*lepB*
flaAII.2	*fliG*	*leuT*	*leuU*
flaAII.3	*fliH*	*liv*	*livS*
flaAII.I	*fliF*	*livA*	*livH*
flaAIII	*fliI*	*livB*	*livJ*
flaB	*fliP*	*livC*	*livK*
flaC	*flhA*	*livEF*	*livM*
flaD	*fliQ*	*livF*	*livG*
flaE	*flhC*	*livG*	*livF*
flaFI	*flgA*	*lnt*	*cutE*
flaFII	*flgB*	*lom*	*pagC*
flaFIII	*flgC*	*lys*	*lysA*
flaFIV	*flgD*	*lys*	*sucA*
flaFIX	*flgI*	*malB*	*malE*
flaFV	*flgE*	*manA*	*ptsM*
flaFVI	*flgF*	*metI*	*metA*
flaFVII	*flgG*	*metP*	*metD*
flaFVIII	*flgH*	*mglD*	*galS*
flaFX	*flgJ*	*mkaA*	*spvB*
flaK	*flhD*	*mkaB*	*spvA*
flaL	*fliA*	*mkaC*	*spvR*
flaM	*flhB*	*mkaD*	*spvC*
flaN	*fliN*	*mkfA*	*spvC*
flaP	*fliO*	*mkfB*	*spvB*
flaQI	*fliL*	*motC*	*fliG*
flaQII	*fliM*	*musA*	*rfbA*
flaR	*fliK*	*musB*	*rfbA*
flaS	*fliJ*	*mutB*	*mutY*
flaU	*flgL*	*mviB*	*mviM*
flaV	*fliD*	*mviS*	*flgM*
flaW	*flgK*	*nadI*	*nadR*

Continued

TABLE 2—*Continued*

Former or alternative symbol	Current symbol	Former or alternative symbol	Current symbol
nag	*nagA*	*spcA*	*rpsE*
nalA	*gyrA*	*ssc*	*lpxD*
nfsI	*nfnB*	*strA*	*rpsL*
nic	*nadB*	*stx*	*stn*
nicA	*nadA*	*suc*	*sucA*
nml	*fliB*	*sufB*	*proL*
ntrA	*rpoN*	*sufC*	*sufB*
O-5	*oafA*	*sufJ*	*thrT*
ofi	*oafA*	*sufS*	*glyT*
ompB	*envZ*	*sulB*	*ftsZ*
ompB	*ompR*	*supC*	*tyrT*
omsA	*lpxD*	*supF*	*tyrT*
optA	*opdA*	*supH*	*supJ*
orf5	*pefK*	*supI*	*sufG*
orf6	*pefL*	*supK*	*prfB*
orf8	*pefS*	*supM*	*tyrU*
osmZ	*hns*	*supT*	*prfB*
oxrA	*fnr*	*supX*	*topA*
oxrB	*rpoA*	*supY*	*supE*
oxrC	*pgi*	*thiA*	*thiC*
parA	*gyrB*	*thiB*	*thiH*
pasA	*pgi*	*thiC*	*thiI*
pck	*pckB*	*thiG*	*thiA*
phs	*phsA*	*thrA*	*thrB*
pil	*fimA*	*thrB*	*thrC*
pilG	*hns*	*thrC*	*thrA*
pmi	*manA*	*thrD*	*thrA*
pnu	*deoD*	*tlp*	*tlpB*
pnuA	*nadR*	*top*	*topA*
poh	*oriC*	*tpp*	*deoA*
pox	*ply*	*tppA*	*envZ*
proT	*proM*	*tppA*	*ompR*
proU	*proV*	*tppB*	*envZ*
proU	*proW*	*tre*	*treA*
proU	*proX*	*triM*	*tctIII*
proW	*proL*	*triR*	*tctIII*
prp	*prpA*	*trpA*	*trpE*
prsB	*prsA*	*trpB*	*trpD*
psu	*rho*	*trpC*	*trpA*
ptdD	*pepD*	*trpD*	*trpB*
ptdN	*pepN*	*trpE*	*trpC*
ptdP	*pepP*	*trz*	*cysK*
pup	*deoD*	*umpA*	*lgt*
putB	*putA*	*unc*	*atp*
pyrA	*carA*	*uncA*	*atp*
pyrA	*carB*	*use*	*argX*
rbsP	*rbsB*	*vh2*	*hin*
RC	*relA*	*ViA*	*viaA*
rfbL	*cpsG*	*virA*	*spvC*
rfbT	*rfbP*	*virB*	*spvD*
rff	*rffM*	*visA*	*hemH*
rff	*rffT*	*vsdA*	*spvR*
rflB	*flgM*	*vsdB*	*spvA*
rhaC1	*rhaR*	*vsdC*	*spvB*
rhaC2	*rhaS*	*vsdD*	*spvC*
rhl	*fljA*	*vsdE*	*spvD*
rif	*rpoB*	*wrkA*	*divA*
rnsA	*rna*		
rol	*cld*		
rouC	*rfc*		
sapG	*trkA*		
sapK	*sapJ*		
selA	*selD*		
sinA	*stiA*		
smoA	*divC*		

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[a] The alternative symbols have been used in past publications. It is recommended that their use be abandoned and that the current symbols, listed and described in Table 1 and in the associated references, be used in the future.

TABLE 3. Sequenced genes of *S. typhimurium*[a]

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
STCARAB	(+)	78000	1.622	SP	1,886	X13200	
carA	(+)	78696	1.637	W	382	SG10032/P14845	343
carB	(+)	79863	1.661	F	8	SG10033/P14846	343
araDstyM	(+)	115391	2.400	MG	5,947	SS1001	
STYARABAD	(−)	115392	2.400	C	4,790	M11047	
araD	(−)	115954	2.412	W	248	SG10015/P06190	394
araA	(−)	116841	2.430	W	500	SG10012/P06189	395
araB	(−)	118354	2.462	W	569	SG10013/P06188	396
STYARALC	(+)	120053	2.497	C	1,286	J01797	
araC	(+)	120404	2.504	W	281	SG10014/P03022	92, 93
leuDstyM	(+)	137999	2.870	MP	6,168	SS1020	
STLEUD	(−)	138000	2.870	C	1,074	X02528	
leuD	(−)	138454	2.880	W	201	SG10198/P04787	177
STLEUC	(−)	139053	2.892	C	1,432	X51476	
leuC	(−)	139070	2.892	W	464	SG10197/P15717	570
STLEUB	(−)	140445	2.921	C	1,122	X53376	
leuB	(−)	140467	2.922	W	359	SG10196/P37412	19
STYLEUA	(−)	141545	2.944	C	1,569	X51583	
leuA	(−)	141546	2.944	W	522	SG10195/P15875	198, 553
STYLEUOP	(−)	143024	2.975	C	497	J01807	
STYLEUP	(−)	143313	2.981	C	855	M12892	
STILVIHO	(+)	144299	3.001	SG	348	X68562	
STFRURG	(+)	144721	3.010	SG	2,497	X55456	
ilvI	(+)	144722	3.010	F	52	SG10129/P40811	307
ilvH	(+)	144904	3.014	W	163	SG10182/P21622	307
fruR	(+)	145679	3.030	W	334	SG10133/P21930	307, 722
STYNADC	(−)	172126	3.580	SG	1,403	L07292	
nadC	(−)	172264	3.583	W	297	SG10242/P30012	291
ampD	(+)	173245	3.603	F	94	SG10010/P30013	291
ompHstyM	(+)	193281	4.020	MG	2,332	SS1025	
STYOMPH	(+)	193282	4.020	C	992	J05101	
ompH	(+)	193593	4.026	W	161	SG10265/P16974	266, 350, 351
STYSSCA	(+)	194063	4.036	C	1,551	M35193	
lpxD	(+)	194082	4.037	W	341	SG10209/P18482	267, 268, 593, 726
fabZ	(+)	195213	4.060	F	134	SG10096/P21773	267
STLPXGNA	(+)	200974	4.180	SG	812	Z25462	
lpxA	(+)	200975	4.180	W	262	SG10208/P32200	726
STPEPMG	(−)	205782	4.280	SG	1,811	X55778	
glnD	(−)	206054	4.286	F	201	SG10144/P23679	460
pepM	(−)	206623	4.297	W	264	SG10283/P10882	460, 742
STYHEML	(−)	240400	5.000	SG	1,658	M60064	
hemL	(−)	240548	5.003	W	426	SG10152/P21267	139
STSPHSPG	(+)	245000	5.096	SH	1,980	X54548	
dgt	(+)	245001	5.096	F	87	SG10473/P40733	317
htrA	(+)	245395	5.104	W	475	SG10173/P26982	317
STYPOL3A	(+)	284000	5.907	SP	3,763	M26046	
rnhB	(+)	284001	5.907	F	55	SG10493/P40675	369
dnaE	(+)	284159	5.910	W	1,160	SG10087/P14567	369
accA	(+)	287654	5.983	F	36	SG10496/P40674	369
rnhAstyM	(+)	329999	6.864	MH	927	SS1031	
STDNAQRN	(−)	330000	6.864	C	545	X57159	
rnhA	(−)	330001	6.864	W	155	SG10360/P23329	
STYPOL3E	(+)	330473	6.873	C	454	M26045	

Continued on following page

TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
dnaQ	(+)	330532	6.875	F	100	SG10090/P14566	368
STGHPT	(+)	356273	7.410	SG	845	X63336	
gpt	(+)	356466	7.414	W	152	SG10147/P26972	
yafA	(+)	357013	7.425	F	35	SG10415/P37722	
STPHOE	(−)	365408	7.600	SG	1,232	X68023	
phoE	(−)	365413	7.600	W	350	SG10291/P30705	644
STYP22ATB	(+)	375000	7.800	SG	320	M10894	
proA	(+)	375001	7.800	F	23	SG10301/P40861	379
thrW (*ataA*)	(+)	375188	7.803	W	RNA	SG30013/tRNA	
STYDDLA	(−)	420000	8.735	SH	1,197	M20793	
ddlA	(−)	420004	8.736	W	364	SG10084/P15051	115
brnQstyM	(+)	429999	8.943	MG	2,645	SS1003	
STYBRNQ	(+)	430000	8.943	C	1,603	D00332	
brnQ	(+)	430220	8.948	W	439	SG10029/P14931	490
STPROY	(+)	431457	8.974	C	1,188	X74420	
proY	(+)	431551	8.976	W	292	SG10314/P37460	
STTSXOMP	(−)	435000	9.047	SH	2,244	Z26657	
yajD	(+)	435015	9.048	W	109	SG10517/P40777	
tsx	(−)	435987	9.068	W	287	SG10516/P40776	
STU09529	(+)	480000	9.983	SH	1,030	U09529	
apbA	(+)	480102	9.985	W	281	SG10001/P37402	
STHUPB	(+)	547831	11.394	SH	478	X07844	
hupB	(+)	547951	11.397	W	90	SG10175/P05515	436
STYADK	(+)	555324	11.550	SG	1,590	L26246	
adk	(+)	555536	11.554	W	214	SG10003/P37407	
hemH	(+)	556409	11.573	F	168	SG10151/P37408	
STUSHA0	(+)	585614	12.180	SG	2,607	X04651	
ushA	(+)	585780	12.183	W	550	SG10412/P06196	59
ybaK	(−)	587549	12.220	W	159	SG10416/P37174	59
STNITRD	(−)	652330	13.568	SG	1,690	X17250	
nfnB	(−)	653069	13.583	W	217	SG10246/P15888	736
STYAHPCFA	(+)	678000	14.101	SP	2,610	J05478	
ahpC	(+)	678166	14.105	W	187	SG10004/P19479	306, 687, 688
ahpF	(+)	678971	14.122	W	521	SG10005/P19480	306, 688
STYFIMCLUS	(+)	721200	15.000	SG	12,168	L19338	
fimA	(+)	722263	15.022	W	185	SG10275/P37921	
fimI	(+)	722934	15.036	W	164	SG10508/P37922	
fimC	(+)	723472	15.047	W	230	SG10504/P37923	
fimD	(+)	724195	15.062	W	870	SG10505/P37924	
fimH	(+)	726822	15.117	W	335	SG10507/P37925	
fimF	(+)	727839	15.138	W	172	SG10506/P37926	
fimZ	(−)	728403	15.150	W	210	SG10099/P26319	678
fimY	(−)	729639	15.176	W	240	SG10098/P26318	678
fimW	(−)	730853	15.201	W	198	SG10509/P37928	
argU	(+)	731705	15.218	W	RNA	SG30004/tRNA	
STU12808	(−)	750048	15.600	SG	1,124	U12808	
cobC	(−)	750261	15.604	W	234	SG10479/P39701	
STPHRG	(+)	814000	16.930	SH	1,353	X60662	
phrB	(+)	814001	16.930	W	450	SG10295/P25078	384
STYCITA	(+)	815437	16.960	SG	2,119	D90203	

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
citB	(+)	815438	16.960	F	58	SG10059/P37463	610
citA	(+)	815667	16.965	W	434	SG10058/P24115	610
STYNADAPCU	(+)	826000	17.180	SP	2,330	M85180	
nadA	(+)	826142	17.183	W	365	SG10241/P24519	169
pnuC	(+)	827209	17.205	W	322	SG10306/P24520	169
STYGALOPA	(−)	856000	17.804	SP	3,219	M33681	
galK	(−)	856001	17.804	W	380	SG10137/P22713	280
galT	(−)	857147	17.828	W	348	SG10138/P22714	280
galE	(−)	858206	17.850	W	337	SG10135/P22715	280
STYBIOAB	(+)	871000	18.116	SP	117	M21923	
bioA	(−)	871001	18.116	F	5	SG10026/P12677	611
bioB	(+)	871103	18.118	F	5	SG10027/P12678	611
STU02273	(+)	920000	19.135	SH	495	U02273	
lrp	(+)	920001	19.135	W	164	SG10210/P37403	
STYAROAPM	(+)	956000	19.884	SG	1,332	M10947	
aroA	(+)	956027	19.884	W	427	SG10019/P07637	647
STOMPFGE	(−)	1094000	22.754	SH	1,306	Z31594	
ompF	(−)	1094013	22.754	W	363	SG10264/P37432	
STYPNCB	(−)	1114000	23.170	SP	1,837	M55986	
pncB	(−)	1114398	23.178	W	400	SG10305/P22253	724
STYNEUR	(+)	1140000	23.710	SP	1,803	M55342	
nanH	(+)	1140263	23.716	W	382	SG10244/P29768	110, 281, 690
ycdD	(−)	1141482	23.741	F	106	SG10500/P40784	281
STPYRDDD	(+)	1160000	24.126	SP	1,286	X55636	
pyrD	(+)	1160149	24.130	W	336	SG10326/P25468	176
sulAstyM	(+)	1169999	24.334	MG	2,236	SS1032	
STOMPA	(−)	1170000	24.334	C	1,400	X02006	
ompA	(−)	1170148	24.338	W	350	SG10263/P02936	175
STYSULA	(−)	1171364	24.363	C	874	M16324	
sulA	(−)	1171557	24.367	W	169	SG10386/P08847	174
putAstyM	(+)	1229999	25.582	MP	6,077	SS1029	
STPUTA	(−)	1230000	25.582	C	4,102	X70843	
putA	(−)	1230140	25.585	W	1,320	SG10321/P10503	11, 236
STPUTPA	(−)	1234022	25.666	C	546	X12569	
STPUTP	(+)	1234473	25.675	C	1,604	X52573	
putP	(+)	1234524	25.676	W	502	SG10322/P10502	236, 448
STPYRC	(−)	1260000	26.206	SP	1,672	X03928	
pyrC	(−)	1260209	26.211	W	348	SG10325/P06204	472
yceB	(−)	1261363	26.235	F	103	SG10459/P40822	472
mviMstyM	(+)	1264987	26.310	MP	15,013	SS1008	
STYFLGA	(−)	1264988	26.310	C	4,943	D25292	
STMVIMN	(+)	1264989	26.310	C	3,120	Z26133	
mviM	(+)	1265263	26.316	W	307	SG10239/P37168	
mviN	(+)	1266451	26.340	W	524	SG10240/P37169	
STU03631	(+)	1268096	26.375	C	893	U03631	
flgN	(−)	1268107	26.375	W	140	SG10113/P37406	591
flgM	(−)	1268534	26.384	W	97	SG10112/P26477	203, 591
flgA	(−)	1268919	26.392	W	219	SG10503/P40131	364
STYFLG	(+)	1269578	26.406	C	1,000	D13703	
STFLGBC	(+)	1269700	26.408	C	878	X52093	
flgB	(+)	1269735	26.409	W	138	SG10101/P16437	276, 323, 362
flgC	(+)	1270155	26.418	W	134	SG10102/P16438	276, 323, 362
STYFLGD	(+)	1270377	26.422	C	1,147	D25293	

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
flgD	(+)	1270571	26.426	W	232	SG10103/P16321	274, 359
STFLGE	(+)	1271235	26.440	C	1,320	X51737	
flgE	(+)	1271296	26.441	W	403	SG10104/P16322	274
STFLGFG	(+)	1272467	26.466	C	1,687	X52094	
flgF	(+)	1272528	26.467	W	251	SG10105/P16323	274, 276, 323
flgG	(+)	1273297	26.483	W	260	SG10106/P16439	276, 323
STYFLGH	(+)	1274076	26.499	C	2,947	M24466	
flgH	(+)	1274137	26.500	W	232	SG10107/P15929	276, 321
flgI	(+)	1274847	26.515	W	365	SG10108/P15930	275, 321
flgJ	(+)	1275944	26.538	W	316	SG10109/P15931	274, 321
STFLGK	(+)	1276878	26.557	C	1,765	X51738	
flgK	(+)	1276959	26.559	W	553	SG10110/P15932	274, 321, 323
STFLGL	(+)	1278574	26.593	C	1,427	X51739	
flgL	(+)	1278635	26.594	W	317	SG10111/P16326	274
STPTSG	(+)	1293000	26.893	SP	1,434	X74629	
ptsG	(+)	1293001	26.893	W	477	SG10316/P37439	
STYPEPT	(+)	1312178	27.292	SG	2,551	M62725	
potA	(−)	1312179	27.292	F	63	SG10489/P40790	447
pepT	(+)	1312618	27.301	W	409	SG10284/P26311	447
STYPHOPQ	(−)	1315063	27.352	SG	2,190	M24424	
phoQ	(−)	1315084	27.352	W	451	SG10294/P14147	450
phoP	(−)	1316439	27.380	W	224	SG10293/P14146	217, 450
STYGDHA	(−)	1401000	29.139	SP	1,603	M24021	
topB	(+)	1401001	29.139	F	49	SG10495/P40687	25
gdhA	(−)	1401180	29.143	W	447	SG10140/P15111	25
STYINFCA	(+)	1450000	30.158	SH	570	L11254	
infC	(+)	1450019	30.158	W	180	SG10185/P33321	407
STHIMA	(+)	1458747	30.340	SG	420	X16739	
pheT	(+)	1458748	30.340	F	17	SG10290/P15434	385
himA	(+)	1458808	30.341	W	99	SG10155/P15430	385
STU09502	(−)	1475000	30.678	SH	376	U09502	
sodB	(−)	1475001	30.678	F	56	SG10514/P40726	
STU03842	(+)	1482000	30.824	SG	714	U03842	
slyA	(+)	1482167	30.827	W	146	SG10526/P40676	387
STPMIPHI	(−)	1502500	31.250	SG	1,650	X57117	
manA	(−)	1502544	31.251	W	391	SG10217/P25081	560
fumA	(+)	1503919	31.280	F	38	SG10462/P40720	560
STYDCP	(+)	1562000	32.488	SP	2,841	M84575	
ydfG	(−)	1562001	32.488	F	96	SG10499/P40864	240
dcp	(+)	1562427	32.496	W	680	SG10083/P27236	240
STYRFC	(−)	1714533	35.660	SG	1,750	M60066	
rfc	(−)	1714600	35.661	W	407	SG10352/P26479	98
STFNR	(+)	1761000	36.626	SP	1,360	U05668	
ogt	(+)	1761001	36.626	F	115	SG10262/P37429	
fnr	(+)	1761546	36.638	W	250	SG10131/P37428	
STSAP	(+)	1785400	37.134	SG	5,714	X74212	
sapA	(+)	1785516	37.136	W	549	SG10377/P36634	525
sapB	(+)	1787162	37.171	W	321	SG10378/P36668	525
sapC	(+)	1788114	37.190	W	296	SG10379/P36669	525
sapD	(+)	1789004	37.209	W	330	SG10380/P36636	525
sapF	(+)	1789998	37.230	W	268	SG10381/P36638	525
STYENVM	(+)	1805000	37.542	SH	1,656	M31806	

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
ycjE	(+)	1805259	37.547	W	99	SG10440/P16656	708
fabI	(+)	1805676	37.556	W	262	SG10095/P16657	708
STPYRF	(−)	1808000	37.604	SP	1,459	X05382	
osmB	(+)	1808001	37.604	F	20	SG10272/P37723	691
yciH	(−)	1808185	37.608	W	108	SG10419/P20770	691
pyrF	(−)	1808966	37.624	W	245	SG10328/P07691	691
STYCYSB	(−)	1810000	37.646	SP	1,759	M15040	
cysB	(−)	1810342	37.653	W	324	SG10072/P06614	506
topA	(−)	1811727	37.682	F	10	SG10515/P40686	506
STYATPCA	(−)	1824636	37.950	SG	993	L08890	
cobA	(−)	1824854	37.955	W	196	SG10031/P31570	144, 672
trpEstyM	(+)	1827293	38.005	MP	6,783	SS1035	
STYTRPOP	(+)	1827294	38.005	C	105	M10673	
STYTRPEA	(+)	1827370	38.007	C	294	M24960	
STYTRPE	(+)	1827547	38.011	C	1,563	J01812	
trpE	(+)	1827548	38.011	W	520	SG10392/P00898	378, 382, 475, 763
STYTRPDC1	(+)	1829109	38.043	C	1,596	M30285	
trpD	(+)	1829110	38.043	W	531	SG10399/P00905	279, 475
STYTRPDC2	(+)	1830709	38.076	C	1,359	M30286	
trpC	(+)	1830710	38.076	W	452	SG10398/P00910	279
STYTRPCBI	(+)	1832031	38.104	C	82	M24299	
STYTRPBA	(+)	1832077	38.105	C	2,000	J01810	
trpB	(+)	1832078	38.105	W	397	SG10397/P00933	109, 296, 476, 597
trpA	(+)	1833271	38.130	W	268	SG10396/P00929	
STTONB	(+)	1838098	38.230	SG	950	X56434	
tonB	(+)	1838219	38.233	W	242	SG10391/P25945	242, 335
yciA	(−)	1839007	38.249	F	13	SG10418/P25944	242
STOPPAF	(−)	184000	38.270	SP	6,006	X05491	
oppF	(−)	1840244	38.275	W	334	SG10271/P08007	261
oppD	(−)	1841245	38.295	W	335	SG10270/P04285	257, 261
oppC	(−)	1842264	38.317	W	302	SG10269/P08006	261, 529
oppB	(−)	1843187	38.336	W	306	SG10268/P08005	261, 529
oppA	(−)	1844229	38.358	W	542	SG10267/P06202	261, 262
hns-styM	(+)	1846388	38.402	MG	926	SS1009	
STYOSMZ	(+)	1846389	38.402	C	909	M37891	
STHNS	(+)	1846489	38.405	C	827	X14375	
hns	(+)	1846767	38.410	W	137	SG10171/P17428	294, 437
STYNARK	(+)	1856000	38.602	SH	4,183	D26057	
narK	(−)	1856001	38.602	F	130	SG10245/P37593	
smvA	(+)	1857300	38.629	W	496	SG10384/P37594	
nmpC	(−)	1859335	38.672	F	282	SG10249/P37592	
prfAstyM	(+)	1863999	38.769	MP	5,845	SS1028	
STYHEMAPRF	(−)	1864000	38.769	C	3,341	J04243	
hemK	(−)	1864001	39.769	F	77	SG10534/P40816	136
prfA	(−)	1864231	38.773	W	360	SG10309/P13654	136
hemA	(−)	1865354	38.797	W	418	SG10149/P13581	136
STYPRS	(+)	1866603	38.823	C	2,060	M77236	
hemM	(+)	1866928	38.830	W	207	SG10153/P30752	136, 539
ychB	(+)	1867548	38.842	W	283	SG10417/P30753	48, 539
STYPRSA	(+)	1868101	38.854	C	1,740	M19488	
prsA	(+)	1868665	38.866	W	315	SG10315/P15849	48
STYDADB	(−)	1975000	41.077	SP	1,140	K02119	
dadB	(−)	1975010	41.078	W	356	SG10082/P06191	735

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
STYGAPA	(+)	1977000	41.119	SH	882	M63369	
gapA	(+)	1977001	41.119	F	294	SG10139/P24165	374
STYPABB	(+)	2000000	41.597	SH	1,815	M22079	
pabB	(+)	2000207	41.602	W	454	SG10274/P12680	212
flhEstyM	(+)	2003810	41.677	MP	5,097	SS1004	
STYFLHB	(−)	2003811	41.677	C	4,023	D32203	
flhE	(−)	2004025	41.677	W	130	SG10528/P40728	456
flhA	(−)	2004417	41.689	W	692	SG10529/P40729	456
flhB	(−)	2006488	41.732	W	383	SG10530/P40727	456
STYCHEZ	(−)	2007000	41.743	C	1,506	M16691	
cheZ	(−)	2007833	41.760	W	214	SG10057/P07800	662
STYCHEY	(−)	2008456	41.773	C	452	M12131	
cheY	(−)	2008488	41.774	W	129	SG10056/P06657	253, 658, 660, 661
STYCHER	(−)	2012629	41.860	SG	896	J02757	
cheB	(−)	2012630	41.860	W	349	SG10053/P04042	253, 613, 614
cheR	(−)	2012635	41.860	W	288	SG10054/P07801	615
tar-styM	(+)	2015513	41.920	MG	4,475	SS1033	
STYTAR	(−)	2015514	41.920	C	1,922	J01809	
tar	(−)	2015540	41.921	W	552	SG10387/P02941	577
STYCHEW	(−)	2017195	41.955	C	770	J02656	
cheW	(−)	2017439	41.960	W	167	SG10055/P06110	659
STYCHEA	(−)	2017939	41.970	C	2,050	J03611	
cheA	(−)	2017963	41.971	W	671	SG10052/P09384	657
STYFLIA	(−)	2040000	42.429	SG	1,244	D00497	
fliA	(−)	2040321	42.436	W	239	SG10114/P17168	491
fliCstyM	(+)	2043999	42.512	MP	14,084	SS1010	
STYFLGH1I	(−)	2044000	42.512	C	1,485	M11332	
fliC	(−)	2044001	42.513	W	490	SG10115/P06179	274, 328
STFLID	(+)	2045409	42.542	C	1,766	X51740	
fliD	(+)	2045730	42.548	W	467	SG10116/P16328	274
STYFLGPRO	(+)	2047047	42.576	C	965	M85241	
fliS	(+)	2047148	42.578	W	135	SG10127/P26609	337
fliT	(+)	2047555	42.586	W	122	SG10128/P26611	337
STYFTAA	(+)	2047894	42.593	C	1,700	L01643	
amyA	(+)	2047995	42.596	W	494	SG10011/P26613	337, 546
STYAMYA	(+)	2049418	42.625	C	2,940	L13280	
yedD	(−)	2049519	42.627	W	141	SG10420/Q06399	547
yedE	(+)	2050130	42.640	W	401	SG10421/Q06400	547
yedF	(+)	2051332	42.665	W	77	SG10422/P31065	547
STYFLIE	(−)	2052299	42.685	C	647	M84993	
fliE	(−)	2052337	42.686	W	104	SG10117/P26462	321, 462
STYFLIG	(+)	2052807	42.696	C	2,755	M24462	
fliF	(+)	2052868	42.697	W	560	SG10118/P15928	321
fliG	(+)	2054543	42.732	W	331	SG10119/P15933	171, 342, 725
STYFLIHIJ	(+)	2055430	42.750	C	2,654	M62408	
fliH	(+)	2055531	42.752	W	235	SG10120/P15934	342, 725
fliI	(+)	2056238	42.767	W	456	SG10121/P26465	130, 725
fliJ	(+)	2057630	42.796	W	147	SG10122/P26463	725
STYFLIL	(+)	2058550	42.815	SG	2,013	M24463	
fliK	(+)	2058551	42.815	F	10	SG10123/P26416	342, 725
fliL	(+)	2058671	42.818	W	155	SG10124/P26417	342
fliM	(+)	2059143	42.827	W	334	SG10125/P26418	342
fliN	(+)	2060144	42.848	W	137	SG10126/P26419	342
STYUMUDC	(−)	2062151	42.890	SG	2,574	M57431	
cspG	(−)	2062152	42.890	W	40	SG10445/P39818	
umuC	(−)	2062825	42.904	W	422	SG10410/P22494	623, 694

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
umuD	(−)	2064096	42.930	W	139	SG10411/P22493	623, 694, 750
cobTstyM	(+)	2086671	43.400	MP	22,490	SS1005	
STYCOB	(−)	2086672	43.400	C	2,760	L35477	
asnT?	(+)	2087023	43.407	W	RNA	SG30008/tRNA	
yeeG	(−)	2087325	43.414	W	309	SG10484/P40680	
cobT	(−)	2088332	43.435	W	366	SG10062/Q05603	571
STYVB12AA	(−)	2088675	43.442	C	17,442	L12006	
cobS	(−)	2089429	43.457	W	247	SG10061/Q05602	571
cobU	(−)	2090169	43.473	W	180	SG10063/Q05599	571
cbiP	(−)	2090711	43.484	W	506	SG10048/Q05597	571
cbiO	(−)	2092228	43.516	W	271	SG10047/Q05596	571
cbiQ	(−)	2093052	43.533	W	225	SG10049/Q05598	571
cbiN	(−)	2093716	43.547	W	93	SG10046/Q05595	571
cbiM	(−)	2093999	43.552	W	245	SG10045/Q05594	571
cbiL	(−)	2094733	43.568	W	237	SG10044/Q05593	571
cbiK	(−)	2095443	43.582	W	264	SG10043/Q05592	571
cbiJ	(−)	2096240	43.599	W	263	SG10042/Q05591	571
cbiH	(−)	2097028	43.615	W	241	SG10041/Q05590	571
cbiG	(−)	2097753	43.630	W	351	SG10040/Q05631	571
cbiF	(−)	2098789	43.652	W	257	SG10039/Q05630	571
cbiT	(−)	2099546	43.668	W	192	SG10050/Q05632	571
cbiE	(−)	2100114	43.680	W	201	SG10038/Q05629	571
cbiD	(−)	2100713	43.692	W	379	SG10037/Q05628	571
cbiC	(−)	2101852	43.716	W	210	SG10036/Q05601	571
cbiB	(−)	2102495	43.729	W	319	SG10035/Q05600	571
cbiA	(−)	2103451	43.749	W	459	SG10034/P29946	557, 571
STYPDUC	(−)	2105401	43.790	C	3,761	L31414	
pocR	(−)	2105428	43.790	W	303	SG10307/Q05587	571
pduF	(−)	2106556	43.814	W	264	SG10281/P37451	
pduA	(+)	2107876	43.841	W	97	SG10278/P37448	
pduB	(+)	2108266	43.849	W	233	SG10279/P37449	
pduC	(+)	2108986	43.864	F	59	SG10280/P37450	
STYPBCDEF	(−)	2124655	44.190	SG	3,282	L31538	
phsE	(−)	2125087	44.199	W	390	SG10300/P37604	
phsD	(−)	2126288	44.224	W	84	SG10299/P37603	
phsC	(−)	2126542	44.229	W	199	SG10298/P37602	
phsB	(−)	2127138	44.242	W	198	SG10297/P37601	
phsA	(−)	2127731	44.254	F	68	SG10296/P37600	
hisGstyM	(+)	2148461	44.685	MP	33,958	SS1013	
STYHISOGD	(+)	2148462	44.685	C	4,443	J01804	
STHISOP	(+)	2149090	44.698	C	7,439	X13464	
hisG	(+)	2149366	44.704	W	299	SG10162/P00499	65, 91, 428, 534
hisD	(+)	2150368	44.725	W	434	SG10160/P10370	65, 222
hisC	(+)	2151669	44.752	W	359	SG10159/P10369	65
hisB	(+)	2152745	44.774	W	354	SG10158/P10368	65
hisH	(+)	2153809	44.796	W	194	SG10163/P10376	65
hisA	(+)	2154393	44.809	W	246	SG10157/P10372	65
hisF	(+)	2155115	44.824	W	258	SG10161/P10374	65
hisI	(+)	2155885	44.840	W	203	SG10164/P10367	65, 83
SECLDB	(−)	2156446	44.851	C	2,948	Z17278	
cld	(−)	2156576	44.854	W	327	SG10060/Q04866	26, 27
yefA	(−)	2157699	44.877	W	388	SG10439/Q04873	26
STYGNDA	(−)	2158970	44.904	C	1,705	M64332	
gnd	(−)	2159104	44.906	W	468	SG10146/P14062	314, 551
SERFBB	(−)	2160340	44.932	C	22,080	X56793	
rfbP	(−)	2160674	44.939	W	476	SG10351/P26406	314
rfbK	(−)	2162176	44.970	W	477	SG10349/P26405	314
rfbM	(−)	2163596	45.000	W	479	SG10350/P26404	314
rfbN	(−)	2165036	45.030	W	314	SG10455/P26403	314
rfbU	(−)	2165981	45.050	W	353	SG10446/P26402	314
rfbV	(−)	2167361	45.078	W	333	SG10454/P26401	314
rfbX	(−)	2168367	45.099	W	430	SG10453/P26400	314

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
rfbJ	(−)	2169741	45.128	W	299	SG10348/P22716	314, 755
rfbH	(−)	2170668	45.147	W	437	SG10452/P26398	314
rfbG	(−)	2172008	45.175	W	359	SG10347/P26397	314
rfbF	(−)	2173092	45.197	W	257	SG10346/P26396	314
rfbI	(−)	2173862	45.213	W	330	SG10451/P26395	314
rfbC	(−)	2174860	45.234	W	183	SG10450/P26394	314
rfbA	(−)	2175412	45.246	W	292	SG10449/P26393	314
rfbD	(−)	2176338	45.265	W	299	SG10344/P26392	314
rfbB	(−)	2177237	45.284	W	361	SG10345/P26391	314
galF	(−)	2178699	45.314	W	297	SG10136/P26390	314
yefK	(−)	2179770	45.336	W	467	SG10448/P26389	314
yefL	(−)	2181184	45.366	W	406	SG10447/P26388	314
STCPSBG	(−)	2185000	45.445	SH	3,069	X59886	
cpsG	(−)	2185011	45.445	W	456	SG10067/P26341	652
cpsB	(−)	2186492	45.476	W	480	SG10066/P26340	652
mglBsty	(−)	2307000	47.983	SH	1,810	SS3004	
mglA	(−)	2307001	47.983	F	42	SG10228/P23924	34
mglB	(−)	2307259	47.988	W	332	SG10229/P23905	34
galS	(−)	2308754	48.019	F	18	SG10521/P41030	34
STFRUF	(+)	2310725	48.060	SG	1,610	X14243	
yeiO	(−)	2310726	48.060	F	22	SG10423/P33027	197
fruB	(+)	2311160	48.069	W	376	SG10132/P17127	197
STRNAP	(+)	2360247	49.090	SG	1,041	X63777	
yejM	(+)	2360248	49.090	F	190	SG10463/P40709	646
proL	(+)	2360895	49.103	W	RNA	SG30015/tRNA	
STGYRA	(−)	2367940	49.250	SG	261	X78977	
gyrA	(−)	2367941	49.250	F	86	SG10148/P37411	
STNRDABA	(+)	2370000	49.293	SH	4,967	X72948	
ubiG	(+)	2370001	49.293	F	209	SG10405/P37431	326
nrdA	(+)	2370987	49.313	W	761	SG10250/P37426	326
nrdB	(+)	2373385	49.363	F	122	SG10251/P37427	326
STU02281	(−)	2408808	50.100	SG	1,329	U02281	
pmrD	(−)	2409096	50.106	W	85	SG10304/P37589	
menE	(−)	2409451	50.113	F	228	SG10221/P37418	
STYADA	(−)	2411000	50.146	SH	1,266	D90221	
alkB	(−)	2411001	50.146	F	24	SG10006/P37462	237
ada	(−)	2411078	50.147	W	352	SG10002/P26189	237
STYNUOD	(−)	2449676	50.950	SG	3,950	L22504	
nuoG	(−)	2449677	50.950	F	612	SG10257/P33900	20
nuoF	(−)	2451586	50.990	W	431	SG10256/P33901	20
nuoE	(−)	2452878	51.017	W	166	SG10255/P33903	20
nuoD	(−)	2453381	51.027	F	81	SG10254/P33902	20
hisPstyM	(+)	2459999	51.165	MP	5,228	SS1014	
STYHIS3P	(−)	2460000	51.165	C	789	M32273	
STYHISTO	(−)	2460578	51.177	C	4,483	J01805	
hisP	(−)	2460899	51.183	W	258	SG10168/P02915	256
hisM	(−)	2461686	51.200	W	235	SG10167/P02912	256
hisQ	(−)	2462390	51.214	W	228	SG10169/P02913	256
hisJ	(−)	2463259	51.233	W	260	SG10165/P02910	254, 256, 272
argT	(−)	2464279	51.254	W	260	SG10018/P02911	254, 330
STYARGTR	(−)	2465061	51.270	C	467	J01798	
ubiX	(−)	2465352	51.276	F	58	SG10481/P40787	255
pgtAstyM	(+)	2501999	52.038	MP	7,612	SS1027	
STYPGTA	(−)	2502000	52.038	C	2,680	M13923	
pgtE	(−)	2502268	52.044	W	296	SG10288/P06185	216, 765

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
pgtA	(−)	2503374	52.067	W	415	SG10285/P06184	762, 765
STYPGTBC	(−)	2504534	52.091	C	3,388	M21279	
pgtB	(−)	2504611	52.093	W	593	SG10286/P37433	313, 762
pgtC	(−)	2506615	52.134	W	397	SG10287/P37591	313, 762
STYPGTP	(+)	2507601	52.155	C	2,011	M21278	
pgtP	(+)	2508243	52.168	W	406	SG10289/P12681	211
cysZstyM	(+)	2538995	52.808	MP	11,006	SS1006	
STYCYSPTS	(+)	2538995	52.808	C	3,812	M21450	
cysZ	(+)	2539214	52.812	W	290	SG10081/P12673	61
cysK	(+)	2540250	52.834	W	323	SG10078/P12674	61
ptsH	(+)	2541605	52.862	W	85	SG10317/P07006	61, 540, 598, 739
STYENZI	(+)	2541910	52.868	C	1,728	M76176	
ptsI	(+)	2541911	52.868	W	575	SG10318/P12654	61, 389, 598
STCRR	(+)	2543473	52.901	C	733	X05210	
crr	(+)	2543679	52.905	W	169	SG10069/P02908	470
STU11243	(+)	2544185	52.916	C	4,471	U11243	
yfeI	(−)	2544573	52.924	W	287	SG10475/P40192	
ptsJ	(+)	2545519	52.943	W	430	SG10474/P40193	
yfeJ	(+)	2546826	52.971	W	170	SG10476/P40194	
yfeK	(+)	2547623	52.987	W	120	SG10477/P40195	
yfeL	(+)	2547998	52.995	W	179	SG10478/P40196	
STCYSM	(−)	2548650	53.009	C	1,351	X59595	
cysM	(−)	2548668	53.009	W	303	SG10079/P29848	
cysA	(−)	2549647	53.029	F	117	SG10518/P40860	
cysPsty	(−)	2553600	53.112	SH	1,401	SS3006	
cysU	(−)	2553601	53.112	F	15	SG10520/P41032	283, 284
cysP	(−)	2553645	53.112	W	338	SG10519/P40131	283, 284
yfeF	(−)	2554819	53.137	F	60	SG10424/P37441	283, 284
STYHEMF	(+)	2556414	53.170	SG	2,398	L19503	
amiA	(+)	2556641	53.175	W	289	SG10008/P33772	757
hemF	(+)	2557513	53.193	W	299	SG10150/P33771	
STYEUTBC	(−)	2560000	53.245	SP	2,526	J05518	
eutC	(−)	2560149	53.248	W	286	SG10093/P19265	152
eutB	(−)	2561028	53.266	W	452	SG10092/P19264	152
STGLYAG	(−)	2691000	55.969	SP	1,903	X15816	
glyA	(−)	2691238	55.974	W	417	SG10145/P06192	651, 711
hmpA	(+)	2692817	56.007	F	29	SG10170/P26353	652
STYASRABC	(+)	2745368	57.100	SG	3,360	M57706	
asrA	(+)	2745678	57.106	W	347	SG10021/P26474	287
asrB	(+)	2746725	57.128	W	272	SG10022/P26475	287
asrC	(+)	2747554	57.145	W	337	SG10023/P26476	287
STLEPG	(−)	2770000	57.612	SH	1,294	X54933	
lepB	(−)	2770196	57.616	W	324	SG10194/P23697	720
lepA	(−)	2771187	57.637	F	35	SG10193/P23698	720
STU05669	(−)	2776000	57.737	SH	744	U05669	
rpoE	(−)	2776024	57.738	W	191	SG10370/P37401	
STGENES	(−)	2782000	57.862	SG	2,169	X74933	
rplS	(−)	2782029	57.862	W	115	SG10365/P36240	
trmD	(−)	2782417	57.871	W	255	SG10395/P36245	
yfjA	(−)	2783229	57.887	W	183	SG10425/P36246	
rpsP	(−)	2783799	57.899	W	82	SG10375/P36242	
STYAROF	(−)	2817488	58.600	SG	1,235	M31302	
aroF	(−)	2817489	58.600	W	356	SG10020/P21307	461
STHINZ	(+)	2889127	60.090	SG	1,149	V01370	

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
hin	(+)	2889227	60.092	W	190	SG10156/P03013	155, 249, 612, 772
STYTCTD	(+)	2924000	60.815	SP	829	M28368	
tctD	(+)	2924155	60.819	W	224	SG10388/P22104	741
nrdEstyM	(+)	2947999	61.314	MP	5,654	SS1024	
STNRD	(+)	2948000	61.314	C	4,894	X73226	
nrdE	(+)	2948863	61.332	W	714	SG10252/Q08698	326
nrdF	(+)	2950991	61.377	W	319	SG10253/P17424	326, 656
STPROVW	(+)	2951644	61.390	C	2,010	X52693	
proV	(+)	2952305	61.404	W	400	SG10312/P17328	326, 517, 656
proW	(+)	2953500	61.429	F	51	SG10313/P17327	656
STTRNADNA	(−)	2980960	62.000	SG	650	X64175	
argQ	(−)	2980961	62.000	W	RNA	SG30002/tRNA	
argZ	(−)	2981210	62.005	W	RNA	SG30015/tRNA	
argY	(−)	2981349	62.008	W	RNA	SG30006/tRNA	
argV	(−)	2981488	62.011	W	RNA	SG30005/tRNA	
serV	(−)	2981568	62.013	W	RNA	SG30012/tRNA	
STU16278	(+)	3018943	62.790	SG	1,085	U16278	
fhlA	(+)	3018944	62.790	W	253	SG10480/P40734	
STYORG	(+)	3022790	62.870	SG	1,898	L33855	
orgA	(+)	3022998	62.874	W	412	SG10502/P40823	319
spaTstyM	(+)	3026612	62.950	MG	12,917	SS1018	
STSPA	(−)	3026613	62.950	C	6,387	X73525	
spaT	(−)	3026614	62.950	F	32	SG10472/P40703	218
spaS	(−)	3026848	62.954	W	356	SG10471/P40702	218
spaR	(−)	3027905	62.976	W	263	SG10470/P40701	218
spaQ	(−)	3028700	62.993	W	82	SG10469/P40704	218
spaP	(−)	3028986	62.999	W	224	SG10468/P40700	218
spaO	(−)	3029650	63.013	W	303	SG10467/P40699	218
spaN	(−)	3030561	63.032	W	336	SG10466/P40613	218
spaM	(−)	3031571	63.053	W	147	SG10465/P40612	218
STU08279	(−)	3031903	63.060	C	1,835	U08279	
spaL	(−)	3031996	63.061	W	432	SG10464/P39444	133, 218
spaK	(−)	3033284	63.088	C	134	SG10532/P39443	133
STYINVA	(−)	3033677	63.096	C	2,176	M90846	
invA	(−)	3033712	63.097	W	665	SG10186/P35657	185
STYEPI	(−)	3035753	63.140	C	1,313	M90714	
invE	(−)	3035794	63.140	W	372	SG10187/P35671	206, 331
STU08280	(−)	3036700	63.159	C	2,830	U08280	
STINVGE	(−)	3036896	63.163	C	1,736	X75302	
invG	(−)	3036909	63.164	W	562	SG10188/P35672	331
invF	(−)	3038594	63.199	W	216	SG10130/P39437	331
STINVH	(+)	3047000	63.374	SG	884	Z17242	
invH	(+)	3047114	63.376	W	147	SG10189/P37423	14
STKATFR	(−)	3060000	63.644	SH	1,574	X77752	
rpoS	(−)	3060278	63.650	W	330	SG10372/P37400	354
nlpD	(−)	3061333	63.672	F	98	SG10513/P40827	354
STU16303	(+)	3073265	63.920	SP	3,141	U16303	
mutS	(+)	3073812	63.931	W	854	SG10237/P10339	94, 231, 232
STYCYSJIHA	(+)	3085080	64.166	SG	6,050	M23007	
cysJ	(+)	3085470	64.174	W	599	SG10077/P38039	505, 510
cysI	(+)	3087269	64.211	W	570	SG10076/P17845	356, 510
cysH	(+)	3089063	64.248	W	244	SG10075/P17853	510
ygcC	(−)	3089885	64.265	W	317	SG10485/P40722	510
STYLGTX	(−)	3120392	64.900	SG	1,473	L13259	

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
lgt	(−)	3120516	64.903	W	291	SG10201/Q07293	190, 584
ygdF	(−)	3121606	64.925	F	85	SG10426/P37178	190
STYPRF2	(−)	3180492	66.150	SG	1,351	M38590	
lysS	(−)	3180493	66.150	F	31	SG10211/P28354	338
prfB	(−)	3180595	66.152	W	365	SG10310/P28353	338
recJ	(−)	3181797	66.177	F	14	SG10332/P28355	346
SEANSBSQA	(−)	3227000	67.117	SH	147	X69868	309
STYMUTB	(+)	3230495	67.190	SG	1,170	M86634	
mutY	(+)	3230568	67.192	W	350	SG10238/Q05869	122
metCsty	(+)	3322000	69.093	SP	2,186	SS3002	
exbB	(−)	3322001	69.093	F	110	SG10094/P18950	524
metC	(+)	3322583	69.105	W	395	SG10223/P18949	524
yghB	(+)	3323910	69.133	F	92	SG10427/P18951	524
parFstyM	(+)	3328097	69.220	MG	6,409	SS1026	
STU09309	(−)	3328098	69.220	C	3,184	U09309	
ygiK	(+)	3328407	69.226	W	435	SG10523/P40800	
ygiJ	(−)	3329771	69.255	W	465	SG10522/P40799	
STYPARCF	(−)	3330980	69.280	C	3,527	M68936	
parF	(−)	3331242	69.285	W	245	SG10303/P26974	
parC	(−)	3332236	69.306	W	752	SG10276/P26973	424
STYPARE	(−)	3337000	69.405	SG	1,981	L05544	
parE	(−)	3337037	69.406	W	630	SG10277/P31598	645
STCPDB	(−)	3341079	69.490	SG	1,311	X54009	
cpdB	(−)	3341080	69.490	F	250	SG10065/P26265	403
cysQ	(+)	3342097	69.511	F	98	SG10080/P26264	403
STYUGDOP	(+)	3365000	69.988	SH	4,631	M14427	
ygjD	(−)	3365001	69.988	F	44	SG10491/P40731	142
rpsU	(+)	3365359	69.995	W	71	SG10376/P02379	142
dnaG	(+)	3365810	70.004	W	581	SG10088/P07362	142
rpoD	(+)	3367705	70.044	W	615	SG10369/P07336	142
tdcBsty	(−)	3410000	70.923	SH	72	SS3008	
tdcB	(−)	3410001	70.923	F	24	SG10390/P11954	344
STYM1R1	(−)	3420000	71.131	SG	555	M10888	
rnpB	(−)	3420128	71.134	W	RNA	SG30001/M1-RNA	23
STYM1R2	(−)	3420705	71.146	SG	225	M10889	
STYNUSAINF	(−)	3459700	71.963	SH	228	M28868	
STYNUSA	(−)	3460000	71.963	SH	1,503	M61008	
nusA	(−)	3460001	71.963	W	500	SG10258/P37430	108
STYSIG54	(+)	3473299	72.240	SG	1,955	M68571	
rpoN	(+)	3473375	72.242	W	477	SG10371/P26979	537
yhbH	(+)	3474831	72.272	W	95	SG10428/P26983	537
mdh-styM	(+)	3528999	73.399	MP	2,075	SS1022	
STYLT2MDH	(−)	3529000	73.399	C	1,122	M95049	
mdh	(−)	3529064	73.400	W	312	SG10218/P25077	417
STYARGR	(+)	3529934	73.418	C	1,141	M75913	
argR	(+)	3530415	73.428	W	156	SG10017/P37170	419
STU03101	(+)	3559000	74.022	SH	1,757	U03101	
yhdG	(+)	3559286	74.028	W	321	SG10429/P37405	
fis	(+)	3560260	74.049	W	98	SG10100/P37404	

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
STSAPG	(+)	3578215	74.422	SG	1,785	X80501	
trkA	(+)	3578464	74.427	W	458	SG10533/P39445	526
mscL	(+)	3579980	74.459	F	7	SG10531/P39446	526
STYRPOA	(−)	3582000	74.501	SG	1,065	M77750	
rpoA	(−)	3582041	74.502	W	329	SG10367/P00574	412
rpsD	(−)	3583056	74.523	F	2	SG10525/NA[h]	412
STYSPCA	(−)	3587806	74.622	SH	201	M36266	
rplE	(−)	3587807	74.622	F	43	SG10362/P37436	
rplX	(−)	3587951	74.625	F	18	SG10366/P37438	
tufAstyM	(+)	3589171	74.650	MG	3,963	SS1036	
STTUFA	(−)	3589172	74.650	C	1,281	X55116	
tufA	(−)	3589198	74.651	W	394	SG10403/P21694	706
STRPSG	(−)	3590382	74.675	C	2,753	X64591	
fusA	(−)	3590454	74.677	W	704	SG10134/P26229	315
rpsG	(−)	3592665	74.723	W	156	SG10373/P26230	315
STYRPSL	(−)	3592944	74.728	C	605	M68548	
rpsL	(−)	3593051	74.731	W	124	SG10374/P02367	290
STYCRP	(+)	3604000	74.958	SP	959	M13773	
crp	(+)	3604283	74.964	W	210	SG10068/P06170	599
STYPABAA	(−)	3610327	75.090	SG	1,669	M32355	
argD	(−)	3610328	75.090	F	17	SG10488/P40732	700
pabA	(−)	3610464	75.093	W	187	SG10273/P06193	334, 700
fic	(−)	3611059	75.105	W	200	SG10097/P20751	700
yhfG	(−)	3611651	75.118	W	55	SG10430/P37771	700
ppiA	(−)	3611914	75.123	F	26	SG10308/P20753	700
STYCYSAA	(+)	3629000	75.478	SP	5,280	M64606	
nirD	(+)	3629001	75.478	F	67	SG10487/P40789	751
nirC	(+)	3629469	75.488	W	269	SG10248/P25926	751
cysG	(+)	3630290	75.505	W	457	SG10074/P25924	751
yhfI	(+)	3631997	75.541	W	416	SG10437/P25927	751
yhfJ	(+)	3633433	75.571	W	264	SG10438/P25928	751
STENVZ	(−)	3653599	75.990	SG	3,293	X12374	
pckA	(+)	3653600	75.990	F	287	SG10497/P41033	391
envZ	(−)	3654543	76.010	W	450	SG10091/P08982	391
ompR	(−)	3655892	76.038	W	239	SG10266/P08981	391
glgAstyM	(+)	3712737	77.220	MG	1,838	SS1011	
STYGLGC	(−)	3712738	77.220	C	1,410	M17363	
glgA	(−)	3712739	77.220	F	29	SG10141/P05416	380
glgC	(−)	3712826	77.222	W	431	SG10142/P05415	380
STGLGCG	(−)	3714118	77.249	C	458	X59281	
livFstyM	(+)	3723795	77.450	MG	7,630	SS1021	
STYLIV	(−)	3723796	77.450	C	4,072	D12589	
yhhV	(−)	3723797	77.450	F	68	SG10457/P40819	440
livF	(−)	3724127	77.457	W	237	SG10202/P30294	440
livG	(−)	3724842	77.472	W	255	SG10203/P30293	440
livM	(−)	3725606	77.488	W	425	SG10207/P30296	440
livH	(−)	3726880	77.514	W	308	SG10204/P30295	440
STYLIVBC	(−)	3727808	77.533	C	3,618	D00478	
livK	(−)	3727866	77.535	W	369	SG10206/P17216	493
livJ	(−)	3729975	77.579	W	365	SG10205/P17215	493
STYOPDA	(+)	3832000	79.700	SP	2,842	M84574	
opdA	(+)	3832603	79.713	W	239	SG10266/P08981	101
STYCSPSA	(+)	3848000	80.033	SH	481	L23115	
cspA	(+)	3848268	80.039	W	70	SG10070/P37410	

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
STCYSE	(−)	3892557	80.960	SG	1,497	X59594	
cysE	(−)	3892627	80.961	W	273	SG10073/P29847	
gpsA	(−)	3893535	80.980	F	171	SG10456/P40716	
kbl-styM	(+)	3903999	81.198	MP	10,168	SS1019	
STRFADF	(+)	3904000	81.198	C	2,700	U06472	
kbl	(−)	3904001	81.198	F	162	SG10191/P37419	617
rfaD	(+)	3904690	81.212	W	310	SG10335/P37420	617
rfaF	(+)	3906016	81.240	W	348	SG10336/P37421	617
STYRFAC	(+)	3906070	81.241	C	1,574	M95927	
rfaC	(+)	3906672	81.254	W	317	SG10334/P26469	427, 616
STYRFALK	(+)	3907310	81.267	C	4,280	M73826	
rfaL	(+)	3907665	81.274	W	404	SG10340/P26471	427
rfaK	(−)	3908936	81.301	W	381	SG10339/P26470	427
rfaZ	(−)	3910182	81.327	W	269	SG10343/P26473	427
rfaY	(−)	3911141	81.347	C	232	SG10342/P26472	427
rfaYsty	(−)	3911590	81.356	C	2,578	SS3007	
rfaJ	(−)	3911935	81.363	W	336	SG10338/P19817	67
rfaI	(−)	3912891	81.383	W	337	SG10337/P19816	67
rfaB	(−)	3913910	81.404	F	81	SG10333/Q06994	67
S56361	(−)	3914809	81.423	SP	815	S56361	
rfaB	(−)	3914810	81.423	F	70	SG10333/Q06994	346
yibR	(−)	3915089	81.429	W	77	SG10512/P40824	346
rfaP	(−)	3915354	81.434	F	89	SG10341/Q06995	346
pyrEstyM	(+)	3915999	81.448	MG	1,047	SS1030	
STOPPRBST	(−)	3916000	81.448	C	645	Z19547	
pyrE	(−)	3916001	81.448	W	213	SG10327/P08870	473, 585
M28333	(+)	3916462	81.457	C	585	M28333	
rph	(+)	3916463	81.457	F	108	SG10361/P26155	473
STYUHPABCT	(−)	3940637	81.960	SG	5,465	M89480	
uhpT	(−)	3940837	81.964	W	463	SG10409/P27670	304
uhpC	(−)	3942369	81.996	W	442	SG10408/P27669	304
uhpB	(−)	3943707	82.024	W	500	SG10407/P27668	304
uhpA	(−)	3945209	82.055	W	196	SG10406/P27667	304
STYMGTBC	(+)	3946406	82.080	SG	4,586	M57715	
mgtC	(+)	3947009	82.093	W	231	SG10232/P22037	633
mgtB	(+)	3947924	82.112	W	908	SG10231/P22036	633
STRECF	(−)	4012276	83.450	SG	1,068	X62505	
recF	(−)	4012277	83.450	W	355	SG10331/P24900	338
STYDNAA	(−)	4019488	83.600	SG	1,946	M17352	
dnaN	(−)	4019489	83.600	F	64	SG10089/P26464	618
dnaA	(−)	4019679	83.604	W	466	SG10085/P35891	618
STYORI	(+)	4080550	84.870	SG	552	J01808	
rbsBsty	(+)	4085357	84.970	SH	891	SS3005	
rbsB	(+)	4085358	84.970	W	297	SG10330/P02926	57
STYILVPA	(+)	4098000	85.233	SP	329	J01806	
ilvL	(+)	4098120	85.235	W	32	SG10183/P03060	375, 682
ilvEsty	(+)	4098500	85.243	SP	927	SS3001	
ilvE	(+)	4098501	85.243	W	308	SG10181/P15168	153
ilvAstyM	(+)	4099499	85.264	MP	1,756	SS1017	
STYILVAPRI	(+)	4099500	85.264	C	240	M25498	
ilvD	(+)	4099501	85.264	F	68	SG10458/P40810	414
STYILVA	(+)	4099711	85.269	C	1,545	M26670	
ilvA	(+)	4099712	85.269	W	514	SG10179/P20506	681

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
STYILVYCR	(+)	4100000	85.275	SP	378	K03522	
ilvY	(−)	4100001	85.275	F	42	SG10184/P05988	740
ilvC	(+)	4100295	85.281	F	28	SG10180/P05989	740
Z21789	(+)	4102040	85.317	SG	2,558	Z21789	
trxA	(+)	4102391	85.324	W	109	SG10402/P00274	296, 353, 383, 477, 478, 597
rho	(+)	4103139	85.340	W	419	SG10359/P26980	353, 455
rhlB	(−)	4104393	85.366	F	56	SG10498/P40863	455
STYCARABA	(+)	4112282	85.530	SG	4,378	M95047	
rffT	(+)	4112283	85.530	F	426	SG10354/P37458	
rffM	(+)	4113560	85.557	W	246	SG10353/P37457	
yifK	(+)	4114507	85.576	W	461	SG10431/P37456	
argX	(+)	4115995	85.607	W	RNA	SG30007/tRNA	
hisR	(+)	4116125	85.610	W	RNA	SG30009/tRNA	
leuU	(+)	4116222	85.612	W	RNA	SG30010/tRNA	
proM	(+)	4116351	85.615	W	RNA	SG30011/tRNA	
cyaAstyM	(+)	4120000	85.691	SG	1,664	SS1002	
STCYAG	(+)	4120001	85.691	C	489	X55783	
cyaAsty	(+)	4120404	85.699	C	1,260	SS3009	
cyaA	(+)	4120404	85.699	F	28	SG10071/Q05878	273, 696
STYCRA	(+)	4126226	85.820	SG	1,921	L11043	
uvrD	(+)	4126227	85.820	F	13	SG10414/Q05311	627
corA	(+)	4126740	85.831	W	316	SG10064/P31138	627
yigF	(−)	4127739	85.851	W	126	SG10432/P31139	627
STPLDA	(+)	4133000	85.961	SH	1,254	X76900	
yigI	(−)	4133001	85.961	F	25	SG10461/P40725	53
pldA	(+)	4133241	85.966	W	289	SG10302/P37442	53
recQ	(+)	4134194	85.986	F	22	SG10460/P40724	53
STYMETR	(−)	4137284	86.050	SG	1,203	M17356	
metR	(−)	4137397	86.052	W	276	SG10227/P05984	535
metE	(+)	4138479	86.075	F	2	SG10483/NA	535
STHEMN	(+)	4165170	86.630	SG	3,055	U06779	
yihI	(+)	4165987	86.647	W	171	SG10433/P37130	758
hemN	(+)	4166691	86.662	W	457	SG10154/P37129	758
glnAstyM	(+)	4208423	87.530	MP	1,965	SS1012	
STYGLNA2	(−)	4208424	87.530	C	395	J01803	
glnA	(−)	4208754	87.536	W	469	SG10143/P06201	308, 761
STYGLNA	(−)	4208756	87.537	C	1,407	M14536	
STYGLNA1	(−)	4210121	87.565	C	120	J01802	
STYGLNAA	(−)	4210201	87.567	C	188	M11196	
STRHABC2	(−)	4234406	88.070	SG	2,816	X57299	
rhaA	(−)	4234407	88.070	F	70	SG10355/P27031	479
rhaB	(−)	4234615	88.074	W	489	SG10356/P27030	479
rhaS	(+)	4236372	88.111	W	277	SG10357/P27029	479
STYRHAT	(−)	4237806	88.141	SG	2,388	M85157	
rhaR	(+)	4237807	88.141	F	106	SG10524/P40865	689
rhaT	(−)	4238124	88.147	W	344	SG10358/P27135	689
STUSHB	(+)	4247000	88.332	SH	1,453	X13380	
sbp	(+)	4247001	88.332	W	311	SG10382/P02906	195, 303, 532, 533
ushB	(+)	4247358	88.339	W	251	SG10051/P26219	195
STMETJ	(−)	4295000	89.330	SP	656	X01961	

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
metJ	(−)	4295063	89.332	W	104	SG10226/P06203	712
metB	(+)	4295645	89.344	F	4	SG10482/NA	712
metFstyM	(+)	4296999	89.372	MP	3,726	SS1023	
STMETF	(+)	4297000	89.372	C	1,735	X07689	
metF	(+)	4297435	89.381	W	296	SG10224/P11003	757
STKATG	(+)	4298339	89.400	C	2,387	X53001	
katG	(+)	4298490	89.403	W	727	SG10190/P17750	411
trmAstyM	(+)	4310371	89.650	MG	2,604	SS1034	
STYTRMA	(−)	4310372	89.650	C	639	M57569	
trmA	(−)	4310373	89.650	F	102	SG10394/P22038	229
STYBTUB	(+)	4310480	89.652	C	2,496	M89481	
btuB	(+)	4311049	89.664	W	614	SG10030/P37409	738
murI	(+)	4312838	89.701	F	46	SG10494/P40723	738
STYMURBIRA	(+)	4326000	89.975	SP	1,746	L14816	
rrfB	(+)	4326018	89.975	W	RNA	SG30014/rRNA	
murB	(+)	4326317	89.982	W	342	SG10235/P37417	125
birA	(+)	4327342	90.003	W	135	SG10028/P37416	125
STTUFB	(+)	4329681	90.052	SG	1,308	X55117	
tufB	(+)	4329772	90.053	W	394	SG10404/P21694	706
STRPLJL	(+)	4334412	90.150	SG	1,131	X53072	
rplJ	(+)	4334602	90.154	W	165	SG10363/P17352	527, 528, 771
rplL	(+)	4335166	90.166	W	121	SG10364/P18081	527, 771
STRPOB	(+)	4338258	90.230	SG	4,185	X04642	
rpoB	(+)	4338279	90.230	W	1,342	SG10368/P06173	400, 677
STYHUPA	(+)	4360500	90.693	SH	584	M22975	
hupA	(+)	4360711	90.697	W	90	SG10174/P15148	260
hydGstyM	(+)	4362999	90.745	MP	4,784	SS1016	
STYHYDGG	(+)	4363000	90.745	C	2,088	M64988	
hydH	(+)	4363001	90.745	F	208	SG10177/P37461	88
hydG	(+)	4363635	90.758	W	441	SG10176/P25852	88
STYPURHD	(−)	4364597	90.778	C	3,187	M66160	
purD	(−)	4364957	90.785	W	429	SG10319/P26977	89
purH	(−)	4366258	90.812	F	508	SG10320/P26978	89
STYMETA	(+)	4379126	91.080	SG	671	M74188	
yjaB	(−)	4379127	91.080	F	102	SG10486/P40677	435
metA	(+)	4379591	91.090	F	69	SG10222/P37413	435
STICLR	(−)	4387011	91.244	SG	950	X52950	
iclR	(−)	4387086	91.246	W	274	SG10178/P17430	187
metHsty	(+)	4388000	91.265	SH	1,373	SS3003	
metH	(+)	4388261	91.270	F	371	SG10225/P37586	713
U01246	(−)	4392589	91.360	SG	1,088	U01246	
yjbB	(+)	4392590	91.360	F	52	SG10492/P40730	100
pepE	(−)	4392824	91.365	W	229	SG10282/P36936	100
STMAL	(−)	4403243	91.582	SP	8,590	X54292	
malG	(−)	4403507	91.587	W	296	SG10214/P26468	173, 595
malF	(−)	4404412	91.606	W	514	SG10213/P26467	595
malE	(−)	4407203	91.664	W	396	SG10212/P19576	113, 595
malK	(+)	4407639	91.673	W	369	SG10215/P19566	113, 595
lamB	(+)	4408837	91.698	W	452	SG10192/P26466	172, 595
malM	(+)	4410368	91.730	W	305	SG10216/P26478	595
STLEXA	(+)	4420513	91.941	SP	921	X63002	
lexA	(+)	4420626	91.943	W	202	SG10200/P29831	196, 464

Continued on following page

TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
dnaBstyM	(+)	4429257	92.123	MP	3,155	SS1007	
STYDNABA	(+)	4429258	92.123	C	2,013	J03390	
qor	(−)	4429259	92.123	F	168	SG10511/P40783	583, 744
dnaB	(+)	4429827	92.135	W	471	SG10086/P10338	744
STYALR	(+)	4431213	92.163	C	1,200	M12847	
alr	(+)	4431274	92.165	W	359	SG10007/P06655	180
STYUVRA	(−)	4435524	92.253	SP	3,623	M93014	
uvrA	(−)	4435800	92.259	W	941	SG10413/P37434	
ssb	(+)	4438874	92.323	F	91	SG10385/P37435	
STYPMTRAB	(−)	4494834	93.487	SP	3,824	L13395	
proP	(+)	4494835	93.487	F	17	SG10510/P40862	563
pmrB	(−)	4495055	93.491	W	356	SG10025/P36557	563
pmrA	(−)	4496135	93.514	W	222	SG10024/P36556	563
yjdB	(−)	4496800	93.527	W	547	SG10434/P36555	563
STMELB	(+)	4507574	93.752	SP	1,714	X62101	
melA	(+)	4507575	93.752	F	43	SG10219/P30877	457
melB	(+)	4507790	93.756	W	476	SG10220/P30878	457
STPHON	(−)	4529711	94.212	SP	1,408	X63599	
phoN	(−)	4529821	94.214	W	250	SG10292/P26976	220, 336
STYMUTL	(+)	4566000	94.967	SP	2,446	M29687	
amiB	(+)	4566001	94.967	F	100	SG10009/P26366	434
mutL	(+)	4566313	94.973	W	618	SG10236/P14161	434
miaA	(+)	4568160	95.012	F	95	SG10233/P37724	434
STU07843	(+)	4645490	96.620	SG	4,989	U07843	
treR	(−)	4645965	96.630	W	315	SG10393/P36674	
mgtA	(+)	4647296	96.658	F	42	SG10228/P23924	
STPYRBIG	(−)	4658000	96.880	SP	1,812	X05641	
pyrI	(−)	4658031	96.881	W	153	SG10329/P08421	444
pyrB	(−)	4658505	96.891	W	311	SG10324/P08420	444
pyrL	(−)	4659476	96.911	W	33	SG10323/P08522	444
STMIAE	(+)	4672000	97.171	SP	4,531	X73368	
argI	(−)	4672001	97.171	F	218	SG10016/Q08016	531
yjgD	(+)	4672820	97.188	W	138	SG10435/Q08019	531
miaE	(+)	4673248	97.197	W	270	SG10234/Q08015	531
ytgA	(−)	4674295	97.219	W	162	SG10441/Q08020	531
yjgM	(−)	4674890	97.231	W	167	SG10442/Q08021	531
yjgN	(+)	4675726	97.249	F	268	SG10443/Q08022	
hsdSstyM	(+)	4732999	98.440	MP	3,010	SS1015	
STHSDS	(−)	4733000	98.440	C	1,650	Y00524	
hsdS	(−)	4733016	98.440	W	469	SG10172/P06187	179, 191
STYHSDMB	(−)	4734420	98.470	C	1,590	L02506	
hsdM	(−)	4734421	98.470	W	529	SG10501/P40813	
STYNADR	(+)	4800788	99.850	SG	2,496	M85181	
sms	(+)	4800789	99.850	F	298	SG10444/P24517	169
nadR	(+)	4801836	99.872	W	409	SG10243/P24518	169, 769
STYTRPR	(+)	4804154	99.920	SG	748	L13768	
slt	(+)	4804155	99.920	F	54	SG10490/P39434	
trpR	(+)	4804411	99.925	W	108	SG10401/P37444	
yjjX	(−)	4804799	99.933	F	35	SG10436/P39432	
STY326F	(+)	ND[i]	ND	S	326	D12814	
STYNHOA	(+)	ND	ND	S	2,134	D90301	
nhoA	(+)	ND	ND	W	281	SG10247/Q00267	737

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TABLE 3—*Continued*

Locus	Ori[b]	Left End[c]		Code[d]	Length[e]	Accession no.[f]	Reference(s)[g]
		bp	Cs				
yzzJ	(−)	ND	ND	F	132	SG10500/P40788	531
STYOADGABA	(+)	ND	ND	S	4,053	M96434	
oadG	(+)	ND	ND	W	83	SG10261/Q03032	743
oadA	(+)	ND	ND	W	591	SG10259/Q03030	743
oadB	(+)	ND	ND	W	433	SG10260/Q03031	743
STYSINRPHO	(+)	ND	ND	S	4,880	L04307	
sinR	(+)	ND	ND	W	315	SG10383/P37459	221
STYTCPCHEM	(+)	ND	ND	S	1,840	L06029	
tcp	(+)	ND	ND	W	547	SG10389/Q02755	760
SEANSP	(+)	ND	ND	S	1,887	U04851	
ansP	(+)	ND	ND	W	497	SG10527/P40812	

[a] GenBank LOCUS field, StySeq contig name, or gene name. The StySeq contigs are generally composites created by merging overlapping GenBank entries and are usually named by using the first gene present in the contig. This gene name is followed by the organism code sty and an M to denoted a merged (melded) contig. Three-letter gene names have a hyphen instead of a fourth letter, following the conventions established for the EcoSeq data collection. The LOCUS and contig names are mnemonic, but they are subject to change, and therefore one should use the accession numbers for retrieval and identification purposes.

[b] Ori, orientation of genes on the chromosome. (+), clockwise; (−), counterclockwise. Orientation of GenBank entries on the chromosome. (+), 5′ to 3′ is the clockwise direction; (−), 5′ to 3′ is the counterclockwise direction. If the orientation is unknown, the orientation of the corresponding *E. coli* sequence is used as the default orientation (see text). All melded contigs are constructed to be in the (+) orientation.

[c] Left end denotes the genomic coordinate (base pairs) of the left (counterclockwise) end of an aligned DNA sequence entry or gene in base pairs and centisomes. A centisome is a physical map unit equal to 1% of the length of a chromosome. We estimate 1 Cs for the chromosome of *S. typhimurium* to be 48,080 bp. For genetically pinned genes, the estimated centisome value is used to calculate a left-end genomic coordinate in base pairs. We do not mean to imply that genomic positions are known to single-base-pair accuracy. In contrast, the relative positions of genes within a contig are known to single-base-pair accuracy. Persons wishing to quote a centisome map position for *S. typhimurium* genes should use the centisome values presented in Table 1.

[d] Codes: P, physically anchored contig; G, genetically pinned; H, roughly located by using mapping information from the homologous chromosome of *E. coli*; M, melded StySeq meld; S, single StySeq (GenBank) entry; C, constituent GenBank sequence used in assembly of a StySeq meld; W, whole gene sequence; F, fragment of a gene, partial sequence. StySeq1 master contigs are preceded by spaces and have two codes.

[e] Length, number of base pairs for DNA sequences or number of codons (amino acids) for genes. The number of codons is not given for the structural RNA genes, labeled RNA.

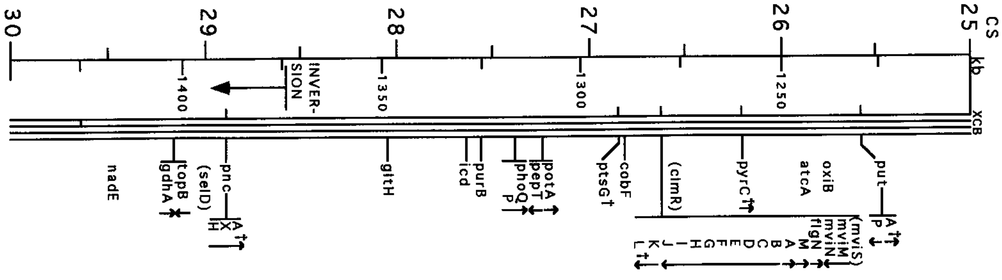
[f] GenBank, SWISS-PROT, and StyGene (SG) accession numbers; completely overlapping (redundant) GenBank entries omitted here are listed in the SWISS-PROT records. Structural RNA genes do not have corresponding SWISS-PROT records; the type of structural RNA gene is indicated instead.

[g] DNA sequence and characterization citations from SWISS-PROT. Additional sequence-related references, including unpublished sources, can be obtained from GenBank and SWISS-PROT records. Additional references are also listed in Table 1.

[h] NA, not available.

[i] ND, not done.

FIG. 1. Genetic map of *S. typhimurium* LT2. The gene designations used here are described in Table 1. The map is shown as 20 linear segments representing the circular chromosome and 1 linear segment representing the circular plasmid pSLT. The chromosome is composed of 100 centisomes (Cs); a scale covering 5 Cs is shown to the left of each segment. The scale is also designated in kilobases; the entire chromosome is designated as 4,808 kb (404). In the middle of the segment are vertical lines which show the restriction maps for the endonucleases *Xba*I, *Ceu*I, and *Bln*I, indicated by X, C, and B, respectively; a horizontal line indicates a restriction site. These sites were determined from PFGE (404, 406, 745, 746). The positions of many genes around the chromosome were anchored by PFGE, through the *Xba*I and *Bln*I sites in Tn*10* transposons which had transposed into these genes (404, 406, 746). Genes which have been mapped in this way are indicated by a short horizontal bar to the left of the *Xba*I map and the gene name is flagged with a superscript †; e.g., the *carAB* genes at 1.6 Cs, the *leu* genes at 2.8 Cs, and the *pan* genes at 4.5 Cs, have been mapped through analysis of Tn*10* insertions in these genes (404). Other genes are anchored through a specific restriction site which falls into a known gene; e.g., *Ceu*I sites are found only in the *rrn* genes; thus, at Cs 6.2 the *Ceu*I site indicates the location of the *rrnH* operon, at 58.1 Cs it indicates the location of the *rrnG* operon, and so on. In these cases, too, we show a short horizontal bar to the left of the *Xba*I map. The locations of the genes between these fixed points are based on several types of data (see the text). In many cases, the location is based on phage-mediated transduction; the distance between genes was determined by assuming that the lengths of P22 and of P1 transducing fragments are 1 and 2 Cs, respectively, and applying the formula developed by Wu (752) to convert the percentage of joint transduction to map distance in centisomes with modifications described in Fig. 2 of Sanderson and Roth (581). Parentheses around a gene symbol indicate that the location of the gene is known only approximately, usually from conjugation studies or sequence comparison with *E. coli*. An asterisk indicates that the gene has been mapped more precisely, usually by phage-mediated transduction, but that its position with respect to adjacent markers is not known. Arrows to the extreme right of the genes and operons indicate the direction of mRNA transcription at these loci. The endpoints of the region of the chromosome inverted with respect to *E. coli* (between 28.6 and 41.1 Cs) are denoted by the word “inversion” and by arrows. The region of the chromosome for which high-resolution restriction mapping data have been published (749) (between 91.5 and 96.5 Cs) is delimited by HR.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kb
XCB
25
26
27
28
29
30
1250
1300
1350
1400
INVER-SION
put
A
P
oxiB
atcA
(mviS)
mviM
mviN
flgN
M
A
B
C
D
E
F
G
H
I
J
K
L
pyrC
(clmR)
cobF
ptsG
potA
pepT
phoQ
P
purB
icd
gltH
pnc
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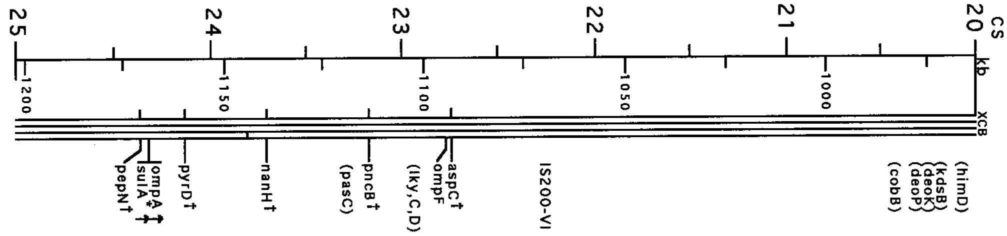
X
H
topB
gdhA
nadE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kb
XCB
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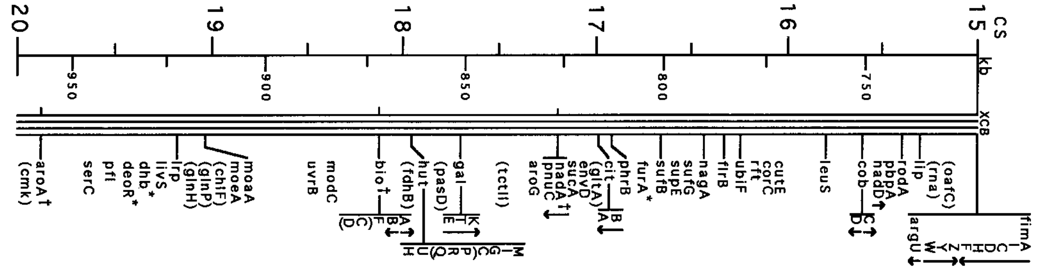
21
22
23
24
25
1000
1050
1100
1150
1200
(himD)
(kdsB)
(deoK)
(deoP)
(cobB)
IS200-VI
aspC
ompF
(lky,C,D)
pncB
(pasC)
nanH
pyrD
ompA
sulA
pepN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XCB
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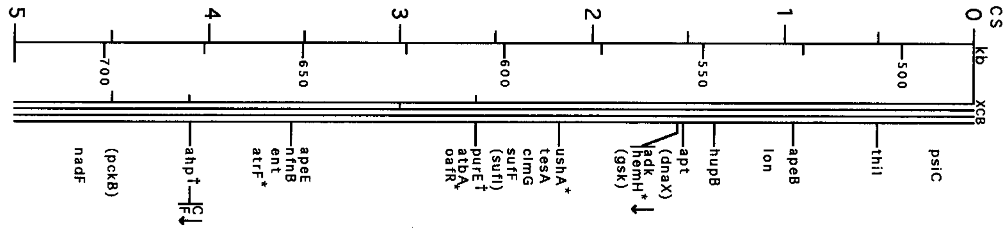
16
17
18
19
20
750
800
850
900
950
fimA
C
D
H
F
Z
Y
W
argU
(oafC)
(rna)
lip
rodA
pbpA
nadD
cob
C
D
leuS
cutE
corC
rft
ubiF
flrB
nagA
sufG
supE
sufB
furA
phrB
cit
B
A
(gltA)
envD
sucA
nadA
pnuC
aroG
(tctII)
gal
K
E
T
(pasD)
hut
(fdhB)
G
M
C
P
R
(Q
U
H
bio
A
B
F
C
D
modC
uvrB
moaA
moeA
(chlF)
(glnP)
(glnH)
lrp
livS
dhb
deoR
pfl
serC
aroA
(cmk)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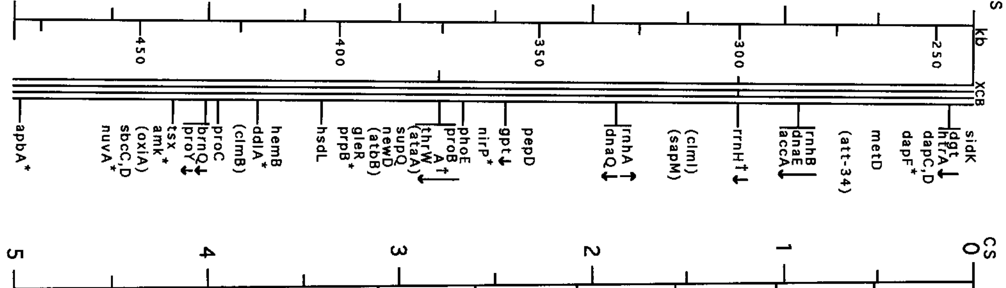
kb
XCB
10
11
12
13
14
15
500
550
600
650
700
psiC
thiI
apeB
lon
hupB
apt
(dnaX)
adk
hemH
(gsk)
ushA
tesA
clmG
sufF
(sufI)
purE
atbA
oafR
apeE
nfnB
ent
atrF
ahp
C
F
(pckB)
nadF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XCB
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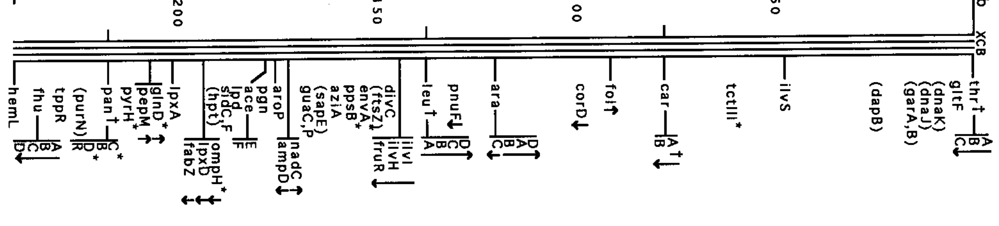
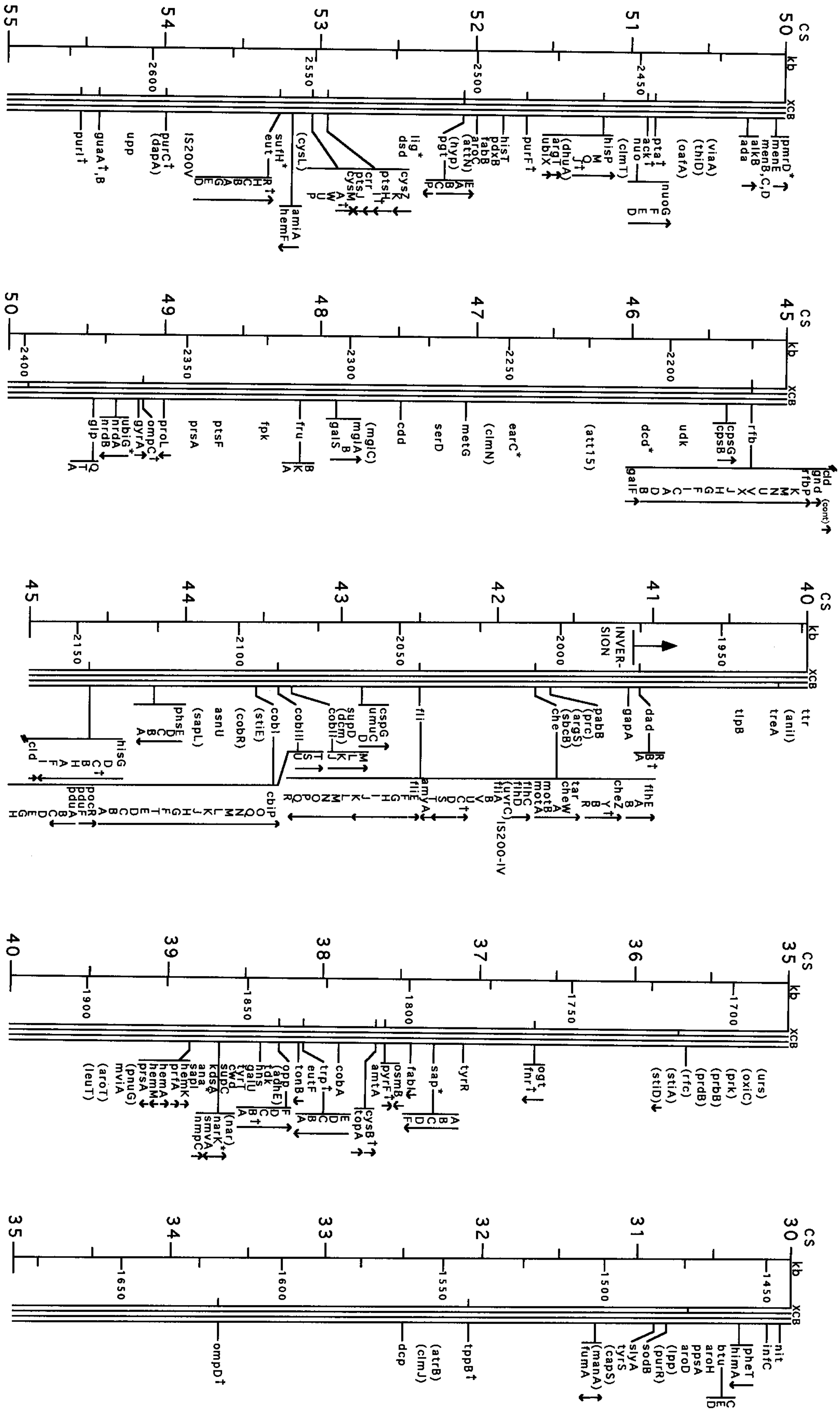
6
7
8
9
10
250
300
350
400
450
sidK
dgt
htrA
dapC,D
dapF
metD
(att-34)
rnhB
dnaE
accA
rrnH
(clmI)
(sapM)
rnhA
dnaQ
pepD
gpt
nirP
phoE
proB
A
thrW
(ataA)
supQ
newD
(atbB)
gleR
prpB
hsdL
hemB
ddlA
(clmB)
proC
brnQ
proY
tsx
amk
(oxiA)
sbcC,D
nuvA
apbA


CS
kb
XCB
0
1
2
3
4
5
50
100
150
200
thr
A
B
C
gltF
(dnaK)
(dnaJ)
(garA,B)
(dapB)
ilvS
tctIII
car
A
B
fol
corD
ara
D
A
B
C
pnuF
D
C
B
A
leu
divC
(ftsZ)
envA
ppsB
aziA
(sapE)
guaC,P
ilvI
ilvH
fruR
aroP
nadC
ampD
pgn
ace
E
F
lpd
sfdC,F
(hpt)
ompH
lpxD
fabZ
lpxA
glnD
pepM
pyrH
pan
C
B
D
(purN)
R
tppR
fhu
A
C
B
D
hemL


CS
kb
XCB
50
51
52
53
54
55
2450
2500
2550
2600
pmrD*
menE
menB,C,D
alkB
ada
(viaA)
(thiD)
(oafA)
pta
ack
nuo
nuoG
F
E
D
(clmT)
hisP
M
Q
J
(dhuA)
argT
ubiX
purF
hisT
pdxB
fabB
aroC
(attN)
(hyp)
pgt
lig*
dsd
cysZ
K
ptsH
I
crr
ptsJ
cysM
A
W
U
P
(cysL)
sufH*
eut
R
H
C
B
G
A
E
D
amiA
hemF
IS200V
upp
purC
(dapA)
guaA,B
purI
45
46
47
48
49
2200
2250
2300
2350
2400
rfb
cld
gnd
rfbP
K
M
N
U
V
X
J
H
G
F
I
C
A
D
B
galF
(cont)
cpsG
cpsB
udk
dcd*
(att15)
earC*
(clmN)
metG
serD
cdd
(mglC)
mglA
B
galS
fru
B
K
A
fpk
ptsF
prsA
proL
ompC
gyrA*
ubiG
nrdA
nrdB
glp
Q
T
A
40
41
42
43
44
1950
2000
2050
2100
2150
INVERSION
ttr
(anil)
treA
tlpB
dad
R
B
A
gapA
flhE
A
B
cheZ
Y
B
R
tar
cheW
A
motB
motA
flhC
flhD
(uvrC)
fliA
B
IS200-IV
pabB
(prc)
(argS)
(sbcB)
che
fli
amyA
fliE
fliF
G
H
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J
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O
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M
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T
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asnU
(sapL)
phsE
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A
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hisG
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pocR
pduF
pduA
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C
D
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39
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1800
1850
1900
(urs)
(oxiC)
(prk)
(prbB)
(prdB)
(rfc)
(stiA)
(stiD)
ogt
fnr
tyrR
sap
*
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B
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D
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osmB
pyrF
amtA
cysB
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cobA
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tonB
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prsA
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(leuT)
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33
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1450
1500
1550
1600
1650
nit
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pheT
himA
btu
E
C
D
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ppsA
aroD
(lpp)
(purR)
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(atrB)
(clmJ)
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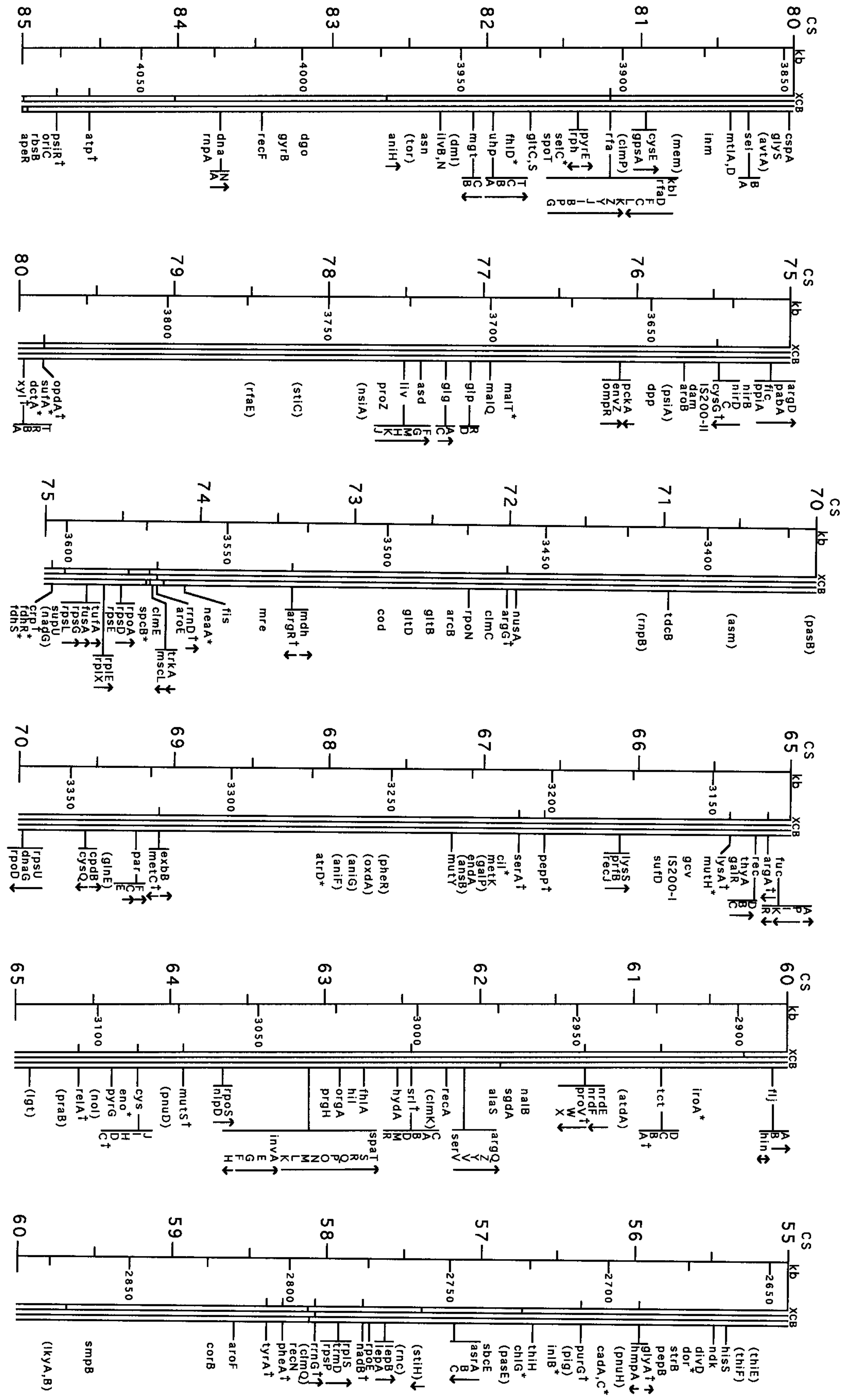
ompD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3950
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4050
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glyS
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inm
sel
B
A
mtlA,D
(mem)
cysE
gpsA
(clmP)
kbl
rfaD
F
C
L
K
Z
Y
J
I
B
P
G
pyrE
rph
selC*
rfa
spoT
gltC,S
fhlD*
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A
B
C
T
mgt
C
B
(dml)
ilvB,N
asn
(tor)
aniH
recF
gyrB
dgo
dna
N
A
rnpA
atp
psiR
oriC
rbsB
apeR
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76
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78
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3700
3750
3800
argD
pabA
fic
ppiA
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dam
aroB
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dpp
pckA
envZ
ompR
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malQ
glp
R
D
glg
A
C
asd
F
liv
G
M
H
K
J
proZ
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(stiC)
(rfaE)
opdA
sufA*
dctA
xylT
T
R
B
A
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72
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3550
3600
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tdcB
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argG
clmC
rpoN
arcB
gltB
gltD
cod
mdh
argR
mre
fis
neaA*
rrnD
aroE
clmE
spcB*
trkA
mscL
rpoA
rpsD
rpsE
rplE
rplX
tufA
fusA
rpsG
rpsL
supU
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crp
fdhR*
tdhS*
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66
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3300
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P
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K
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argA
rec
D
thyA
B
galR
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lysA
mutH*
gcv
IS200-I
sufD
lysS
prfB
recJ
pepT
serA
cil*
metK
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endA
(ansB)
mutY
(pheR)
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(aniG)
(aniF)
atrD*
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metC
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cysQ
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dnaG
rpoD
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2900
2950
3000
3050
3100
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iroA*
tct
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C
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nrdF
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nalB
sgdA
alaS
argQ
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serV
recA
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fhlA
hil
orgA
prgH
spaT
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nlpD
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(lgt)
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(thiF)
hisS
ndk
divD
dor*
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pepB
glyA
hmpA
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(pig)
inlB*
thiH
chlG*
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sbcE
asrA
B
C
(stiH)
(rnc)
lepB
lepA
rpoE
nadB
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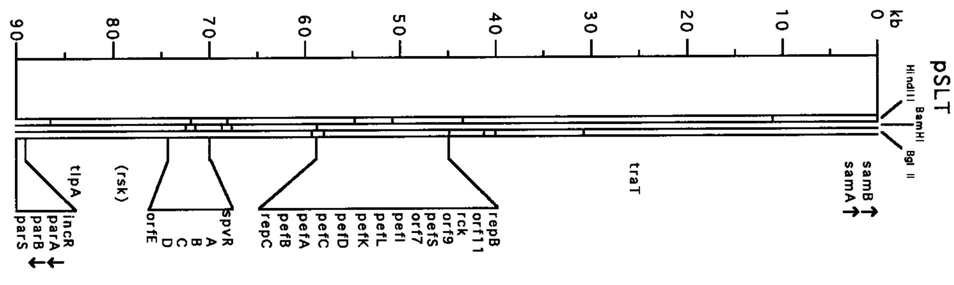
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traT
repB
orf11
rck
orf9
pefS
orf7
pefI
pefL
pefK
pefD
pefC
pefA
pefB
repC
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incR
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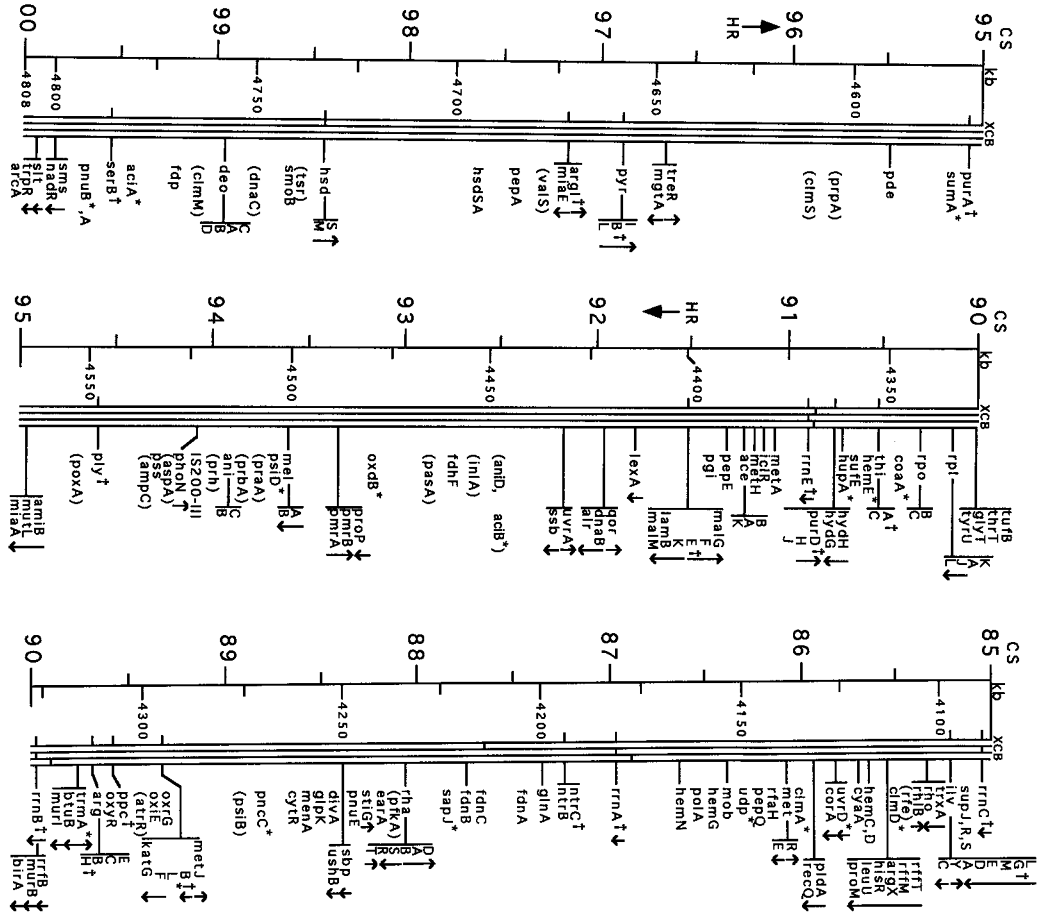
parB
parS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XCB
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sumA*
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(prpA)
(clmS)
treR
mgtA
pyr
B
I
L
pepA
(valS)
argI
miaE
hsdSA
hsd
S
M
(tsr)
smoB
(dnaC)
deo
C
A
B
D
(clmM)
fdp
aciA*
serB
pnuB*, A
sms
nadR
slt
trpR
arcA
90
91
92
93
94
4350
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4500
4550
rpl
tufB
thrT
glyT
tyrU
K
A
J
L
rpo
B
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coaA*
thi
A
hemE*
C
hydH
hydG
hupA*
purD
H
rrnE
metA
iclR
metH
ace
B
A
K
pepE
pgi
malG
F
E
lamB
K
malM
lexA
qor
dnaB
alr
uvrA
ssb
(aniD, aciB*)
(iniA)
fdhF
(pasA)
oxdB*
proP
pmrB
pmrA
mel
psiD*
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(prbA)
ani
C
B
(prh)
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pss
(ampC)
ply
(poxA)
amiB
mutL
miaA
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86
87
88
89
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4150
4200
4250
4300
rrnC
supJ,R,S
ilv
L
G
M
E
D
A
Y
C
trxA
rho
rhlB
(rfe)
clmD*
rffT
rffM
argX
hisR
leuU
proM
hemC,D
cyaA
uvrD*
corA
pldA
recQ
clmA*
met
R
E
rfaH
pepQ
udp
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ntrB
glnA
fdnA
fdnC
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menA
cytR
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oxrG
oxiE
(atrR)
metJ
B
L
F
katG
ppc
oxyR
C
E
B
H
arg
trmA*
btuB
murI
rrnB
rrfB
murB
birA

ACKNOWLEDGMENTS

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