

Linkage Map of *Escherichia coli* K-12, Edition 10: The Traditional Map

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INTRODUCTION

Previously, Berlyn et al. (323) presented the traditional map, the EcoMap physical map, and a map by Singer and Low showing the distribution of the Gross-Singer transposon set around the chromosome. The map in this paper is a revision of that traditional map of *Escherichia coli* K-12, the linkage map of known genes and other functional sites (Fig. 1), and the physical map, EcoMap 10, of Kenneth Rudd is presented in the companion article (3763a).

The linkage map in this presentation includes genes located primarily by restriction, sequence, and cotransduction data reported in the literature and databases. It uses coordinates based on the complete sequence released by the Blattner laboratory. Obviously, the sequence is now the major resource for placing genes on the map. In some regions the placement represents a shift from the edition 9 map, which was based on coordinates of Rudd's EcoMap 7 composite of sequenced genes and regions (27, 33, 395, 568, 569, 926, 3308, 3465, 4127, 4128), placed on the physical map of *Escherichia coli* (2291, 3763b) by restriction and sequence comparisons. Those map positions were based on the results in the literature and on EcoMap and GenBank database entries. EcoMap 10 coordinates are of course also based on the completed sequence, and cross-consulting this summary map and the EcoMap that follows should be straightforward.

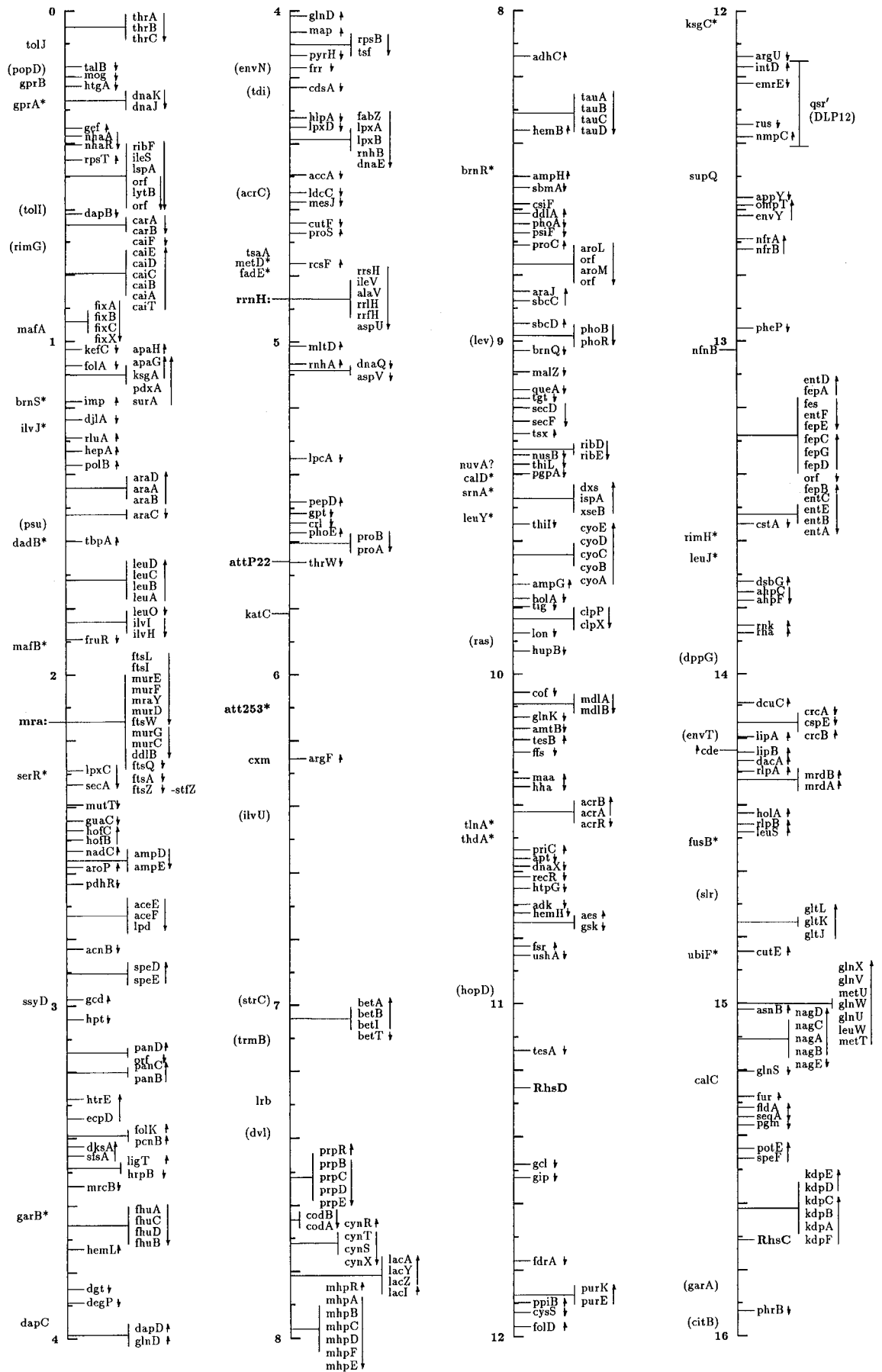
The linkage map of Fig. 1 includes 2,220 genes and about 40 other chromosomal markers, such as phage attachment sites, defective-phage elements, replication origins and termini, and other features traditionally included on the published linkage map. It does not include open reading frames (ORFs) lacking evidence for expression, with unknown functions or putative functions inferred by sequence homologies only. A few exceptions occur for *Salmonella* genes where the inference is strong that they are also expressed in *E. coli*. The ORFs not included

in this map can be found on EcoMap 10. The Fig. 1 map places the genes that can be found in sequence annotation and EcoMap 10 on the right side of the line. On the left side are genes not present on physical maps or the sequence, and in most cases these are not connected to a specific point on the axis to indicate that the localization is only approximate. As in previous editions of the *E. coli* linkage map (187, 188, 189, 190, 190a, 323, 4368, 4369, 4370, 4371), an asterisk indicates that the gene is not precisely located with respect to near neighbors and parentheses indicate that the location is even more uncertain and that the gene is located only within that general region. I have been very conservative about removing these from the map; even though the usefulness of some of these may be quite limited, there will probably be cases where the old, sometimes poorly characterized phenotype may be helpful in ascribing functions and phenotypic effects to ORFs. Also shown on the left side in boldface followed by colons are operon names that are distinct from any gene name within the operon and termination and attachment sites. The arrows indicate the direction of transcription and span genes included within a transcription unit.

Updates of map information are available in electronic form from several sites. These include the *E. coli* Genetic Stock Center's (CGSC's) World Wide Web server at URL <http://cgsc.biology.yale.edu>, which provides an interface for querying the database and retrieving formatted reports about genes, map regions, strains, and mutations, etc. (323a); the National Center for Biotechnology Information ftp site for EcoSeq and EcoMap, ncbi.nlm.nih.gov/repository/Eco/EcoMap7; the Colibri map at <http://www.pasteur.fr/Bio/Colibri.html>, the ECDC map at <http://susi.bio.uni-giessen.de/ecdc.html>, the site for the sequencing project at the University of Wisconsin, <http://www.genetics.wisc.edu>, a gene-protein database, <http://www.mbl.edu/html/ecoli.html>, Genome Information Broker at <http://mol.genes.nig.ac.jp/ecoli>, and others. See also Rudd (3673). The references attempt to document map information, the basic definition of the gene's function, and expression information and do not include information relating to detailed physical structure, active site in vitro mutagenesis, or enzyme

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FIG. 1. Linear drawing of circular linkage map of *E. coli* K-12. Symbols are defined in Table 1. Arrows show the direction of transcription. Where T-bars are used to display groups of genes, the length of the T shows the approximate length and position of the group in terms of the map coordinates, allowing visual ordering of closely packed groups.



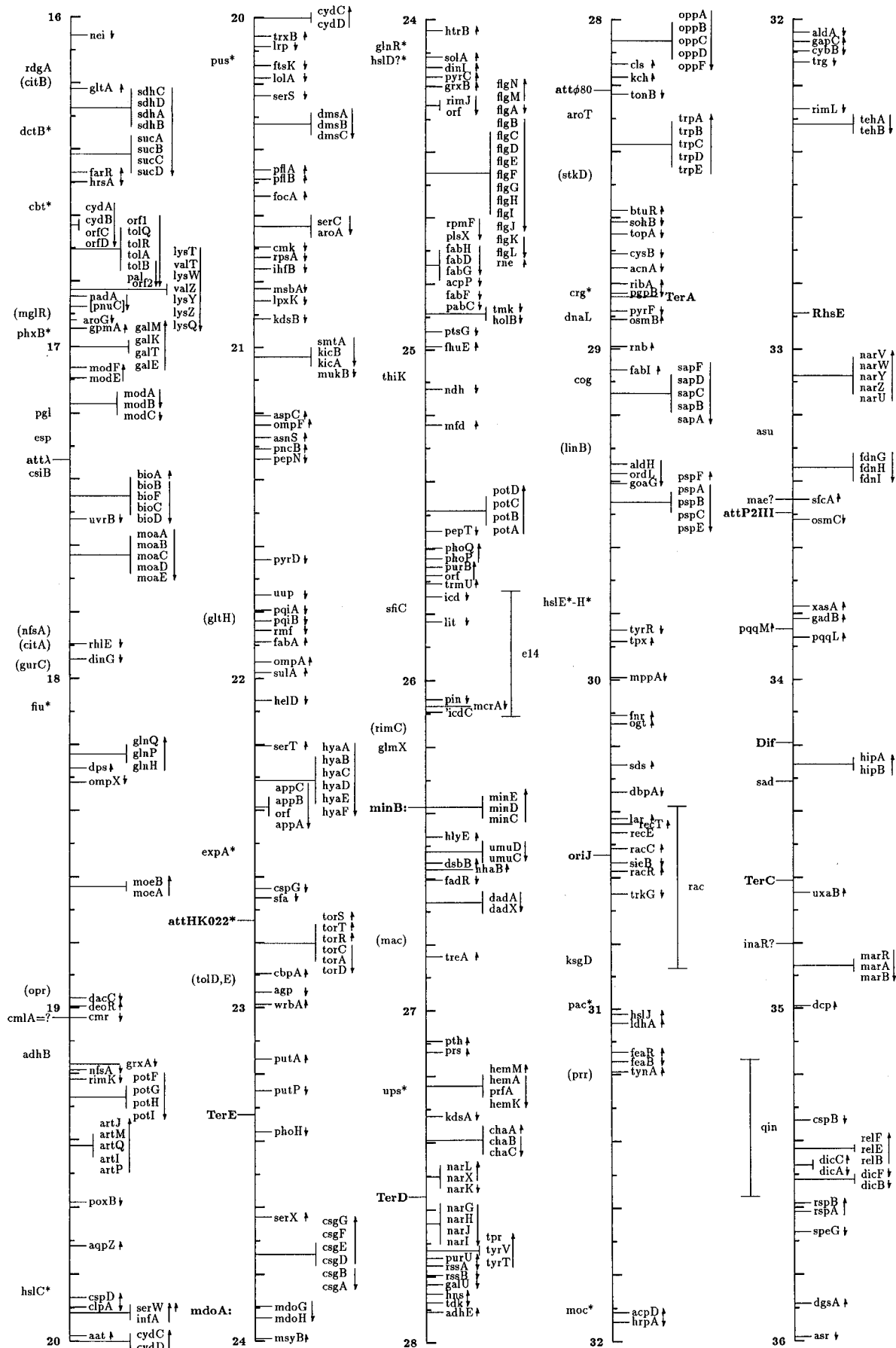


FIG. 1—Continued.

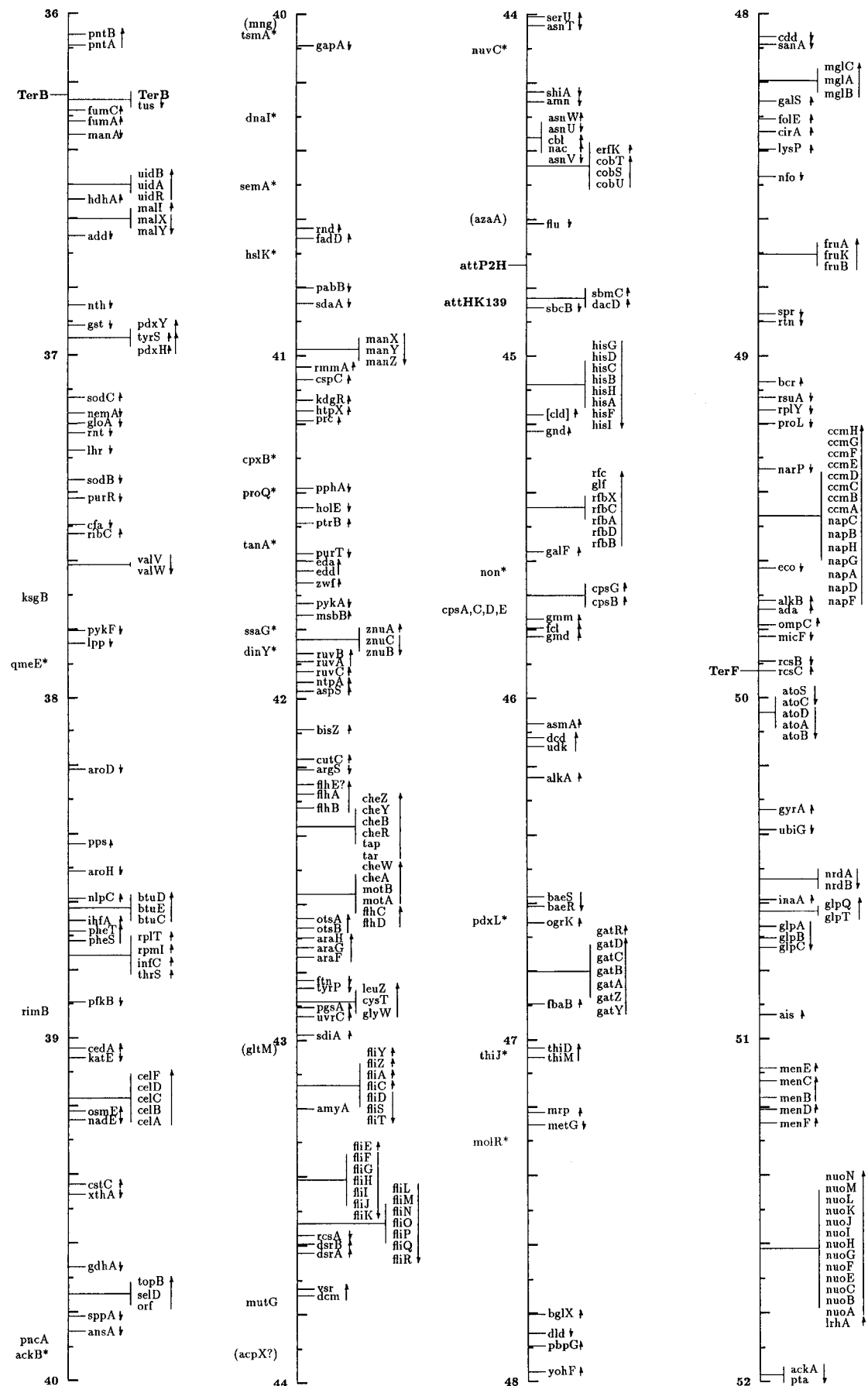


FIG. 1—Continued.

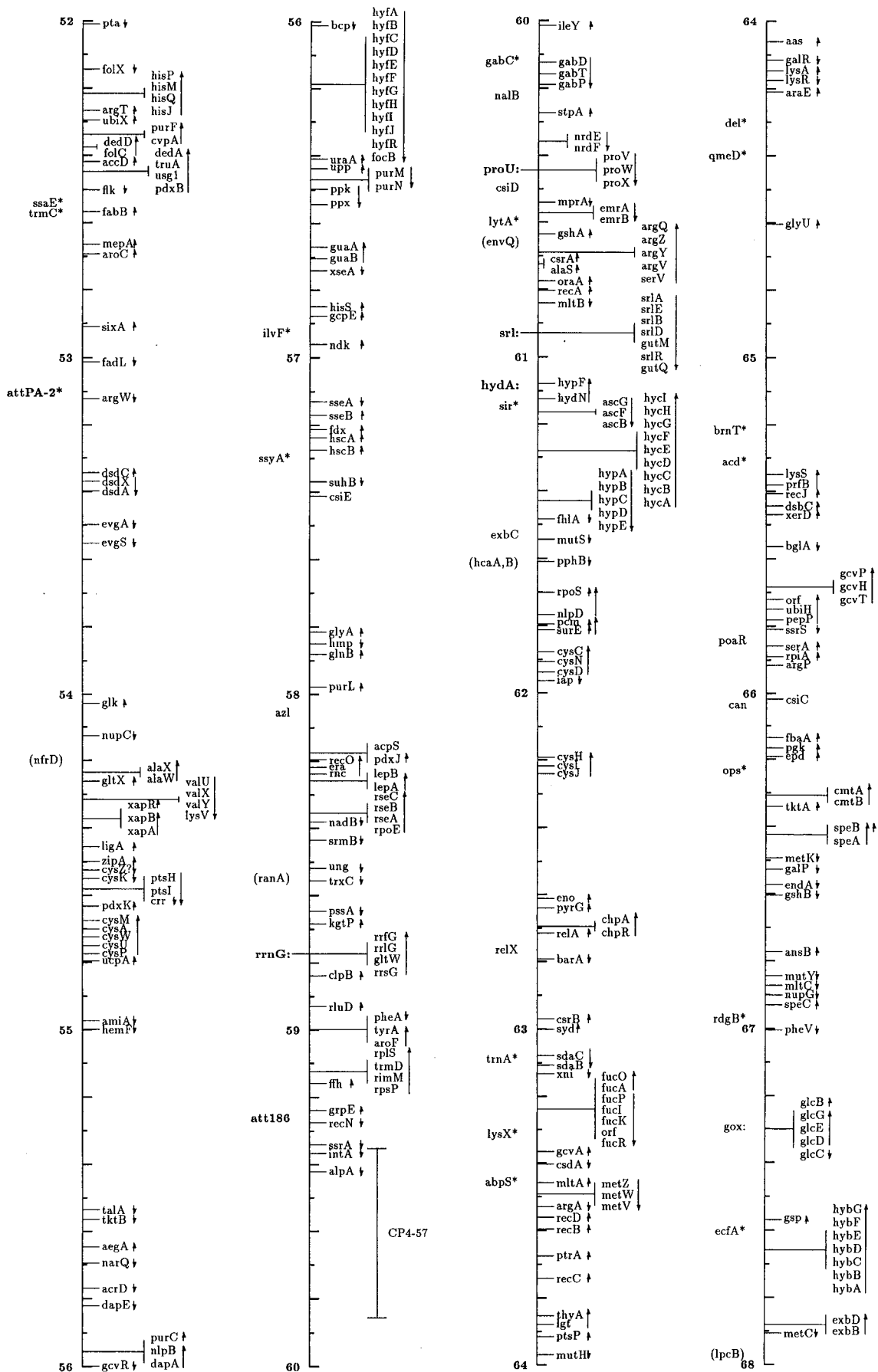


FIG. 1—Continued.

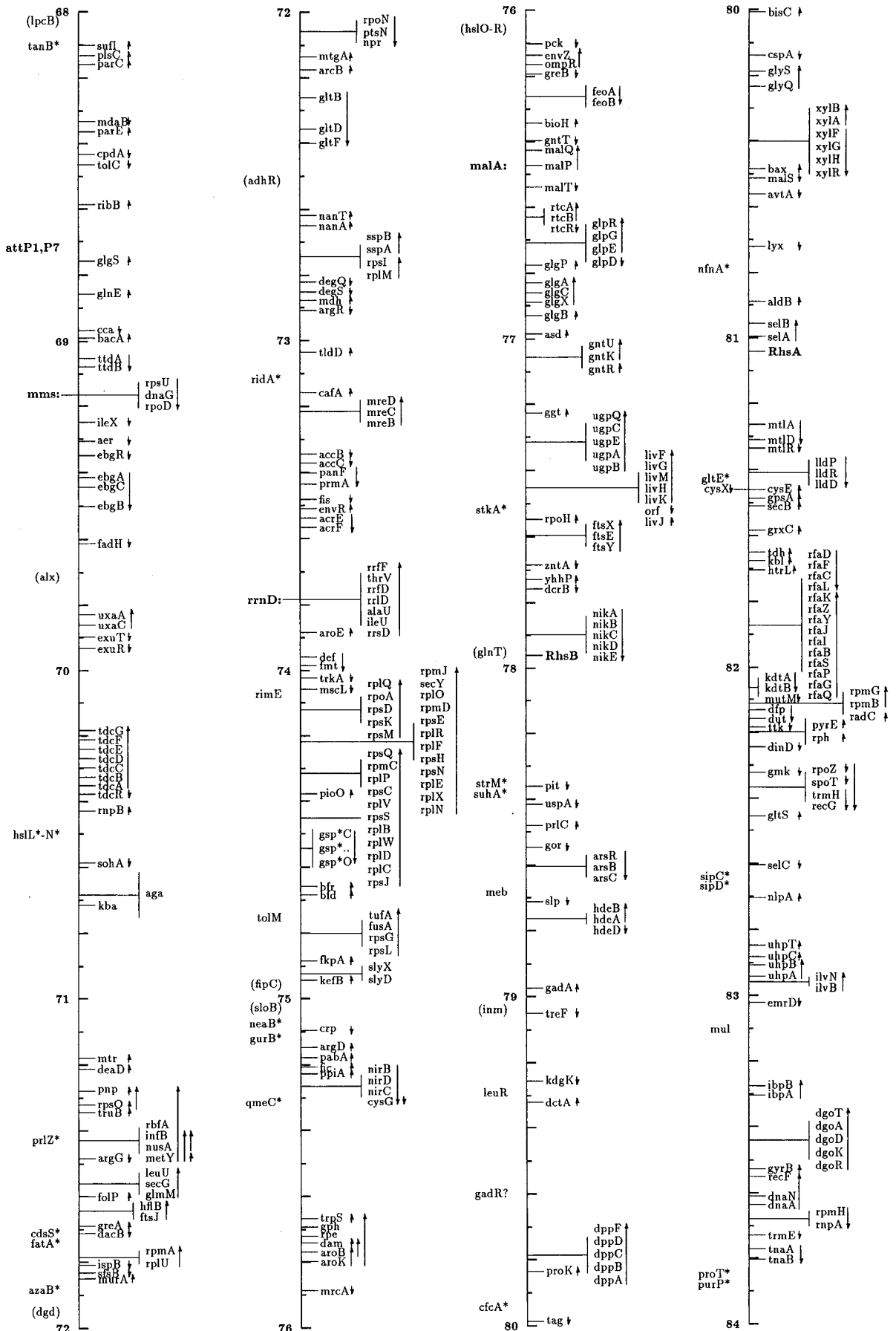


FIG. 1—Continued.

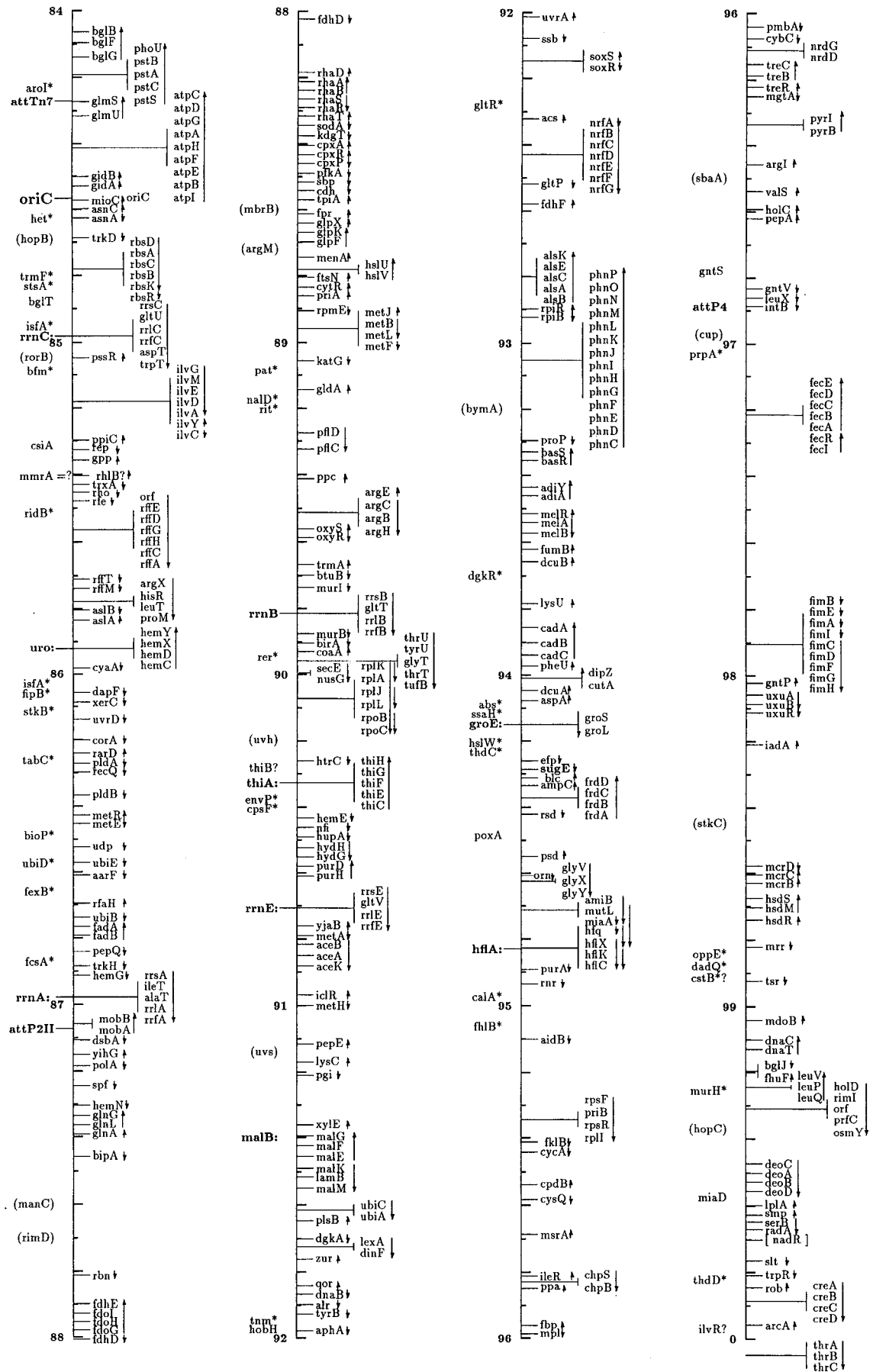


FIG. 1—Continued.

mechanism. Earlier map papers contain additional references for some of the loci (188–190a, 323).

MAP UNITS

Since the 1976 recalibration of the linkage map in terms of minutes required for time of entry of markers in interrupted conjugation experiments, the standard representation of the map has used the basic units of minutes and a total length of 100 minutes (190a). This has been a convenient and accepted coordinate system for the map, and although the current map units are based on restriction and sequence data rather than time of entry, we retain the term minute for 1/100 of the length of the chromosome. Both the CGSC database and EcoMap use as “left endpoints” the counterclockwise boundary of the coding region, and genes in Fig. 1 are placed approximately at these coordinates, with the higher-resolution map of Rudd (3763a) providing more exact placement, showing nucleotide and minute coordinates for the physically mapped genes.

NOMENCLATURE

Gene Symbol Convention

The standard genetic nomenclature for *E. coli* is that of Demerec et al. (1016), as subsequently amended through use, and as described in Instructions to Authors for the *Journal of Bacteriology* (see also reference 3821). This map, like those preceding it, follows those nomenclatural conventions. Accordingly, we have adhered to a three-letter lowercase mnemonic symbol, with an uppercase letter added when there are two or more genes in that mnemonic category. If authors have added an uppercase letter for a gene in a single-instance category, we have used that published four-letter symbol. For attachment sites and noncoding features of the chromosome, etc., the same standard has not been used, and we have continued to use the variable-length symbols historically applied to these sites. We have continued the convention proposed for sites of termination of replication and repetitive sequences, by using italicized symbols with the first letter uppercase.

The Issue of Stability

Many names have been changed by investigators since the 1990 map was published. When those changes were part of a systematic revision of nomenclature (often aimed at clarifying usage and resolving conflicts) for a group of related genes and were in compliance with the current *E. coli* gene nomenclature system, or were changed for compelling mnemonic reasons or for resolution of redundancy or conflict, also in conformance with the standard system, we have adopted those changes. We have not adopted and we wish to discourage changes of valid preexisting names proposed by authors simply because they

believe that theirs is a symbol signifying a more apt or accurate mnemonic. For example, a previously published name based on the pathway or phenotype is valid and should not, simply as a matter of course, be replaced by an alternate mnemonic based on the name of the enzyme that the gene codes for once that functional information has been determined. In general, the stability of a name has more value than improved nuances. In a few cases, we have been compelled to use a new name, despite the apparent validity of the original name, simply because the new name has been widely adopted in the literature. In a number of cases, a new gene has been assigned a symbol which has already been used or which is simultaneously proposed for another gene, with the two mnemonics having entirely different meanings. These names have had to be resolved, usually by changing the newer assignment. In a few cases, a uniquely named gene has been shown later to belong to a category for which a symbol already exists, and the latter symbol has been used instead of the earlier assignment. There is one case in this paper where use of a symbol already assigned to a different gene was strongly preferred by authors, and I was very reluctant to suggest a new symbol for the earlier, published gene name to the earlier authors, since that symbol has been used in a number of publications; for the interim I have broken convention to assign the newer genes temporary symbols with asterisks (*gsp**), in order to show them on the map and in the hope of resolving that naming with the usual precedence custom in the near future. Some synonymy is unavoidable, since a gene under study may be named and described in print before its identity to a known gene is discovered. However, a common practice in the recent literature seems to allow publication of an author's preliminary name for a gene even if its identity to a known gene has been discovered before publication, and that practice creates unnecessary synonymy. Alternate gene symbols are listed in Table 1, and Table 2 provides an alphabetized list of such symbols with cross-references to the symbols used in Table 1.

There is a standing tradition of coordinating gene symbols between the CGSC and the *Salmonella* Genetic Stock Center to avoid the assignment of the same symbol to different genes in the two organisms and the assignment of different symbols to homologous genes, insofar as this coordination is feasible. We have not, however, changed names of *E. coli* genes in order to extend this tradition to other bacteria or other organisms. The desirability and feasibility of uniform nomenclature conventions for all bacteria or other microbial groupings are currently only topics of discussion and conjecture, and changes to enhance similarities in an ad hoc, piecemeal fashion seem counterproductive at the present time. Readers are reminded that symbol changes create discontinuity with previous literature concerning genes, with even more serious ramifications for allele designations, since unique allele numbers are assigned on the basis of the three letter mnemonic and changes in a symbol may necessitate renumbering of alleles as well.

TABLE 1. *E. coli* genes and replication- or phage-related sites^a

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>aarF</i>	86.6	Aminoglycoside acetyltransferase regulator	<i>yigQR</i> ; regulator of 2'-N-acetyltransferase; involved in respiratory cofactor ubiquinone production	53879	2696
<i>aas</i>	64.1	Acyl-ACP synthase	2-Acyl-glycerophosphoethanolamine acyltransferase; acyl-ACP synthetase; salvage pathway for reacylation; inner membrane; bifunctional for turnover/incorporation	29780	1831, 1972
<i>aat</i>	20.0	Amino acyl-tRNA-protein transferase	Aminoacyl-tRNA-protein-transferase (EC 2.3.2.6)	1054	4045
<i>abpS</i>	63.5	Arg binding protein	Low-affinity transport system for arginine and ornithine; periplasmic binding protein	18562	664
<i>abs</i>	94.1	Antibiotic sensitivity	Sensitivity and permeability to antibiotics and dyes	18559	763
<i>accA</i>	4.5	Acetyl-CoA carboxylase	Acetyl-CoA carboxylase α -carboxyltransferase subunit; (EC 6.4.1.2)	29829	2536, 2537
<i>accB</i>	73.4	Acetyl-CoA carboxylase	<i>fabE</i> ; acetyl-CoA carboxylase, biotin carboxyl carrier protein (EC 6.4.1.2)	796	2537, 2712, 3057, 4302, 4616
<i>accC</i>	73.4	Acetyl-CoA carboxylase	<i>fabG</i> ; acetyl-CoA carboxylase, biotin carboxylase (BC) subunit (EC 6.4.1.2)	29834	2315, 2537, 3253
<i>accD</i>	52.4	Acetyl-CoA carboxylase	<i>dedB</i> , <i>usg</i> ; acetyl-CoA carboxylase β -carboxyltransferase subunit (EC 6.4.1.2)	28570	2534, 2537, 3081
<i>acd</i>	65.1	Acetaldehyde-CoA deHase	Acetaldehyde-CoA dehydrogenase (EC 1.2.1.10)	1053	764
<i>aceA</i>	90.8	Acetate	<i>icl</i> ; isocitrate lyase (EC 4.1.3.1); acetate utilization	1052	2744, 2811, 3674, 754, 841
<i>aceB</i>	90.8	Acetate	<i>mas</i> ; malate synthase A (EC 4.1.3.2)	1051	2744, 591, 592, 840, 841
<i>aceE</i>	2.7	Acetate	<i>aceE1</i> ; pyruvate dehydrogenase (decarboxylase component) E1p; (EC 1.2.4.1); acetate requirement	1050	1553, 1555, 1556, 1558, 2934, 4150, 4204, 655
<i>aceF</i>	2.7	Acetate	<i>aceE2</i> ; pyruvate dehydrogenase (dihydropolyltransacetylase component) E2p (EC 1.6.4.3, EC 2.3.1.12); acetate requirement	26530	1554, 2934, 655
<i>aceK</i>	90.9	Acetate	Isocitrate dehydrogenase kinase/phosphatase	17770	1343, 1897, 2274, 2418, 2419, 753, 842, 754
<i>ackA</i>	52.0	Acetate kinase	Acetate kinase (EC 2.7.2.1); mutants fluoroacetate resistant	1048	1548, 2094, 2512, 2812, 530, 224
<i>ackB</i>	39.9	Acetate kinase	Acetate kinase activity* (EC 2.7.2.1)	1047	3379
<i>acnA</i>	28.8	Aconitase	Aconitase A (EC 4.2.1.2)	28218	3542, 3543
<i>acnB</i>	2.8	Aconitase	Aconitase B (EC 4.2.1.2)	36955	1538, 2141, 474
<i>acpD</i>	31.9	Acyl carrier protein	ACP phosphodiesterase	52896	1256, 394
<i>acpP</i>	24.8	Acyl carrier protein	ACP (acyl carrier protein)	31871	2183, 3621
<i>acpS</i>	58.2	Acyl carrier protein	<i>dpp</i> ; holo-ACP synthase (EC 2.7.8.7)	32953	2397, 2400, 2401, 3471, 4340
<i>acpX</i>	43.9	Acyl carrier protein	<i>acpS</i> ; originally thought to be holo-ACP synthase; perhaps cryptic second gene or regulator	1046	3471
<i>acrA</i>	10.4	Acridine	<i>Mb</i> , <i>lir</i> , <i>mbl</i> , <i>mtcA</i> , <i>sipB</i> ; AcrAB efflux system effects Mar multiple resistance	1045	1291, 1726, 2684, 2685, 3282, 3563, 4723, 808
<i>acrB</i>	10.4	Acridine	<i>acrE</i> ; AcrAB system has major role in Mar multiple resistance to NAL, TET, AMP, etc.; beware renamings of <i>acrE</i> , <i>acrB</i> , and <i>envC</i>	35806	1291, 2684, 2685, 3282, 4723
<i>acrC</i>	4.5	Acridine	Sensitivity to acriflavine; transmembrane protein	1044	3104
<i>acrD</i>	55.7	Acridine	Sensitivity to acriflavine	35697	3188
<i>acrE</i>	73.5	Acridine	<i>envC</i> ; anomolous cell division; chain formation; splits cross-wall to form new poles; see <i>acrB</i>	813	2133, 2255, 2256, 2516, 3702
<i>acrF</i>	73.6	Acridine	<i>envD</i> ; encodes lipoprotein with signal peptide; osmotically remedial envelope defect	33608	2255, 2256, 2516, 2684
<i>acrR</i>	10.5	Acridine	Regulatory protein for <i>acrA</i> and <i>acrB</i>	35809	2686
<i>acs</i>	92.3	Acetyl-CoA synthetase	Acetyl CoA synthetase 2 (EC 6.2.1.1)	34317	2367, 395
<i>ada</i>	49.7	Adaptive (response)	O ⁶ -methylguanine-DNA methyltransferase, inducible; DNA repair against methylating and alkylating agents; transcription factor	1043	1184, 2001, 2158, 2410, 2489, 2698, 2760, 2967, 3078, 3094, 3795, 3812, 3815, 3957, 3958, 3959, 4330, 4385
<i>add</i>	36.6	Adenine deaminase	Adenosine deaminase (EC 3.5.4.4.); mutants affect growth on deoxyadenosine in <i>purA</i> , <i>B</i> mutants	1042	2024, 765

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>adhB</i>	19.1	Alcohol dehydrogenase	Alcohol dehydrogenase	36932	E, 763a
<i>adhC</i>	8.1	Alcohol dehydrogenase	Alcohol-acetaldehyde dehydrogenase; <i>adhC</i> has also been used for <i>adhE</i> control region	52901	2070, 394
<i>adhE</i>	27.9	Alcohol/acetaldehyde dehydrogenase	<i>ana</i> ; <i>adhC</i> ; alcohol dehydrogenase, acetaldehyde dehydrogenase, CoA-linked (EC 1.1.1.1) allyl alcohol resistance; deactivase for PFL	1041	129, 1457, 2203, 2495–2497, 2634, 710, 887, 1582
<i>adhR</i>	72.5	Alcohol/acetaldehyde dehydrogenase	Regulatory gene for <i>acd</i> and <i>adhE</i>	18556	723, 767
<i>adiA</i>	93.5	Arginine decarboxylase, induced	<i>adi</i> ; arginine decarboxylase, inducible by acid; homology with CadA, SpeC, SpeF	34495	1665, 4022, 4023, 4024, 4223, 4224
<i>adiY</i>	93.4	Arginine decarboxylase, induced	Sequence similarity with XylS/AraC family, including EnvY and AppY regulates <i>adiA</i>	35597	4224
<i>adk</i>	10.7	Adenylate kinase	<i>dnaW</i> , <i>plsA</i> ; adenylate kinase (EC 2.7.4.3) pleiotropic effects on glycerol-3-phosphate acyltransferase activity	1040	1176, 1725, 541
<i>aegA</i>	55.6	Anaerobically expressed gene	<i>air</i> ; induced by anaerobiosis, repressed by NO ₃ ; control mediated by Fnr, NarX, Q, L; nonessential in respiration, N source utilized	50847	662
<i>aer</i>	69.3	Aerotaxis	<i>air</i> ; possibly flavoprotein, mediates positive aerotactic responses; signal transducer	47273	347
<i>aes</i>	10.7	Acetyl esterase	Esterase affecting maltose system expression	53369	2114, 3393
<i>aga</i>	70.7	Acetylgalactosamine	Cluster of putative <i>N</i> -acetylgalactosamine pathway genes, including the <i>kba</i> gene, and mannose permease homologs	55305	3649
<i>agp</i>	23.0	Acid glucose-1-phosphatase	Homology with <i>appA</i> ; periplasmic	31830	3521, 3524, 3525, 3526
<i>ahpC</i>	13.8	Alkyl hydroperoxide	<i>tpx</i> ; alkyl hydroperoxide reductase small subunit	31190	4106, 4241, 667, 668
<i>ahpF</i>	13.8	Alkyl hydroperoxide	Alkyl hydroperoxide reductase large subunit	31194	4106, 4241, 668
<i>aidB</i>	95.1	Alkylating agent induced	Adaptive response	18553	2408, 2409, 4602, 4603
<i>ais</i>	50.9	Aluminum inducible	An aluminum-inducible protein	53490	1589
<i>alaS</i>	60.7	Alanine	<i>act</i> , <i>ala-act</i> , <i>lovB</i> ; alanyl-tRNA synthetase 1B (ligase) (EC 6.1.1.7)	1039	2132, 2317, 3556, 3557, 3558, 458, 4590
<i>alaT</i>	87.0	Alanine	<i>talA</i> ; alanine tRNA 1B; <i>rmA</i> operon	1038	2313, 926
<i>alaU</i>	73.8	Alanine	<i>talD</i> ; alanine tRNA 1B; <i>rmD</i> operon	1037	2313
<i>alaV</i>	4.8	Alanine	Alanine tRNA 1B; <i>rmH</i> operon	1036	1146
<i>alaW</i>	54.2	Alanine	<i>alaWα</i> ; alanine tRNA 2; tandemly duplicated; see <i>alaX</i>	32851	539
<i>alaX</i>	54.2	Alanine	<i>alaWβ</i> ; alanine tRNA 2; tandemly duplicated <i>alaW</i>	18547	2313, 539
<i>aldA</i>	32.0	Aldehyde dehydrogenase	<i>ald</i> ; aldehyde dehydrogenase, NAD linked	17767	1749, 3571, 712
<i>aldB</i>	80.9	Aldehyde dehydrogenase	Aldehyde dehydrogenase	35668	4813, 4815
<i>aldH</i>	29.3	Aldehyde dehydrogenase	Putative aldehyde dehydrogenase, by homology; transcribed in operon with <i>goaG</i>	35320	1697, 2066
<i>alkA</i>	46.2	Alkylation	<i>aidA</i> ; 3-methyl-adenine DNA glycosylase II, inducible; repairs by single- and double-strand excision of 3-methyl adenine	1035	1184, 3093, 3095, 365, 4385, 4602, 773
<i>alkB</i>	49.7	Alkylation	<i>aidD</i> ; DNA repair specific for alkylated DNA; mutants extremely sensitive to MMS	18544	2157, 2158, 2316, 4602, 4689, 693
<i>alpA</i>	59.4	Activation of Lon protease	Alp protease; cryptic prophage CP4-57 element; regulates <i>intA</i> (<i>slp</i> [suppressor of Lon])	33086	2241, 4455
<i>alr</i>	91.9	Alanine racemase	Alanine racemase (EC 5.1.1.1)	1034	2549, 395
<i>alsA</i>	92.8	Allose	Allose transport ABC protein	53362	2223
<i>alsB</i>	92.9	Allose	Allose-binding protein	53365	2223
<i>alsC</i>	92.8	Allose	Allose transport, membrane component	53357	2223
<i>alsE</i>	92.8	Allose	Allulose-6-P 3-epimerase	53353	2223
<i>alsK</i>	92.8	Allose	Allose kinase	53345	2223
<i>alx</i>	70.0	Alkaline-induced expression	pH-regulated locus; induced in alkaline medium	36513	356
<i>amiA</i>	55.0	Amidase	<i>N</i> -Acetylmuramyl-L-alanine amidase activity	18541	4425
<i>amiB</i>	94.7	Amidase	Cell wall amidase (EC 3.5.1.28?); overexpression causes lysis, osmotic hypersensitivity, autolysis	34432	4489, 4490
<i>amn</i>	44.3	AMP nucleosidase	AMP nucleosidase (EC 3.2.2.4)	17764	2503, 2504
<i>ampC</i>	94.3	Ampicillin	<i>ampA</i> ; β-lactamase; penicillin resistance; affects peptidoglycan synthesis; cell morphology	1033	1116, 1117, 1167, 1540, 1541, 1713, 1993–1995, 3213, 796
<i>ampD</i>	2.6	Ampicillin	<i>ampC</i> regulation	30478	1794, 2561
<i>ampE</i>	2.6	Ampicillin	Ampicillin resistance; membrane protein	30481	1794, 2561

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>ampG</i>	9.7	Ampicillin	Ampicillin resistance; membrane protein	31027	2560
<i>ampH</i>	8.5	Ampicillin	Probable role in peptidoglycan, cell wall synthesis; cell morphology	51873	1713
<i>amtB</i>	10.2	Ammonia transport	Putative ammonia transporter	47403	4557
<i>amyA</i>	43.2	Amylase	α -amylase, cytoplasmic	30745	3581, 3582
<i>ansA</i>	39.9	Asparaginase	L-Asparaginase I; (EC 3.5.1.1)	1030	1005, 4167
<i>ansB</i>	66.8	Asparaginase	L-Asparaginase II; (EC 3.5.1.1)	30045	427, 2008
<i>apaG</i>	1.1	ad-P-ad	Expressed as part of complex <i>ksgA</i> operon	30310	3683, 380
<i>apaH</i>	1.1	ad-P-ad	Diadenosine tetraphosphatase; stress response; complex operon	17761	1205, 2034, 2509, 2861, 3683, 380
<i>aphA</i>	92.0	Acid phosphatase	Acid phosphatase/phosphotransferase, class B	45401	4390
<i>appA</i>	22.4	Acid (poly)phosphatase	Acid phosphatase, pH 2.5, exopolyphosphatase (EC 3.1.3.2, 3.6.1.11); <i>agp</i> homology; phytase P2	17758	1514, 432, 945, 946, 4446
<i>appB</i>	22.4	Acid (poly)phosphatase	<i>cyxB</i> ; cytochrome oxidase, putative additional one	31813	161, 947
<i>appC</i>	22.4	Acid (poly)phosphatase	<i>cyxA</i> ; cytochrome oxidase, putative additional one	31810	161, 947
<i>appY</i>	12.6	Acid (poly)phosphatase	Regulates <i>hya</i> and <i>appA</i> operons; induced by PO ₄ starvation and stationary phase	31146	160, 161, 162, 1786, 2195, 516
<i>apt</i>	10.6	ad-P transferase	Adenine phosphoribosyltransferase (EC 2.4.2.7); adenine salvage, AMP from PRPP + Ad	1029	1733, 1734, 577
<i>aqpZ</i>	19.7	Aquaporin	Aquaporin Z, bacterial water channel	40930	607, 608
<i>araA</i>	1.4	Arabinose	L-Arabinose isomerase (EC 5.3.1.4)	1028	2469
<i>araB</i>	1.5	Arabinose	Ribulokinase (EC 2.7.1.16)	1027	1102, 2169, 2469, 2470, 2970, 3247, 4110
<i>araC</i>	1.5	Arabinose	Regulatory gene: activator and repressor	1026	1102, 1158, 2169, 2300, 2470, 2971, 3247, 4018, 4110, 4237, 4642, 643, 651
<i>araD</i>	1.4	Arabinose	L-Ribulosephosphate 4-epimerase (EC 5.1.3.4)	1025	2469, 2949
<i>araE</i>	64.2	Arabinose	Low-affinity L-arabinose transport; L-arabinose proton symport	1024	2299, 2300, 2708, 2724, 4238
<i>araF</i>	42.7	Arabinose	L-Arabinose-binding protein	1023	2299, 2300, 2328, 3953, 3954, 758
<i>araG</i>	42.7	Arabinose	High-affinity L-arabinose transport	1022	2299, 2300, 2328, 3953
<i>araH</i>	42.7	Arabinose	High-affinity L-arabinose transport, membrane protein	18535	3953
<i>araJ</i>	8.8	Arabinose	Function unknown, arabinose inducible, not affecting Ara transport or utilization	29861	1716, 3636
<i>arcA</i>	100.0	Aerobic pathways control	<i>dye</i> , <i>fexA</i> , <i>msp</i> , <i>seg</i> , <i>sfzA</i> ; negative regulatory gene for aerobic path genes, anaerobic repression; activates <i>cydAB</i>	831	1089, 1955, 333, 4069, 587, 588, 689
<i>arcB</i>	72.2	Aerobic pathways control	Activates ArcA in response to anoxia; probable histidine kinase phosphorylating ArcA	29063	1953, 1956, 1958, 3886, 689
<i>argA</i>	63.5	Arginine	<i>Arg1</i> , <i>Arg2</i> , <i>argB</i> ; N-acetylglutamate synthase (EC 2.3.1.1); growth on acetylornithine; see <i>argE</i>	1021	1107, 3152, 3870, 528, 862
<i>argB</i>	89.5	Arginine	Acetylglutamate kinase (EC 2.7.2.8); see <i>argA</i>	1020	255, 3000, 3374, 862, 863
<i>argC</i>	89.5	Arginine	<i>Arg2</i> , <i>argH</i> ; N-acetyl- γ -glutamyl-phosphate reductase (EC 1.2.1.38)	1019	255, 3000, 311, 3374, 3433, 862, 863
<i>argD</i>	75.2	Arginine	<i>Arg1</i> , <i>argG</i> ; acetylornithine aminotransferase (EC 2.6.1.11); see <i>argF</i>	1018	2191, 315, 3676, 862
<i>argE</i>	89.5	Arginine	<i>Arg4</i> , <i>argA</i> ; acetylornithine deacetylase (EC 3.5.1.16); see <i>argG</i>	1017	2187, 255, 3000, 311, 3433, 863
<i>argF</i>	6.2	Arginine	<i>Arg5</i> , <i>argD</i> ; ornithine transcarbamylase (EC 2.1.3.3); see duplicate locus, <i>argI</i>	1016	1597, 1838, 2015, 2476, 2997, 2998, 3434, 4561, 4892, 863, 1717
<i>argG</i>	71.5	Arginine	<i>Arg6</i> , <i>argE</i> ; argininosuccinate synthetase (EC 6.3.4.5); see <i>argD</i>	1015	4560, 1717
<i>argH</i>	89.5	Arginine	Argininosuccinate lyase (EC 4.3.2.1); see <i>argC</i>	1014	255, 3000, 863, 1717
<i>argI</i>	96.5	Arginine	Ornithine transcarbamylase (EC 2.1.3.3); see <i>argF</i>	1013	295, 3434, 3729
<i>argM</i>	88.7	Arginine	Acetylornithine transaminase; cryptic gene; may be duplicate of <i>argD</i>	18532	3676
<i>argP</i>	65.9	Arginine	<i>iciA</i> (inhibitor of chromosome initiation); transport of arginine, ornithine, and lysine; canavanine sensitivity	1012	1614, 1871, 1873, 1874, 2474, 2691, 3427, 3733, 665, 4405

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>argQ</i>	60.7	Arginine	<i>Rarg</i> ; arginine tRNA ₂ tandem quadruple genes	2313	35604
<i>argR</i>	72.9	Arginine	<i>xerA</i> ; repressor of Arg regulon; <i>cer</i> -mediated site-specific recombination	1011	1114, 2187, 2481, 254, 2552, 2690, 315, 3399, 3427, 4225
<i>argS</i>	42.2	Arginine	<i>lov</i> ; arginyl-tRNA synthetase (EC 6.1.1.19);	1010	1164, 1772, 3147, 4590
<i>argT</i>	52.3	Arginine	<i>Salmonella</i> homolog codes for Lys-, Arg-, and Orn-binding proteins	18529	3211
<i>argU</i>	12.1	Arginine	<i>dnaY</i> , <i>pin</i> ; arginine tRNA ₄	17755	1285, 1360, 1415, 2313, 2563, 3888, 4140, 505, 696
<i>argV</i>	60.7	Arginine	<i>argV</i> α; arginine tRNA ₂ tandem quadruple genes	2313	11650
<i>argW</i>	53.1	Arginine	Arginine tRNA ₅	17752	2313
<i>argX</i>	85.8	Arginine	Arginine tRNA ₃	17749	1832, 2313, 926
<i>argY</i>	60.7	Arginine	<i>argV</i> β; arginine tRNA ₂ tandem quadruple genes	2313	35610
<i>argZ</i>	60.7	Arginine	<i>argV</i> γ; arginine tRNA ₂ tandem quadruple genes	2313	35607
<i>aroA</i>	20.7	Aromatic	3-Enolpyruvylshikimate-5-phosphate synthetase (EC 2.5.1.19)	1008	1098, 1099
<i>aroB</i>	75.8	Aromatic	3-Dehydroquinate synthase (EC 4.6.1.3)	1007	2937
<i>aroC</i>	52.7	Aromatic	Chorismate synthase (EC 4.6.1.4)	1006	683
<i>aroD</i>	38.2	Aromatic	3-Dehydroquinate dehydratase (EC 4.2.1.10)	1005	2240, 433
<i>aroE</i>	73.9	Aromatic	Dehydroshikimate reductase (EC 1.1.1.25)	1004	116, 2865
<i>aroF</i>	59.0	Aromatic	DAHP synthetase (tyrosine repressible) (EC 4.1.2.15)	1003	1371, 1847, 4047
<i>aroG</i>	16.9	Aromatic	DAHP synthetase (phenylalanine repressible) (EC 4.1.2.15); TyrR regulon	1002	1189, 1704, 1903, 2819, 958, 959
<i>aroH</i>	38.5	Aromatic	DAHP synthetase (tryptophan repressible) (EC 4.1.2.15)	1001	1100, 1848, 3030, 433, 4968, 958
<i>aroI</i>	84.2	Aromatic	Function unknown	1000	1422
<i>aroK</i>	75.8	Aromatic	Shikimate kinase I	30224	1516, 2604, 2605, 4586, 4719
<i>aroL</i>	8.7	Aromatic	Shikimate kinase II (EC 2.7.1.71)	999	2436, 2936, 4719, 998, 999
<i>aroM</i>	8.8	Aromatic	Function unknown; regulated by <i>aroR</i>	18523	998, 999
<i>aroP</i>	2.6	Aromatic	General aromatic amino acid transport; TyrR regulon	998	1553, 1556, 1558, 1657, 2131, 2415, 2416, 3689, 529, 755, 756, 83, 1795
<i>aroT</i>	28.3	Aromatic	<i>trpR</i> ; <i>aroR</i> ; indole acrylic acid resistant mutants; transport	997	4410
<i>arsB</i>	78.6	Arsenate resistance	<i>arsF</i> ; resistance to arsenate, arsenite, and antimonite	35996	1055, 4128, 600, 637
<i>arsC</i>	78.6	Arsenate resistance	<i>arsG</i> ; resistance to arsenate, arsenite, and antimonite	35999	1055, 4128, 600, 637
<i>arsR</i>	78.6	Arsenate resistance	<i>arsE</i> ; resistance to arsenate, arsenite, and antimonite	35993	1055, 4128, 4812, 600, 637
<i>artI</i>	19.4	Arginine transport	Periplasmic binding protein of Arg transport system	31674	4759, 4760
<i>artJ</i>	19.4	Arginine transport	Periplasmic binding protein of Arg transport system	31664	4759
<i>artM</i>	19.4	Arginine transport	Arg periplasmic transport system; similarity to transmembrane proteins, BPC ATPases	31667	4759, 4760
<i>artP</i>	19.4	Arginine transport	Arg periplasmic transport system; similarity to transmembrane proteins, BPC ATPases	31677	4759, 4760
<i>artQ</i>	19.4	Arginine transport	Arg periplasmic transport system; similarity to transmembrane proteins, BPC ATPases	31670	4759, 4760
<i>ascB</i>	61.2	Arbutin, salicin, cellobiose	<i>sac</i> ; cryptic; paralogous to cryptic <i>bglFB</i> ; expressed when <i>AscG</i> is mutated	33236	1606, 3365
<i>ascF</i>	61.2	Arbutin, salicin, cellobiose	<i>sac</i> ; cryptic; paralogous to cryptic <i>bglFB</i> ; expressed when <i>AscG</i> is mutated	33233	1606, 3365
<i>ascG</i>	61.1	Arbutin, salicin, cellobiose	Repressor of cryptic <i>asc</i> operon; <i>galR</i> paralog	33230	1606
<i>asd</i>	77.0	Aspartate semialdehyde deHase	<i>dap</i> , <i>hom</i> ; aspartate semialdehyde dehydrogenase (EC 1.2.1.11)	996	1679, 1680, 3281, 3940
<i>aslA</i>	85.8	Arylsulfatase-like	<i>gppB</i> ; suppresses <i>gpp</i> mutants	33957	3069
<i>aslB</i>	85.8	Arylsulfatase-like	<i>gppB</i> ; suppresses <i>gpp</i> mutants	33960	3069
<i>asmA</i>	46.1	Assembly suppressor mutant	Membrane protein; suppressor of <i>ompF</i> assembly mutants	41068	1021; 2957, 4811
<i>asnA</i>	84.6	Asparagine	Asparagine synthetase A (EC 6.3.1.1)	995	1769, 1861, 2295, 3111, 4610, 4621, 556
<i>asnB</i>	15.0	Asparagine	Asparagine synthetase B (EC 6.3.1.1)	994	1861, 3454, 3952
<i>asnC</i>	84.6	Asparagine	Regulatory gene for <i>asnA</i> , <i>asnC</i> , <i>gidA</i>	18520	1033, 2294, 556, 729

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>asnS</i>	21.3	Asparagine	<i>lcs, tss</i> ; asparaginyl-tRNA synthetase (EC 6.1.1.22)	993	1917, 4433
<i>asnT</i>	44.0	Asparagine	Asparagine tRNA	992	1285, 2313, 3324
<i>asnU</i>	44.4	Asparagine	Asparagine tRNA	17746	2313
<i>asnV</i>	44.4	Asparagine	Asparagine tRNA	17743	2313
<i>asnW</i>	44.3	Asparagine	Asparagine tRNA	51238	2313
<i>aspA</i>	94.1	Aspartate	Aspartate ammonia-lyase (aspartase) (EC 4.3.1.1)	991	1557, 4327
<i>aspC</i>	21.2	Aspartate	Aspartate aminotransferase (EC 2.6.1.1)	990	1283, 2317, 2373, 2740
<i>aspS</i>	42.0	Aspartate	<i>tls</i> ; aspartyl-tRNA synthetase	32508	1165, 1351, 4000
<i>aspT</i>	85.0	Aspartate	<i>tasC</i> ; aspartate tRNA ₁ triplicated gene	989	2313, 2777, 4904, 926
<i>aspU</i>	4.8	Aspartate	Aspartate tRNA ₁ triplicated gene, in <i>rmH</i> operon	988	1146, 2313, 2777
<i>aspV</i>	5.1	Aspartate	Aspartate tRNA ₁ triplicated gene	987	1806, 2313, 2777, 3324
<i>asr</i>	35.9	Acid shock RNA	Acid shock RNA; expression controlled by <i>phoBR</i>	53672	1986
<i>asu^e</i>	33.3	Asparagine utilization	Utilizes asparagine as sole nitrogen source	18517	723
<i>atoA</i>	50.1	Acetoacetate	Acetate CoA-transferase (EC 2.8.3.-)	986	2321
<i>atoB</i>	50.1	Acetoacetate	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	985	2005
<i>atoC</i>	50.0	Acetoacetate	Az; positive regulator in two-component system, with AtoS sensor kinase	984	395a, 1949a, 3985a, 2005, 2006, 3382, 3817, 629
<i>atoD</i>	50.0	Acetoacetate	Acetyl-CoA:acetoacetyl-CoA transferase β -subunit	18514	2005
<i>atoS</i>	50.0	Acetoacetate	AtoS sensor kinase, with AtoC response regulator in 2-component system	37061	395a, 1949a, 3985a
<i>atpA</i>	84.4	ATP	<i>papA, uncA</i> ; membrane-bound ATP synthase, F ₁ sector, α -subunit (EC 3.6.1.3)	33	1390, 1570, 2275, 4187, 4635
<i>atpB</i>	84.5	ATP	<i>papD, uncB</i> ; membrane-bound ATP synthase, F ₀ sector, subunit a (EC 3.6.1.3)	32	1570, 1830, 2993, 3180, 3860, 4609, 4635
<i>atpC</i>	84.3	ATP	<i>papG, uncC</i> ; membrane-bound ATP synthase, F ₁ sector, ϵ -subunit (EC 3.6.1.3)	31	1570, 4635, 4809, 4810
<i>atpD</i>	84.4	ATP	<i>papB, uncD</i> ; membrane-bound ATP synthase, F ₁ sector, β -subunit (EC 3.6.1.3)	30	1570, 3296, 4635
<i>atpE</i>	84.5	ATP	<i>papH, uncE</i> ; membrane-bound ATP synthase, F ₀ sector, subunit c; DCCD ⁻ (EC 3.6.1.3)	29	1570, 1992, 2836, 2993, 3860, 3900, 4635
<i>atpF</i>	84.5	ATP	<i>papF, uncF</i> ; membrane-bound ATP synthase, F ₀ sector, subunit b (EC 3.6.1.3)	28	1570, 2993, 4635
<i>atpG</i>	84.4	ATP	<i>papC, uncG</i> ; membrane-bound ATP synthase, F ₁ sector, γ -subunit (EC 3.6.1.3)	27	1570, 2275, 2692, 3860, 4635
<i>atpH</i>	84.4	ATP	<i>papE, uncH</i> ; membrane-bound ATP synthase, F ₁ sector, δ -subunit (EC 3.6.1.3)	26	1570, 2994, 3380, 4635
<i>atpI</i>	84.5	ATP	<i>uncI</i> ; membrane-bound ATP synthase subunit, F ₁ -F ₀ -type proton-ATPase (EC 3.6.1.34)	18511	1830, 2040, 2156, 3180, 3491, 4609, 4635, 544, 3923
<i>att186</i>	59.3	Attachment	Integration site for phage HK186	972	D
<i>att253</i>	6.1	Attachment	Integration site for phage HK253	18508	3484
<i>attHK139</i>	44.8	Attachment	Attachment site for phage HK139	981	1035
<i>attHK022</i>	22.7	Attachment	<i>autht</i> ; lambdaoid prophage HK022 attachment site	982	1034, 2301
<i>attλ</i>	17.3	Attachment	<i>att92, att434</i> ; lambda attachment site	980	1470, 18, 1035, 1836, 2940
<i>attP1,P7</i>	68.7	Attachment	<i>loxB</i> ; attachment site for phage P1 and P7	979	4205, 722
<i>attP22</i>	5.6	Attachment	<i>ata</i> ; phage P22 attachment site, within <i>thrW</i> gene	975	2562
<i>attP2H</i>	44.7	Attachment	Integration site H for phage P2	978	241a, 4291, D
<i>attP2II</i>	87.1	Attachment	Integration site II for phage P2	977	241a, 37, D
<i>attP2III</i>	83.5	Attachment	Integration site III for phage P2	32179	241a
<i>attP4</i>	96.9	Attachment	Integration site for phage P4	976	611, 3431
<i>attPA-2</i>	53.1	Attachment	Integration site for phage PA-2	974	C
<i>attϕ80</i>	28.2	Attachment	Integration site for phage phi80	973	3794a
<i>attTn7</i>	84.3	Attachment	Specific site for Tn7 insertion	37363	1520, 2852
<i>avtA</i>	80.6	Alanine-isoketoveralate transaminase	Alanine- α -ketoisovalerate transaminase, transaminase C	971	1196, 2585, 4656, 4718
<i>azaA</i>	44.6	Azaserine	Mutants azaserine resistant	970	4744
<i>azaB</i>	71.9	Azaserine	Mutants azaserine resistant	969	4744
<i>azl</i>	58.1	Azaleucine	Mutants azaleucine resistant; regulates <i>ilv</i> and <i>leu</i>	967	3452

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>bacA</i>	69.0	Bacitracin resistance	A lipid kinase; may confer resistance by phosphorylation of undecaprenol	29739	606
<i>baeR</i>	46.6	Bacterial adaptive <i>envZ</i> regulator	Suppresses <i>envZ</i> and <i>phoR/creC</i> mutations	30764	3083
<i>baeS</i>	46.6	Bacterial adaptive <i>envZ</i> regulator	Suppresses <i>envZ</i> and <i>phoR/creC</i> mutations	30761	3083
<i>barA</i>	62.8	Bacterial adaptive response	Has sensory kinase and response regulator domains like OmpR and EnvZ	33320	1924, 3084
<i>basR</i>	93.4	Bacterial adaptive sensor	BasRS two-component regulatory system homologous with OmpR-EnvZ family	28168	3083, 3716
<i>basS</i>	93.3	Bacterial adaptive sensor	BasRS two-component regulatory system homologous with OmpR-EnvZ family	28171	3083
<i>bax</i>	80.5		Gene transcribed divergently from <i>malS</i>	54736	3922
<i>bcp</i>	56.0	Bacterioferritin comigratory protein	Probable bacterioferritin	33035	112
<i>bcr</i>	49.1	Bicyclomycin resistance	<i>bicA</i> , <i>bicR</i> , <i>sur</i> , <i>suxA</i> ; transmembrane; affects sulfathiazole-sulfonamide resistance	32582	309
<i>betA</i>	7.0	Betaine	Choline dehydrogenase	17740	104, 2399, 4257, 470
<i>betB</i>	7.0	Betaine	Betaine aldehyde dehydrogenase (EC 1.2.1.8)	17737	104, 2399, 470
<i>betI</i>	7.1	Betaine	Regulatory gene, perhaps repressor for choline regulation of <i>bet</i> genes	30692	2399
<i>betT</i>	7.1	Betaine	High-affinity choline transport	18505	104, 2399
<i>bfd</i>	74.7	Bfr regulating	Regulatory or redox component complexing with Bfr in iron storage and mobility [2Fe-2S]	43017	1369
<i>bfm</i>	85.9	BF23 multiplication	Controls phage BF23 multiplication	966	A, 4041a
<i>bfr</i>	74.7	Bacterioferritin	Bacterioferritin	32528	111
<i>bglA</i>	65.6	β -Glucoside	<i>bglD</i> ; phospho- β -glucosidase A; growth on arbutin or salicin when activated	965	2076, 3239
<i>bglB</i>	84.1	β -Glucoside	<i>bglA</i> ; phospho- β -glucosidase B; growth on arbutin or salicin when activated	964	2718, 3528, 3658, 3924, 3925, 4611
<i>bglF</i>	84.1	β -Glucoside	<i>bglC</i> , <i>bglB</i> ; BglG kinase; transport	18502	2718, 3924, 476, 704
<i>bglG</i>	84.1	β -Glucoside	<i>bglC</i> , <i>bglS</i> ; positive regulatory gene, RNA-binding protein; regulated by phosphorylation	963	1818, 2718, 3658, 3659, 3924, 3825, 4077, 4506
<i>bglJ</i>	99.2	β -Glucoside	Mutation <i>bglJ4</i> activates silent <i>bgl</i> operon, allowing arbutin and salicin transport and utilization	45483	1424, 4506
<i>bglT</i>	84.9	β -Glucoside	<i>bglE</i> ; regulatory gene for BglA	961	3890
<i>bglX</i>	47.8	β -Glucoside	Periplasmic β -glucosidase (EC 3.2.1.21)	4858	48154
<i>bioA</i>	17.4	Biotin	Diaminopelargonic acid synthetase	959	18, 232, 2331, 235, 3312, 4246, 4319
<i>bioB</i>	17.4	Biotin	Biotin synthetase; dethiobiotin to biotin pathway	958	18, 232, 2331, 235, 3312, 4246, 4319
<i>bioC</i>	17.5	Biotin	Blocked prior to pimeloyl CoA formation	957	18, 2488, 4246, 4319
<i>bioD</i>	17.5	Biotin	Dethiobiotin synthetase	956	18, 2488, 4246, 4319, 4852
<i>bioF</i>	17.5	Biotin	7-Keto-8-aminopelargonic acid synthetase	955	18, 2488, 4246, 4319
<i>bioH</i>	76.3	Biotin	<i>bioB</i> ; blocked prior to pimeloyl CoA formation	954	232, 2488, 3303, 3940
<i>bioP</i>	86.6	Biotin	<i>bir</i> , <i>birB</i> ; biotin transport	953	1298, 624
<i>bipA</i>	87.4	BPI-induced protein	<i>yihK</i> ; in EPEC strains, it mediates interactions with epithelial cells; tyrosine-phosphorylated GTPase	37329	1206
<i>birA</i>	89.9	Biotin retention	<i>bioR</i> , <i>dhbB</i> ; biotin-[acetyl-CoA carboxylase] holoenzyme synthetase, and repressor	952	1825, 232–234, 2743, 3337, 4817, 624
<i>bisC</i>	80.0	Biotin sulfoxide	Biotin sulfoxide reductase, structural gene	951	1003, 3430
<i>bisZ</i>	42.1	Biotin sulfoxide	Responsible for background activity of biotin sulfoxide reductase in <i>bisC</i> mutants	50496	1004
<i>blc</i>	94.3	Bacterial lipocalin	Membrane protein, first prokaryotic lipocalin; cell division and growth, <i>rpoS</i> regulon; shares translation termination codons with <i>sugE</i>	40887	361
<i>bolA</i>	9.8	Bolus	Morphogene; overexpression produces osmotically stable spherical cells; FtsZ dependent	31032	2413, 55–57
<i>brnQ</i>	9.0	Branched chain	<i>hrbA</i> ; mutants valine and <i>o</i> -methylthreonine resistant, glycylvaline sensitive; transport system I for Ile, Leu, and Val	950	1542, 1543
<i>brnR</i>	8.5	Branched chain	Mutants valine resistant, glycylvaline sensitive	949	1542
<i>brnS</i>	1.2	Branched chain	Mutants valine resistant, glycylvaline sensitive	948	1542

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>brnT</i>	65.2	Branched chain	Low-affinity transport of Ile	947	1876a
<i>btuB</i>	89.7	B12 uptake	<i>bfe</i> , <i>cer</i> ; receptor for vitamin B ₁₂ , E colicins, and phage BF23; also C1 phage absorption	946	1545, 1546, 166, 167, 1705, 1850, 2082, 2430, 2546, 3000, 585
<i>btuC</i>	38.6	B12 uptake	Vitamin B ₁₂ transport	945	1029, 1031, 1315
<i>btuD</i>	38.6	B12 uptake	B ₁₂ transport, membrane associated	18499	1029, 1031, 1315
<i>btuE</i>	38.6	B12 uptake	Not required for vitamin B ₁₂ transport, perhaps periplasmic protein	18496	1029, 1315, 3679
<i>btuR</i>	28.6	B12 uptake	Regulatory gene affecting <i>btuB</i>	18493	2667
<i>bymA</i>	93.2	Bypass maltose	Growth on maltose in MalT ⁻ cells	944	1781
<i>cadA</i>	93.9	Cadaverine	Lysine decarboxylase (EC 4.1.1.18)	943	168, 169, 2886, 2887, 3144, 4022, 4325, 4680
<i>cadB</i>	93.9	Cadaverine	Arginine/ornithine antiporter, probably	34228	2886, 3144, 4680
<i>cadC</i>	93.9	Cadaverine	Regulatory gene	34231	2887, 3144, 4680
<i>cafA</i>	73.2	Cytoplasmic axial filaments	Cell division and growth, overexpression forms minicells and chains with long axial structures	31358	3278
<i>caiA</i>	0.8	Carnitine inducible	Carnitine metabolism, oxidoreductase	36825	1134, 550
<i>caiB</i>	0.8	Carnitine inducible	Carnitine dehydratase	36800	1135, 550
<i>caiC</i>	0.8	Carnitine inducible	Crotonobetain/carnitine-CoA ligase	36828	1134, 550
<i>caiD</i>	0.8	Carnitine inducible	Putative enoyl hydratase/isomerase with carnitine racemase activity	36831	1134, 550
<i>caiE</i>	0.8	Carnitine inducible	Stimulates carnitine racemase activity of CaiD and CaiB activity	36834	1134, 550
<i>caiF</i>	0.7	Carnitine inducible	Regulatory gene; transcriptional activation of <i>cai</i> operon	42995	1133, 550
<i>caiT</i>	0.9	Carnitine inducible	Putative carnitine/betaine transport	36822	1134, 550
<i>calA</i>	95.0	Calcium	Calcium-proton antiport activity	941	4417, 499
<i>calC</i>	15.2	Calcium	Calcium transport; mutants defective in chemotaxis	940	4417, 499
<i>calD</i>	9.4	Calcium	Calcium transport; mutants defective in chemotaxis	939	4417, 499
<i>can</i>	66.0	Canavanine	Resistance to canavanine	938	A, 2691a
<i>carA</i>	0.6	Carbamoyl P	<i>arg+ura</i> , <i>cap</i> , <i>pyrA</i> ; carbamoylphosphate synthase (glutamine-hydrolysing) light subunit (EC 6.3.5.5)	936	1427, 3432, 465, 861
<i>carB</i>	0.7	Carbamoyl P	<i>arg+ura</i> , <i>cap</i> , <i>pyrA</i> ; carbamoylphosphate synthase (ammonia), heavy subunit (EC 6.3.4.16)	935	1427, 3234, 861
<i>cbl</i>	44.4	<i>cysB</i> -like	<i>cys</i> regulon member; perhaps an accessory regulatory circuit within the <i>cys</i> regulon	50175	1964, 4550
<i>cbpA</i>	22.9	Curved-DNA binding protein	Recognizes a curved DNA sequence; sequence similarity to DnaJ	31822	4505
<i>cbt</i>	16.6	Colicin B (and D) tolerance	Dicarboxylate binding protein production; ColB and ColD tolerance	934	334
<i>cca</i>	69.0	CCA tRNA terminus	tRNA nucleotidyl transferase	933	880
<i>ccmA</i>	49.5	Cytochrome <i>c</i> maturation	ABC transporter, ATPase subunit	36574	1537, 4406, 4411, 739, 740
<i>ccmB</i>	49.5	Cytochrome <i>c</i> maturation	ABC transporter, ATPase subunit	36577	1537, 4406, 4411, 739, 740
<i>ccmC</i>	49.4	Cytochrome <i>c</i> maturation	ABC transporter, heme binding	36581	1537, 4406, 4411, 739, 740
<i>ccmD</i>	49.4	Cytochrome <i>c</i> maturation	Cytochrome <i>c</i> related	36584	1537, 4406, 739, 740
<i>ccmE</i>	49.4	Cytochrome <i>c</i> maturation	Cytochrome <i>c</i> related	36587	1537, 4406, 739, 740
<i>ccmF</i>	49.4	Cytochrome <i>c</i> maturation	Required for synthesis of <i>c</i> -type cytochromes; similarity with NrfE	36590	1536, 1537, 4406, 4411, 739, 740
<i>ccmG</i>	49.4	Cytochrome <i>c</i> maturation	<i>dsbE</i> ; thioredoxin homolog; thiol-disulfide interchange protein	36594	1192, 1537, 4406, 4411, 739, 740
<i>ccmH</i>	49.3	Cytochrome <i>c</i> maturation	Required for synthesis of <i>c</i> -type cytochromes; similarity with NrfF and NrfG	36597	1536, 1537, 4406, 739, 740
<i>cdd</i>	48.1	Deoxycytidine deaminase	Deoxycytidine deaminase (EC 3.5.4.5); mutants 5-fluorodeoxycytidine resistant	932	1075, 2057, 2058, 2925, 3241, 429, 4325, 4851
<i>cde</i>	14.2	Control of <i>dam</i> expression	Affects growth rate control of <i>dam</i> expression; near or within <i>lipB</i>	37102	3616
<i>cdh</i>	88.5	CDP diglyceride hydrolase	CDP-diglyceride hydrolase	931	1710, 1884, 51, 559, 560
<i>cdsA</i>	4.2	CDP diglyceride synthase	CDP-diglyceride synthase	930	1356, 1886
<i>cdsS</i>	71.7	CDP diglyceride synthase	Stability of CDP diglyceride synthase	18490	1355
<i>cedA</i>	39.1	Cell division	Modulates cell division, affects inhibition after overreplication of chromosome in <i>dnaAcos</i> mutants	55374	2161

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>celA</i>	39.2	Cellobiose	<i>chbB</i> ; member of cryptic <i>cel</i> operon	34873	2205, 3366
<i>celB</i>	39.2	Cellobiose	<i>chbC</i> ; phosphotransferase system enzyme II _{cel} , PEP dependent; cryptic operon; cellobiose, arbutin, and salicin transport	18487	2205, 2340, 2341, 3366, 3647
<i>celC</i>	39.2	Cellobiose	<i>chbA</i> ; phosphotransferase system enzyme III _{cel} , PEP dependent; cryptic operon; cellobiose, arbutin, and salicin transport	18484	2205, 2340, 2341, 3366, 3547
<i>celD</i>	39.2	Cellobiose	<i>chbR</i> ; Cel regulatory protein	18481	2205, 2340, 2341, 3366
<i>celF</i>	39.1	Cellobiose	<i>chbF</i> ; phospho-β-glucosidase B; cryptic operon	17734	2205, 2340, 2341, 3366
<i>cfa</i>	37.5	Cyclopropane fatty acid	<i>cdfA</i> ; cyclopropane fatty acid synthase	10810	1527, 1528, 1529, 4649
<i>cfcA</i>	79.9	Control frequency of cell division	Controls cell division frequency per round of DNA replication	36615	3194
<i>chaA</i>	27.4	Ca ²⁺ /H ⁺ antiporter	Ca ²⁺ /H ⁺ antiporter	30293	1961, 3271, 3330
<i>chaB</i>	27.4	Ca ²⁺ /H ⁺ antiporter	Accessory and regulatory protein for <i>chaA</i>	37193	4792a
<i>chaC</i>	27.4	Ca ²⁺ /H ⁺ antiporter	Accessory and regulatory protein for <i>chaA</i>	37196	4792a
<i>cheA</i>	42.5	Chemotaxis	Autophosphorylating histidine kinase of chemotactic response; clockwise and counterclockwise signals; Fla regulon	928	2285, 2679, 3757, 3830, 4064, 4101, 4119, 4363, 4652, 84
<i>cheB</i>	42.4	Chemotaxis	Protein methylesterase; flagellar regulon member	927	2349, 3076, 4101, 4214, 468, 923
<i>cheR</i>	42.4	Chemotaxis	<i>cheX</i> ; protein methyltransferase (in chemotactic response); flagellar regulon	926	2951, 3076, 4101, 468
<i>cheW</i>	42.5	Chemotaxis	Signal transduction; couples CheA to chemoreceptor control by promoting CheW/CheA/Tsr; flagellar regulon	925	3076, 3757, 4064, 4101
<i>cheY</i>	42.4	Chemotaxis	Response regulator CheY for chemotactic signal transduction; flagellar regulon member	924	2679, 2809, 3076, 3757, 3857, 4046, 4101, 468, 776
<i>cheZ</i>	42.3	Chemotaxis	Chemotactic signal transduction; flagellar regulon member	923	3076, 3856, 3857, 4101, 468
<i>chpA</i>	62.7	Chromosomal homolog of <i>pem</i>	<i>chpAK</i> , <i>mazF</i> ; ChpAB growth inhibitor, homology to R100 <i>pemK</i> gene, programmed cell death? toxic protein	33287	2794, 35
<i>chpB</i>	95.8	Chromosomal homolog of <i>pem</i>	<i>chpBK</i> , <i>yjfB</i> ; ChpAB growth inhibitor, homology to <i>pemK</i>	33290	2793, 2794
<i>chpR</i>	62.7	Chromosomal homolog of <i>pem</i>	<i>chpAI</i> , <i>mazE</i> ; homology to R100 <i>pemI</i> , which suppresses <i>pemK</i> ; suppresses ChpA inhibition	33283	2794, 35
<i>chpS</i>	95.8	Chromosomal homolog of <i>pem</i>	<i>chpBI</i> , <i>yjfA</i> ; homology to <i>pemI</i> ; suppresses ChpB	33293	2793, 2794
<i>cirA</i>	48.3	Colicin I resistance/receptor	<i>feuA</i> ; colicin I receptor production	916	1518, 2925, 428, 4783
<i>citA</i>	17.9	Citrate	Cryptic gene for citrate transport system	18469	1604
<i>citB</i>	16.0	Citrate	Cryptic gene for citrate transport system	18466	1604
<i>clid</i>	45.2	Chain length determination	<i>rol</i> ; regulator of lipopolysaccharide O-chain length; gene studied in <i>Salmonella</i> and non-K-12 strains	56819	1061a, 1293a
<i>clpA</i>	19.9	Caseinolytic protease	Clp ATP-dependent protease, ATP-binding subunit	31293	1472, 3972, 3973, 3990
<i>clpB</i>	58.8	Caseinolytic protease	ClpB protease, ATP dependent (EC 1.17.4.-, 3.4.21.-)	32875	1327, 2244, 3359, 3478, 4178, 4772
<i>clpP</i>	9.8	Caseinolytic protease	F21.5, LopP; ClpP ATP-dependent protease proteolytic subunit	31280	2344, 2822, 2824, 3973, 4765
<i>clpX</i>	9.8	Caseinolytic protease	LopC; ClpX protease, which activates ClpP	31287	1297, 1473, 2505, 4765, 4891
<i>cls</i>	28.1	Cardiolipin synthase	<i>nov</i> ; cardiolipin synthase; mutants dihydroxybutylphosphonate resistant; novobiocin sensitivity	915	1690, 1765, 1766, 1876, 1960, 3193, 3267, 3600, 4462, 4463
<i>cmk</i>	20.7	CMP kinase	<i>mssA</i> ; multicopy suppressor; CMP kinase	31736	1308, 4843
<i>cmlA</i>	19.0	Chloramphenicol	Probably same as <i>cmr</i> ; resistance or sensitivity to chloramphenicol, also tetracycline resistance	914	187, 3637, 4043
<i>cmr</i>	19.0	Chloramphenicol resistance	<i>cmlA?</i> , <i>mdfA</i> ; transmembrane multidrug/chloramphenicol efflux transporter	55066	1115, 3189, 3637
<i>cmtA</i>	66.3	Cryptic mannitol	Similar to mannitol phosphotransferase enzymes	33362	4163
<i>cmtB</i>	66.3	Cryptic mannitol	<i>tolM</i> ; protein-Nπ-phosphohistidine sugar P-transferase; enzyme III of PEP-PTS cryptic mannitol transport	33365	4163
<i>coaA</i>	89.9	CoA	<i>panK</i> , <i>ris</i> ; pantothenate kinase	17731	1259, 4134, 4135, 4538
<i>cobS</i>	44.5	Cobalamin, coenzyme B12	Partial cobalamin biosynthesis pathway present in <i>E. coli</i>	40912	2439

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>cobT</i>	44.4	Cobalamin, coenzyme B12	Partial cobalamin biosynthesis pathway present in <i>E. coli</i>	40908	2439
<i>cobU</i>	44.5	Cobalamin, coenzyme B12	Partial cobalamin biosynthesis pathway present in <i>E. coli</i>	40916	2439
<i>codA</i>	7.7	Cytosine deaminase	Cytosine deaminase (EC 3.5.4.1)	913	23, 4562, 927, 95
<i>codB</i>	7.6	Cytosine deaminase	Cytosine transport	912	23, 927, 95
<i>cof</i>	10.1	Complementation of <i>fur</i>	Complements deletion mutant for growth on succinate	53227	1640
<i>cog</i>	29.1	Control of <i>ompG</i>	Probable repressor of <i>ompG</i>	37297	2956
<i>corA</i>	86.2	Cobalt resistance	Mg ²⁺ transport system; mutants resistant to Co ²⁺ , Mn ²⁺ , and Ni ²⁺ , insensitive to Ca ²⁺	911	2750, 3242, 3243, 3353, 4120, 4683, 58, 926
CP4-57	59.4	Cryptic prophage	Cryptic prophage; see <i>intA</i> and <i>alpA</i>	33089	2241, 3653
<i>cpdA</i>	68.4	Cyclic nucleotide P-diesterase	<i>icc</i> ; affects cAMP requirement during growth on maltose; 3',5' cAMP phosphodiesterase	37437	1907
<i>cpdB</i>	95.5	Cyclic nucleotide P-diesterase	2',3'-Cyclic nucleotide 2'-phosphodiesterase (EC 3.1.4.16)	909	1996, 2580, 259
<i>cpsA</i>	45.4	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	18463	4460
<i>cpsB</i>	45.7	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis; mannose 1-P guanyltransferase	18460	4460
<i>cpsC</i>	45.8	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	18457	4460
<i>cpsD</i>	45.8	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	18454	4460
<i>cpsE</i>	45.8	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	51241	4460
<i>cpsF</i>	90.2	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	18448	4460
<i>cpsG</i>	45.7	Capsular polysaccharide synthesis	Phosphomannomutase isozyme; colanic acid biosynthesis	37429	1999
<i>cpxA</i>	88.4	Conjugative plasmid expression	<i>ecfB</i> , <i>eup</i> , <i>ssd</i> ; membrane sensor in two-component <i>cpxAR</i> signal transduction system; Kan ^r , phage Q resistant; L-serine growth	908	1952, 2844, 2845, 3011, 3166, 3448, 3595, 3596, 4066–4068, 4408, 4684, 50, 52, 843
<i>cpxB</i>	41.3	Conjugative plasmid expression	Phage Q resistance, membrane protein	907	2844, 2845, 4066
<i>cpxP</i>	88.4	Conjugative plasmid expression	Periplasmic protein, CpxA/R activated, induced in alkaline pH; suppresses toxic envelope protein effects	54751	922
<i>cpxR</i>	88.4	Conjugative plasmid expression	Regulator in two-component <i>cpxAR</i>	34166	1065, 3596, 843
<i>crcA</i>	14.1	Camphor resistance and chromosome condensation	High-copy <i>crc-csp</i> restores normal chromosome condensation in presence of camphor or <i>mukB</i> mutations	41127	1837
<i>crcB</i>	14.2	Camphor resistance and chromosome condensation	See <i>crcA</i>	41131	1837
<i>creA</i>	99.9	Catabolite regulation	Function unknown; transcribed with <i>cre</i> operon	34809	81
<i>creB</i>	99.9	Catabolite regulation	<i>phoM-orf2</i> ; structurally homologous to <i>creC</i> (<i>phoM</i>)	34803	81, 82
<i>creC</i>	99.9	Catabolite regulation	<i>phoM</i> ; sensor in Pho regulon	395	2654, 2733, 2734, 4431, 4660, 4661, 4664, 4666, 4667, 81
<i>creD</i>	99.9	Catabolite regulation	<i>cet</i> (colicin E2 tolerance), <i>refII</i>	929	1090, 1284, 1462, 1568, 81
<i>crg</i>	28.8	Cold resistant growth	Allows cold-resistant growth	18445	2175
<i>crl</i>	5.6	Curli	Regulatory protein for curli (cryptic <i>csgA</i>)	30625	137, 1722, 3291, 3545
<i>crp</i>	75.1	cAMP receptor protein	<i>cap</i> , <i>csm</i> ; cAMP receptor protein	906	1404, 147, 1559, 2233, 2365, 258, 2627, 32, 3610, 3279, 3559, 3617, 4108, 4394, 500, 8, 844, 924
<i>crr</i>	54.6	Carrier?	<i>gsr</i> , <i>iex</i> , <i>tgs</i> ; phosphocarrier protein for glucose of the PTS; III _{glc}	905	1023, 2326, 2859, 3150, 3369, 3370, 3793, 508, 539, 557, 562, 982, 983b
<i>csdA</i>	63.4	Cysteine, selenocysteine decomposition	Cysteine sulfinate desulfinate	52073	2926
<i>csgA</i>	23.8	Curlin σ^S -dependent growth	Curlin, σ^S (stationary phase) dependent, cryptic	30620	137, 138, 1619, 2612, 3289–3291, 3725, 4584
<i>csgB</i>	23.8	Curlin σ^S -dependent growth	Curlin nucleator protein, homology with major curlin, CsgA	36735	138, 2612, 3725

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>csgD</i>	23.7	Curlin σ^S -dependent growth	<i>csgD</i> insertions eliminate σ^S -dependent transcription from <i>csgBA</i> promoter	50655	1619, 3725
<i>csgE</i>	23.7	Curlin σ^S -dependent growth	Possible secretion or assembly protein for bacterial fibers	50658	1619, 3725
<i>csgF</i>	23.7	Curlin σ^S -dependent growth	Possible assembly or transport protein for curli	50661	1619
<i>csgG</i>	23.7	Curlin σ^S -dependent growth	Possible assembly or transport protein for curli; novel lipoprotein	50664	1619, 2612, 3725
<i>csiA</i>	85.3	Carbon starvation induced	Stationary phase inducible protein	36892	4690
<i>csiB</i>	17.4	Carbon starvation induced	Stationary phase inducible protein	36895	4690
<i>csiC</i>	66.0	Carbon starvation induced	Stationary phase inducible protein	36898	4690
<i>csiD</i>	60.5	Carbon starvation induced	Stationary phase inducible protein	36904	2775, 4690
<i>csiE</i>	57.4	Carbon starvation induced	Stationary phase inducible protein	36901	2774, 4690
<i>csiF</i>	8.6	Carbon starvation induced	Stationary phase inducible protein	36998	4690
<i>cspA</i>	80.1	Cold shock protein	Cold shock protein CS7.4; similar to Y-box DNA binding proteins of eukaryotes; transcription factor	29540	1199, 1200, 1443, 1452, 194, 2019, 2046, 2473, 478, 4841a, 4347
<i>cspB</i>	35.3	Cold shock protein	Cold shock protein with similarity to CspA	32231	1200, 2473
<i>cspC</i>	41.1	Cold shock protein	<i>msmB</i> ; multicopy suppresses <i>mukB</i> mutants	35339	2043, 2473, 4842
<i>cspD</i>	19.9	Cold shock protein	Similarity to CspA but not cold shock induced	31688	2473, 4841
<i>cspE</i>	14.2	Cold shock protein	<i>msmC</i> ; with <i>crcAB</i> , high copy promotes or protects chromosome condensation	31528	1837, 4841, 4842
<i>cspG</i>	12.6	Cold shock protein	Cold-induced CspA/B analog	53423	194, 3119
<i>csrA</i>	60.7	Carbon storage regulator	<i>zfiA</i> , regulatory gene inhibiting glycogen biosynthesis; global regulatory protein	34504	2586, 3061, 3723, 3724, 3787, 4854
<i>csrB</i>	62.9	Carbon storage regulator	CsrA-binding RNA, antagonizing CsrA regulation		2585a
<i>cstA</i>	13.5	Carbon starvation	Starvation induced stress response protein	31179	1523, 2798, 3937, 403
<i>cstC^b</i>	39.4	Carbon starvation	<i>astC</i> ; starvation gene regulated by cAMP and RpoS, T; induced by ornithine; arginine succinyltransferase	54626	1290a, 1290b, 1950a, 3921a
<i>cup</i>	97.0	Carbohydrate uptake	Mutants have defective carbohydrate uptake	18442	2720
<i>cutA</i>	94.0	Cu tolerance	<i>cycY</i> , <i>cutA1</i> ; copper sensitivity; possible role in cytochrome <i>c</i> maturation; cytochrome <i>c</i> -like	34216	1271, 1921, 875
<i>cutC</i>	42.2	Cu tolerance	Copper sensitivity	36974	1574
<i>cutE</i>	14.8	Cu tolerance	<i>lnt</i> ; copper sensitivity; apolipoprotein <i>N</i> -acetyltransferase	31471	3710
<i>cutF</i>	4.6	Cu tolerance	<i>nlpE</i> ; copper sensitivity	35748	1574, 4122
<i>cvpA</i>	52.3	Colicin V production	<i>dedE</i> ; member of <i>purF</i> operon; affects Col V production	32727	1207
<i>cxm</i>	6.3	Carbon-xylose metabolism	<i>cxr</i> ; methyl glyoxal synthesis; D-xylose utilization	903	8
<i>cyaA</i>	86.0	Cyclase, adenylate	Adenylate cyclase (EC 4.6.1.1)	902	1008, 219, 2233, 2275, 2321, 2365, 26, 29, 30, 3559, 3758, 3759, 3760, 4401, 500, 58, 924, 926
<i>cybB</i>	32.1	Cytochrome <i>b</i>	Cytochrome <i>b</i> ₅₆₁	17728	3052, 3054, 3105
<i>cybC</i>	96.1	Cytochrome <i>b</i>	Cytochrome <i>b</i> ₅₆₂	34583	4465
<i>cycA</i>	95.4	Cycloserine	<i>dagA</i> ; D-alanine, D-serine, glycine permease	900	3685, 3686, 3939, 4671, 569
<i>cydA</i>	16.6	Cytochrome <i>d</i>	Cytochrome <i>d</i> terminal oxidase, polypeptide subunit I	10369	1060, 1447, 1491, 1492, 1493, 1494, 3039, 3611, 615, 847
<i>cydB</i>	16.6	Cytochrome <i>d</i>	Cytochrome <i>d</i> terminal oxidase, polypeptide subunit II	9469	1009, 1010, 1011, 1060, 1447, 1491, 1492, 1494, 1495, 3039, 3611, 4638, 615, 847
<i>cydC</i>	20.0	Cytochrome <i>d</i>	<i>mdrA</i> , <i>mdrH</i> , <i>surB</i> ; cytochrome <i>d</i> terminal oxidase, possibly heme d component	17725	1009, 1405, 1447, 3763, 4054, 4055
<i>cydD</i>	20.0	Cytochrome <i>d</i>	ATP-binding cassette membrane transporter; bd-type oxidase	31720	1009, 1447, 262, 3479–3481
<i>cynR</i>	7.7	Cyanase; cyanate metabolism	Transcriptional activator of <i>cyn</i> operon	31255	102, 2403, 4288
<i>cynS</i>	7.7	Cyanase; cyanate metabolism	Cyanate aminohydrolase (EC 3.5.5.3)	15267	102, 1564, 1565, 2403, 4286, 4288, 4289
<i>cynT</i>	7.7	Cyanase; cyanate metabolism	Carbonic anhydrase	31258	102, 1564, 1566, 2333, 4286, 4287, 4289
<i>cynX</i>	7.7	Cyanase; cyanate metabolism	Apparent hydrophobic protein, member of <i>cyn</i> operon	31261	102, 1564
<i>cyoA</i>	9.7	Cytochrome <i>o</i> oxidase	Cytochrome <i>o</i> oxidase subunit II; cytochrome <i>bo</i> ₃ ubiquinol oxidase subunit II	18439	164, 165, 2687, 615
<i>cyoB</i>	9.7	Cytochrome <i>o</i> oxidase	Cytochrome <i>o</i> oxidase subunit I	30997	164, 3106, 615

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>cyoC</i>	9.6	Cytochrome <i>o</i> oxidase	Cytochrome <i>o</i> oxidase subunit III	31005	164, 615, 720, 721
<i>cyoD</i>	9.6	Cytochrome <i>o</i> oxidase	Cytochrome <i>o</i> oxidase subunit IV	31008	164, 615, 720
<i>cyoE</i>	9.6	Cytochrome <i>o</i> oxidase	Cytochrome <i>o</i> oxidase subunit, protoheme IX farnesyltransferase	31014	164, 3799, 615, 720, 721
<i>cysA</i>	54.7	Cysteine	Sulfate permease; chromate resistance	898	3793, 4082, 4172, 47, 539
<i>cysB</i>	28.7	Cysteine	Positive regulator for <i>cys</i> regulon	897	1980, 3310, 4382
<i>cysC</i>	61.9	Cysteine	Adenylylsulfate kinase (EC 2.7.1.25)	896	2520, 3879, 4380
<i>cysD</i>	61.9	Cysteine	Sulfate adenylyltransferase (EC 2.7.7.4)	895	1862, 2742, 4380
<i>cysE</i>	81.5	Cysteine	Serine acetyltransferase (EC 2.3.1.30)	894	1021, 4381
<i>cysG</i>	75.3	Cysteine	Uroporphyrinogen III methyltransferase; transcribed from <i>nirB</i> operon and <i>cysG</i> promoters	893	1647, 1973, 2693, 2694, 3386, 3387, 4148, 4380, 792
<i>cysH</i>	62.2	Cysteine	Adenylylsulfate reductase (EC 1.8.99.2)	892	1862, 2345, 2346, 2522, 4380
<i>cysI</i>	62.2	Cysteine	<i>cysQ</i> ; sulfite reductase, α -subunit (EC 1.8.1.2)	891	1175, 1862, 2522, 4380, 4795
<i>cysJ</i>	62.3	Cysteine	<i>cysP</i> ; sulfite reductase, β -subunit (EC 1.8.1.2)	890	1175, 1862, 2522, 2637, 4380, 4795
<i>cysK</i>	54.5	Cysteine	<i>cysZ</i> ; cysteine synthase (EC 4.2.99.8); homodimer; selenate resistance, azaserine resistance	889	1247, 3370, 3793, 4082, 438, 47, 4731, 508, 539
<i>cysM</i>	54.7	Cysteine	<i>o</i> -Acetylserine sulfhydrylase B (EC 4.2.99.8)	17722	3793, 4082, 47, 539
<i>cysN</i>	61.9	Cysteine	ATP sulfurylase (ATP:sulfate adenylyltransferase)	18436	2520
<i>cysP</i>	54.8	Cysteine	Periplasmic sulfate binding protein; see <i>cysJ</i>	27367	1828, 4081
<i>cysQ</i>	95.6	Cysteine	<i>amt</i> , <i>amtA</i> ; requirement for sulfite or cysteine during aerobic growth; see also <i>cysI</i>	34409	1193, 1996, 1997, 3159
<i>cysS</i>	11.9	Cysteine	CysteinyI-tRNA synthetase (EC 6.1.1.16)	888	176, 413, 1816
<i>cysT</i>	42.9	Cysteine	Cysteine tRNA; see also <i>cysU</i>	17719	1285, 2313
<i>cysU</i>	54.7	Cysteine	Cysteine transport system; may also transport molybdate (see <i>mod</i>)	37093	4081
<i>cysW</i>	54.7	Cysteine	Membrane-bound sulfate transport protein; may also transport molybdate (see <i>mod</i>)	27371	4081
<i>cysX</i>	81.5	Cysteine	Reading frame in opposite orientation within <i>cysE</i> gene; polypeptide synthesized in maxicells	55332	4381
<i>cysZ</i>	54.5	Cysteine	putative; ORF upstream of <i>cysK</i> may be <i>cysZ</i>	33018	593
<i>cytR</i>	88.8	Cytosine resistant?	Regulatory gene for <i>deo</i> , <i>udp</i> , and <i>cdd</i> ; mutants show improved growth on uridine	887	226, 3048, 3617, 4128, 4529
<i>dacA</i>	14.3	D-Alanine carboxypeptidase	<i>pfv</i> ; D-alanine carboxypeptidase IA (EC 3.4.12.11); penicillin-binding protein; deletion suppresses <i>ftsK</i> mutant block	886	2801, 2802, 3198, 3360, 4157, 4232, 520
<i>dacB</i>	71.7	D-Alanine carboxypeptidase	D-Alanine carboxypeptidase IB; penicillin-binding protein (EC 3.4.12.11)	885	2322, 2803, 3021, 3022, 4075, 4337
<i>dacC</i>	19.0	D-Alanine carboxypeptidase	Penicillin-binding protein 6 (EC 3.4.17.8)	34706	276, 3421, 520
<i>dacD</i>	44.8	D-Alanine carboxypeptidase	<i>phsE</i> ? Penicillin-binding protein 6b	50486	223
<i>dadA</i>	26.7	D-Amino acid dehydrogenase	<i>dadR</i> ; D-amino acid dehydrogenase subunit	884	2357, 2607, 2797, 4736, 4737, 4739, 4740
<i>dadB</i>	1.6	D-Amino acid dehydrogenase	<i>alnA</i> ; D-amino acid dehydrogenase subunit	883	1298
<i>dadQ</i>	98.9	D-Amino acid dehydrogenase	<i>alnR</i> ; regulator of <i>dad</i> regulon	882	1298
<i>dadX</i>	26.7	D-Amino acid dehydrogenase	<i>msuA</i> ? alanine racemase (EC 5.1.1.1)	17716	1526, 2607, 2797, 4739
<i>dam</i>	75.7	DNA adenine methylase	DNA adenine methylase	881	145, 1609, 2851, 3411, 518
<i>dapA</i>	56.0	Diaminopimelate (lysine path)	Dihydrodipicolinate synthase (EC 4.2.1.52)	880	3667
<i>dapB</i>	0.6	Diaminopimelate (lysine path)	Dihydrodipicolinate reductase (EC 1.3.1.26); see <i>dapE</i> and <i>lspA</i>	879	2699, 464
<i>dapC</i>	3.9	Diaminopimelate (lysine path)	Tetrahydrodipicolinate succinylase	878	1359, 558
<i>dapD</i>	4.0	Diaminopimelate (lysine path)	Succinyl-diaminopimelate aminotransferase	877	1000, 1359, 296, 3665
<i>dapE</i>	55.8	Diaminopimelate (lysine path)	<i>dapB</i> ; <i>N</i> -succinyl-diaminopimelate deacylase	876	3364, 3667
<i>dapF</i>	86.1	Diaminopimelate (lysine path)	Diaminopimelate epimerase	17713	3664, 3666, 926
<i>dbpA</i>	30.3	DNA binding protein	Binds DNA, RNA, only hydrolyses ATP in presence of 23S rRNA	32058	1337, 3177
<i>dcd</i>	46.1	dCTP deaminase	<i>paxA</i> ; dCTP deaminase (EC 3.5.4.13); mutants suppress lethal <i>dut</i> mutants	875	1180, 3156, 4655
<i>dcm</i>	43.7	DNA cytosine methylation	<i>mec</i> ; DNA cytosine methylase; internal cytosine methylated	874	1314, 1625, 337
<i>dcp</i>	35.0	Dipeptidyl carboxypeptidase	Dipeptidyl carboxypeptidase II (EC 3.4.15.1)	873	1027, 1723, 269
<i>dcrB</i>	77.8	C resistance	Resistant to lytic phage C1; periplasmic protein perhaps anchored to inner membrane	46606	2546

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>dctA</i>	79.3	Dicarboxylic acid transport	Uptake of C-4 dicarboxylic acids; 3-fluoromalate resistance, D-tartrate resistant	872	206, 2181, 2602, 3897
<i>dctB</i>	16.4	Dicarboxylic acid transport	Uptake of C-4 dicarboxylic acids; 3-fluoromalate resistance, D-tartrate resistant	871	2181, 3897
<i>dcuA</i>	94.0	Dicarboxylate uptake	<i>genA</i> ; C4-dicarboxylate transporter, anaerobic	34476	4084
<i>dcuB</i>	93.7	Dicarboxylate uptake	<i>genF</i> ; C4-dicarboxylate transporter, anaerobic	34479	4084
<i>dcuC</i>	14.1	Dicarboxylate uptake	C4-dicarboxylate carrier, anaerobic; W3110 has an IS5 insertion	50968	4956
<i>ddlA</i>	8.6	D-Alanine ligase	D-Alanine:D-alanine ligase, ADP-forming	30966	3350, 4921
<i>ddlB</i>	2.2	D-Alanine ligase	<i>ddl</i> ; D-Alanine:D-alanine ligase	870	1893, 2071, 2675, 2676, 3350, 3692
<i>deaD</i>	71.2	Dead-box protein	<i>csdA</i> , <i>mssB</i> ; gene dosage-dependent suppressor of <i>rpsB(ts)</i> mutations; putative RNA helicase	33472	1200, 2045, 4437, 4843
<i>dedA</i>	52.4	Downstream, expressed?	Temporary designation for genes in <i>pxdB</i> and <i>folC</i> operons; unknown function	32742	3211
<i>dedD</i>	52.4	Downstream, expressed?	Temporary designation for genes in <i>pxdB</i> and <i>folC</i> operons; unknown function	32739	3211
<i>def</i>	74.0	Deformylase	<i>fms</i> ; peptide deformylase, N-formylmethionylaminoacyl-tRNA deformylase (EC 3.4.11.-, EC 3.5.1.27)	33619	2830, 2869, 2871, 2872, 2873, 3597
<i>degP</i>	3.9	Degradative protease	<i>htrA</i> ; DegP periplasmic serine endoprotease (EC 3.4.99-), protease Do, required for high-temperature growth; σ^E promoter	30554	1767, 2570, 2571, 2572, 3974, 4092, 4251, 660
<i>degQ</i>	72.8	Degradative protease	<i>hhoA</i> ; periplasmic serine endoprotease	36675	2296, 250, 4643
<i>degS</i>	72.8	Degradative protease	<i>htrH</i> , <i>hhoB</i> ; periplasmic serine endoprotease	36678	250, 4643
<i>del</i>	64.3	Deletion	Affects frequency of IS1-mediated deletions; 1,000-fold reduction in deletion frequency	869	3164
<i>deoA</i>	99.5	Deoxyribose	<i>tpg-75</i> ; thymidine phosphorylase (EC 2.4.2.4)	868	1255, 22, 4270, 4528, 4530, 4531, 4532
<i>deoB</i>	99.5	Deoxyribose	<i>drm</i> , <i>thyR</i> , <i>tlr</i> ; deoxyribouratase (EC 2.7.5.6), phosphopentomutase	867	1255, 22, 2616, 3705, 4527, 4530, 4532
<i>deoC</i>	99.5	Deoxyribose	<i>dra</i> , <i>thyR</i> , <i>tlr</i> ; deoxyribose-phosphate aldolase (EC 4.1.2.4)	866	1255, 2616, 3705, 4526, 4527, 4528, 4532, 54, 920
<i>deoD</i>	99.6	Deoxyribose	<i>pup</i> ; purine-nucleoside phosphorylase PNP (EC 2.4.2.1)	865	1255, 22, 2282, 2422, 3705, 4528, 4532
<i>deoR</i>	19.0	Deoxyribose	<i>nucR</i> , <i>nupG</i> , <i>tse</i> ; regulatory gene for <i>deo</i> operon	864	3017, 3048, 4533
<i>dfp</i>	82.1	DNA synthesis flavoprotein	<i>dnaS</i> , <i>dut</i> ; flavoprotein affecting DNA synthesis and pantothenate metabolism	18430	4154, 4155
<i>dgd</i>	72.0	D-Galactose dehydrogenase	D-Galactose dehydrogenase production	863	4803
<i>dgkA</i>	91.7	Diglyceride kinase	Diglyceride kinase	862	2544, 2545
<i>dgkR</i>	93.7	Diglyceride kinase	Regulatory	861	3578
<i>dgoA</i>	83.4	D-Galactonate	2-Oxo-3-deoxygalactonate 6-phosphate aldolase (EC 4.1.2.21)	36891	182
<i>dgoD</i>	83.4	D-Galactonate	Galactonate dehydratase (EC 4.2.1.6)	859	182
<i>dgoK</i>	83.5	D-Galactonate	2-Oxo-3-deoxygalactonate kinase (EC 2.7.1.58)	858	182
<i>dgoR</i>	83.5	D-Galactonate	Regulatory; growth on 2-keto-3-deoxygalactonate, <i>dgoR^e</i>	857	830
<i>dgoT</i>	83.4	D-Galactonate	Galactonate transport	856	182
<i>dgsA</i>	35.9	D-Glucosamine	<i>mlc</i> (makes large colonies); affects function of phosphotransferase system enzyme IIA/IIB, anaerobic growth on glucosamine; binds NagC promoters; regulates <i>manX</i>	855	1813, 3012, 3453, 3707
<i>dgt</i>	3.9	dGTP triphosphohydrolase	<i>optA</i> ; deoxyguanosine 5'-triphosphate triphosphohydrolase (EC 3.1.5.1)	30546	261, 3572, 3573, 4806
<i>dicA</i>	35.5	Division control	Regulatory for <i>dicB</i>	18427	282, 283
<i>dicB</i>	35.5	Division control	Control of cell division	18424	282, 283, 622
<i>dicC</i>	35.5	Division control	Regulatory for <i>dicB</i>	18421	282, 283
<i>dicF</i>	35.5	Division control	DicF antisense RNA; inhibits Qin	32240	1208, 1209, 4389, 453
<i>dif</i>	34.2	Deletion-induced filamentation	Recombination site in terminus, <i>recA</i> independent	30208	1675, 2354, 2356, 376, 378, 835, 836, 4378
<i>dinB</i>	5.4	Damage inducible	<i>dinP</i> ; increased mutagenesis, apparently independent of <i>umuDC</i> ; SOS related	53389	2232, 526
<i>dinD</i>	82.2	Damage inducible	<i>orfY</i> , <i>pcsA</i> , <i>yicD</i> ; mutant cs phenotype filamentous with large nucleoid	33582	2200, 2352, 2353, 2664, 3262, 4877
<i>dinF</i>	91.7	Damage inducible	Induced by UV and mitomycin C; SOS, <i>lexA</i> regulon	854	2200, 2348, 2928

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>dinG</i>	17.9	Damage inducible	LexA regulated (SOS) repair enzyme	31247	2318, 2518, 2519
<i>dinI</i>	24.1	Damage inducible	Multicopy suppresses phenotype of cold-sensitive <i>dinD</i> filamentous mutation	53428	4877
<i>dinY</i>	41.9	Damage inducible	Repair gene	36880	3412
<i>dipZ</i>	94.0	Disulfide isomerase	<i>cycZ</i> , <i>dsbD</i> , <i>cutA2</i> ; may be involved in cytochrome maturation, see <i>ccm</i> genes; affects disulfide binding	34213	1921, 268, 2910, 874, 875
<i>djlA</i>	1.2	DnaJ-like	Proposed to dock and interact with variety of membrane proteins; mutants rapidly accumulate suppressors	51192	2188, 769, 770
<i>dksA</i>	3.5	<i>dnaK</i> suppressor	<i>msmA</i> ; high copy suppresses <i>muk</i> and TS growth and filamentation of <i>dnaK</i> mutant	30521	2122, 4842
<i>dld</i>	47.9	D-Lactate dehydrogenase	<i>ldh</i> ; D-lactate dehydrogenase (EC 1.1.1.28); vinylglycolate resistance, FAD enzyme	852	2058, 3768, 4012, 626
<i>dmsA</i>	20.3	DMSO reductase	DMSO reductase subunit A, anaerobic	17710	353, 354, 3749
<i>dmsB</i>	20.3	DMSO reductase	DMSO reductase subunit B; apparent Fe-S binding domain; anaerobic	31724	354, 3749
<i>dmsC</i>	20.3	DMSO reductase	DMSO reductase subunit C, membrane bound	31727	354, 3749
<i>dnaA</i>	83.6	DNA	DNA biosynthesis; initiation; binding protein	851	1372, 1630, 1631, 1872, 1873, 1875, 2160, 2235, 2272, 2275, 2474, 2927, 2985, 2986, 3051, 3261, 3400, 3541, 3569, 3570, 3809, 3813, 4087, 4300, 4301, 4611, 471, 4910, 1790
<i>dnaB</i>	91.9	DNA	<i>groP</i> , <i>grpA</i> , <i>grpD</i> ; DNA biosynthesis; chain elongation	850	1406, 2259, 2545, 3126, 3333, 3804, 3951, 4449, 561
<i>dnaC</i>	99.1	DNA	<i>dnaD</i> ; DNA biosynthesis; initiation and chain elongation	849	2786, 3125, 3753
<i>dnaE</i>	4.4	DNA	<i>polC</i> , <i>sdgC</i> (suppressor of <i>dnaG</i> mutation); DNA polymerase III, α -subunit	373	1239, 1240, 2194, 296, 3889, 4016, 4424, 4708, 4761
<i>dnaG</i>	69.2	DNA	<i>dnaP</i> , <i>parB</i> , <i>sdgA</i> ; primase; primer synthesis for leading- and lagging-strand synthesis	847	1531, 2671, 2672, 2673, 3055, 3113, 3125, 3216, 3753, 4105, 4376, 4449, 4578, 4766, 579
<i>dnaI</i>	40.3	DNA	DNA biosynthesis	846	334a
<i>dnaJ</i>	0.3	DNA	<i>groP</i> , <i>grpC</i> ; chain elongation; stress-related DNA biosynthesis, responsive to heat shock; chaperone with DnaK	845	1406, 2069, 231, 3256, 3257, 3258, 3333, 3804, 4252, 4293, 4830, 972
<i>dnaK</i>	0.3	DNA	<i>gro</i> , <i>groP</i> , <i>groPAB</i> , <i>groPC</i> , <i>groPF</i> , <i>grpC</i> , <i>grpF</i> , <i>seg</i> ; stress-related heat-shock DNA biosynthesis, ATP-regulated binding and release of polypeptide substrates; HSP-70-type molecular chaperone, with DnaJ	844	1143, 1186, 1187, 1875, 2120, 227, 2837, 3035, 3158, 3257, 3332, 3807, 4252, 567, 3697
<i>dnaL</i>	28.9	DNA	DNA biosynthesis	843	3982
<i>dnaN</i>	83.6	DNA	DNA biosynthesis; sliding clamp subunit, required for high processivity; DNA polymerase III β subunit	842	132, 1630, 2194, 2235, 3261, 3626, 3627, 3809, 3810, 3813, 4910, 564
<i>dnaQ</i>	5.1	DNA	<i>mutD</i> ; DNA polymerase III ϵ -subunit; streptomycin, azaserine resistant; 3' to 5' proofreading, <i>lexA</i> regulon	840	1047, 1113, 1239, 1706, 1804, 2194, 2730, 2783, 3209, 3568, 3903, 4052, 779, 855, 856, 4331
<i>dnaT</i>	99.1	DNA	Primasomal protein i	839	2786, 2787, 3125
<i>dnaX</i>	10.6	DNA	<i>mutH</i> , <i>dnaZ</i> ; subunit of DNA polymerase III holoenzyme; DNA elongation factor III; τ and γ subunits	838	1264, 1265, 1266, 1669, 1845, 2194, 2228, 2229, 2283, 2421, 2471, 2472, 2511, 2731, 3043, 3753, 398, 399, 4485, 4486, 4885, 701, 912, 913
<i>dppA</i>	79.8	Dipeptide permease	<i>alu</i> , <i>tpp?</i> ; uptake of dipeptides	35111	3294, 4, 4576
<i>dppB</i>	79.8	Dipeptide permease	Uptake of dipeptides	33771	4, 4118, 4576
<i>dppC</i>	79.8	Dipeptide permease	Uptake of dipeptides	33768	4, 4118, 4576
<i>dppD</i>	79.8	Dipeptide permease	Uptake of dipeptides	33765	4, 4118, 4576
<i>dppF</i>	79.7	Dipeptide permease	Uptake of dipeptides	33752	4

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>dppG</i>	14.0	Dipeptide permease	Uptake of dipeptides; dipeptide permease	835	1453, 3384, 997
<i>dps</i>	18.3	DNA-binding protein, stationary phase	<i>pexB</i> ; stress response DNA-binding protein; starvation induced resistance to H ₂ O ₂	31650	1226, 2620, 71
<i>dsbA</i>	87.1	Disulfide bond	<i>iarA</i> , <i>ppfA</i> ; disulfide oxidoreductase, periplasmic protein disulfide-isomerase; role in cytochrome <i>c</i> synthesis (EC 5.3.4.1)	34063	1560, 2243, 229, 230, 2778, 287, 2910, 3549, 3550, 3823, 45, 4805, 4840, 67, 904
<i>dsbB</i>	26.6	Disulfide bond	<i>iarB</i> ; PDI or PDI-like protein; DTT-sensitive phenotype; periplasm/inner membrane	31933	1560, 1989, 2243, 229, 288, 2960, 3823, 67
<i>dsbC</i>	65.4	Disulfide bond	<i>xprA</i> ; periplasmic disulfide oxidoreductase, protein disulfide isomerase	33355	2639, 2641, 2962, 4019
<i>dsbG</i>	13.8	Disulfide bond	Thiol-disulphide oxidase; multicopy resistance to DTT; mutants accumulate reduced proteins, corrected by DsbA/B overexpression	53792	92
<i>dsdA</i>	53.4	D-Serine deaminase	D-Serine deaminase	834	2751, 2846, 2847, 3215, 3339, 436, 48, 642
<i>dsdC</i>	53.3	D-Serine deaminase	LysR-type transcriptional regulator; previously cited as D-serine permease; <i>dsdC/X</i> order reversed in different sequence entries	833	2847, 3215, 3339, 436, 48, 642
<i>dsdX</i>	53.4	D-Serine deaminase	Homology with gluconate permease; D-serine tolerance; <i>dsdC/A</i> order reversed in different sequence entries	35717	3215
<i>dsrA</i>	43.6	Small RNA	Regulatory RNA; positive regulation of promoters sensitive to HNS negative regulation	48173	2249, 4098
<i>dsrB</i>	43.6	Small RNA	Regulatory RNA; regulated by DsrA and HNS, under control of RpoS	48176	4099
<i>dut</i>	82.2	dUTPase	<i>dnaS</i> , <i>sof</i> ; deoxyuridinetriphosphatase (EC 3.6.1.23)	832	2661, 2662, 4154, 4367
<i>dvl</i>	7.4	Dye-visible light?	Sensitivity to SDS and toluidine blue plus light	18418	4632
<i>dxs</i>	9.4	Deoxy-xylulose-P synthase	DXP synthase; DXP is precursor to isoprenoids, thiamin, pyridoxol	52930	2615, 4166
<i>e14</i>	25.7	Prophage element 14	Defective prophage element; includes loci <i>sfiC</i> , <i>lit</i> , <i>pin</i> , <i>mcrA</i>	18409	2128, 2715, 3447, 3448, 3604, 4544, 511, 512, 625
<i>ebgA</i>	69.4	Evolved β-galactosidase	Cryptic β-galactoside utilization	830	1607, 4234, 4235, 627
<i>ebgB</i>	69.5	Evolved β-galactosidase	Cryptic β-galactoside utilization, possible paralog of <i>lacY</i>	18415	1607, 4234
<i>ebgC</i>	69.5	Evolved β-galactosidase	Phospho-β-D-galactosidase, β-subunit; cryptic gene	18412	1607
<i>ebgR</i>	69.4	Evolved β-galactosidase	Regulatory gene from <i>ebg</i> cryptic operon	829	1607, 4234
<i>ecfA</i>	67.6	Energy coupling factor	With <i>metC</i> mutation, <i>ecf</i> mutation abolishes coupling of energy with active transport	828	4434
<i>eco</i>	49.6	Ecotin	Ecotin, serine protease inhibitor	32630	1173
<i>ecpD</i>	3.4	<i>E. coli papD</i> homolog	Possible pilin chaperone	30513	3593
<i>eda</i>	41.6	Entner-Doudoroff aldolase	<i>hga</i> , <i>kdgA</i> , <i>kga</i> ; 2-keto-3-deoxygluconate 6-phosphate aldolase (EC 4.1.2.14); 2-keto-4-hydroxyglutarate aldolase	826	1154, 1290
<i>edd</i>	41.6	Entner-Doudoroff dehydratase	Phosphogluconate dehydratase (EC 4.2.1.12); growth on gluconate	825	1121, 1289, 1290, 4594
<i>efp</i>	94.3	Elongation factor P	Elongation factors P and EF-P; prokaryotic	34470	118, 119, 1357
<i>emrA</i>	60.6	E-multidrug resistance	Multidrug resistance pump family	33259	2619, 2621
<i>emrB</i>	60.6	E-multidrug resistance	Hydrophobic, inner membrane-spanning domains; multidrug resistance pump family	33262	2619, 2621
<i>emrD</i>	83.0	E-multidrug resistance	Multidrug resistance pump family	36938	3132
<i>emrE</i>	12.2	E-multidrug resistance	<i>envB</i> , <i>mvrC</i> , <i>mon</i> , <i>rodY</i> ; multidrug resistance pump family; cell shape; methylviologen sensitivity	36935	2452, 4879, 4880, 300
<i>endA</i>	66.6	Endonuclease	DNA-specific endonuclease I; extensive DNA breakdown	824	2002, 4785
<i>eno</i>	62.6	Enolase	Enolase (EC 4.2.1.11)	823	158, 2257, 4709
<i>entA</i>	13.5	Enterochelin	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase	822	1262, 1777, 2394, 2395, 2581, 3090, 3091, 3424, 4180
<i>entB</i>	13.5	Enterochelin	2,3-Dihydro-2,3-dihydroxybenzoate synthetase	821	1262, 2394, 2395, 3090, 3091, 3326, 5424
<i>entC</i>	13.5	Enterochelin	Isochorismate synthetase	820	1262, 2394, 2395, 2582, 3090, 3091, 3325, 3326, 3424, 4644

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>entD</i>	13.1	Enterochelin	Enterochelin synthetase, component D; facilitates secretion of enterobactin peptide	819	1261, 133, 1534, 2394, 2395, 2400, 786, 787
<i>entE</i>	13.5	Enterochelin	Enterochelin synthetase, component E	818	1262, 2394, 2395, 3090, 3091, 3424
<i>entF</i>	13.2	Enterochelin	Enterochelin synthetase, component F	817	1262, 2394, 2395, 3415, 3770, 286
<i>envN</i>	4.2	Envelope	Affects envelope; defects osmotically remedied	811	1120
<i>envP</i>	90.4	Envelope	Affects envelope; defects osmotically remedied	810	1120
<i>envQ</i>	60.7	Envelope	Affects envelope; defects osmotically remedied	809	1120
<i>envR</i>	73.5	Envelope	<i>acrS</i> ; regulatory gene for <i>envCD</i> (<i>acrEF</i>)	33605	2516, 2684
<i>envT</i>	14.2	Envelope	Affects envelope; defects osmotically remedied	808	1120
<i>envY</i>	12.6	Envelope	Envelope protein involved with thermoregulation of porin	18406	2666, 2668
<i>envZ</i>	76.1	Envelope	<i>ompB</i> , <i>perA</i> , <i>tpo</i> ; inner membrane osmosensor protein; regulates production of outer membrane proteins	807	1373, 1374, 1610, 1611, 2665, 2978, 2979, 2983, 3349, 3769, 4647, 4662, 4681, 4807, 661, 816
<i>epd</i>	66.2	Erythrose-4-P dehydrogenase	<i>gapB</i> ; erythrose-4-P dehydrogenase	32089	1071, 3980, 444, 4946, 61
<i>epp</i>		E-pentapeptide	Minigene within 23S rRNA encoding functional pentapeptide; erythromycin resistance	51135	4383
<i>era</i>	58.2	<i>E. coli ras</i> -like	<i>sdgE</i> ; GTP-binding protein, essential gene	29010	2498, 25, 4137, 708
<i>esp</i>	17.3	Efficiency site for phage	Site for efficient packaging of phage T1	805	1085a
<i>evgA</i>	53.5	<i>E. coli</i> homolog of virulence gene	Multicopy on plasmid in <i>envZ</i> -deleted strain induces <i>ompC</i> expression; see <i>evgS</i>	32763	4519
<i>evgS</i>	53.5	<i>E. coli</i> homolog of virulence gene	With <i>evgA</i> , two-component regulatory system, environmentally responsive	32766	4519
<i>exbB</i>	67.9	Export	Uptake of enterochelin; resistance or sensitivity to colicins; similarity with TolQ	804	1136, 1137, 1254, 1580, 2109, 2136, 2221, 24, 3554, 481, 482
<i>exbC</i>	61.5	Export	Uptake of enterochelin; resistance or sensitivity to colicins	803	1580, 3554
<i>exbD</i>	67.9	Export	Uptake of enterochelin; resistance or sensitivity to colicins; similarity with TolR	33384	1137, 1254, 1721, 2221, 24, 482
<i>expA</i>	22.2	Export	Expression of a group of export proteins	802	944
<i>exuR</i>	69.9	Hexuronate	Negative regulatory gene for <i>exu</i> regulon (<i>exu</i> , <i>uxu</i> , <i>uxa</i>)	801	1852, 1853, 2795, 3489, 3490, 3682, 3687
<i>exuT</i>	69.9	Hexuronate	Transport of hexuronates	800	1852, 2795, 2796, 3489, 3490, 3682, 382
<i>fabA</i>	21.9	Fatty acid biosynthesis	β -hydroxydecanoylthioester dehydrase (EC 4.2.1.60)	799	870, 872
<i>fabB</i>	52.6	Fatty acid biosynthesis	<i>fabC</i> ; β -ketoacyl-acyl carrier protein synthase I (EC 2.3.1.41)	798	1380, 1381, 4056
<i>fabD</i>	24.8	Fatty acid biosynthesis	Malonyl-CoA-acyl carrier protein transacylase (EC 2.3.1.39)	797	1381, 2713, 4579
<i>fabF</i>	24.8	Fatty acid biosynthesis	<i>cvc</i> , <i>fabJ</i> , <i>vtr</i> ; β -ketoacyl-acyl carrier protein synthase II (EC 2.3.1.41)	795	1380, 1381, 3621, 4057, 4512
<i>fabG</i>	24.8	Fatty acid biosynthesis	3-Ketoacyl-ACP reductase (EC 1.1.1.100); reuse of <i>fabG</i> synonym for <i>accC</i>	31865	2315, 3253, 3621
<i>fabH</i>	24.7	Fatty acid biosynthesis	ACP synthase III	31860	3253, 3466, 4481
<i>fabI</i>	29.1	Fatty acid biosynthesis	<i>gts</i> , <i>envM</i> , <i>qmeA</i> ; enoyl-ACP reductase, NADH dependent (EC 1.3.1.9)	812	1687, 2251, 321, 322, 4502, 4734, 4735
<i>fabZ</i>	4.4	Fatty acid biosynthesis	<i>sefA</i> ; 3R-hydroxymyristoyl acyl carrier protein dehydrase	30597	2990, 3212
<i>fadA</i>	86.8	Fatty acid degradation	Thiolase I (EC 2.3.1.16)	794	1057, 3099, 4160, 4860, 4862, 762, 926
<i>fadB</i>	86.8	Fatty acid degradation	<i>oldB</i> ; 3-hydroxyacyl-CoA dehydrogenase: 3-hydroxyacyl-CoA epimerase; dodecenoyl-CoA- Δ -isomerase, enoyl-CoA hydratase; fatty acid oxidation complex, α -subunit (EC 1.1.1.35, 4.2.1.17, 5.1.2.3, and 5.3.3.8); four activities	793	1057, 3099, 3098, 4160, 4860–4862, 926
<i>fadD</i>	40.7	Fatty acid degradation	Acyl-CoA synthetase (EC 6.2.1.3)	792	1336, 371
<i>fadE</i>	4.8	Fatty acid degradation	Electron transport flavoprotein of β -oxidation	791	762
<i>fadH</i>	69.6	Fatty acid degradation	2,4-Dienoyl CoA reductase	54705	1686
<i>fadL</i>	53.0	Fatty acid degradation	<i>ttr</i> ; fatty acid transport protein, outer membrane	790	3010, 3222, 370, 372, 3796

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>fadR</i>	26.6	Fatty acid degradation	<i>dec</i> , <i>ole</i> , <i>thdB</i> ; negative regulatory gene for <i>fad</i> regulon, positive regulator of <i>fabA</i> ; regulates <i>aceBAK</i> , glyoxylate shunt	789	1056, 1058, 1204, 1729, 2744, 3, 4073, 4074, 4739, 762
<i>farR</i>	16.5	Fatty acyl responsive	Fatty acyl responsive regulator	36837	3566, 551
<i>fatA</i>	71.7	Fatty acid	Utilization of <i>trans</i> unsaturated fatty acids	18403	1030
<i>fabA</i>	66.1	Fructose bis-P aldolase	<i>ald</i> , <i>fdA</i> ; fructose-bisphosphate aldolase	786	326, 3560, 4076, 62
<i>fabB</i>	46.9	Fructose bis-P aldolase	<i>dhnA</i> ; fructose 1,6-bisphosphate aldolase	54836	4404, 4076
<i>fbp</i>	96.0	Fructose-bisphosphatase	<i>fdp</i> ; fructose-bisphosphatase (EC 3.1.3.11)	784	2275, 3961
<i>fcf</i>	45.8	Fucose, FX-like	Colanic acid gene cluster, fucose synthetase	55074	113
<i>fcsA</i>	86.9	Filamentous, cold sensitive	Cold-sensitive cell division mutant	787	2352
<i>fdhD</i>	88.0	Formate dehydrogenase	Homologous to <i>fdnC</i> and <i>-B</i> of <i>Salmonella</i> spp.	33972	2746, 3465, 3912, 4221
<i>fdhE</i>	87.9	Formate dehydrogenase	Homologous to <i>fdnC</i> and <i>-B</i> of <i>Salmonella</i> spp.	33978	2746, 3193, 3465, 3912, 4221
<i>fdhF</i>	92.6	Formate dehydrogenase	<i>chlF</i> , <i>fdh</i> ; formate dehydrogenase-N selenopolypeptide subunit molybdate dependence (EC 1.2.2.1), part of FHL complex	18400	3388, 360, 3736, 4798, 4799, 4964, 4965, 697
<i>fdnG</i>	33.3	Formate dehydrogenase-N	Formate dehydrogenase-N major subunit	32160	2527, 312, 313, 314, 3575, 3678, 4221
<i>fdnH</i>	33.4	Formate dehydrogenase-N	Formate dehydrogenase-N Fe-S subunit	32164	2527, 312, 313, 314, 3575, 3678, 4221, 859
<i>fdnI</i>	33.4	Formate dehydrogenase-N	Formate dehydrogenase-N cytochrome subunit	32168	2527, 312, 313, 314, 3575, 3678, 4221
<i>fdoG</i>	88.0	Formate dehydrogenase-O	Formate dehydrogenase-O subunit, major	33985	2, 3465
<i>fdoH</i>	87.9	Formate dehydrogenase-O	Formate dehydrogenase-O subunit, Fe-S	33988	2, 3465
<i>fdoI</i>	87.9	Formate dehydrogenase-O	Formate dehydrogenase-O subunit cytochrome b ₅₅₆	33991	2, 3465
<i>fdx</i>	57.2	Ferredoxin	In multicopy, suppresses negative <i>ftsH</i> mutations	40877	44
<i>feaB</i>	31.2	Phenylethylamine	Ferredoxin, cotranscribed with <i>hscBA</i> , presumably cold inducible	32984	2484, 4320, 4321
<i>feaR</i>	31.1	Phenylethylamine	<i>padA</i> ; catabolism of phenylethylamine	50925	1230, 1629
<i>fecA</i>	97.3	Iron (citrate dependent)	<i>maoB</i> ; regulates expression of <i>tynA</i> and <i>padA</i>	783	114, 1870, 3536, 4558, 4569, 4629, 4962
<i>fecB</i>	97.2	Iron (citrate dependent)	Citrate-dependent iron transport, outer membrane receptor	782	1870, 3536, 4190, 4569, 4962
<i>fecC</i>	97.2	Iron (citrate dependent)	Citrate-dependent iron transport, periplasmic protein	35620	4190, 4569, 4558
<i>fecD</i>	97.2	Iron (citrate dependent)	Transport gene	18394	3536, 4190, 4569, 4558
<i>fecE</i>	97.2	Iron (citrate dependent)	Citrate-dependent iron transport, membrane bound	35617	4190, 4569, 4558
<i>fecI</i>	97.3	Iron (citrate dependent)	Transport gene	35630	114, 4569, 4558
<i>fecR</i>	97.3	Iron (citrate dependent)	Transport gene mediating induction by iron	35627	4558, 4569
<i>feoA</i>	76.3	Ferrous iron	Regulatory gene mediating induction by iron	28964	1638, 2107
<i>feoB</i>	76.3	Ferrous iron	Ferrous iron uptake system	28967	1638, 2107
<i>fepA</i>	13.1	Ferrienterobactin permease	Membrane protein of ferrous iron uptake system	18388	1261, 1863, 2669, 3325, 3416, 3429, 3554, 4013, 4780, 786
<i>fepB</i>	13.4	Ferrienterobactin permease	<i>cbr</i> , <i>cbr</i> ; outer membrane component of ferribactin transport system	18385	3325, 3428, 3429, 4013, 4202, 4780, 486, 501
<i>fepC</i>	13.3	Ferrienterobactin permease	Periplasmic component of ferrienterobactin transport system	4987	3325, 3326, 3428, 4013
<i>fepD</i>	13.4	Ferrienterobactin permease	Cytoplasmic membrane component of ferrienterobactin transport	18382	1863, 3325, 4013
<i>fepE</i>	13.3	Ferrienterobactin permease	Ferrienterobactin permease, membrane-bound subunit	18379	3325, 4013
<i>fepG</i>	13.4	Ferrienterobactin permease	Ferric enterobactin uptake	31162	717, 4013
<i>fes</i>	13.2	Iron	Ferrienterobactin permease, membrane-bound subunit	780	1261, 1777, 1863, 2394, 2395, 3415, 3416, 786
<i>fexB</i>	86.7	F exclusion	Enterochelin esterase	778	2499
<i>ffh</i>	59.2	54-kDa homolog (4.5S particle)	Affects ArcA phenotype	33006	2695, 325, 3407, 3419, 3488, 3520
<i>ffs</i>	10.2	4.5S	4.5S-RNP protein; RNP has mammalian protein-targeting counterpart: SRP	18373	1064, 1834, 2695, 534
<i>fhIA</i>	61.5	Formate hydrogen-lyase	4.5S rRNA; mammalian counterpart, SRP, includes 4.5S RNA; cotranslational integration of proteins into membrane	18370	1800, 1801, 1957, 3745, 3852, 3853, 3907, 3909
<i>fhIB</i>	95.1	Formate hydrogen-lyase	Transcription factor, formate hydrogen lyase system activator, global regulator, <i>hyc</i> , <i>hyp</i>	36851	2821
<i>fhuA</i>	3.6	Ferric hydroxamate uptake	Formate hydrogen-lyase; activated by <i>fhIA</i>	777	1216, 2081, 2219, 2221, 2220, 2652, 2653, 457, 483, 485, 486, 849, 850

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>fhuB</i>	3.7	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component; mutants albomycin resistant	776	1216, 2081, 2330, 3544, 486
<i>fhuC</i>	3.7	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component; mutants albomycin resistant	11187	1216, 486, 566, 848
<i>fhuD</i>	3.7	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component; mutants albomycin resistant	11184	1216, 3712, 486, 566, 848
<i>fhuE</i>	25.0	Ferric hydroxamate uptake	Outer membrane receptor for ferric-rhodotorulic acid	18367	1636, 3881, 3882
<i>fhuF</i>	99.2	Ferric hydroxamate uptake	Ferric hydroxamate transport	18364	1639, 3033
<i>fic</i>	75.2	Filamentation-cAMP	Filamentation in presence of cyclic AMP, in mutants	18361	2302, 4521
<i>fimA</i>	97.9	Fimbriae	<i>fimD</i> , <i>pilA</i> ; fimbrin type 1, major structural subunit; phase variation	18358	1142, 1304, 1305, 1634, 2261, 2264, 5
<i>fimB</i>	97.8	Fimbriae	<i>pil</i> ; recombinase? regulatory gene for <i>fimA</i>	18355	1072, 1142, 1347, 1348, 2262, 2264, 2838
<i>fimC</i>	97.9	Fimbriae	<i>pil</i> , <i>pilB</i> ; biosynthesis of fimbriae; periplasmic chaperone for type 1 fimbriae	18352	2038, 2263, 2264
<i>fimD</i>	97.9	Fimbriae	<i>pil</i> , <i>pilC</i> ; export and assembly of type 1 fimbrial outer membrane protein	18349	2264
<i>fimE</i>	97.9	Fimbriae	<i>pilH</i> ; recombinase? regulatory gene for expression of <i>fimA</i>	18346	1072, 1142, 1347, 1348, 2262, 2838
<i>fimF</i>	98.0	Fimbriae	<i>pilD</i> ; fimbrin type 1 minor component; fimbrial morphology, assembly	18343	2265, 3779
<i>fimG</i>	98.0	Fimbriae	<i>pilD</i> ; fimbrin type 1 minor component; pilus length; perhaps inhibits polymerization in pilus assembly	18340	2265, 3779
<i>fimH</i>	98.0	Fimbriae	<i>pilE</i> ; membrane-specific adhesin (lectin); major fimbrial subunit; mediates mannose-binding	18337	1634, 1655, 2265, 2343, 6
<i>fimI</i>	97.9	Fimbriae	Fimbria related	35633	2261
<i>fipB</i>	86.0	F1 phage	Morphogenesis of phage F1	18334	2629
<i>fipC</i>	75.0	F1 phage	Morphogenesis of phage F1	18331	2629
<i>fis</i>	73.5	Factor for inversion stimulation	<i>nbp</i> ; transcriptional activator for rRNA operons; bends DNA; interacts with RNAP; nucleoid-associated protein	18328	1195, 1244, 1430, 1456, 1464, 1465, 1496, 170, 2280, 2779, 3403, 3742, 443, 4767, 4814, 4815, 4943
<i>fiu</i>	18.1	Ferric iron uptake	Outer membrane protein, ferric iron uptake	18325	1636
<i>fixA</i>	0.9	Sequence similar to those of N-fixation genes	Related to carnitine metabolism; amino acid similarity to <i>Rhizobium fix</i> gene	53111	1132, 550
<i>fixB</i>	0.9	Sequence similar to those of N-fixation genes	Related to carnitine metabolism; amino acid similarity to <i>Rhizobium fix</i> gene	53114	1132, 550
<i>fixC</i>	1.0	Sequence similar to those of N-fixation genes	Related to carnitine metabolism; amino acid similarity to <i>Rhizobium fix</i> gene	53117	1132, 550
<i>fixX</i>	1.0	Sequence similar to those of N-fixation genes	Related to carnitine metabolism; amino acid similarity to <i>Rhizobium fix</i> gene	53121	1132, 550
<i>flkB</i>	95.4	FKBP-like	Periplasmic PPIase, of FK506-binding protein type (EC 5.2.1.8); contains pipecolic acid residue	48137	3584
<i>fkpA</i>	74.9	FK506-binding protein	Protein that binds immunosuppressive drug FK506, a peptidomacrolide, MIP-like	36042	1809, 2964
<i>fldA</i>	15.3	Flavodoxin	Flavodoxin	31496	3306
<i>flgA</i>	24.3	Flagella	<i>flaU</i> ; flagellar synthesis; flagellar regulon member	756	1892, 2305
<i>flgB</i>	24.4	Flagella	<i>flbA</i> ; flagellar synthesis; flagellar regulon member	750	2309
<i>flgC</i>	24.4	Flagella	<i>flaW</i> ; flagellar synthesis; flagellar regulon member; basal body protein	754	2309
<i>flgD</i>	24.4	Flagella	<i>flaV</i> ; flagellar synthesis; flagellar regulon member; basal body rod modification	755	2309, 2307
<i>flgE</i>	24.4	Flagella	<i>flaK</i> ; flagellar hook subunit protein; flagellar regulon member	766	2308, 2309, 2307
<i>flgF</i>	24.4	Flagella	<i>flaX</i> ; flagellar synthesis; flagellar regulon member; basal body rod protein	753	2309
<i>flgG</i>	24.4	Flagella	<i>flaL</i> ; flagellar synthesis; flagellar regulon member; basal body rod protein	765	2307, 2309
<i>flgH</i>	24.5	Flagella	<i>flaY</i> ; flagellar synthesis, basal body L-ring protein	752	2039, 2309

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>flgI</i>	24.5	Flagella	<i>flaM</i> ; flagellar regulon member; basal body P-ring protein	764	2039, 2307, 2309
<i>flgJ</i>	24.5	Flagella	<i>flaZ</i> ; flagellar synthesis; flagellar regulon member	751	2704
<i>flgK</i>	24.5	Flagella	<i>flaS</i> ; flagellar synthesis; flagellar regulon member; hook-associated protein I	758	2307
<i>flgL</i>	24.6	Flagella	<i>flaT</i> ; flagellar synthesis; flagellar regulon member; hook-associated protein	757	2307
<i>flgM</i>	24.3	Flagella	<i>anti-σ</i> factor regulator of FlhD	53436	532
<i>flgN</i>	24.3	Flagella	FlgN flagellar synthesis protein	53440	532
<i>flhA</i>	42.3	Flagella	<i>flaH</i> ; flagellar synthesis; flagellar regulon member	768	2704
<i>flhB</i>	42.3	Flagella	<i>flaG</i> ; flagellar synthesis; flagellar regulon member	769	2704, 86
<i>flhC</i>	42.6	Flagella	<i>flaI</i> ; flagellar synthesis; regulatory gene	767	246, 2589, 2590, 40
<i>flhD</i>	42.6	Flagella	<i>flbB</i> ; regulatory gene, flagellum-specific σ factor, transcriptional activator of Fla class II operons	749	246, 2589, 2590, 3547
<i>fliA</i>	43.1	Flagella	<i>flaD</i> , <i>rpoF</i> ; regulation of late gene expression; σ transcription factor for class 3a and 3b operons	771	1925, 2083, 2305, 2369, 2591, 2623, 2704
<i>fliC</i>	43.1	Flagella	<i>flaF</i> , <i>hag</i> ; flagellin, structural gene; flagellar regulon member	649	1623, 2382, 4316
<i>fliD</i>	43.2	Flagella	<i>flbC</i> ; hook-associated protein 2, axial family; flagellar regulon member	748	2172
<i>fliE</i>	43.3	Flagella	<i>flaN</i> ; flagellar synthesis; basal body component	763	2704, 3041
<i>fliF</i>	43.4	Flagella	<i>flaBI</i> ; flagellar basal body M-ring protein	17707	1891, 2304, 2306, 247, 4065
<i>fliG</i>	43.4	Flagella	<i>flaBII</i> ; motor switching and energizing	18322	1891, 2304, 2306, 247, 2601, 2785, 3720, 4065
<i>fliH</i>	43.4	Flagella	<i>flaBIII</i> ; flagellar biosynthesis	18319	1891, 2304, 2306, 247, 4065
<i>fliI</i>	43.4	Flagella	<i>flaC</i> ; flagellar biosynthesis	772	247
<i>fliJ</i>	43.5	Flagella	<i>flaO</i> ; flagellar biosynthesis	762	247
<i>fliK</i>	43.5	Flagella	<i>flaE</i> ; hook filament junction; controls hook length	770	2171, 2172, 247, 2704
<i>fliL</i>	43.5	Flagella	<i>flaAI</i> ; flagellar biosynthesis	18316	2370, 247, 2739, 3580
<i>fliM</i>	43.5	Flagella	<i>cheC</i> , <i>flaA</i> ; flagellar synthesis, motor switching and energizing	774	2370, 2785, 777
<i>fliN</i>	43.5	Flagella	<i>motD</i> ; flagellar switch protein	18313	2739
<i>fliO</i>	43.5	Flagella	<i>flbD</i> ; flagellar synthesis; flagellar regulon member	17510	2704, 2738, 2739
<i>fliP</i>	43.5	Flagella	<i>flaR</i> ; flagellar synthesis; flagellar regulon member	759	2738, 2739
<i>fliQ</i>	43.6	Flagella	<i>flaQ</i> ; flagellar synthesis; flagellar regulon member	760	2739
<i>fliR</i>	43.6	Flagella	<i>flaP</i> ; flagellar synthesis; flagellar regulon member	761	2738, 2739
<i>fliS</i>	43.2	Flagella	Flagellar synthesis; flagellar regulon member	30736	2172
<i>fliT</i>	43.2	Flagella	Flagellar synthesis; flagellar regulon member	30739	2172
<i>fliY</i>	43.1	Flagella	Not required for motility; may regulate FliA (σ^F)	49936	3080
<i>fliZ</i>	43.1	Flagella	Not required for motility; may regulate FliA (σ^F)	49933	3080
<i>flk</i>	52.5	Flagella	<i>div</i> ; transcribed divergently from <i>pdxB</i> , promoters overlapping, <i>Salmonella</i> homolog functions in sensing flagellar assembly stage	32751	2134, 3930
<i>flu</i>	44.6	Flagella	Antigen 43, phase-variable bipartite outer membrane protein; affects surface properties, piliation, colonial morphology; unstable gene	746	1712, 1712a, 2704
<i>fmt</i>	74.0	fMet-tRNA formyltransferase	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	33616	1562, 1563, 2748, 2830, 2870, 3609
<i>fnr</i>	30.1	Fumarate-nitrate-reductase	<i>frdB</i> , <i>nirA</i> , <i>nirR</i> , <i>ossA</i> ; regulatory gene for nitrite and nitrate reductases, hydrogenase, fumarate reductase	745	2878, 3611, 3863, 4008, 4009, 4010, 4153, 4216
<i>focA</i>	20.5	Formate channel	Membrane protein	31732	2088, 4294
<i>focB</i>	56.3	Formate channel	Membrane protein, formate transporter of <i>hyf</i> operon	55723	108a

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>folA</i>	1.1	Folate	<i>tmrA</i> ; trimethoprim resistance; dihydrofolate reductase (EC 1.5.1.3)	744	106, 1962, 3437, 3728, 380, 4014, 4112, 4113, 4114
<i>folC</i>	52.4	Folate	Dihydrofolate:folylpolyglutamate synthetase (EC 6.3.2.12)	17704	1228, 3211, 409
<i>folD</i>	12.0	Folate	<i>ads</i> ; methenyltetrahydrofolate dehydrogenase/cyclohydrolase (EC 1.5.1.5, EC 3.5.4.9)	31127	1052, 932
<i>folE</i>	48.3	Folate	GTP cyclohydrolase I	32718	2170
<i>folK</i>	3.4	Folate	Dihydro-hydroxymethylpterin pyrophosphokinase	29572	4341
<i>folP</i>	71.6	Folate	Dihydropteroate synthase (EC 2.5.1.15)	29566	4312, 910, 911
<i>folX</i>	52.1	Folate	Dihydroneopterin triphosphate epimerase	54773	1668
<i>fpr</i>	88.6	Ferredoxin NADP ⁺ reductase	<i>mvrA</i> ; ferredoxin NADP ⁺ reductase; anaerobic	18127	3002, 344, 4474
<i>frdA</i>	94.4	Fumarate reductase	Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	742	1116, 1540, 2041, 2614, 396, 793, 796, 797, 798, 801
<i>frdB</i>	94.4	Fumarate reductase	Fumarate reductase iron-sulfur protein subunit (EC 1.3.99.1)	741	1540, 2041, 2614, 663, 796, 797, 801
<i>frdC</i>	94.3	Fumarate reductase	Fumarate reductase membrane anchor polypeptide (EC 1.3.99.1)	740	1540, 2041, 2486, 663, 796
<i>frdD</i>	94.3	Fumarate reductase	Fumarate reductase membrane anchor polypeptide (EC 1.3.99.1)	739	1540, 2041, 2486, 663, 796
<i>frr</i>	4.2	Factor for ribosome recycling	Ribosome recycling factor; essential gene; dissociates ribosomes from mRNA after termination of translation	30590	1739, 1880, 1881, 1991, 4033
<i>fruA</i>	48.7	Fructose	<i>ptsF</i> ; fructosephosphotransferase enzyme II	350	1396, 3538
<i>fruB</i>	48.7	Fructose	<i>fruF</i> ; fructosephosphotransferase enzyme III	17515	1396, 3646
<i>fruK</i>	48.7	Fructose	<i>fpk</i> , <i>fruF</i> ; fructose-1-phosphate kinase (EC 2.7.1.3)	743	1061, 1396, 2925, 428
<i>fruR</i>	1.9	Fructose	<i>fruC</i> , <i>shl</i> , <i>cra</i> ; regulatory gene for <i>fru</i> operon, other catabolite-regulated genes	18304	1396, 1982, 2324, 3611, 3797, 397
<i>fsr</i>	10.8	Fosmidomycin resistance	Amplification confers fosmidomycin resistance	49279	1329
<i>ftn</i>	42.8	Ferritin	<i>gen-165</i> , <i>rsgA</i> ; ferritin	32521	1846, 1970
<i>ftsA</i>	2.2	Filamentation, temperature sensitive	<i>divA</i> ; cell division, septation	738	1024, 17, 2036, 2675, 2676, 2689, 279, 3691, 3693, 4274, 4589, 4882, 57, 621
<i>ftsE</i>	77.6	Filamentation, temperature sensitive	Cell division; ATP-binding protein	736	1429, 3821
<i>ftsI</i>	2.0	Filamentation, temperature sensitive	<i>pbpB</i> , <i>sep</i> ; peptidoglycan synthetase; penicillin-binding protein 3	423	1439, 1642, 2071, 279, 2889, 3107
<i>ftsJ</i>	71.7	Filamentation, temperature sensitive	Cell division and growth; heat inducible	33511	3250
<i>ftsK</i>	20.1	Filamentation, temperature sensitive	Cell division and growth, septation; NA-binding membrane protein; homology with <i>B. subtilis</i> SpoIIIE protein; filamentous growth mutants, suppressed by <i>dacA</i> deletion; promoter region <i>dinH</i>	40896	1046, 2519, 278, 4908
<i>ftsL</i>	2.0	Filamentation, temperature sensitive	Cell division and growth; essential gene; cytoplasmic membrane protein	30402	1588, 1929, 2071, 238
<i>ftsN</i>	88.8	Filamentation, temperature sensitive	<i>msgA</i> ; essential gene; cell division and growth; multicopy suppresses <i>ftsA12</i>	34153	16, 903
<i>ftsQ</i>	2.2	Filamentation, temperature sensitive	Cell division and growth of wall at septum	734	1024, 2071, 277, 279, 3691, 3692, 4240, 4882, 57
<i>ftsW</i>	2.1	Filamentation, temperature sensitive	Cytoplasmic membrane required for PBP 2 expression; homology to <i>rodA</i>	30409	1896, 2071, 2209, 2210
<i>ftsX</i>	77.6	Filamentation, temperature sensitive	<i>ftsS</i> ; cell division	18298	1429
<i>ftsY</i>	77.6	Filamentation, temperature sensitive	Cell division	18295	1429, 2381, 2656, 3520
<i>ftsZ</i>	2.3	Filamentation, temperature sensitive	<i>sfkB</i> , <i>sulB</i> ; cell division and growth; initiation of septation; GTP binding protein	143	1024, 1377, 17, 1978, 2036, 2071, 2674, 2677, 2689, 279, 339, 341, 3443, 3516, 3614, 3623, 4274, 4589, 4881, 4882, 57, 621, 901, 902
<i>fucA</i>	63.2	Fucose	<i>fucC</i> ; L-fucose-1-phosphate aldolase	17701	2650, 4089, 4955, 669, 713, 714
<i>fucI</i>	63.2	Fucose	L-Fucose isomerase	10878	2650, 4955, 713, 714
<i>fucK</i>	63.3	Fucose	L-Fucose kinase (EC 2.7.1.51)	10881	2650, 4955, 713, 714
<i>fucO</i>	63.2	Fucose	L-1,2-Propanediol oxidoreductase	17698	2650, 4089, 4955, 713, 714

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>fucP</i>	63.2	Fucose	<i>prd</i> ; fucose permease	10875	2650, 4089, 4955, 669, 713, 714
<i>fucR</i>	63.3	Fucose	Positive regulatory protein for <i>fuc</i> regulon	10884	2650, 4090, 4955, 713, 714
<i>fumA</i>	36.3	Fumarate	Fumarase A, aerobic	18292	1555, 2932, 2933, 3357
<i>fumB</i>	93.6	Fumarate	Fumarase B, anaerobic; regulatory gene?	18289	1552, 1555, 292
<i>fumC</i>	36.3	Fumarate	Fumarase C, aerobic; member of <i>soxRS</i> regulon	15273	1552, 2568, 3357
<i>fur</i>	15.3	Ferric uptake regulation	Ferric iron uptake, negative regulatory gene	18286	1637, 1777, 198, 199, 3178, 3891, 978
<i>fusA</i>	74.8	Fusidic acid	<i>far</i> ; fusidic acid resistance; protein chain elongation factor G	732	1815, 2383, 3498, 4929
<i>fusB</i>	14.5	Fusidic acid	Fusidic acid resistance; pleiotropic effects on RNA synthesis and ribosomes, ribosomal protein S6	731	1923a, 4332a
<i>gabC</i>	60.1	γ -Aminobutyrate	Utilization of GABA as N source; regulatory for <i>gab</i> ?	730	1082, 2911, 2912
<i>gabD</i>	60.1	γ -Aminobutyrate	Succinate-semialdehyde dehydrogenase; NADP dependent (EC 1.2.1.16)	729	2911, 2912, 3179
<i>gabP</i>	60.2	γ -Aminobutyrate	GABA permease, membrane protein	728	2239, 2911, 2912
<i>gabT</i>	60.2	γ -Aminobutyrate	Aminobutyrate aminotransferase (EC 2.6.1.19)	727	249, 2911, 2912
<i>gadA</i>	79.0	Glutamate deCase	<i>gadS</i> ? glutamate decarboxylase (EC 4.1.1.15)	32191	4111
<i>gadB</i>	33.8	Glutamate deCase	Glutamate decarboxylase (EC 4.1.1.15)	32194	4111
<i>gadR</i>	79.6	Glutamate deCase	Regulatory gene for <i>gat</i> ?	726	2670, 2758
<i>galE</i>	17.0	Galactose	UDP-galactose 4-epimerase; hexose-1-phosphate uridylyltransferase (EC 2.7.7.12)	724	2456, 2485, 31, 4678, 4693, 581
<i>galF</i>	45.5	Galactose	<i>wcaN</i> ; not required for colanic acid synthesis; putative UTP-glucose-P-uridylyltransferase (<i>galU</i>) regulatory subunit	53092	2771, 4209
<i>galK</i>	17.0	Galactose	Galactose resistance; galactokinase (EC 2.7.1.6)	723	225, 2456, 3792, 4285, 4693, 4876, 993, 994
<i>galM</i>	17.0	Galactose	Aldose-1-epimerase (mutarotase)	35171	456
<i>galP</i>	66.5	Galactose	D-Galactose/H ⁺ symporter	722	4693
<i>galR</i>	64.1	Galactose	Repressor of <i>galETK</i> operon; regulates low-affinity transport; Gal repressor	721	1395, 2491, 2708, 3792, 4613, 4691, 4692, 4693, 4953, 584
<i>galS</i>	48.3	Methyl-galactoside	<i>mglD</i> ? utilization of methylgalactoside; negative regulation of high-affinity transport; Gal isorepressor; represses <i>mgl</i>	499	1395, 3684, 3751, 4693
<i>galT</i>	17.0	Galactose	<i>galB</i> ; galactose-1-phosphate uridylyltransferase; (EC 2.7.7.10)	720	2095, 2371, 2456, 2485, 2491, 4693, 839
<i>galU</i>	27.8	Galactose	Glucose-1-P uridylyltransferase (UDP-glucose pyrophosphorylase) (EC 2.7.7.9), regulatory	719	1168, 1299, 1547, 3989, 4678, 4704
<i>gapA</i>	40.1	Glyceraldehyde phosphate dehydrogenase	<i>gad</i> ; glyceraldehyde 3-P dehydrogenase A (EC 1.2.1.12); horizontal transfer? similar to eukaryotic GAPDH	718	1071, 2438, 3149, 3980, 480
<i>gapC</i>	32.1	Glyceraldehyde phosphate dehydrogenase	<i>gad</i> ; glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12)	53105	1747
<i>garA</i>	15.8	Glucarate	D-Glucarate utilization	717	3690
<i>garB</i>	3.6	Glucarate	D-Glucarate utilization	716	3690
<i>gatA</i>	46.8	Galactitol	Galactitol-specific enzyme IIA of phosphotransferase system (PTS)	715	1015, 2058, 2565, 2925, 3202, 3644, 429
<i>gatB</i>	46.8	Galactitol	Galactitol-specific enzyme IIB of PTS	32559	3202
<i>gatC</i>	46.8	Galactitol	Galactitol-specific enzyme IIC of PTS	714	2058, 2565, 2925, 3202, 429
<i>gatD</i>	46.8	Galactitol	Galactitol-1-phosphate dehydrogenase	713	2058, 2565, 2925, 3202, 429
<i>gatR</i>	46.7	Galactitol	Regulatory gene for <i>gat</i>	32562	3202
<i>gatY</i>	46.8	Galactitol	D-Tagatose-1,6-bisphosphate aldolase	53142	3202
<i>gatZ</i>	46.8	Galactitol	Function unknown	53139	3202
<i>gcd</i>	3.0	Glucose dehydrogenase	Glucose dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.17); inner membrane	30502	4825, 782
<i>gcl</i>	11.5	Glyoxylate carboligase	Glyoxylate carboligase (EC 4.1.1.47)	31107	677
<i>gcpE</i>	56.9	Gene coding for protein E	Apparently essential gene	32909	205
<i>gcvA</i>	63.4	Glycine cleavage	<i>trans</i> -Acting protein, responsible for glycine-induced activation of <i>gcv</i> , perhaps repression in the presence of inosine	28676	4756, 4757, 4758
<i>gcvH</i>	65.7	Glycine cleavage	Glycine cleavage, carrier of aminomethyl group	28664	4192, 4194
<i>gcvP</i>	65.6	Glycine cleavage	Glycine dehydrogenase (decarboxylating) (EC 1.4.4.2)	28661	3280

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<i>gcvR</i>	56.0	Glycine cleavage	Regulatory gene	40204	1416, 1417
<i>gcvT</i>	65.7	Glycine cleavage	Aminomethyl transferase, tetrahydrofolate dependent (EC 2.1.2.10)	28667	3280, 4192, 4193
<i>gdhA</i>	39.7	Glutamate dehydrogenase	Glutamate dehydrogenase	712	1707, 265, 2857, 3844, 4539, 4540, 853, 968
<i>gef</i>	0.4	Gene expression fatal	Small toxic membrane polypeptide; multimeric	30252	2012, 3507, 3508, 3509, 3510
<i>ggt</i>	77.2	γ -Glutamyltranspeptidase	γ -Glutamyltranspeptidase (EC 2.3.2.2)	18280	1663, 4303, 4304, 4305, 4306
<i>gidA</i>	84.5	Glucose-inhibited division	Glucose effects on cell division, perhaps replication	18277	2275, 3245, 4635, 556
<i>gidB</i>	84.5	Glucose-inhibited division	Glucose effects on cell division, perhaps replication	18274	2275, 3180, 3245, 4635
<i>gip</i>	11.5	Glyoxylate-induced protein	Induced by glyoxylate, downstream of <i>gcl</i>	49283	677
<i>glcB</i>	67.2	Glycolate	Malate synthase G (EC 4.1.3.2)	711	3396
<i>glcC</i>	67.4	Glycolate	Regulatory gene	49985	3396
<i>glcD</i>	67.3	Glycolate	Regulatory protein, transcriptional activator	49982	3396
<i>glcE</i>	67.3	Glycolate	<i>glcF</i> (frameshifted segment of <i>glcE</i>); glycolate oxidase subunit, FeS protein	49979	3396
<i>glcG</i>	67.3	Glycolate	Unknown function	49974	3396
<i>gldA</i>	89.1	Glycerol dehydrogenase	Glycerol dehydrogenase, NAD ⁺ dependent	34147	395, 4473
<i>glf</i>	45.4	Galactofuranose	UDP-galactopyranose mutase (EC 5.4.99.9)	54669	3137
<i>glgA</i>	76.8	Glycogen	Glycogen synthase (EC 2.4.1.21)	710	2084, 2364, 2432, 3281, 3721, 3722, 4854
<i>glgB</i>	76.9	Glycogen	1,4- α -Glucan branching enzyme (EC 2.4.1.18)	709	196, 2432, 3721, 3722, 3820
<i>glgC</i>	76.9	Glycogen	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)	708	195, 2432, 3721, 3722, 3281
<i>glgP</i>	76.8	Glycogen	α -Glucan phosphorylase (EC 2.4.1.1)	33653	4907, 742
<i>glgS</i>	68.8	Glycogen	Glycogen synthesis protein, controlled by σ^S (stationary phase) and cAMP	29727	1719, 4854
<i>glgX</i>	76.9	Glycogen	Glycogen debranching enzyme	53576	4854
<i>glk</i>	54.0	Glucokinase	Glucokinase; (EC 2.7.1.2)	707	539, 890
<i>glmM</i>	71.6	Glucosamine	<i>mrsA</i> ; phosphoglucosamine mutase; essential gene; UDP-GlcNAc path, peptidoglycan, lipopolysaccharide synthesis; mRNA stability effects	47201	2893, 4658
<i>glmS</i>	84.3	Glucosamine	Glucosamine-6-phosphate synthase (EC 2.6.1.16)	706	3464, 4611, 4635
<i>glmU</i>	84.3	Glucosamine	Bifunctional glucosamine-1-phosphate acetyltransferase and <i>N</i> -acetylglucosamine-1-P uridylyltransferase	29106	2891, 2892
<i>glmX</i>	26.2	Glucosamine	Affects suppression of <i>glmS</i> mutations by <i>nagB</i>	36538	4601
<i>glnA</i>	87.4	Glutamine	Glutamine synthetase (EC 6.3.1.2)	705	1579, 192, 2705, 2706, 2710, 2849, 2952, 3072, 3336, 3645, 3695, 3750, 813, 852, 853
<i>glnB</i>	57.9	Glutamine	PII regulatory protein for glutamine synthetase	32933	1683, 2578, 4132, 4555, 555
<i>glnD</i>	4.0	Glutamine	Uridylyltransferase	704	1359, 4556
<i>glnE</i>	68.9	Glutamine	GS adenylyl transferase (EC 2.7.7.42)	33468	4555
<i>glnG</i>	87.3	Glutamine	<i>glnT</i> , <i>ntrC</i> ; nitrogen regulator I	702	192, 2705, 2706, 2707, 2710, 2849, 2952, 3335, 3336
<i>glnH</i>	18.2	Glutamine	Periplasmic glutamine-binding protein	18271	3206, 3207
<i>glnK</i>	10.2	Glutamine	Regulated through NRI/NRII two-component regulatory system	38502	4554, 4557
<i>glnL</i>	87.4	Glutamine	<i>glnR</i> , <i>ntrB</i> ; bifunctional protein kinase/phosphatase nitrogen regulator II, NRII	701	159, 192, 2706, 2707, 2710, 2848, 2849, 2952, 3207, 3336, 3645, 3695, 4510, 711
<i>glnP</i>	18.2	Glutamine	L-Glutamate periplasmic binding protein; transport; methionine sulfoximine resistance	700	2792, 3207, 4695, 4696
<i>glnQ</i>	18.2	Glutamine	Glutamine high-affinity transport system	18268	3207
<i>glnR</i>	24.1	Glutamine	Glutamine transport	699	724
<i>glnS</i>	15.2	Glutamine	Glutamyl-tRNA synthetase (EC 6.1.1.18)	698	136, 3454, 3709, 4846, 1776
<i>glnT</i>	78.0	Glutamine	Levels of glutamine tRNA ₁ and glutamine synthetase	697	3001
<i>glnU</i>	15.0	Glutamine	<i>glnU</i> α ; <i>su_B</i> , <i>supB</i> (ochre [UAA] suppression); glutamine tRNA ₁ , tandem duplication	696	1285, 1915, 2313, 3102, 3103, 3454
<i>glnV</i>	15.0	Glutamine	<i>glnV</i> α ; <i>Su₁₁</i> , <i>Su2</i> , <i>supE</i> (amber suppression); glutamine tRNA ₂ , tandem duplication (VX)	695	1122a, 1285, 1915, 1916, 2313, 3102, 3103, 3454

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>glnW</i>	15.0	Glutamine	<i>glnUβ</i> ; <i>su_B</i> , <i>supB</i> (ochre [UAA] suppression); glutamine tRNA ₁ , tandem duplication (UW)	37440	1122a, 3001
<i>glnX</i>	15.0	Glutamine	<i>glnVβ</i> ; <i>Su₁₁</i> , <i>Su₂</i> , <i>supE</i> (amber suppression); glutamine tRNA ₂ , tandem duplication (VX)	37443	1122a, 1285, 1915, 1916, 2313, 3102, 3103, 3454
<i>gloA</i>	37.2	Glyoxalase	Glyoxalase I	39135	2703, 952
<i>glpA</i>	50.7	Glycerol phosphate	Glycerol-3-phosphate dehydrogenase (anaerobic) large subunit (EC 1.1.99.5)	694	1130, 2424, 3936, 799
<i>glpB</i>	50.7	Glycerol phosphate	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic) subunit (EC 1.1.99.5); membrane anchor	17692	1130, 4566, 799
<i>glpC</i>	50.7	Glycerol phosphate	<i>sn</i> -Glycerol-3-phosphate dehydrogenase (anaerobic) small subunit (EC 1.1.99.5)	17695	1130, 799
<i>glpD</i>	76.7	Glycerol phosphate	<i>glyD</i> ; glycerol-3-phosphate dehydrogenase (aerobic) (EC 1.1.99.5)	693	171, 2491, 3940, 3942, 3947
<i>glpE</i>	76.7	Glycerol phosphate	Gene of <i>glp</i> regulon	18265	3942, 4926
<i>glpF</i>	88.7	Glycerol phosphate	Glycerol facilitator	692	4313
<i>glpG</i>	76.7	Glycerol phosphate	Gene of <i>glp</i> regulon	18262	3942, 4926
<i>glpK</i>	88.7	Glycerol phosphate	Glycerol kinase (EC 2.7.1.30)	691	324, 3413, 3414, 3798, 3940, 827
<i>glpQ</i>	50.6	Glycerol phosphate	Glycerol-3-phosphate diesterase, periplasmic	690	2424, 2426, 4428
<i>glpR</i>	76.7	Glycerol phosphate	Repressor of <i>glp</i> operon	688	3940, 3942, 3950, 4926, 743
<i>glpT</i>	50.6	Glycerol phosphate	<i>sn</i> -Glycerol-3-phosphate permease	689	1130, 1138, 1581, 1620, 2424, 2477, 2931, 334, 3936, 4571, 4753, 4827
<i>glpX</i>	88.6	Glycerol phosphate	May be involved in glycerol metabolism but not required for growth on glycerol	30884	4474
<i>gltA</i>	16.2	Glutamate	<i>glt</i> , <i>icdB</i> ; citrate synthase (EC 4.1.3.7)	687	1549, 1708, 1859, 2396, 3151, 3356, 402, 4149, 4741, 4773
<i>gltB</i>	72.3	Glutamate	<i>aspB</i> , <i>ossB</i> ; glutamate synthase, large subunit (EC 1.4.1.13)	686	1172, 1363, 2644, 3288, 3863, 657, 853
<i>gltD</i>	72.4	Glutamate	<i>aspB</i> , <i>ossB</i> ; glutamate synthase, small subunit	17689	1363, 3288, 3863, 657
<i>gltE</i>	81.4	Glutamate	Glutamyl-tRNA synthetase; possible regulatory subunit	685	3062
<i>gltF</i>	72.4	Glutamate	<i>ossB</i> ; regulatory gene?	18259	657
<i>gltH</i>	21.8	Glutamate	Growth on glutamate	684	2757, 2758, 3897
<i>gltJ</i>	14.8	Glutamate	Membrane protein, transport gene	49541	2659, 3308
<i>gltK</i>	14.8	Glutamate	Membrane protein, transport gene	49537	2659, 3308
<i>gltL</i>	14.7	Glutamate	Membrane protein, transport gene	49528	2659, 3308
<i>gltM</i>	43.0	Glutamate	Affects glutamyl-tRNA synthetase level or activity?	683	3062
<i>gltP</i>	92.5	Glutamate	Proton-glutamate-aspartate transport protein	34330	1001, 2660, 4423, 4639
<i>gltR</i>	92.3	Glutamate	Growth on glutamate at 42°C	682	2758
<i>gltS</i>	82.5	Glutamate	Glutamate permease	681	1001, 1002, 1078, 1178, 2098, 2655, 2757, 2758, 2950, 3897
<i>gltT</i>	89.8	Glutamate	<i>tgtB</i> ; glutamate tRNA ₂	680	2313, 3446, 3579, 522, 523
<i>gltU</i>	85.0	Glutamate	<i>tgtC</i> ; glutamate tRNA ₂	679	2313
<i>gltV</i>	90.7	Glutamate	<i>tgtE</i> ; glutamate tRNA ₂	678	2313
<i>gltW</i>	58.8	Glutamate	Glutamate tRNA ₂	677	1146, 2313
<i>gltX</i>	54.3	Glutamate	Glutamyl-tRNA synthetase (EC 6.1.1.17)	676	2336, 3851, 498, 539
<i>glyA</i>	57.8	Glycine	Serine hydroxymethyltransferase (EC 2.1.2.1)	675	2633, 3444, 3445, 4191, 4522
<i>glyQ</i>	80.2	Glycine	<i>glySα</i> ; glycyl-tRNA synthetase, α-subunit (EC 6.1.1.14)	33775	4127
<i>glyS</i>	80.2	Glycine	<i>act</i> , <i>gly</i> , <i>glySβ</i> ; glycyl-tRNA synthetase, β-subunit (EC 6.1.1.14)	674	2196, 4127, 502
<i>glyT</i>	90.0	Glycine	<i>sumA</i> ; glycine tRNA ₂ , UGA suppression ^f	673	1849, 2313, 2467, 3743, 90
<i>glyU</i>	64.6	Glycine	<i>suA56</i> , <i>sufD</i> , <i>sumA</i> , <i>sumB</i> , <i>supT</i> ; glycine tRNA ₁	672	1122a, 2313
<i>glyV</i>	94.6	Glycine	<i>ins</i> , <i>mutA</i> ; glycine tRNA ₃ (VXY)	35636	1122a, 2921, 2313
<i>glyW</i>	42.9	Glycine	<i>ins</i> , <i>mutC</i> ; glycine tRNA ₃	670	2313, 2921, 4493, 4494
<i>glyX</i>	94.6	Glycine	Glycine tRNA ₃ (VXY)	35639	2313
<i>glyY</i>	94.6	Glycine	Glycine tRNA ₃ (VXY)	35642	2313
<i>gmd</i>	45.8	GDP-D-mannose dehydratase	Fucose biosynthesis; GDP-D-mannose 4,6-dehydratase	51902	4256
<i>gnk</i>	82.3	GMP kinase	Guanylate kinase (EC 2.7.4.8)	33871	1401
<i>gmm</i>	45.8	GDP mannose mannosyl hydrolase	Guanosine diP mannose mannosyl hydrolase	40934	1307

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>gnd</i>	45.2	Gluconate-P dehydrogenase	Gluconate-6-phosphate dehydrogenase (EC 1.1.1.43)	669	3135, 3138, 3156, 4291, 4768
<i>gntK</i>	77.1	Gluconate	Gluconokinase, thermoresistant	35465	1969, 4436, 980
<i>gntP</i>	98.0	Gluconate	Membrane protein, homologous to <i>B. subtilis</i> gluconate permease	50203	2266
<i>gntR</i>	77.1	Gluconate	Controls <i>gntKU</i> induction, also <i>edd</i> and <i>eda</i> ; gluconate transport and P'n	667	1194, 186, 1969, 3391, 3940, 4436, 4970
<i>gntS</i>	96.8	Gluconate	Secondary gluconate transport system; putative regulator of GntV	666	186, 1943, 569
<i>gntT</i>	76.4	Gluconate	<i>gntM</i> , <i>usgA</i> ; high-affinity gluconate transport	668	1942, 3391, 3487, 4826, 981
<i>gntU</i>	77.0	Gluconate	Low-affinity gluconate transport protein, membrane protein	35461	1969, 4436, 4826, 980
<i>gntV</i>	96.8	Gluconate	Glucokinase, thermosensitive	17686	1942, 569
<i>goaG</i>	29.4		GABA aminotransferase (EC 2.6.1.19)	51935	2066
<i>gor</i>	78.5	GSH oxidoreductase	Glutathione oxidoreductase (EC 1.6.4.2)	665	1150, 1513, 270, 964
<i>gph</i>	75.7	Glycolate phosphatase	Phosphoglycolate phosphatase activity, in <i>dam</i> operon	53568	2681
<i>gpmA</i>	16.9	Glycerol P mutase	Phosphoglycerate mutase 1	35790	456, 958
<i>gpp</i>	85.4	Guanosine pentaphosphatase	Guanosine pentaphosphatase activity; exopolyphosphatase	664	289, 58, 926
<i>gprA</i>	0.3	Growth of phage, replication	Replication of certain lambdoid phage	15896	3240, 3829
<i>gprB</i>	0.2	Growth of phage, replication	Replication of certain lambdoid phage	15890	3240
<i>gpsA</i>	81.5	Glycerol phosphate	<i>sn</i> -Glycerol-3-phosphate dehydrogenase [NAD(P) ⁺] (EC 1.1.1.94)	663	3700, 3701, 4032
<i>gpt</i>	5.5	Guanine-xanthine phosphotransferase	<i>glyD</i> , <i>gpp</i> , <i>gxu</i> ; guanine-xanthine phosphoribosyltransferase (EC 2.4.2.22)	662	1469, 1722, 1979, 3221, 3531, 3662, 535
<i>greA</i>	71.7	Growth restorer?	Transcription elongation factor	33506	1166, 1835, 4141, 4142, 4195, 441, 442, 76
<i>greB</i>	76.2	Growth restorer?	Transcription elongation factor	35448	1835, 442, 76
<i>groE</i>	94.2	Growth of phage	<i>hdh</i> , <i>mop</i> , <i>tabB</i> , <i>groS</i> ; operon	13587	See <i>groE</i> , <i>groL</i>
<i>groL</i>	94.2	Growth of phage	<i>groEL</i> , <i>mopB</i> ; <i>hdh</i> ; <i>tabB</i> ; chaperone for assembly of enzyme complexes; phage morphogenesis; large subunit	492	1068, 1215, 1407, 1409, 2119, 2393, 2454, 3146, 4416, 573
<i>groS</i>	94.2	Growth of phage	<i>groES</i> , <i>mopA</i> ; <i>hdh</i> , <i>tabB</i> ; small subunit of GroE chaperone	493	1068, 1409, 2119, 2393, 2475, 3146, 4416
<i>grpE</i>	59.2	Growth after phage induction	GrpE heat shock protein; mutant survives induction of prophage λ; stimulates DnaK ATPase; nucleotide exchange function	660	2569, 3804, 4093, 4252, 4790, 4791
<i>grxA</i>	19.2	Glutaredoxin	Glutaredoxin 1	17683	1796, 2337, 3771, 3778, 4350
<i>grxB</i>	24.2	Glutaredoxin	Glutaredoxin 2	52078	154, 4595
<i>grxC</i>	81.6	Glutaredoxin	Glutaredoxin 3	42921	154, 155
<i>gshA</i>	60.6	GSH, glutathione	γ-Glutamyl-cysteine synthetase; (EC 6.3.2.2)	659	1368, 1504, 1613, 2853, 3060, 4674
<i>gshB</i>	66.6	GSH, glutathione	Glutathione synthetase (EC 6.3.2.3)	33370	966
<i>gsk</i>	10.8	Guanosine kinase	Guanosine kinase	658	1653, 1824
<i>gsp</i>	67.6	Glutathionylspermidine	Glutathionylspermidine synthetase/amidase; bifunctional protein	36859	420
<i>gsp*</i>	74.6	General secretory pathway operon	<i>hopD</i> , <i>hopG</i> ; <i>gsp</i> previously used for glutathionylspermidine (see above), cryptic general secretory pathway; <i>pul</i> in <i>Klebsiella</i> spp.	55310	1292
<i>gst</i>	36.9	GSH S-transferase	Glutathione S-transferase	37217	3192
<i>guaA</i>	56.7	Guanine	GMP synthetase (EC 6.3.4.1)	657	4414, 4503, 955, 4386
<i>guaB</i>	56.7	Guanine	<i>guaR</i> ; IMP dehydrogenase (EC 1.2.1.14)	656	4399, 4400, 4413, 4503, 955, 4386
<i>guaC</i>	2.4	Guanine	GMP reductase (EC 1.6.6.8)	655	110, 2988, 3689
<i>gurB</i>	75.1	Glucuronide	Utilization of glucuronides	654	3219
<i>gurC</i>	18.0	Glucuronide	Utilization of glucuronides	653	3219
<i>gutM</i>	60.9	Glucitol (sorbitol)	Part of <i>srl</i> operon	33198	4824
<i>gutQ</i>	61.0	Glucitol (sorbitol)	Part of <i>srl</i> operon; putative ATP-binding protein	33206	4828, 757
<i>gyrA</i>	50.3	Gyrase	<i>hisW</i> , <i>nalA</i> , <i>parD</i> , <i>nfxA</i> , <i>nora</i> ; nalidixic acid resistance; cold shock regulon; DNA gyrase, subunit A	651	1053, 1626, 1699, 1869, 2046, 2159, 2339, 2900, 2901, 3112, 4189, 4250, 4311, 4475, 4682, 4888, 4893

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>gyrB</i>	83.5	Gyrase	<i>cou</i> , <i>acrB</i> , <i>himB</i> , <i>hisU</i> , <i>nalC</i> , <i>nalD</i> , <i>pcbA</i> , <i>parA</i> ; novobiocin, coumermycin resistance; DNA gyrase, subunit B	650	10, 1053, 11, 1397, 2159, 2900, 2901, 2944, 3112, 3304, 4607, 4611, 4831, 9, 4438
<i>hcaA</i>	61.6	HCA, hydrocinnamic acid	<i>dig</i> , <i>phd</i> ; 3-phenylpropionate dioxygenase	35007	570, 571
<i>hcaB</i>	61.7	HCA, hydrocinnamic acid	<i>dig</i> , <i>phd</i> ; 3-phenylpropionate-2',3'-dihydrodiol deHase	35010	570, 571
<i>hdeA</i>	78.8	H-NS-determined expression	Periplasmic, unknown function, has σ^S -dependent promoter	33734	138, 4894
<i>hdeB</i>	78.8	H-NS-determined expression	Periplasmic, unknown function, has σ^S -dependent promoter	33731	138, 4894
<i>hdeD</i>	78.8	H-NS-determined expression	Periplasmic, unknown function, has σ^S -dependent promoter	33737	4894
<i>hdhA</i>	36.5	Hydroxysteroid dehydrogenase	<i>hsdH</i> ; 7- α -hydroxysteroid dehydrogenase (EC 1.1.1.159)	32248	4897
<i>helD</i>	22.1	Helicase	<i>srjB</i> ; helicase IV	31769	2642, 2883, 2884, 2885, 4774
<i>hemA</i>	27.2	Hemin	Neomycin sensitivity; hemin biosynthesis; glutamyl tRNA dehydrogenase	648	1087, 177, 1898, 2528, 4573, 709, 4575
<i>hemB</i>	8.4	Hemin	<i>ncf</i> ; 5-aminolevulinic acid dehydratase (EC 4.2.1.24)	647	1111, 19, 2517, 2529, 2530, 2839, 2840, 3297
<i>hemC</i>	86.0	Hemin	<i>popE</i> ; porphobilinogen deaminase (EC 4.3.1.8); neomycin sensitivity	646	1596, 2052, 2054, 2055, 2405, 2645, 2840, 3870, 3871, 4042, 4401, 60, 926
<i>hemD</i>	85.9	Hemin	Uroporphyrinogen III cosynthase; neomycin sensitivity	645	2052, 2053, 3870, 3871, 4042, 926
<i>hemE</i>	90.4	Hemin	Uroporphyrinogen decarboxylase (EC 4.1.1.37)	644	1912, 3196, 3874
<i>hemF</i>	55.0	Hemin	<i>popB</i> , <i>sec</i> ; coproporphyrinogen III oxidase (EC 1.3.3.3)	643	2840, 3037, 4464
<i>hemG</i>	86.9	Hemin	Protoporphyrinogen oxidase activity; neomycin sensitivity	642	3197, 3872, 3873, 4853
<i>hemH</i>	10.7	Hemin	<i>popA</i> , <i>visA</i> ; ferrocyclase (EC 4.99.1.1)	641	1323, 3100, 3101, 2974
<i>hemK</i>	27.3	Hemin	Heme biosynthesis	36992	3127
<i>hemL</i>	3.7	Hemin	<i>gsa</i> , <i>popC</i> ; glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)	372	1519, 1899, 1900
<i>hemM</i>	27.2	Hemin	<i>lolB</i> ; glutamyl-tRNA dehydrogenase? novel outer membrane lipoprotein?	31940	1898, 1981, 2815, 2816, 4573, 709
<i>hemX</i>	85.9	Hemin	Uroporphyrinogen III methylase	33965	3875, 926
<i>hemY</i>	85.9	Hemin	Member of <i>uro</i> (<i>hemC</i>) operon	33969	926
<i>hepA</i>	1.3	Helicase-like protein	<i>rapA</i> ; sequence similarity to helicases, downstream of <i>polB</i> , not under <i>lexA</i> control	29491	1139, 2519, 4269a, 435
<i>het</i>	84.6	Heterogeneous size	<i>cop</i> ; possibly structural gene for DNA-binding protein; near <i>ori</i>	640	3249, 4610, 4771
<i>hflA</i>	94.8	High frequency lysogeny	Operon including <i>hfq</i> , <i>hflX</i> , -K, -C; part of complex <i>mutL-hflC</i> transcription unit	34429	4487
<i>hflB</i>	71.6	High-frequency lysogenization	<i>ftsH</i> , <i>mrsC</i> , <i>tolZ</i> ; cell growth, septum formation, λ development, mRNA decay; essential inner membrane ATP-dependent protease, acting on SecY	735	1486, 1727, 1728, 221, 3565, 41, 4435, 4657
<i>hflC</i>	94.9	High-frequency lysogenization	HflA complex cleaves lambda cII; protease	17520	220, 285
<i>hflK</i>	94.8	High frequency lysogenization	HflA complex cleaves lambda cII; protease	639	220, 285
<i>hflX</i>	94.8	High frequency lysogenization	HflX GTPase, putative	34423	220, 3203
<i>hfq</i>	94.8	Host factor for Q β	HF-I, host factor for phage Q β	34450	2090, 2091, 4024, 4487-4490
<i>hha</i>	10.3	High hemolysin activity	Histone-like; downregulates gene expression, stimulates transposition events	31084	1438, 2929, 3182
<i>hipA</i>	34.2	High persistence	Probable role in cell division	18244	2882, 3028, 3029, 367, 368, 3902
<i>hipB</i>	34.3	High persistence	Probable role in cell division	32207	2882, 367, 368
<i>hisA</i>	45.1	Histidine	<i>N</i> -(5'-phospho-L-ribosylformimino)-5-amino-1-(5'-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	636	1202, 65
<i>hisB</i>	45.1	Histidine	Bifunctional enzyme imidazoleglycerolphosphate (IGP) dehydratase, histidinol phosphatase (EC 3.1.3.15, EC 4.2.1.19)	635	1521, 730
<i>hisC</i>	45.1	Histidine	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	634	1521, 1522
<i>hisD</i>	45.0	Histidine	Histidinol dehydrogenase (EC 1.1.1.23)	633	542, 65, 731
<i>hisF</i>	45.1	Histidine	Cyclase component of IGP synthase complex	631	1202, 1263, 1296, 1376, 1451, 2260, 65

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>hisG</i>	45.0	Histidine	ATP phosphoribosyltransferase (EC 2.4.2.17)	630	1322, 3027, 4572, 542
<i>hisH</i>	45.1	Histidine	Amidotransferase component of IGP synthase	629	1263, 1296, 1376, 1451, 2260, 65
<i>hisI</i>	45.2	Histidine	Formerly <i>hisE</i> and <i>hisI</i> ; bifunctional enzyme PR-ATP pyrophosphatase PR-AMP cyclohydrolase (EC 3.5.4.19, EC 3.6.1.31)	628	65, 731
<i>hisJ</i>	52.3	Histidine	Histidine-binding protein of high-affinity histidine transport system	627	126, 2512
<i>hisM</i>	52.2	Histidine	Histidine transport membrane protein M	25879	2335
<i>hisP</i>	52.2	Histidine	Histidine permease	626	126, 2335, 2512
<i>hisQ</i>	52.2	Histidine	Histidine transport gene	32721	126
<i>hisR</i>	85.8	Histidine	<i>hisT</i> ; histidine tRNA	625	1832, 2313, 2535, 926
<i>hisS</i>	56.8	Histidine	Histidyl-tRNA synthetase (EC 6.1.1.21)	624	1140, 1141, 1301
<i>hlpA</i>	4.3	Histone-like protein	<i>ompH</i> ; <i>firA</i> , <i>orf</i> (<i>skp</i>), <i>skp</i> ; histone-like protein HLP-I (cytoplasmic?); early confusion with adjacent <i>lpxD</i> gene	18241	1, 1040, 1773, 1775, 1784, 2429, 2964, 4402, 4403, 706, 804, 1702
<i>hlyE</i>	26.5	Hemolysin (latent)	Latent hemolysin expressed in presence of <i>Actinobacillus glyX</i> or <i>fjr</i> mutant	53859	1498
<i>hmp</i>	57.9	Hemoglobin-like	<i>fsrB</i> ; hemoglobin-like flavoprotein	32917	109, 2879, 2880, 2881, 3482, 3483, 4068
<i>hns</i>	27.8	Histone-like protein, H-NS	<i>bgY</i> , <i>cur</i> , <i>drc</i> , <i>drdX</i> , <i>drs</i> , <i>fimG</i> , <i>irk</i> , <i>msyA</i> , <i>osmZ</i> , <i>pilG</i> , <i>topX</i> , <i>virR</i> ; H-NS (H1a) DNA-binding protein, histone-like; diverse mutant phenotypes affecting transcription, transposition, inversion, cryptic-gene expression; involved in chromosome organization	960	1041, 1195, 1458, 1750, 2160, 2385, 239, 2482, 2483, 2495, 2828, 327, 3476, 4022, 4146, 4173, 4504, 4507, 4821, 887, 2392, 3599
<i>hofB</i>	2.5	Homologous to <i>fim</i>	<i>hopB</i> ; homologous to PilB of <i>Pseudomonas aeruginosa</i> ; function not established, insertion mutation gives no phenotype	33679	4722
<i>hofC</i>	2.5	Homologous to <i>fim</i>	<i>hopC</i> ; homologous to PilC of <i>P. aeruginosa</i> ; function not established, insertion mutation gives no phenotype	33676	4722
<i>holA</i>	14.4	Holoenzyme	DNA polymerase III, δ -subunit	31431	1067, 2194, 3300, 645
<i>holB</i>	24.9	Holoenzyme	DNA polymerase III, δ' -subunit	31447	1067, 2194, 3300
<i>holC</i>	96.6	Holoenzyme	DNA polymerase III, χ -subunit	31456	2194, 3295, 4808, 644
<i>holD</i>	99.3	Holoenzyme	DNA polymerase, ψ -subunit	31460	2194, 3295, 4808, 646
<i>holE</i>	41.5	Holoenzyme	DNA polymerase III, θ -subunit	31439	2194, 2224, 4097, 4254, 647
<i>hopB</i>	84.7	Host plasmid maintenance	<i>hop</i> ; also used for <i>hof</i> loci (homologous to Pil genes in <i>Pseudomonas</i>); required for mini-F plasmid	37343	3184
<i>hopC</i>	99.4	Host plasmid maintenance	Required for maintenance of stable mini-F plasmid; see also <i>hofC</i>	37346	3184
<i>hopD</i>	11	Host plasmid maintenance	Required for maintenance of stable mini-F plasmid	37349	3184
<i>hpt</i>	3.0	HGPRT	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	622	2024, 535
<i>hrpA</i>	31.9	Helicase-related protein	RNA helicase-like; similarity to eukaryotic DEAH family	36987	3005
<i>hrpB</i>	3.5	Helicase-related protein	RNA helicase-like; similarity to eukaryotic DEAH family and <i>araC</i>	36926	3005, 1331
<i>hrsA</i>	16.5	Heat-responsive suppressor	Suppresses <i>ompC</i> mutation's defective thermoresponse	53146	4520
<i>hscA</i>	57.2	Heat shock cognate	Stress response gene; Hsp70 family	32977	2179, 2484, 3956, 4583
<i>hscB</i>	57.3	Heat shock cognate	Stress response gene; heat shock regulon	40196	2484, 4583
<i>hsdM</i>	98.7	Host specificity	<i>hs</i> , <i>hsm</i> , <i>hsp</i> , <i>rm</i> ; host DNA modification; DNA methylase M	621	1014, 2608, 3800, 4909
<i>hsdR</i>	98.7	Host specificity	<i>hs</i> , <i>hsp</i> , <i>hsr</i> , <i>rm</i> ; host DNA restriction; endonuclease R	620	1014, 2608, 3800, 4909
<i>hsdS</i>	98.7	Host specificity	<i>hss</i> ; specificity determinant for <i>hsdM</i> and <i>hsdR</i>	619	1474, 2608, 3071, 3800, 4909
<i>hslC</i>	19.9	Heat shock locus	Protein expressed as heat shock regulon member	36762	749
<i>hslD</i>	24.1	Heat shock locus	Protein expressed as heat shock regulon member	36765	749
<i>hslE-H</i>	29.7	Heat shock loci	Protein expressed as heat shock regulon member	37190	749
<i>hslJ</i>	31.0	Heat shock locus	Protein expressed as heat shock regulon member	41193	323, 749

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>hslK</i>	40.7	Heat shock locus	Protein expressed as heat shock regulon member	36945	749
<i>hslL-N</i>	70.5	Heat shock loci	Protein expressed as heat shock regulon member	37449	749
<i>hslO-R</i>	76.0	Heat shock loci	Heat shock proteins; HslO is HspG21.0	36769	749
<i>hslU</i>	88.8	Heat shock locus	<i>hplI</i> , <i>clpY</i> ; heat shock protein D48.5, protease? required for peptide hydrolysis of HslVU; modulated by catabolite repression	34157	1341, 2121, 2208, 2963, 3408, 3713, 4889, 749, 750
<i>hslV</i>	88.8	Heat-shock locus	<i>hplO</i> ; heat shock regulon	34160	1341, 2121, 2208, 2963, 3713, 4889, 4890, 749, 750
<i>hslW</i>	94.2	Heat shock locus	Heat-inducible; regulatory gene, near <i>groE</i>	41190	749
<i>htgA</i>	0.2	High-temperature growth	<i>hplY</i> ; heat inducible	30233	1987, 2961, 984
<i>htpG</i>	10.7	Heat shock protein	Heat shock protein C62.5; chaperone	17680	228
<i>htpX</i>	41.2	Heat shock protein	Protein expressed as heat shock regulon member	32320	2327
<i>htrB</i>	24.0	High temperature (requirement)	Not under heat shock regulation; membrane protein affecting cell division, growth, and high-temperature survival	31878	2137, 2140, 2141, 781
<i>htrC</i>	90.3	High temperature (requirement)	Essential for growth at high temperature, under α^{32} (heat shock) regulation	34265	2141, 3589
<i>htrE</i>	3.3	High temperature (requirement)	Sequence homology with pilin protein PapC	30510	3593
<i>htrL</i>	81.7	High temperature (requirement)	RfaH-regulated high-temperature gene	54740	3591
<i>hupA</i>	90.5	HU protein	HU- β , HU-2, histone-like protein	34243	1977, 2125, 2126, 2292, 2391, 422
<i>hupB</i>	9.9	HU protein	<i>dpeA</i> , <i>hopD</i> ; HU- α , HU-1, histone-like protein	18235	1463, 1977, 2124, 2127, 2292, 2391, 2749, 4239
<i>hyaA</i>	22.2	Hydrogenase 1	Hydrogenase 1 small subunit [NiFe]	31781	2897, 2898
<i>hyaB</i>	22.3	Hydrogenase 1	Hydrogenase 1 large subunit [NiFe]	31784	2897, 2898
<i>hyaC</i>	22.3	Hydrogenase 1	Possible membrane-spanning protein of <i>hya</i> operon	31788	2897, 2898
<i>hyaD</i>	22.3	Hydrogenase 1	Processing of HyaA and HyaB	31791	2897, 2898
<i>hyaE</i>	22.3	Hydrogenase 1	Processing of HyaA and HyaB	31794	2897, 2898
<i>hyaF</i>	22.3	Hydrogenase 1	Nickel incorporation in hydrogenase 1 proteins	31797	2897, 2898
<i>hybA</i>	67.7	Hydrogenase 2	<i>hydL</i> , <i>hydC</i> ; hydrogenase 2 [Ni, Fe], small subunit, probably	33407	2896
<i>hybB</i>	67.7	Hydrogenase 2	HYD2 cytochrome <i>b</i> type component, probably	33414	2896
<i>hybC</i>	67.7	Hydrogenase 2	Hydrogenase 2 [Ni Fe] large subunit, probably	33418	2896
<i>hybD</i>	67.7	Hydrogenase 2	Processing element for hydrogenase 2, probably	33421	2896
<i>hybE</i>	67.6	Hydrogenase 2	Function undefined	33424	2896
<i>hybF</i>	67.6	Hydrogenase 2	Regulatory gene	33427	2896
<i>hybG</i>	67.6	Hydrogenase 2	May affect maturation of hydrogenase 2 large subunit	33403	2896
<i>hycA</i>	61.4	Hydrogenase 3	Regulatory gene for <i>hyc</i> and <i>hyp</i> ; counteracts activation by FhlA	33143	1801, 2554, 3883, 412, 4294
<i>hycB</i>	61.4	Hydrogenase 3	Formate-hydrogenlyase system, formate regulon, small subunit of hydrogenase 3?	33169	3883, 2554
<i>hycC</i>	61.3	Hydrogenase 3	Formate-hydrogenlyase system, formate regulon, small subunit of hydrogenase 3?	33166	3883, 2554
<i>hycD</i>	61.3	Hydrogenase 3	Hydrogenase 3 subunit	33162	3883, 2554
<i>hycE</i>	61.3	Hydrogenase 3	Hydrogenase 3 subunit, large, precursor	33159	3746, 3883
<i>hycF</i>	61.3	Hydrogenase 3	Hydrogenase 3 subunit	33154	3883
<i>hycG</i>	61.2	Hydrogenase 3	Hydrogenase 3 subunit	33151	3883
<i>hycH</i>	61.2	Hydrogenase 3	Required for converting HycE precursor to Hyd-3 subunit	33140	2678, 3883
<i>hycI</i>	61.2	Hydrogenase 3	Maturation protease for Ni-containing Hyd-3	50402	3747
<i>hydA</i>	61.1	Hydrogenase	<i>hydNF</i> operon	18232	2145, 2465, 2726, 3376, 3852, 4835
<i>hydG</i>	90.6	Hydrogenase	Two-component regulation of Hyd-3 activity	34252	3410, 4231
<i>hydH</i>	90.5	Hydrogenase	Two-component regulation of Hyd-3 activity, sensor kinase	34249	4231
<i>hydN</i>	61.1	Hydrogenase	Iron-sulfur protein required for Hyd-3 activity	33521	2726
<i>hyfA-J</i>	56.2	Hydrogenase 4	Part of 12-cistron operon encoding putative proton-translocating formate hydrogenlyase system	55682	108a
<i>hyfR</i>	56.3	Hydrogenase 4	Formate-sensing regulator for <i>hyf</i> operon	55719	108a

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>hypA</i>	61.4	Hydrogenase	Formate-hydrogenlyase system; guanine-nucleotide-binding protein, Ni donor for Hyd-3 large subunit	33104	1801, 1976, 2678, 3745
<i>hypB</i>	61.4	Hydrogenase	<i>hydE</i> ; formate-hydrogenlyase system; formate regulon	33110	1801, 1976, 2678, 2725, 3745
<i>hypC</i>	61.4	Hydrogenase	Formate-hydrogenlyase system: formate regulon	33113	1801, 1976, 2678, 3745
<i>hypD</i>	61.4	Hydrogenase	<i>hydF</i> ; formate-hydrogenlyase system: formate regulon	33116	1801, 1976, 2678, 3745, 3855
<i>hypE</i>	61.5	Hydrogenase	<i>hydB</i> ; formate-hydrogenlyase system: formate regulon	33119	1801, 1976, 2678, 3745, 3854
<i>hypF</i>	61.1	Hydrogenase	Mutation results in loss of hydrogenase activity; affects maturation of all hydrogenases, formate regulon	50120	2726
<i>iada</i>	98.2	Isoaspartyl dipeptidase	Isoaspartyl dipeptidase	53593	1382
<i>iap</i>	62.0	Isozymic alkaline P'ase	Aminopeptidase, presumably, that generates alkaline phosphatase isozyme	616	1931, 3120
<i>ibpA</i>	83.3	Inclusion body protein	<i>hslT</i> , <i>hlpN</i> ; chaperone, heat-inducible protein of HSP20 family	33847	2427, 69, 750
<i>ibpB</i>	83.3	Inclusion body protein	<i>hslS</i> , <i>hlpE</i> ; chaperone, heat-inducible protein of HSP20 family	33843	2427, 69, 750
<i>icd</i>	25.7	Isocitrate dehydrogenase	<i>icdE</i> ; isocitrate dehydrogenase, NADP ⁺ -specific (EC 1.1.1.42)	615	124, 1709, 1729, 1753, 625
<i>iclR</i>	91.0	Isocitrate lyase	Isocitrate lyase (EC 4.1.3.1)	614	1331, 2744, 3382, 4290, 840
<i>ihfA</i>	38.7	Integration, host factor	<i>himA</i> , <i>hid</i> ; host infection, mutant λ; site-specific recombination; sequence-specific DNA-binding transcriptional activator, IHF, α subunit	638	1156, 1603, 2461, 2860, 2862, 2882, 2939, 2940, 2941, 2942, 2943, 2944, 3231, 4267, 685, 817
<i>ihfB</i>	20.8	Integration, host factor	<i>himD</i> , <i>hip</i> ; see <i>ihfA</i> , β subunit	637	1156, 1258, 1603, 2216, 2461, 2941, 2943, 2944, 4687
<i>ileR</i>	95.8	Isoleucine	<i>avr</i> , <i>flrA</i> ; Ile repressor; regulation of <i>thr</i> and <i>ilv</i> operons; originally placed at 99.9 min; sequence puts it at 95.8 min	15914	2028, 2029, 4702, 569
<i>ileS</i>	0.5	Isoleucine	Isoleucyl-tRNA synthetase (EC 1.1.1.5)	613	2104, 2945, 3640, 4317, 4422, 4820, 4830
<i>ileT</i>	87.0	Isoleucine	Isoleucine tRNA ₁ , triplicate (T, U, V)	612	2313, 926
<i>ileU</i>	73.8	Isoleucine	Isoleucine tRNA ₁ , triplicate (T, U, V)	611	2313
<i>ileV</i>	4.8	Isoleucine	Isoleucine tRNA ₁ , triplicate (T, U, V)	610	1146, 2313
<i>ileX</i>	69.2	Isoleucine	Isoleucine tRNA ₂	17677	3058
<i>ileY</i>	60.0	Isoleucine	Isoleucine tRNA ₂ variant	53508	4837
<i>ilvA</i>	85.2	Isoleucine-valine (requirement)	<i>ile</i> ; threonine deaminase (EC 4.2.1.16)	609	1086, 1490, 1839, 2445, 3824, 4614, 58, 860, 926
<i>ilvB</i>	83.0	Isoleucine-valine (requirement)	Acetolactate synthase I, valine sensitive (EC 4.1.3.18)	608	1309, 1310, 1453, 1667, 2079, 3168, 3169, 3452, 3607, 4006, 4299, 4513, 4705, 681, 960
<i>ilvC</i>	85.3	Isoleucine-valine (requirement)	<i>ilvA</i> ; ketol-acid reductoisomerase (EC 1.1.1.86)	607	257, 351, 4707, 58, 926
<i>ilvD</i>	85.2	Isoleucine-valine (requirement)	Dihydroxyacid dehydrase (EC 4.2.1.9)	606	1086, 1490, 1839, 2445, 317, 58, 860, 926
<i>ilvE</i>	85.1	Isoleucine-valine (requirement)	<i>ilvC</i> , <i>ilvJ</i> ; branched-chain amino acid aminotransferase (EC 2.6.1.42)	605	1086, 149, 1490, 1839, 2374, 2441, 2445, 316, 4263, 4524, 4706, 613, 860, 926
<i>ilvF</i>	57.0	Isoleucine-valine (requirement)	Production of valine-resistant acetolactate synthase activity	604	3452, 960
<i>ilvG</i>	85.1	Isoleucine-valine (requirement)	Acetolactate synthase II, valine insensitive (EC 4.1.3.18)	603	1086, 1393, 1437, 1490, 1839, 2441, 2442, 2443, 2444, 2445, 2648, 3131, 316, 3348, 4262, 4263, 4524, 575, 58, 860, 926
<i>ilvH</i>	1.9	Isoleucine-valine (requirement)	<i>brnP</i> ; acetolactate synthase II, valine sensitive (EC 4.1.3.18)	602	1437, 1453, 184, 1982, 3450, 3607, 4176, 4177, 4299, 4513, 960
<i>ilvI</i>	1.8	Isoleucine-valine (requirement)	Acetolactate synthase II, valine sensitive (EC 4.1.3.18)	601	1453, 1666, 184, 3450, 3607, 4176, 4177, 4299, 4513, 960
<i>ilvJ</i>	1.3	Isoleucine-valine (requirement)	Acetolactate synthase IV, valine resistant (EC 4.1.3.18)	600	1437, 1975, 3694, 960

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>ilvM</i>	85.1	Isoleucine-valine (requirement)	Acetohydroxy acid synthase II (EC 4.1.3.18); valine insensitive, small subunit	1214	1839, 2445, 2628, 2648, 4706, 860, 926
<i>ilvN</i>	83.0	Isoleucine-valine (requirement)	Acetohydroxy acid synthase I, small subunit (EC 4.1.3.18); valine sensitive small subunit; positive regulator for <i>thr</i> and <i>ilv</i>	15441	1310, 4705, 681
<i>ilvR</i>	99.9	Isoleucine-valine		15917	2029
<i>ilvU</i>	6.4	Isoleucine-valine (requirement)	Regulation of <i>ileS</i> and modification of Ile tRNA ₂ and Val tRNA ₂	599	1214
<i>ilvY</i>	85.2	Isoleucine-valine (requirement)	Positive regulator for <i>ilvC</i>	598	351, 3824, 4707, 58, 926
<i>imp</i>	1.2	Increased membrane permeability	<i>ostA</i> ; permeability of outer membrane to large maltodextrins; antibiotic and detergent sensitivity, stress induced	36754	3828
<i>inaA</i>	50.6	Inducible by acid	Protein induced by acid, independent of SoxRS regulation	32692	3737, 4727
<i>inaR</i>	34.8	Inducible by acid	Regulates <i>inaA</i> (may be <i>marA</i> or <i>soxZ</i> ?)	32696	4727
<i>infA</i>	19.9	Initiation factor	<i>hypA1</i> ? protein chain initiation factor IF1	17674	3475, 3849, 885, 886, 899
<i>infB</i>	71.4	Initiation factor	<i>ssyG</i> ; protein chain initiation factor 2, IF2	597	1561, 1928, 2748, 3016, 3108, 3459, 3462, 4026, 4027, 4029
<i>infC</i>	38.8	Initiation factor	<i>fit?</i> , <i>srjA</i> ; protein chain initiation factor 3, IF3	596	1148, 1601, 2500, 2592, 2829, 3056, 3463, 3527, 3788, 4168, 4710, 4801, 514, 582, 583, 732, 942
<i>inm</i>	79.0	Insensitive NG mutagenesis	Susceptibility to mutagenesis by nitrosoguanidine	595	3767
<i>intA</i>	59.4	Integrase	<i>slpA</i> ; from defective prophage CP4-57	33082	2241, 4455
<i>intB</i>	96.9	Integrase	Prophage P4 integrase, defective prophage derivative	53585	394
<i>intD</i>	12.2	Integrase	<i>int</i> (<i>qsr'</i>); integrase locus within defective prophage derivative <i>qsr'</i>	31133	3059
<i>isfA</i>	86.0	Inhibits SOS function	Regulatory gene; SOS-related	41044	263, 264
<i>ispA</i>	9.5	Isoprenoid synthesis	Farnesyl diphosphate synthase (EC 2.5.1.1)	30978	1328, 1330
<i>ispB</i>	71.8	Isoprenoid synthesis	<i>cel</i> ; octaprenyl diphosphate synthase	35712	150, 3277
<i>katC</i>	6.0	Catalase	IS1B and IS20B insertions sensitize to peroxide; deletion or Tn insertion increases resistance	594	4605
<i>katE</i>	39.1	Catalase	Catalase hydroperoxidase III	593	2609, 2611, 3898, 3899, 4612
<i>katG</i>	89.1	Catalase	Catalase hydrogen peroxidase I	14983	2611, 3036, 3898, 4457, 4592, 4456
<i>kba</i>	71.8	Ketose-bis-phosphate aldolase	Ketose-bis-phosphate aldolase, tagatose-bis-phosphate aldolase; part of <i>aga</i> cluster for K ⁺ transport	592	2490, 3649
<i>kbl</i>	81.7	Ketobutyrate ligase	2-Amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29)	18205	140, 3620
<i>kch</i>	28.2	Potassium (K ⁺) channel	Homology to potassium channel proteins	35309	2026, 2935
<i>kdgK</i>	79.3	Ketodeoxygluconate	Ketodeoxygluconokinase (EC 2.7.1.45)	591	3515
<i>kdgR</i>	41.1	Ketodeoxygluconate	Regulator of <i>kdgK</i> , <i>kdgT</i> , and <i>eda</i>	590	2047, 3515
<i>kdgT</i>	88.4	Ketodeoxygluconate	Ketodeoxygluconate transport system, structural gene	589	2047, 2747, 3465, 3515
<i>kdpA</i>	15.7	Potassium dependence	<i>kac</i> ; K ⁺ -translocating ATPase Kdp subunit	588	1225, 4266, 74
<i>kdpB</i>	15.6	Potassium dependence	<i>kac</i> ; high-affinity potassium transport	587	4266, 74
<i>kdpC</i>	15.6	Potassium dependence	<i>kac</i> ; high-affinity potassium transport	586	4266, 74
<i>kdpD</i>	15.5	Potassium dependence	<i>kac</i> ; sensor kinase for K ⁺ - <i>kdp</i> system	585	153, 3117, 3118, 3472, 3555, 4266, 4597, 4633
<i>kdpE</i>	15.5	Potassium dependence	Transcriptional effector of <i>kdp</i> operon	31571	153, 3117, 3118, 3472, 4266, 4597, 4633
<i>kdpF</i>	15.7	Potassium dependence	Inner membrane protein for K ⁺ transport	35751	1735, 74
<i>kdsA</i>	27.3	KDO synthesis	3-Deoxy-D-manno-octulosonic acid 8-P synthetase	17671	4763, 4764
<i>kdsB</i>	20.9	KDO synthesis	CMP-3-deoxy-D-manno-octulosonate cytidyltransferase	18202	1449, 1450, 3420
<i>kdtA</i>	82.0	KDO transfer (to lipid A)	<i>waaA</i> ; 3-deoxy-D-manno-octulosonate-lipid A transferase (EC 2.4.99.-)	33819	293, 3921, 779, 780
<i>kdtB</i>	82.1	KDO transfer (to lipid A)	CMP-deoxy-D-manno-octulosonate-lipid A transferase (EC 2.4.99.-)	33900	3726, 4128
<i>kefB</i>	74.9	K efflux	<i>trkB</i> ; NEM-activatable K ⁺ /H ⁺ antiporter	83	1226, 209
<i>kefC</i>	1.0	K efflux	<i>trkC</i> ; NEM-activatable K ⁺ /H ⁺ antiporter	82	1226, 209, 2946, 3050
<i>kgtP</i>	58.7	Ketoglutarate	<i>witA</i> ; α-ketoglutarate permease	32867	3977, 3975, 3976, 3978

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>kicA</i>	21.0	Kill cell	<i>mukE</i> ; killing protein	31751	1223, 4844, 4845
<i>kicB</i>	21.0	Kill cell	<i>mukF</i> ; Suppressor of killing protein	31748	1223, 4845
<i>ksgA</i>	1.1	Kasugamycin	<i>S</i> -Adenosylmethionine-6- <i>N'</i> , <i>N'</i> -adenosyl (rRNA) dimethyltransferase	583	105, 106, 107, 1711, 380, 4542
<i>ksgB</i>	37.7	Kasugamycin	High-level resistance to kasugamycin	582	1042, 1286, 1529, 4144
<i>ksgC</i>	12.0	Kasugamycin	Resistance to kasugamycin; affects ribosomal protein S2	581	4896
<i>ksgD</i>	30.9	Kasugamycin	Resistance to kasugamycin	580	1286
<i>lacA</i>	7.8	Lactose	Thiogalactoside acetyltransferase; (EC 2.3.1.18)	579	1696, 1805
<i>lacI</i>	7.9	Lactose	Repressor protein of <i>lac</i> operon	578	1203, 1461, 1811, 2202, 2417, 2492, 2501, 2625, 2626, 2767, 3042, 3217, 331, 335, 3798, 4121, 620
<i>lacY</i>	7.8	Lactose	Galactoside permease (M protein)	577	1127, 1685, 1805, 2033, 3042, 3293, 346, 404, 4121, 4647, 549
<i>lacZ</i>	7.8	Lactose	β -D-Galactosidase (EC 3.2.1.23)	576	1597, 1805, 2033, 2101, 2417, 2781, 4021, 4630
<i>lamB</i>	91.5	Lambda	Phage lambda receptor protein; maltose high-affinity uptake system; in <i>malB</i> cluster	575	1152, 1695, 1778, 1779, 1780, 3941, 4394, 488, 778, 814, 987
<i>lar</i>	30.4	Ral inverse	<i>rac</i> locus; restriction alleviation	37053	2238, 4439
<i>ldcC</i>	4.5	Lysine decarboxylase	Lysine decarboxylase	49257	2217, 4836, 4839
<i>ldhA</i>	31.0	Lactate dehydrogenase	<i>hslF</i> , <i>hslI</i> , <i>hslH</i> ; lactate dehydrogenase	37446	2800, 749, 561a
<i>lepA</i>	58.3	Leader peptidase	GTP binding membrane protein, function unknown; <i>lep</i>	18199	1039, 2754, 2755, 4062
<i>lepB</i>	58.3	Leader peptidase	Signal peptidase I (for nonlipoproteins)	573	2754, 4769, 906, 4062
<i>leuA</i>	1.8	Leucine (biosynthesis)	α -Isopropylmalate synthase (EC 4.1.3.12)	572	1399, 4711, 963, 245
<i>leuB</i>	1.7	Leucine (biosynthesis)	β -Isopropylmalate dehydrogenase (EC 1.1.1.85)	571	963
<i>leuC</i>	1.7	Leucine (biosynthesis)	α -Isopropylmalate isomerase subunit	570	963
<i>leuD</i>	1.7	Leucine (biosynthesis)	α -Isopropylmalate isomerase subunit	569	963
<i>leuJ</i>	13.7	Leucine (biosynthesis)	<i>frt</i> ; regulation of <i>leu</i> and <i>ilv</i> operons	18196	2028
<i>leuO</i>	1.8	Leucine (biosynthesis)	Affects expression of small regulatory Dsr-RNA, translational regulation of <i>rpoS</i> , relieves <i>bgl</i> silencing	35918	2249, 4025, 4506
<i>leuP</i>	99.2	Leucine	<i>leuV</i> β tandemly triplicate <i>leuVPQ</i> , duplicate with <i>leuT</i> ; leucine tRNA ₁	38293	2313
<i>leuQ</i>	99.2	Leucine	<i>leuV</i> γ tandemly triplicate, and duplicate with <i>leuT</i> ; leucine tRNA ₁	38296	2313
<i>leuR</i>	79.3	Leucine	Regulates level of leucyl-tRNA synthetase	567	4392
<i>leuS</i>	14.5	Leucine	Leucyl-tRNA synthetase (EC 6.1.1.4)	566	1658, 4157
<i>leuT</i>	85.8	Leucine	Leucine tRNA ₁ , duplicate with <i>leuVPQ</i>	565	1832, 2313, 926
<i>leuU</i>	71.6	Leucine	Leucine tRNA ₂	564	2313, 4631
<i>leuV</i>	99.2	Leucine	<i>leuV</i> α leucine tRNA ₁ , tandemly triplicate <i>leuVPQ</i> , duplicate with <i>leuT</i>	563	1095, 1285, 2313
<i>leuW</i>	15.0	Leucine	<i>feeB</i> ; leucine tRNA ₃	562	2313, 3102, 3103, 3454, 460, 703
<i>leuX</i>	96.9	Leucine	<i>Su-6</i> , <i>supP</i> ; leucine tRNA ₅ (amber [UAG] suppressor)	561	1122a, 135, 2313, 3210, 4407, 4409, 4899
<i>leuY</i>	9.5	Leucine	Regulates level of leucyl-tRNA synthetase	560	2420
<i>leuZ</i>	42.9	Leucine	Leucine tRNA ₄	17668	2313
<i>lev</i>	9.0	Levallorphan	Resistance to levallorphan	559	916
<i>lexA</i>	91.7	Lambda excision	<i>exrA</i> , <i>recA</i> , <i>spr</i> , <i>umuA</i> ; global regulator for SOS regulon (represses ca. 20 genes)	558	1654, 1755, 1802, 2575, 2576, 2765, 2928, 4017, 479, 496, 497
<i>lgt</i>	63.9	(Pro)lipoprotein glyceryl transferase	<i>umpA</i> ; phosphatidylglycerol:prolipoprotein diacylglycerol transferase	33350	1352, 3561, 3562, 4743
<i>lhr</i>	37.2	Long helicase related protein	Probable ATP-dependent helicase	35720	3656
<i>ligA</i>	54.5	Ligase	<i>lig</i> , <i>dnaL</i> , <i>pdeC</i> ; DNA ligase	557	1398, 1932, 1959
<i>ligT</i>	3.5	Ligase tRNA	Name temporary, not published; 2'-5' RNA ligase	50132	134
<i>linB</i>	29.3	Lincomycin	High-level lincomycin resistance	556	120
<i>lipA</i>	14.2	Lipoate	Lipoate biosynthesis	31534	1672, 1673, 3632, 4563
<i>lipB</i>	14.2	Lipoate	Lipoyl-protein ligase	555	3014, 3632, 4157, 4563, 681
<i>lit</i>	25.8	Late induced T4	Locus within defective prophage ϕ 14; expression of T4 late genes	554	2128, 2129, 829

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>livF</i>	77.4	Leucine, isoleucine, valine (transport)	Membrane protein	33713	14
<i>livG</i>	77.4	Leucine, isoleucine, valine (transport)	<i>hrbB</i> , <i>hrbC</i> , <i>hrbD</i> ; high-affinity branched-chain amino acid transport system; membrane component	553	14, 1657, 3141, 3323, 4850
<i>livH</i>	77.5	Leucine, isoleucine, valine (transport)	<i>hrbB</i> , <i>hrbC</i> , <i>hrbD</i> ; high-affinity branched-chain amino acid transport system; membrane component	552	14, 3142, 3323, 4850, 98
<i>livJ</i>	77.5	Leucine, isoleucine, valine (transport)	<i>hrbB</i> , <i>hrbC</i> , <i>hrbD</i> ; binding protein, high-affinity branched-chain amino acid transport system	551	14, 2406, 3317, 3323, 4418, 4850, 98
<i>livK</i>	77.5	Leucine, isoleucine, valine (transport)	<i>hrbB</i> , <i>hrbC</i> , <i>hrbD</i> ; leucine-specific periplasmic binding protein, high-affinity branched-chain amino acid transport	550	14, 2406, 3141, 3142, 332, 3323, 4418, 4850, 98
<i>livM</i>	77.4	Leucine, isoleucine, valine (transport)	High-affinity transport system	18190	14, 3141, 3142
<i>lldD</i>	81.4	L-Lactose dehydrogenase	<i>lct</i> , <i>lctD</i> ; L-lactate dehydrogenase, FMN dependent (EC 1.1.1.27); Arc regulon	574	1066, 1951, 2556, 4012
<i>lldP</i>	81.4	L-Lactose dehydrogenase	<i>lctP</i> ; L-lactate permease	35161	1066, 1951, 2556, 4012, 4128
<i>lldR</i>	81.4	L-Lactose dehydrogenase	<i>lctR</i> ; regulatory gene	35164	1066, 2556, 4012, 4128
<i>lolA</i>	20.2	Localization OM lipoproteins	Periplasmic protein responsible for sorting and transporting lipoproteins to outer membrane	53417	2815, 2816
<i>lon</i>	9.9	Long form	<i>capR</i> , <i>deg</i> , <i>dir</i> , <i>muc</i> ; DNA-binding, ATP-dependent protease LA; <i>lon</i> mutants form long cells	547	1063, 1297, 1324, 1392, 20, 2768, 2769, 2823, 2992, 3929, 4924, 4925, 682, 733, 752, 4396
<i>lpcA</i>	5.4	Lipopolysaccharide core	<i>gmhA</i> ; phosphoheptose isomerase, T-phage resistance	546	1698, 4562, 517
<i>lpcB</i>	68.0	Lipopolysaccharide core	<i>mrc</i> , <i>pon</i> ; T-phage resistance, novobiocin sensitivity	545	10241
<i>lpd</i>	2.8	Lipoamide dehydrogenase	<i>dhl</i> ; lipoamide dehydrogenase (NADH) (EC 1.8.1.4)	544	1553, 1556, 1558, 2415, 2416, 4199, 4150, 4203, 655, 866
<i>lplA</i>	99.6	Lipoprotein ligase	<i>slr</i> ; lipoate-protein ligase A; selenolipoate resistant	33052	3013, 3014, 3633
<i>lpp</i>	37.8	Lipoprotein	<i>mlpA</i> ; murein lipoprotein structural gene	543	1420, 1529, 1671, 3109, 3110, 4792, 4819, 487, 4971, 3748a
<i>lpxA</i>	4.4	Lipid A expression	UDP-N-acetylglucosamine acetyltransferase	17665	1346, 4747, 804, 876, 877
<i>lpxB</i>	4.4	Lipid A expression	<i>pgsB</i> ; lipid A disaccharide synthase	404	4424, 804, 876, 877
<i>lpxC</i>	2.3	Lipid A expression	<i>asmA</i> ; <i>envA</i> ; essential gene; cell envelope and cell separation	815	2071, 2273, 260, 2675, 2676, 2911, 3091, 3921, 4139, 4275, 4903
<i>lpxD</i>	4.3	Lipid A expression	<i>fir</i> , <i>firA</i> , <i>hlpA</i> , <i>omsA</i> , <i>skp</i> , <i>ssc</i> ; UDP-3-O-(R-3-hydroxymyristoyl)-glucosamine N-acetyltransferase	775	1, 1040, 1773, 1775, 2193, 3761, 3921, 804, 1702
<i>lpxK</i>	20.9	Lipid A expression	Lipid A 4' kinase	51784	1375
<i>lrb</i>	7.3	L-Ribose (utilization)	Affects NADPH-linked L-ribose reductase activity	36791	4459
<i>lrhA</i>	51.8	LysR homolog	<i>genR</i> ; regulatory protein, similar to LysR family	32685	421
<i>lrp</i>	20.1	Leucine regulatory protein	<i>mbf</i> , <i>ihb</i> , <i>livR</i> , <i>lrs</i> , <i>lss</i> , <i>lstR</i> , <i>oppI</i> , <i>rblA</i> ; high-affinity branched-chain amino acid transport system; global regulatory protein, Leu responsive; site-specific blocking of methylation	549	100, 117, 1349, 2416, 2555, 2558, 3167, 3450, 3660, 4516, 4551, 473, 4748, 883, 1627
<i>lspA</i>	0.5	Lipoprotein signal peptidase	<i>dapB</i> , <i>ileS</i> ; prolipoprotein signal peptidase (EC 3.4.99.-)	11326	1913, 2104, 2945, 3640, 4422, 466, 4820, 4829, 4830, 4905
<i>lysA</i>	64.1	Lysine	Diaminopimelate decarboxylase (EC 4.1.1.20)	540	4247, 4249, 716
<i>lysC</i>	91.2	Lysine	<i>apk</i> ; aspartokinase III (EC 1.1.1.3)	539	467, 652, 653
<i>lysP</i>	48.4	Lysine	<i>cadR</i> ; lysine permease	942	3143, 3485, 4198, 4325
<i>lysQ</i>	16.8	Lysine	Lysine tRNA (multiple loci, see <i>lysT</i>)	51037	2313
<i>lysR</i>	64.2	Lysine	LysR, prototype of family of global transcriptional regulators	18187	4248
<i>lysS</i>	65.3	Lysine	<i>asuD</i> <i>herC</i> ; lysyl tRNA synthetase, constitutive	17662	1122a, 1151, 1351, 1383, 1771, 1946, 2173, 686, 768
<i>lysT</i>	16.8	Lysine	<i>Suβ</i> , <i>lysTα</i> , <i>supG</i> , <i>supL</i> (ochre suppression); lysine tRNA (multiple loci, <i>lysQTVWYZ</i>)	537	1122a, 1285, 2313, 3530, 4898

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>lysU</i>	93.8	Lysine	Lysyl tRNA synthetase, inducible	16693	1394, 1946, 1948, 2508, 4541, 686, 268
<i>lysV</i>	54.3	Lysine	<i>supN</i> ; lysine tRNA (multiple loci, see <i>lysT</i>)	132	1122a, 2313, 3238, 4509, 539
<i>lysW</i>	16.8	Lysine	<i>lysTβ</i> ; lysine tRNA (multiple loci, see <i>lysT</i>)	28352	2313
<i>lysX</i>	63.3	Lysine	Lysine excretion	536	2007, 2008
<i>lysY</i>	16.8	Lysine	<i>lysTγ</i> ; lysine tRNA (multiple loci, see <i>lysT</i>)	51031	2313
<i>lysZ</i>	16.8	Lysine	lysine tRNA (multiple loci, see <i>lysT</i>)	51034	2313
<i>lytA</i>	60.6	Lytic	Tolerance to β-lactams; autolysis	18184	1649, 1651, 2380, 4035
<i>lytB</i>	0.6	Lytic	Penicillin tolerance and stringent response effects	34696	1575, 1651, 2380, 3506, 466
<i>lyx</i>	80.7	Lyxose	Novel pathway for utilization of lyxose via xylulose through rhamnose and pentose pathways; xylulose kinase	36908	2437, 3843
<i>maa</i>	10.3	Maltose acetylase	<i>mac</i> ; maltose transacetylase	36808	477
<i>mac</i>	26.5	Macrolide	Macrolide resistance, erythromycin resistance; see also <i>maa</i>	535	4143
<i>mae</i>	33.5	Malic enzyme	May be <i>sfcA</i> ; malic enzyme, NAD linked (EC 1.1.1.38)	36710	2719
<i>mafA</i>	0.9	Maintenance of F	Maintenance of F-like plasmids	534	3249, 3313, 4625–4628
<i>mafB</i>	1.9	Maintenance of F	Maintenance of F-like plasmids	533	4625
<i>malA</i>	76.4	Maltose	<i>malQPT</i> cluster	23561	1781
<i>malB</i>	91.5	Maltose	<i>malG-M</i> cluster	18924	
<i>malE</i>	91.5	Maltose	Maltose-binding protein, periplasmic; substrate recognition for transport and chemotaxis	532	1103, 1224, 1293, 271, 272, 273, 274, 3265, 329, 330, 3644, 3668, 810
<i>malF</i>	91.4	Maltose	Maltose transport complex, inner membrane-spanning subunit	531	1128, 1320, 2850, 3798
<i>malG</i>	91.4	Maltose	Maltose/maltodextrin transport complex, inner membrane-spanning subunit	530	1224, 1295, 3798, 943
<i>malI</i>	36.6	Maltose	Regulatory gene whose product has homology to repressors LacI, GalR, CytR	18181	1129, 3642
<i>malK</i>	91.5	Maltose	<i>malB</i> ; maltose transport complex, ATP-binding subunit	529	1224, 1431, 1701, 271, 272, 274, 3265, 3798, 4394, 814
<i>malM</i>	91.5	Maltose	<i>mola</i> ; periplasmic protein	18178	1432
<i>malP</i>	76.5	Maltose	<i>blu</i> ; maltodextrin phosphorylase (EC 2.4.1.1)	528	1778, 1779, 1781, 3340, 3588, 3706, 3940, 990
<i>malQ</i>	76.4	Maltose	Amylomaltase (EC 2.4.1.25)	527	1778, 1779, 1781, 3551, 3940
<i>malS</i>	80.5	Maltose	α-Amylase, periplasmic, MalT dependent	17659	1306, 3922
<i>malT</i>	76.5	Maltose	Lambda sensitivity; positive regulator for <i>mal</i> regulon	526	1224, 1778, 1779, 1780, 1781, 3587, 3588, 3669, 800, 928, 931, 988, 989, 990
<i>malX</i>	36.6	Maltose	PTS enzyme II homolog; <i>malI</i> regulated	32254	3643
<i>malY</i>	36.6	Maltose	Affects induction of maltose system	32257	3643, 4922
<i>malZ</i>	9.1	Maltose	Maltodextrin glucosidase	29868	2651, 3394, 4352
<i>manA</i>	36.4	Mannose	<i>pni</i> ; mannosephosphate isomerase (EC 5.3.1.8)	525	2024, 2491, 2932, 2933, 3207, 386
<i>manC</i>	87.6	Mannose	<i>mni</i> ; D-mannose isomerase	524	4207
<i>manX</i>	41.0	Mannose	<i>gptB</i> , <i>mpt</i> , <i>ptsL</i> , <i>ptsM</i> , <i>ptsX</i> ; mannose phosphotransferase system, protein II-A (III)	17656	1169, 1171, 3344, 4745
<i>manY</i>	41.0	Mannose	<i>pel</i> , <i>ptsM</i> , <i>ptsP</i>	18175	1169, 1171, 1844, 3344, 4745
<i>manZ</i>	41.0	Mannose	<i>gptB</i> , <i>mpt</i> , <i>ptsM</i> , <i>ptsX</i> ; mannosephosphotransferase enzyme IIB	346	1844, 3344, 4745, 890
<i>map</i>	4.1		Methionine aminopeptidase (EC 3.4.11.18)	30569	294, 676
<i>marA</i>	34.9	Multiple antibiotic resistance	<i>soxQ</i> , <i>cfxB</i> ? <i>nfxC</i> , <i>norB</i> ? resistance to tetracycline, other antibiotics; transcription activator of multiple antibiotic resistance system	18172	130, 1350, 1403, 1448, 1505, 1591, 1592, 1984, 2780, 3737, 4724, 790, 791
<i>marB</i>	34.9	Multiple antibiotic resistance	Regulatory gene for <i>mar</i>	32217	130, 1448, 3737, 790
<i>marR</i>	34.9	Multiple antibiotic resistance	<i>cfxB</i> , <i>soxQ</i> ; repressor of <i>mar</i> operon	30935	130, 1448, 2780, 3737, 4271, 790
<i>mbrB</i>	88.6	Mothball resistant	Resistance to camphor vapors; coupling of cell division and replication, growth rate and partitioning	36929	4468, 4469
<i>mcrA</i>	26.1	Methylcytosine restriction	<i>rglA</i> ; within defective prophage e14; restriction of DNA at 5-methylcytosine residues	10961	3602, 3603, 3604, 3618, 1759

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>mcrB</i>	98.6	Methylcytosine restriction	<i>rglB</i> ; restriction of DNA at 5-methylcytosine residues	4978	1050, 2350, 3602, 3603, 3604, 3739, 3740, 3741
<i>mcrC</i>	98.6	Methylcytosine restriction	Modifies specificity of McrB restriction	34613	1050, 2350, 3603, 3740
<i>mcrD</i>	98.6	Methylcytosine restriction	Inhibits McrE restriction resistance to DMP840, adriamycin, etoposide; possibly modulates Topo IV activity	34616	3603, 3740
<i>mdaB</i>	68.3	Modulator of drug activity		53544	688
<i>mdh</i>	72.9	MDH	Malate dehydrogenase (EC 1.1.1.37)	523	1227, 2831, 4298, 4598
<i>mdoA</i>	23.9	Membrane-derived oligosaccharide	<i>modGH</i> operon	4970	
<i>mdoB</i>	99.0	Membrane-derived oligosaccharide	Phosphoglycerol transferase I activity	18169	1234, 1974, 569
<i>mdoG</i>	23.9	Membrane-derived oligosaccharide	<i>mdoA</i> ; periplasmic oligosaccharide synthesis	31849	1235, 2387, 2388, 2636, 411
<i>mdoH</i>	23.9	Membrane-derived oligosaccharide	<i>mdoA</i> ; membrane glycosyltransferase	31852	1235, 2387, 2388, 2636, 411
<i>meb</i>	78.7	<i>malE</i> bypass	Suppressor of <i>malE secB</i> -defective transport of <i>mal</i> -binding protein	28194	1293
<i>melA</i>	93.5	Melibiose	<i>mel-7</i> ; α -galactosidase (EC 3.2.1.22)	522	1624, 2185, 2501, 2548, 4031, 4685
<i>melB</i>	93.6	Melibiose	<i>mel-4</i> ; thiomethylgalactoside permease II	521	1624, 2185, 2501, 252, 4878
<i>melR</i>	93.5	Melibiose	Regulatory	18166	2501, 462, 4685, 659
<i>menA</i>	88.7	Menaquinone (vitamin K ₂)	Dimethylmenaquinone formation in vitamin K ₂ biosynthesis	520	3465, E
<i>menB</i>	51.2	Menaquinone	1,4-Dihydroxy-2-naphthoate synthase	519	1548, 1550, 3997, 4007, 4011
<i>menC</i>	51.2	Menaquinone	<i>o</i> -Succinylbenzoate synthase II	518	1548, 1550, 310, 4007, 4011
<i>menD</i>	51.2	Menaquinone	<i>o</i> -Succinylbenzoate synthase I (EC 4.1.3.-)	517	1548, 1550, 3338, 3486, 4007, 4011
<i>menE</i>	51.1	Menaquinone	<i>o</i> -Succinylbenzoate-CoA synthase	17653	2384, 3998, 4011
<i>menF</i>	51.2	Menaquinone	Menaquinone pathway-specific isochorismate synthase	35955	3040, 310, 936
<i>mepA</i>	52.7	Murein peptidase	Murein DD-endopeptidase	17650	1890, 2184
<i>mesJ</i>	4.6		Cell cycle protein	49262	3423a
<i>metA</i>	90.8	Methionine	Homoserine transsuccinylase (EC 2.3.1.46)	516	1094, 2919, 2920, 358, 35
<i>metB</i>	88.9	Methionine	<i>met</i> ₁ , <i>met-1</i> ; cystathionine γ -synthase (EC 4.2.99.9)	515	1093, 1508, 1509, 2242, 2347, 2547, 3802, 4917
<i>metC</i>	67.9	Methionine	Cystathionine β -lyase; (EC 4.4.1.8)	514	284, 2918
<i>metD</i>	4.8	Methionine	Methionine sulfoximine sensitivity, D-methionine transport	513	2078
<i>metE</i>	86.5	Methionine	Tetrahydropteroyltryglutamate methyltransferase (EC 2.1.1.14)	512	3284, 58, 66, 926
<i>metF</i>	89.0	Methionine	5,10-Methylenetetrahydrofolate reductase (EC 1.1.1.68)	511	1509, 2242, 2347, 3802, 3803, 4454, 4917
<i>metG</i>	47.3	Methionine	Methionyl-tRNA synthetase; ethionine effects	510	125, 929, 930
<i>metH</i>	91.0	Methionine	B ₁₂ -dependent homocysteine-N ⁵ -methyltetrahydrofolate transmethylase	509	218, 2756, 3283, 3284
<i>metJ</i>	88.9	Methionine	Methionine sulfoximine plus methylmethionine sensitivity; repressor	508	1509, 2078, 2242, 2336, 2347, 2547, 3802, 4109, 4917
<i>metK</i>	66.5	Methionine	Methionine adenosyltransferase (EC 2.5.1.6); ethionine sensitivity	507	1510, 1598, 2336, 2766, 3878, 472
<i>metL</i>	89.0	Methionine	<i>metM</i> ; aspartokinase II-homoserine dehydrogenase II	506	1093, 1508, 1509, 2242, 2347, 3802, 3877, 4916, 4917, 789, 953
<i>metR</i>	86.4	Methionine	Positive regulatory gene for <i>metE</i> and <i>metH</i> and autogenous regulation	18163	2825, 4515, 4703, 601, 926, 4515
<i>metT</i>	15.0	Methionine	<i>metT</i> α ; duplicate gene; methionine tRNA _m ; see <i>metU</i>	505	1285, 1915, 2313, 3102, 3103, 3454
<i>metU</i>	15.0	Methionine	<i>metT</i> β ; duplicate gene; methionine tRNA _m	28349	2313
<i>metV</i>	63.5	Methionine	<i>metZ</i> β ; triplicate gene; initiator methionine tRNA _{i1} (<i>metVWZ</i>)	35659	2198, 2199, 2313
<i>metW</i>	63.5	Methionine	Triplicate gene; methionine tRNA _{i1}	35656	2313, 2198
<i>metY</i>	71.5	Methionine	Methionine tRNA _{i2}	504	1487, 1927, 1928, 2197, 2313
<i>metZ</i>	63.5	Methionine	<i>metZ</i> α ; triplicate gene; initiator methionine tRNA _{i1} ; <i>metVWZ</i>	503	2198, 2199, 2313, 3085
<i>mfd</i>	25.2	Mutation frequency decline	Transcription repair coupling factor	35179	3964–3969

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>mgIA</i>	48.2	Methyl-galactoside	<i>mgIP</i> ; PMG; methyl-galactoside transport and galactose taxis; cytoplasmic membrane protein	502	1158, 1645, 1783, 2925, 3156, 3302, 3751, 3932, 428, 429, 758
<i>mgIB</i>	48.2	Methyl-galactoside	PMG; galactose-binding protein; receptor for galactose taxis	501	1158, 1645, 1783, 2925, 3156, 3302, 3751, 3932, 3938, 3954, 758
<i>mgIC</i>	48.2	Methyl-galactoside	<i>mgIP</i> ; PMG; methyl-galactoside transport and galactose taxis	500	1158, 1645, 1783, 2925, 3156, 3302, 3751, 758
<i>mgIR</i>	16.9	Methyl-galactoside	R-MG; regulatory gene	498	1354
<i>mgsA</i>	22.1 ^b	Methylglyoxal synthase	Methylglyoxal synthase (not shown on map)	57077	4444a
<i>mgtA</i>	96.2	Magnesium transport	<i>corB</i> ; cobalt resistance, magnesium transport	497	3353, 569
<i>mhpA</i>	7.9	<i>m</i> -Hydroxyphenylpropionic acid	3-(3-Hydroxyphenyl)propionate 2-hydroxylase; utilizes MHP	29024	1229, 570, 571
<i>mhpB</i>	8.0	<i>m</i> -Hydroxyphenylpropionic acid	3-(2,3-Dihydroxyphenyl)propionate dioxygenase; utilizes MHP	29027	1229, 4147, 570, 571
<i>mhpC</i>	8.0	<i>m</i> -Hydroxyphenylpropionic acid	Dihydroxyphenylpropionate-ring-fission-product hydrolase; utilizes MHP	29030	1229, 570, 571
<i>mhpD</i>	8.0	<i>m</i> -Hydroxyphenylpropionic acid	<i>mhpS</i> ; 2-keto-4-pentenoate hydratase; utilizes MHP	29033	1229, 570, 571
<i>mhpE</i>	8.0	<i>m</i> -Hydroxyphenylpropionic acid	4-Hydroxy-2-oxovalerate aldolase; utilizes MHP	51197	1229
<i>mhpF</i>	8.0	<i>m</i> -Hydroxyphenylpropionic acid	Acetaldehyde dehydrogenase, acylating; utilizes MHP	53814	1228, 1229
<i>mhpR</i>	7.9	<i>m</i> -Hydroxyphenylpropionic acid	Regulatory gene for MHP utilization	29021	1228, 1229, 570, 571
<i>miaA</i>	94.8	Me-isopentyl-adenine	<i>trpX</i> ; 2-methylthio- <i>N</i> ⁶ -isopentyladenosine tRNA hypermodification	18160	1345, 4487, 4489, 4490, 563, 605, 825, 826
<i>miaD</i>	99.6	Me-isopentyl-adenine	Suppresses leaky <i>miaA</i> (Oc) mutation	35254	826
<i>micF</i>	49.8	mRNA interfering cRNA	<i>stc</i> ; regulatory antisense RNA affecting <i>ompF</i> ; member of <i>soxRS</i> regulon	18157	2955, 2982, 3008, 3608, 3918, 4309, 4520, 93, 4335
<i>minB</i>	26.4	Minicell	<i>min</i> operon; formation of minicells containing no DNA; positioning division septum	495	3895, 954, 971a
<i>minC</i>	26.4	Minicell	Inhibition of FtsZ ring at division site	31329	340, 3614, 970, 971, 971a
<i>minD</i>	26.4	Minicell	Affects cell division and growth; membrane ATPase that activates MinC	31326	2386, 340, 3614, 948, 969, 970, 971a
<i>minE</i>	26.4	Minicell	Reverses inhibition by MinC of FtsZ ring	31317	3614, 948, 970, 993, 971a
<i>mioC</i>	84.6	Minimal origin	Initiation of replication; transcription of 16-kDa protein proceeds through <i>oriC</i>	18154	2603, 2606, 3245, 408
<i>mltA</i>	63.5	Membrane-bound lytic transglycosylase	<i>waaN</i> ; lipoprotein lytic transglycosylase; membrane-bound murein hydrolase, affecting sacculus maturation	53524	1789, 2618, 4517
<i>mltB</i>	60.8	Membrane-bound lytic transglycosylase	<i>slt</i> ; murein hydrolase lipoprotein; Slt35, soluble lytic transglycosylase	41040	1124, 1154, 1789, 1048a
<i>mltC</i>	66.9	Membrane-bound lytic transglycosylase	Peptidoglycan hydrolase activity, lytic transglycosylase family	54700	1049
<i>mltD</i>	5.0	Membrane-bound lytic transglycosylase	<i>dniR</i> (dissimilatory nitrite reductase); reduced amounts of hexaheme nitrite reductase; membrane transglycosylase	1575	2089
<i>mmrA</i>	85.4	Minimal medium recovery	Same as <i>rhlB</i> ? RNA helicase motif	18151	2099, 3993, 926, 4508
<i>mms</i>	69.2	Macromolecular synthesis	Complex operon, macromolecular synthesis	36863	3154
<i>mng</i>	40.0	Manganese	Manganese resistance	494	4063
<i>moaA</i>	17.6	Molybdenate	<i>bisA</i> , <i>chlA</i> , <i>narA</i> ; MPT synthesis; chlorate resistance protein A	922	1003, 1245, 1434, 18, 187, 2030, 207, 2402, 3534, 3986, 4570, 72
<i>moaB</i>	17.6	Molybdenate	MPT synthesis; chlorate resistance protein B	31222	3986
<i>moaC</i>	17.6	Molybdenate	MPT synthesis; chlorate resistance protein C	31225	3986
<i>moaD</i>	17.6	Molybdenate	<i>chlM</i> ; MPT synthesis; chlorate resistance	18475	2030, 3986, 4373
<i>moaE</i>	17.6	Molybdenate	MPT synthesis; chlorate resistance	31228	3986
<i>mobA</i>	87.1	Molybdenum	<i>chlB</i> , <i>narB</i> ; MPT guanine dinucleotide synthesis; chlorate resistance	921	1003, 1245, 1434, 18, 187, 1922, 2402, 3342, 3343, 3465, 3534, 3749, 3986, 654
<i>mobB</i>	87.0	Molybdenum	Molybdenum cofactor biosynthesis, putative nucleotide binding site	43961	1922, 3343
<i>moc</i>	31.9	Modification of CCA	Modification of CCA at 3' end of tRNA	36923	3237
<i>modA</i>	17.1	Molybdenum	Molybdate uptake; chlorate resistance; periplasmic molybdate binding protein	37372	2060, 2820, 2973, 4634

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>modB</i>	17.1	Molybdenum	<i>chlJ</i> ; molybdate uptake; chlorate resistance; membrane-spanning ABC protein	18478	2025, 2060, 2820, 2973, 3630, 3986, 4634
<i>modC</i>	17.2	Molybdenum	<i>chlD</i> , <i>narD</i> ; molybdate uptake; chlorate resistance	920	1003, 1245, 1434, 18, 187, 2025, 2060, 2820, 2973, 3630, 3986, 4634
<i>modE</i>	17.1	Molybdenum	<i>chlD</i> , <i>modR</i> , <i>narD</i> ; molybdate uptake	37366	1539, 2855, 4634
<i>modF</i>	17.1	Molybdenum	<i>chlD</i> , <i>narD</i> , <i>phrA</i> ; molybdate uptake	37369	1539, 4634
<i>moeA</i>	18.6	Molybdenum	<i>bisB</i> , <i>chlE</i> ; MPT synthesis; chlorate resistance	919	1003, 1245, 1434, 1664, 18, 187, 2030, 2402, 3208, 3378, 3534, 3986, 4219
<i>moeB</i>	18.6	Molybdenum	<i>chlN</i> ; MPT synthesis; chlorate resistance	18472	2030, 3208, 3986, 4373
<i>mog</i>	0.2	Molybdenum	<i>bisD</i> , <i>chlG</i> ; unknown function; chlorate resistance	917	1003, 1245, 1434, 18, 187, 2003, 2004, 2060, 3986, 4219
<i>molR</i>	47.3	Molybdate	Unknown function, probably related to molybdate transport	32567	2464, 3736
<i>motA</i>	42.6	Motility	<i>flaJ</i> ; flagellar-regulon member; flagellar rotation	491	374, 375, 4064, 4101, 985
<i>motB</i>	42.5	Motility	<i>flaJ</i> ; flagellar-regulon member; flagellar rotation	490	373, 4064, 4101, 4183
<i>mpl</i>	96.0	<i>meso</i> -Diaminopimelate ligase	UDP- <i>N</i> -acetylmuramate:L-alanyl- γ -D-glutamyl- <i>meso</i> -diaminopimelate ligase; recycles cell wall peptidoglycan (EC 6.3.2.13)	46610	2894
<i>mppA</i>	30.0	Murein peptide permease	Murein tripeptide (L-Ala- γ -D-Glut- <i>m</i> -DAP) permease	53908	3352
<i>mprA</i>	60.5	Microcin peptide regulation	<i>emrR</i> ; controls level of microcin synthesis; negative regulation of EmrAB	33255	1006, 1007, 2622
<i>mraA</i>	2.0	Murein cluster a	D-Alanine carboxypeptidase	489	
<i>mraY</i>	2.1	Murein cluster a	UDP- <i>N</i> -acetylmuramoyl-pentapeptide:undecaprenyl-PO ₄ phosphatase (EC 2.7.8.13)	30466	1894, 1895
<i>mrcA</i>	75.9	Murein cluster c	<i>ponA</i> ; penicillin-binding protein 1A	484	1930, 4337, 519
<i>mrcB</i>	3.6	Murein cluster c	<i>pbpF</i> , <i>ponB</i> ; peptidoglycan synthetase; penicillin-binding protein 1Bs	483	2166, 3096, 3097, 3601, 3714, 4307, 4337, 4346, 4957, 519
<i>mrda</i>	14.3	Murein cluster d	<i>pbpA</i> ; penicillin-binding protein PBP 2, mecillinam resistance	18148	156, 157, 279, 4157, 4232, 4233, 4343, 4587, 545
<i>mrdb</i>	14.3	Murein cluster d	<i>rodA</i> ; affects cell shape; mecillinam sensitivity	18145	156, 157, 279, 2818, 4232, 4233
<i>mreB</i>	73.2	Murein cluster e; mecillinam resistance	<i>envB</i> , <i>mon</i> , <i>rodY</i> ; mecillinam resistance; cell shape, affects division versus elongation	31343	1062, 1968, 2624, 434, 4616, 4617, 4619, 4716
<i>mreC</i>	73.2	Mecillinam resistance	Cell division and growth; mecillinam resistance; rod shape-determining protein	31348	4617, 4618
<i>mreD</i>	73.2	Mecillinam resistance	Mecillinam resistance; rod shape-determining protein	31351	4617, 4618
<i>mrp</i>	47.2	Methionine-related protein	Putative ATPase; in <i>Salmonella</i> , homolog is part of alternative pyrimidine pathway to Thi (<i>apbC</i>)	32572	3409, 930
<i>mrr</i>	98.8	Methyl-purine restriction	Restriction of methylated adenine	18139	1700, 3603
<i>msbA</i>	20.8	Multicopy suppressor of <i>htrB</i>	ABC transporter homology; biogenesis of outer membrane	31743	2139, 3474
<i>msbB</i>	41.8	Multicopy suppressor of <i>htrB</i>	Role in outer membrane structure or function	32359	2138
<i>mscL</i>	74.1	Mechanosensitive channel	Cytoplasmic membrane channel protein, opens large pore in response to mechanical stress	35417	400, 401, 4267, 4268, 4269
<i>msrA</i>	95.7	Methionine sulfoxide reductase	<i>pmsR</i> ; methionine sulfoxide reductase	34400	3018, 3585, 3586, 525
<i>msyB</i>	24.0	Multicopy suppressor of <i>secY</i>	In multicopy restores growth and protein export functions of <i>secY</i> and <i>secA</i> mutants	34718	4504
<i>mtgA</i>	72.1	Monofunctional transglycolase	Monofunctional biosynthetic peptidoglycan transglycosylase	54732	4159
<i>mtlA</i>	81.3	Mannitol	<i>mtlC</i> (promoter/operator); mannitol-specific enzyme II of PTS	481	2018, 2459, 2468, 965
<i>mtlD</i>	81.3	Mannitol	Mannitol-1-phosphate dehydrogenase (EC 1.1.1.17)	479	2018, 2347, 965
<i>mtlR</i>	81.3	Mannitol	Mannitol repressor	36774	1236
<i>mtr</i>	71.2	Methyltryptophan	High-affinity Trp permease; TyR regulon	478	1689, 1764, 1688, 3864
<i>mukB</i>	21.0	Mukaku (anucleate)	Required for chromosome partitioning; DNA binding; kinesin-like motor protein?	31516	1188, 1761, 1977, 3183, 1185, 3819, 4589
<i>mul</i>	83.1	Mutability lambda	Mutability in UV-radiated lambda phage	477	4620

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>murA</i>	71.8	Murein	<i>mrba</i> , <i>murZ</i> ; UDP- <i>N</i> -acetylglucosamine enolpyruvyl transferase (EC 2.5.1.7); phosphomycin resistance	33518	2773, 3548, 4571, 527
<i>murB</i>	89.9	Murein	UDP- <i>N</i> -acetylglucosaminyl-3-enolpyruvate reductase (EC 1.1.1.158)	34141	308, 3548, 395
<i>murC</i>	2.2	Murein	L-Alanine adding enzyme	476	1183, 1893, 2021, 2071, 2675, 2676
<i>murD</i>	2.1	Murein	UDP- <i>N</i> -acetylmuramoyl-L-alanine:D-glutamate ligase (EC 6.3.2.9)	30450	1894, 2889, 2890, 3533
<i>murE</i>	2.0	Murein	<i>meso</i> -Diaminopimelate adding enzyme	475	1183, 2071, 2889, 2923, 4349
<i>murF</i>	2.0	Murein	<i>mra</i> ; D-alanyl:D-alanine adding enzyme	474	101, 1183, 2071, 2889, 3368
<i>murG</i>	2.1	Murein	UDP-NAc-glucosamine: NAc-muramyl-(pentapeptide) pyrophosphoryl-undecaprenol NAc-glucosamine transferase	473	1893, 2071, 2889, 2895, 3820
<i>murH</i>	99.3	Murein	Terminal stage in peptidoglycan synthesis, incorporating disaccharide peptide units into wall	18136	3204, 900
<i>murI</i>	89.7	Murein	<i>mbrC</i> , <i>dga</i> , <i>glr</i> ; glutamate racemase (EC 5.1.1.3); D-glutamate synthesis, essential for peptidoglycan	29401	1076, 1077, 1078, 212, 2584, 4900, 523
<i>mutG</i>	43.7	Mutator	Mutation causes high C-to-T mutation in second C of CCAGG; near but distinct from <i>vsr</i> ; provisionally termed <i>mutG</i>	28933	3766
<i>mutH</i>	64.0	Mutator	<i>mutR</i> , <i>prv</i> ; methyl-directed mismatch repair; see also <i>dnaX</i>	471	1222, 1484, 1485, 1706, 4052, 4488, 856
<i>mutL</i>	94.7	Mutator	Methyl-directed mismatch repair	470	1088, 1222, 139, 1706, 4052, 4487, 4489, 4490, 856
<i>mutM</i>	82.1	Mutator	<i>fpg</i> ; repair; GC to TA; formamidopyrimidine-DNA glycosylase	18133	1221, 1489, 1706, 2434, 3717, 4052, 4128, 416, 417, 568, 599, 805, 856
<i>mutS</i>	61.5	Mutator	<i>ant?</i> <i>fdv</i> (formate dehydrogenase 2?); methyl-directed mismatch repair	469	1222, 1706, 2587, 3615, 3853, 4052, 4488, 4802, 856
<i>mutT</i>	2.4	Mutator	AT to GC transversions	468	1288, 1706, 2729, 338, 39, 4052, 856
<i>mutY</i>	66.8	Mutator	<i>micA</i> ; GC to TA transversions; adenine glycosylase, G-A repair	18130	1706, 2922, 3172, 3576, 4052, 856, 4476, 4477
<i>nac</i>	44.4	Nitrogen assimilation control	Regulatory gene, binding <i>ntrC</i>	50182	3073
<i>nadA</i>	16.8	Nicotinamide adenine dinucleotide	Quinolinate synthetase, A protein	467	1257, 2819, 4246
<i>nadB</i>	58.4	Nicotinamide adenine dinucleotide	Quinolinate synthetase, B protein	466	1257, 3015, 4379, 3963
<i>nadC</i>	2.5	Nicotinamide adenine dinucleotide	<i>nic</i> ; quinolinate phosphoribosyl transferase	465	1553, 1556, 1558, 2415, 2416, 3689
<i>nadE</i>	39.2	Nicotinamide adenine dinucleotide	<i>efg</i> , <i>ntrL</i> ; NAD synthetase, ammonia dependent	28576	4752, 70
<i>nagA</i>	15.1	<i>N</i> -Acetylglucosamine	<i>N</i> -acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	464	2491, 3402, 3454–3456, 4599, 4726
<i>nagB</i>	15.1	<i>N</i> -Acetylglucosamine	<i>glmD</i> ; glucosamine-6-phosphate deaminase (EC 5.3.1.10)	463	3402, 3454, 3455, 3456, 3464, 3709, 4601, 4726
<i>nagC</i>	15.1	<i>N</i> -Acetylglucosamine	<i>nagR</i> ; transcriptional regulator of <i>nag</i> operon	31479	3402, 3455, 3456, 3457, 4593, 3458
<i>nagD</i>	15.1	<i>N</i> -Acetylglucosamine	Function unknown, expressed as part of <i>nag</i> operon	36240	3455
<i>nagE</i>	15.2	<i>N</i> -Acetylglucosamine	<i>pstN</i> ; <i>N</i> -acetylglucosamine-specific enzyme II of phosphotransferase system	462	2048, 2491, 3401, 3402, 3454, 3709, 4599, 4726, 4600
<i>nalB</i>	60.2	Nalidixic acid	Sensitivity to nalidixic acid (NAL)	460	1626
<i>nalD</i>	89.2	Nalidixic acid	NAL sensitivity; NAL and glycerol penetration	18124	1827
<i>nanA</i>	72.6	<i>N</i> -Acetylneuraminic acid	<i>N</i> -Acetylneuraminic acid lyase (aldolase) (EC 4.1.3.3)	17647	2782, 3270, 4585
<i>nanT</i>	72.6	<i>N</i> -Acetylneuraminic acid	Sialic acid transport	18121	2782, 4585
<i>napA</i>	49.5	NitrAte reductase, periplasmic	Nitrate reductase homolog	36550	1537, 739, 740
<i>napB</i>	49.5	NitrAte reductase, periplasmic	Cytochrome <i>c</i> homolog	36560	1537, 739, 740
<i>napC</i>	49.5	NitrAte reductase, periplasmic	Cytochrome <i>c</i> homolog	36566	1537, 739, 740
<i>napD</i>	49.6	NitrAte reductase, periplasmic	Unknown function, <i>nap</i> operon	36547	1537, 739, 740

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>napF</i>	49.6	NitrAte reductase, periplasmic	Ferredoxin homolog	36544	1537, 739, 740
<i>napG</i>	49.5	NitrAte reductase, periplasmic	Ferredoxin homolog	36553	1537, 739, 740
<i>napH</i>	49.5	Nitrate reductase, periplasmic	Ferredoxin homolog	36556	1537, 739, 740
<i>narG</i>	27.6	Nitrate reductase, nitrate regulation	<i>chlC</i> , <i>narC</i> ; nitrate reductase α -subunit (EC 1.7.99.4)	459	1118, 1595, 240, 2495, 2532, 2533, 2856, 3727, 391, 4125
<i>narH</i>	27.7	Nitrate reductase, nitrate regulation	<i>chlC</i> ; nitrate reductase β -subunit	18118	1118, 1246, 1433, 240, 2495, 392, 4125
<i>narI</i>	27.7	Nitrate reductase, nitrate regulation	<i>chlI</i> ; cytochrome <i>b_{NR}</i> , structural gene; γ subunit	458	1595, 2495, 3305, 3727, 4125, 4126, 4219, 425, 735
<i>narJ</i>	27.7	Nitrate reductase, nitrate regulation	Nitrate reductase δ -subunit; chaperone	18115	1092, 2495, 2588, 3343, 392, 4125
<i>narK</i>	27.5	Nitrate reductase, nitrate regulation	Nitrate/nitrite antiporter (probably)	18112	1017, 2495, 391, 4220
<i>narL</i>	27.5	Nitrate reductase, nitrate regulation	<i>frdR</i> , <i>narR</i> ; regulatory protein	18109	1122, 1569, 1954, 2096, 2097, 2495, 4008, 4215, 4220
<i>narP</i>	49.3	Nitrate reductase, nitrate regulation	Regulatory protein	32598	3575, 4217
<i>narQ</i>	55.7	Nitrate reductase, nitrate regulation	Nitrate sensor-transmitter protein, anaerobic respiratory path; function redundant with <i>narX</i>	36333	3574, 3575, 3935, 726–728
<i>narU</i>	33.2	Nitrate reductase, nitrate regulation	Nitrate sensor-transmitter protein, anaerobic respiratory path	52770	423
<i>narV</i>	33.1	Nitrate reductase, nitrate regulation	Cryptic nitrate reductase II, γ -subunit	32136	391, 393
<i>narW</i>	33.1	Nitrate reductase, nitrate regulation	Cryptic nitrate reductase II, δ -subunit	32139	391, 393, 423
<i>narX</i>	27.5	Nitrate reductase, nitrate regulation	<i>frdR</i> , <i>narR</i> ; nitrate sensor-transmitter protein; functional redundancy with <i>narQ</i>	18106	2096, 2097, 2495, 4215, 4220, 4746, 728
<i>narY</i>	33.1	Nitrate reductase, nitrate regulation	Cryptic NR II, β -subunit	32142	391, 393, 423
<i>narZ</i>	33.1	Nitrate reductase, nitrate regulation	Cryptic NR II, α -subunit	18103	391, 393, 424
<i>ndh</i>	25.1	NADH dehydrogenase	Respiratory NADH dehydrogenase	457	1497, 2888, 4901, 615
<i>ndk</i>	57.0	Nucleoside diphosphate kinase	Nucleoside diphosphate kinase (EC 2.7.4.6)	32926	1615, 1616, 2649, 3985
<i>neaB</i>	75.0	Neamine	Neamine sensitivity	456	630
<i>nei</i>	16.0	Endonuclease VIII	DNA glycosylase/apurinic lyase, deoxyinosine-specific; endonuclease VIII	53314	1656, 2016, 2017, 2875, 3805
<i>nemA</i>	37.2	<i>N</i> -Ethylmaleimide	<i>N</i> -Ethylmaleimide reductase	52714	2968
<i>nfi</i>	90.5	Endonuclease V	Endonuclease V, specific for single-stranded DNA or duplex DNA with damaged U	45426	1018, 1571, 1572, 4874
<i>nfnA</i>	80.8	Nitrofurantoin	Nitrofurantoin sensitivity	18100	3876
<i>nfnB</i>	13.0	Nitrofurantoin	<i>nfsI</i> , <i>nfsB</i> ; resistance to nitrofurantoin; a nitroreductase	18097	2832, 2917, 3876, 490, 4931, 4932
<i>nfo</i>	48.5	Endonuclease IV	Endonuclease IV; member of <i>soxRS</i> regulon	14161	889
<i>nfrA</i>	12.7	N4 (phage) resistant	Outer membrane protein, putative structural receptor for N4 adsorption	31154	2213, 2214
<i>nfrB</i>	12.7	N4 (phage) resistant	Phage N4 susceptibility; membrane protein	31157	2213, 2214
<i>nfrD</i>	54.2	N4 (phage) resistant	Phage N4 susceptibility	36113	2215
<i>nfsA</i>	21.9	Nitrofurazone sensitivity	<i>mdaA</i> ; nitrofurantoin reductase I activity B; overexpression results in resistance to cytotoxic drugs	454	688, 2832, 490, 4930
<i>nhaA</i>	0.4	Na ⁺ /H ⁺ antiporter	<i>ant</i> ; Na ⁺ /H ⁺ antiporter; stress response to high salinity and pH	15893	1081, 1410, 1440, 1909, 2142, 2143, 3272, 3329, 3330, 3583, 4326, 4393, 4577
<i>nhaB</i>	26.6	Na ⁺ /H ⁺ antiporter	Regulator of intracellular pH	30269	2182, 3272, 3329, 3330, 3438, 3439, 4393, 4577
<i>nhaR</i>	0.4	Na ⁺ /H ⁺ antiporter	Positive regulator of Na ⁺ -dependent transcription of <i>nhaA</i> ; DNA-binding; LysR family of regulatory proteins	30281	3330, 3583, 641
<i>nikA</i>	77.8	Nickel	<i>hydC</i> , <i>hydD</i> ; affects formate hydrogen-lyase activity, hydrogenase, and hydrogenase-related fumarase	18226	1340, 3139, 4230, 4796, 4797, 4800
<i>nikB</i>	77.9	Nickel	<i>hydC</i> , <i>hydD</i> ; activity as <i>nikA</i>	33180	3139, 4796

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>nikC</i>	77.9	Nickel	<i>hydC</i> , <i>hydD</i> ; activity as <i>nikA</i>	33183	3139, 4796
<i>nikD</i>	77.9	Nickel	<i>hydC</i> , <i>hydD</i> ; activity as <i>nikA</i>	33186	3139, 4796
<i>nikE</i>	77.9	Nickel	<i>hydD</i> , <i>lipP</i> ? formate hydrogen-lyase activity	18223	3139, 4796, 4797
<i>nirB</i>	75.3	Nitrite reductase	Nitrite reductase [NAD(P)H] subunit (EC 1.6.6.4)	451	1647, 1973, 1998, 2693, 2694, 3386
<i>nirC</i>	75.3	Nitrite reductase	Membrane protein affecting nitrite reductase [NAD(P)H] activity	452	1647, 3386
<i>nirD</i>	75.3	Nitrite reductase	Nitrite reductase [NAD(P)H] subunit (EC 1.6.6.4)	35425	1647, 3386
<i>nlpA</i>	82.7	New lipoprotein	Lipoprotein in outer membrane vesicles	35704	2022, 3563, 4833, 4906
<i>nlpB</i>	56.0	New lipoprotein	Nonessential lipoprotein in outer membrane vesicles	33030	463
<i>nlpC</i>	38.6	New lipoprotein	Lipoprotein	35802	4792a
<i>nlpD</i>	61.8	New lipoprotein	May function in cell wall formation	33225	1879, 2414
<i>nmpC</i>	12.4	New membrane protein	<i>phmA</i> ; locus of defective phage <i>qsr'</i> ; porin, outer membrane, not expressed in K-12 due to IS5 insertion	447	1751, 389, 390, 809
<i>non</i>	45.7	Nonmucoid	Affects capsule formation	446	3577
<i>npr</i>	72.1	N-regulated protein	<i>ptsO</i> ; NPr, N-regulated HPr-like protein	43864	3517
<i>nrdA</i>	50.5	Nucleotide reductase	<i>dnaF</i> ; ribonucleoside diphosphate reductase subunit B1 (EC 1.17.4.1); class I enzyme, aerobic, physiologically active	445	1326, 3190, 3451, 4085, 4278, 4279, 4280, 4495, 4496, 4827, 640, 1242, 1243, 1487, 1628
<i>nrdB</i>	50.6	Nucleotide reductase	<i>ftsB</i> ; ribonucleoside diphosphate reductase subunit B2 (EC 1.17.4.1); class I enzyme, aerobic	444	1326, 2338, 3451, 4279, 4357, 4496, 4827, 640, 1242, 1243, 1487, 1628, 3822
<i>nrdD</i>	96.1	Nucleotide reductase	Ribonucleotide reductase, class III, anaerobic	34589	4284
<i>nrdE</i>	60.3	Nucleotide reductase	Nonessential ribonucleoside-diP reductase 2, subunit α , class I, function unknown	53512	2050, 2051
<i>nrdF</i>	60.3	Nucleotide reductase	Nonessential ribonucleoside-diP reductase 2, subunit β , class I, function unknown	53515	2050, 2051
<i>nrdG</i>	96.1	Nucleotide reductase	NrdD activating enzyme, generating glycylic radical	54766	4283
<i>nrfA</i>	92.4	Nitrite reductase, formate-dependent	<i>aidC</i> ; formate-dependent nitrite reduction; tetraheme cytochrome <i>c</i> ₅₅₂ ; <i>aidC</i> mutation complemented by <i>nrfG</i>	34336	1868, 1921, 3334, 937, 11a, 4602
<i>nrfB</i>	92.4	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; pentaheme cytochrome <i>c</i>	34364	1868, 938
<i>nrfC</i>	92.4	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; nonheme FE-S protein, probably transmembrane	34352	1868, 938
<i>nrfD</i>	92.4	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; transmembrane protein similar to QOR	34355	1868, 938
<i>nrfE</i>	92.5	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; membrane protein	34358	1536, 1868, 938
<i>nrfF</i>	92.5	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; periplasmic protein; NrfA/B synthesis?	34361	1536, 1868, 938
<i>nrfG</i>	92.5	Nitrite reductase, formate-dependent	<i>aidC</i> ; function unknown, required for Nrf pathway; <i>aidC</i> mutation complemented by <i>nrfG</i>	34345	1536, 1868, 3334, 11a, 4602
<i>nth</i>	36.9	Endonuclease III	DNA glycosylase/aprimidinic (AP) lyase, specific for damaged pyrimidine sites, particularly Thy; endonuclease III	13070	1656, 202, 2434, 3717, 3805, 4701, 888
<i>ntpA</i>	42.0	Nucleoside triphosphatase	dATP-preferring nucleoside tri-P pyrophosphohydrolase	46700	1950, 3254
<i>nuoA</i>	51.8	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.-)	32679	1197, 4694, 4918, 616
<i>nuoB</i>	51.8	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.-)	32676	1197, 4694, 4918, 616
<i>nuoC</i>	51.7	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.-)	32673	1197, 4694, 616
<i>nuoE</i>	51.7	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.-)	32667	4694, 616
<i>nuoF</i>	51.7	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.-)	32664	1197, 3546, 4694, 616
<i>nuoG</i>	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.-)	32661	1197, 3546, 4694, 616

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>nuoH</i>	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32658	1197, 3546, 4694, 616
<i>nuoI</i>	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32655	1197, 3546, 4694, 616
<i>nuoJ</i>	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32652	3546, 4694, 616
<i>nuoK</i>	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32649	3546, 4694, 616
<i>nuoL</i>	51.5	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32646	3117, 3546, 616
<i>nuoM</i>	51.5	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32639	1197, 4694, 616
<i>nuoN</i>	51.5	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	29354	1197, 4694, 616
<i>nupC</i>	54.1	Nucleoside permease	<i>cru</i> ; transport of nucleosides, except guanosine	443	2303, 3046, 3047, 4944, 539, 586, 864
<i>nupG</i>	66.9	Nucleoside permease	Transport of nucleosides	442	3046, 3047, 3172, 4715
<i>nusA</i>	71.4	N (λ protein) utilization substance	Survives lambda prophage induction; transcription termination/antitermination L factor	441	1312, 1506, 1507, 1513, 1927, 1928, 2375, 2566, 3108, 3459, 3462, 4670, 4945, 939, 3804a
<i>nusB</i>	9.4	N (λ protein) utilization substance	<i>groNB</i> , <i>ssaD</i> , <i>ssyB</i> ; survives prophage induction; transcription termination L factor	440	1313, 1366, 1408, 1926, 3285, 3598, 4004, 4315, 4361, 4670, 851
<i>nusG</i>	90.0	N (λ protein) utilization substance	Stabilizes λ -N-NusA-RNAP antitermination complex	31308	2525, 2526, 2566, 4276, 576, 939
<i>nuvA</i>	9.4	Near UV (sensitivity)	Uridine thiolation factor A activity	439	1210, 2573, 3606, 609
<i>nuvC</i>	44.1	Near UV (sensitivity)	Uridine thiolation factor C activity	438	3781
<i>ogrK</i>	46.7	P2 <i>ogr</i> gene	Positive regulator of P2 growth (insertion of P2 <i>ogr</i> gene)	53483	4100
<i>ogt</i>	30.1	O-methylguanine transferase	O ⁶ -methylguanine-DNA methyltransferase, constitutive	31984	1990, 2698, 2761, 3006, 3503, 3504, 3505, 3629, 7
<i>ompA</i>	21.9	Outer membrane protein	<i>con</i> , <i>tolG</i> , <i>tut</i> ; outer membrane protein 3a (II*; G;d) structural gene	437	1501, 1694, 267, 280, 3023, 3024, 3025, 493, 707, 795, 949, 986
<i>ompC</i>	49.8	Outer membrane protein	<i>meoA</i> , <i>par</i> ; outer membrane protein 1b (Ib, c)	436	2954, 2980, 2981, 3880, 4520, 4574, 4811
<i>ompF</i>	21.2	Outer membrane protein	<i>cmlB</i> , <i>coa</i> , <i>cry</i> , <i>tolF</i> ; outer membrane protein 1a (Ia;b;F)	435	1652, 1841, 1842, 1917, 1918, 258, 2740, 2954, 3075, 3077, 3225, 3550, 3637, 3738, 3880, 4375, 4433, 4492, 4574, 905
<i>ompG</i>	29.7	Outer membrane protein	Novel porin; not shown in Fig. 1; see EcoMap10 (3763a) at 29.75 min	57349	2987, 1194a
<i>ompR</i>	76.2	Outer membrane protein	<i>cry</i> , <i>envZ</i> , <i>ompB</i> ; activator protein for osmoregulation of OmpC and OmpF	434	1374, 1610, 1611, 2110, 1167, 2978, 2979, 2983, 3129, 3946, 4374, 4491, 4584, 4681, 4807, 816, 4038
<i>ompT</i>	12.6	Outer membrane protein	Outer membrane protein 2b; protease VII; cleaves T7 RNA polymerases, Ada, SecY	4984	1462, 1524, 1525, 1715, 2786, 3769, 4265
<i>ompX</i>	18.3	Outer membrane protein	Outer membrane protein, with role in inducing RNAP- σ^E production	35913	2863
<i>oppA</i>	28.0	Oligopeptide permease	Oligopeptide permease	18094	108, 1782, 2494, 3351, 4188
<i>oppB</i>	28.0	Oligopeptide permease	Oligopeptide transport	18091	108, 1782, 2494
<i>oppC</i>	28.1	Oligopeptide permease	Oligopeptide transport	18088	108, 1782
<i>oppD</i>	28.1	Oligopeptide permease	Oligopeptide transport	18085	108, 1782
<i>oppE</i>	98.9	Oligopeptide permease	Oligopeptide transport	18082	108
<i>oppF</i>	28.1	Oligopeptide permease	Oligopeptide transport; ATP hydrolysis	35799	1344
<i>opr</i>	19.0	<i>rpo</i> reversed	Rate of degradation of aberrant RNAP-subunit proteins	18079	3983
<i>ops</i>	66.1	Overproduction of polysaccharide	Level of exopolysaccharide production	18076	4963
<i>oraA</i>	60.8	<i>orf-recA</i>	Putative RecX regulatory protein	33246	4914
<i>ordL</i>	29.4	Oxidoreductase	Putative oxidoreductase	51940	2066

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>oriC</i>	84.6	Origin of replication	<i>poh</i> ; origin of DNA replication	431	148, 1633, 1769, 2075, 2084, 2275, 253, 2635, 2711, 2805, 2905, 2985, 3273, 3275, 3276, 3981, 4131, 4255, 4322, 452, 4610, 4611, 4635, 556, 628
<i>oriJ</i>	30.5	Origin of replication	Locus in defective prophage <i>rac</i>	430	1037, 1038, 2086
<i>orn</i>	94.6	Oligoribonuclease	3' to 5' oligoribonuclease	54868	4942
<i>osmB</i>	28.9	Osmotically inducible	OsmB lipoprotein	31965	1054, 2072, 2073
<i>osmC</i>	33.5	Osmotically inducible	Nonessential gene	32184	1460, 1584
<i>osmE</i>	39.2	Osmotically inducible	<i>anr</i> ; promoter overlaps <i>nadE</i> promoter; regulated by growth phase as well as osmotic pressure	36628	1585, 828
<i>osmY</i>	99.3	Osmotically inducible	<i>csi-5</i> ; periplasmic, σ^S dependent protein (stationary phase)	34640	1054, 2412, 4883, 4884
<i>otsA</i>	42.6	Osmoregulated trehalose synthesis	Trehalose phosphate synthase (EC 2.4.1.15)	18073	1419, 2077
<i>otsB</i>	42.7	Osmoregulated trehalose synthesis	Trehalose phosphate phosphatase (EC 3.1.3.12)	18070	1419, 2077
<i>oxyR</i>	89.6	Oxygen	<i>mor</i> , <i>momR</i> ; bifunctional regulatory protein sensor for oxidative stress	28841	1455, 1712, 2358, 2359, 4242, 4951, 4356
<i>oxyS</i>	89.6	Oxygen	Regulatory RNA; activator for genes that detoxify oxidative damage; small RNA	28844	77
<i>pabA</i>	75.2	<i>para</i> -Aminobenzoate	Sulfonamide resistance; <i>p</i> -aminobenzoate biosynthesis	429	2130, 4593, 535, 4450
<i>pabB</i>	40.8	<i>para</i> -Aminobenzoate	Sulfonamide resistance; <i>p</i> -aminobenzoate biosynthesis	428	1454, 3624, 4593, 535
<i>pabC</i>	24.8	<i>para</i> -Aminobenzoate	Sulfonamide resistance; aminodeoxychorismate lyase	31889	1499, 1500
<i>pac</i>	31.0	Phenylacetate	Phenylacetate degradation	18067	831
<i>pal</i>	16.8	Peptidoglycan-associated lipoprotein	<i>excC</i> ; essential lipoprotein associated with peptidoglycan	35129	1270, 2448, 2450, 4581, 705
<i>panB</i>	3.2	Pantothenate	Ketopantoate hydroxymethyltransferase (EC 4.1.2.12)	427	2037, 2903, 871
<i>panC</i>	3.2	Pantothenate	Pantothenate synthetase (EC 6.3.2.1)	426	2903, 871
<i>panD</i>	3.2	Pantothenate	Aspartate 1-decarboxylase (EC 4.1.1.11)	425	2903, 871
<i>panF</i>	73.4	Pantothenate	Pantothenate permease (symporter)	10818	1971, 4537, 4565
<i>parC</i>	68.2	Partition	Cell partitioning; topoisomerase IV subunit A	33440	1699, 2163, 2164, 2165, 2211, 2360, 3397, 3398, 4923, 695, 4213
<i>parE</i>	68.4	Partition	<i>nfxD</i> ; topoisomerase IV subunit B	33451	2163, 2165, 2211, 2511, 3397, 3398, 491, 4923
<i>pat</i>	89.1	Putrescine aminotransferase	Putrescine aminotransferase	18064	3984
<i>pbpG</i>	47.9	Penicillin-binding protein	Penicillin-binding protein 7 (PBP7)	36349	1714
<i>pck</i>	76.1	PEP carboxykinase	Phosphoenolpyruvate carboxykinase (ATP); (EC 4.1.1.49)	422	1444, 1445, 1446, 2864
<i>pcm</i>	61.8	Protein carboxyl methyltransferase	L-Isoaspartyl protein carboxyl methyltransferase (EC 2.1.1.77); repair of isoaspartyl residues	33221	1325, 2524, 4591
<i>pcnB</i>	3.4	Plasmid copy number	Replication and cell division; poly(A) polymerase I; controls plasmid copy number	13584	13584 2583, 2631, 2572, 2790, 2791, 3625, 631, 632, 1682
<i>pdhR</i>	2.6	Pyruvate-dehydrogenase	Pyruvate-dehydrogenase repressor	30488	1674, 3567, 655
<i>pdxA</i>	1.1	Pyridoxine	Isoniazid resistance; pyridoxine biosynthesis	420	1020, 105, 106
<i>pdxB</i>	52.5	Pyridoxine	Isoniazid resistance; erythronate-4-phosphate dehydrogenase? pyridoxine biosynthesis	419	1020, 143, 144, 3930
<i>pdxH</i>	37.0	Pyridoxine	Isoniazid resistance; pyridoxine-phosphate oxidase	417	1020, 1526, 1529, 2398, 4034
<i>pdxJ</i>	58.2	Pyridoxine	Codon overlap with <i>recO</i> ; complex operon	416	2397, 4340
<i>pdxK</i>	54.6	Pyridoxine	Vitamin B ₆ kinase	51757	4866
<i>pdxL</i>	46.6	Pyridoxine	Pyridoxine kinase	50836	2977
<i>pdxY</i>	37	Pyridoxine	Pyridoxal kinase	53757	4867
<i>pepA</i>	96.6	Peptidase	<i>xerB</i> , <i>carP</i> ; amino-exopeptidase A	30215	2842, 3732, 4226, 4227, 684
<i>pepD</i>	5.5	Peptidase	Peptidase D, a dipeptidase	415	1698, 1722, 2254, 2938, 3384, 724
<i>pepE</i>	91.1	Peptidase	α -Aspartyl dipeptidase (EC 3.4.11.–)	34261	822
<i>pepN</i>	21.3	Peptidase	Amino-peptidase N	414	1233, 1269, 213, 214, 215, 2431, 2833, 2834, 2835, 3384

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>pepP</i>	65.8	Peptidase	Proline aminopeptidase II	28682	4897a, 3100
<i>pepQ</i>	86.8	Peptidase	Proline dipeptidase (EC 3.4.13.9)	34071	3098, 926
<i>pepT</i>	25.5	Peptidase	Putative peptidase T	31914	2617
<i>pfkA</i>	88.5	Phosphofructokinase	6-Phosphofructokinase I (EC 2.7.1.11)	413	1710, 3706, 907
<i>pfkB</i>	38.9	Phosphofructokinase	Suppresses <i>pfkA</i> mutations; phosphofructokinase, Pfk-2	412	817, 908, 909
<i>pflA</i>	20.5	Pyruvate formate-lyase	<i>act</i> ; pyruvate formate lyase I activase	35839	1085, 3699
<i>pflB</i>	20.5	Pyruvate formate-lyase	Pyruvate formate lyase I; induced anaerobically	410	3389, 3699, 3884, 3885, 3886
<i>pflC</i>	89.3	Pyruvate formate-lyase	Pyruvate formate lyase II activase	35847	395, 396
<i>pflD</i>	89.3	Pyruvate formate-lyase	Pyruvate formate lyase II	35843	395, 396
<i>pfs</i>	3.8	PNP similarity	5'-Methylthioadenosine/S-adenosylhomocysteine nucleosidase	54950	834
<i>pgi</i>	91.2	Phosphoglucose isomerase	Glucosephosphate isomerase (EC 5.3.1.9)	409	1311, 1319, 3706, 4678
<i>pgk</i>	66.2	Phosphoglycerate kinase	Phosphoglycerate kinase (EC 2.7.2.3)	408	3148
<i>pgl</i>	17.2	Phosphogluconolactonase	<i>blu</i> ; 6-phosphogluconolactonase (EC 3.1.1.31)	407	3706
<i>pgm</i>	15.4	Phosphoglucomutase	<i>blu</i> ; phosphoglucomutase (EC 5.4.4.2)	406	2647, 3706
<i>pgpA</i>	9.5	Phosphatidylglycerophosphate phosphatase	Phosphatidylglycerophosphate phosphatase, membrane bound, nonessential	17644	1338, 1882, 1885
<i>pgpB</i>	28.8	Phosphatidylglycerophosphate phosphatase	Phosphatidylglycerophosphate phosphatase, membrane bound, nonessential	17641	1051, 1338, 1883, 1885
<i>pgsA</i>	42.9	Phosphatidylglycerophosphate synthase	Phosphatidylglycerophosphate synthetase (EC 2.7.8.5)	405	1459, 3266, 4493, 4518
<i>pheA</i>	59.0	Phenylalanine	Chorismate mutase-P-prephenate dehydratase (EC 5.4.99.5, EC 4.2.1.51) FPA resistance	403	1386, 1388, 1389, 1479, 1480, 1847
<i>pheP</i>	13.0	Phenylalanine	Phenylalanine-specific permease	402	3422, 4720
<i>pheS</i>	38.7	Phenylalanine	<i>phe-act</i> ; phenylalanyl-tRNA synthetase α -subunit (EC 6.1.1.20)	400	1148, 1201, 1213, 2132, 2860, 2862, 3460, 3461, 3463, 4168, 4169, 4171, 4801
<i>pheT</i>	38.7	Phenylalanine	Phenylalanyl-tRNA synthetase β -subunit (EC 6.1.1.20)	399	1148, 1213, 2860, 2862, 3460, 3461, 3463, 4168, 4169, 4801
<i>pheU</i>	94.0	Phenylalanine	<i>pheR</i> , <i>pheW</i> ; phenylalanine tRNA	18061	1345, 1387, 1388, 2313, 3938, 4755, 603, 3442
<i>pheV</i>	67.0	Phenylalanine	Phenylalanine tRNA	18058	2313, 4755, 602, 604, 3442
<i>phnC</i>	93.2	Phosphonate	Phosphonate transporter subunit I (cryptic in K-12); member Pho regulon	34553	2737, 2906, 2908, 4669, 694
<i>phnD</i>	93.1	Phosphonate	<i>psiD</i> ; phosphonate transporter subunit, periplasmic (cryptic in K-12)	17638	2737, 2906, 2907, 2908, 2909, 4621, 4665, 4669, 694
<i>phnE</i>	93.1	Phosphonate	Phosphonate transporter subunit, integral membrane component (cryptic in K-12)	34550	2737, 2906, 2908, 4669, 694
<i>phnF</i>	93.1	Phosphonate	Phosphonate utilization (cryptic in K-12); putative regulatory gene, member of <i>pho</i> regulon	34547	2737, 2906, 2908, 4669, 694
<i>phnG</i>	93.1	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34544	2737, 2906, 2908, 4669, 694
<i>phnH</i>	93.1	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34541	2737, 2906, 2908, 4669, 694
<i>phnI</i>	93.1	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34538	2737, 2906, 2908, 4669, 694
<i>phnJ</i>	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34535	2737, 2906, 2908, 4669, 694
<i>phnK</i>	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34532	2737, 2906, 2908, 4669, 694
<i>phnL</i>	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34529	2737, 2906, 2908, 4669, 694
<i>phnM</i>	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34526	2737, 2906, 2908, 4669, 694
<i>phnN</i>	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34523	2737, 2906, 2908, 4669, 694
<i>phnO</i>	93.0	Phosphonate	Probably regulatory for C-P lyase complex (phosphonate utilization cryptic in K-12)	34520	2737, 2906, 2908, 4669, 694
<i>phnP</i>	92.9	Phosphonate	Carbon-phosphorus lyase complex membrane-bound subunit (utilization cryptic in K-12)	34514	2737, 2906, 2908, 4669, 694
<i>phoA</i>	8.6	Phosphate	Alkaline phosphatase (EC 3.1.3.1)	398	1303, 1597, 1740, 1919, 1920, 2105, 2218, 319, 3866, 3867, 4050, 415, 4443, 4667, 4668, 475, 4816, 674

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>phoB</i>	9.0	Phosphate	<i>phoRc</i> , <i>phoT</i> ; positive response regulator for <i>pho</i> regulon, two-component system	397	1597, 2230, 2732, 2734, 2735, 4040, 415, 4426, 4430, 4661, 4663, 4667, 4668
<i>phoE</i>	5.6	Phosphate	<i>ompE</i> ; outer membrane porin protein E	396	1676, 1722, 3221, 3319, 4426, 4429, 4432, 4433, 4553
<i>phoH</i>	23.4	Phosphate	<i>psiH</i> ; member of <i>pho</i> regulon, P starvation induced	31841	2231, 2320, 2909, 4661
<i>phoP</i>	25.6	Phosphate	In <i>Salmonella</i> , a sensor in the two-component regulatory system, with <i>phoQ</i>	31919	1530, 2146
<i>phoQ</i>	25.6	Phosphate	In <i>Salmonella</i> two-component regulatory system with <i>phoP</i>	31922	2146
<i>phoR</i>	9.0	Phosphate	<i>nmpB</i> , <i>phoR1</i> , <i>R1pho</i> ; positive and negative regulatory gene for <i>pho</i> regulon; sensor of two-component system for <i>pho</i> regulon	394	1112, 2734, 2736, 4040, 4427, 4430, 4661, 4663, 4667, 4753
<i>phoU</i>	84.2	Phosphate	<i>phoT</i> ; P uptake, high-affinity P-specific transport system, regulatory gene	18055	3121, 4196, 4295, 79, 80
<i>phrB</i>	15.9	Photoreactivation	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	391	1073, 1826, 1866, 2632, 2683, 3327, 3841, 3842
<i>phxB</i>	17.0	Phage ϕ X	Adsorption of ϕ X154	389	3049
<i>pin</i>	26.1	Prophage-derived inversion	Locus in defective prophage ϵ 14; calcium-binding protein required for initiation of replication	18049	1159, 2168, 3447, 3448, 4544
<i>pioO</i>	74.4	Protein, initiation?	<i>pinO</i> ; calcium-binding protein, may have a role in initiation of replication	53557	1586, 1587
<i>pit</i>	78.4	P _i transport	Low-affinity P _i transport	385	1149, 1150, 300, 4156
<i>pldA</i>	86.3	Phospholipase, detergent resistant	Detergent-resistant phospholipase A activity	384	1648, 1791, 1792, 2277, 4606, 513, 58, 926, 973, 974
<i>pldB</i>	86.4	Phospholipase, detergent resistant	Lysophospholipase L2	5001	1792, 2277, 2278, 58, 926
<i>plsB</i>	91.6	Phospholipid synthesis	Glycerolphosphate acyltransferase activity	382	2544, 2545
<i>plsC</i>	68.1	Phospholipid synthesis	1-Acyl- <i>sn</i> -glycerol-3-phosphate acyltransferase (EC 2.3.1.51); affects partitioning	33443	802, 803
<i>plsX</i>	24.7	Phospholipid synthesis	Glycerol P auxotrophy in <i>plsB</i> background	18046	2425
<i>pmbA</i>	96.0	Peptide MccB17	<i>mcb</i> , <i>lldE</i> ; antibiotic peptide MccB17	34577	2619, 3061, 3703
<i>pncA</i>	39.9	Pyridine nucleotide cycle	<i>nam</i> ; nicotinamide deamidase (EC 3.5.1.19)	381	1321, 2487, 3347
<i>pncB</i>	21.3	Pyridine nucleotide cycle	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	380	2487
<i>pnp</i>	71.3	Polynucleotide phosphorylase	Polynucleotide phosphorylase (EC 2.7.7.8)	379	1182, 1787, 2854, 290, 3492, 3493, 3494, 3638, 3639, 4333, 868, 869, 4940
<i>pntA</i>	36.1	Pyridine nucleotide transhydrogenase	Pyridine nucleotide transhydrogenase α subunit (EC 1.6.1.1)	18043	771, 772
<i>pntB</i>	36.1	Pyridine nucleotide transhydrogenase	Pyridine nucleotide transhydrogenase β subunit (EC 1.6.1.1)	18040	1436, 771, 772
<i>pnuC</i>	16.9	Putative NMN uptake	Nicotinamide mononucleotide transporter, putative, by homology with <i>Salmonella</i>	53409	1280, 4954
<i>poaR</i>	65.9	Proline oxidase	Regulation of proline oxidase production	377	819a
<i>polA</i>	87.2	Polymerase	<i>resA</i> ; DNA polymerase I (EC 2.7.7.7)	375	2068, 2189, 2190, 3072, 4869, 4941, 4966
<i>polB</i>	1.4	Polymerase	<i>dinA</i> ; DNA polymerase II (EC 2.7.7.7)	374	1174, 1967, 2519, 3385, 4039, 426, 698, 699
<i>popD</i>	0.2	Porphyrin	5-Aminolevulinate dehydratase (EC 4.2.1.24)	371	2839, 3518
<i>potA</i>	25.5	Putrescine-ornithine transporter	ATP-binding membrane protein; putrescine/spermidine-ornithine transporter	31899	1339, 2148, 2150, 2617
<i>potB</i>	25.5	Putrescine-ornithine transporter	Membrane protein, channel-forming, for spermidine uptake	31902	1339, 2150, 2617
<i>potC</i>	25.5	Putrescine-ornithine transporter	Membrane protein, channel-forming, for spermidine uptake	31905	1339, 2150, 2617
<i>potD</i>	25.5	Putrescine-ornithine transporter	Spermidine-binding membrane protein	31908	1339, 2150, 2617
<i>potE</i>	15.4	Putrescine-ornithine transporter	Putrescine-lyase antiporter	31552	2149, 2151, 2152
<i>potF</i>	19.2	Putrescine-ornithine transporter	Apparent periplasmic putrescine-specific binding protein	31694	3440
<i>potG</i>	19.3	Putrescine-ornithine transporter	Apparent nucleotide-binding subunit of putrescine-ornithine transporter	31697	3440
<i>potH</i>	19.3	Putrescine-ornithine transporter	Transmembrane-spanning subunit	31700	3440
<i>potI</i>	19.3	Putrescine-ornithine transporter	Apparent transmembrane-spanning subunit	31703	3440

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>poxA</i>	94.5	Pyruvate oxidase	Regulator of <i>poxB</i>	370	679
<i>poxB</i>	19.6	Pyruvate oxidase	Pyruvate oxidase (EC 1.2.2.2)	369	1482, 1483, 678, 680, 681
<i>ppa</i>	95.8	Pyrophosphatase	Inorganic pyrophosphatase (EC 3.6.1.1)	34394	2389, 2390, 700
<i>ppc</i>	89.4	PEP carboxylase	<i>asp, glu</i> ; phosphoenolpyruvate carboxylase (EC 4.1.1.31)	368	1332, 3000, 3786
<i>pphA</i>	41.4	Phosphoprotein phosphatase	Phosphoprotein phosphatase involved in signalling protein misfolding; heat shock regulon	54632	2966
<i>pphB</i>	61.5	Phosphoprotein phosphatase	As above; heat shock regulon	54636	2966
<i>ppiA</i>	75.2	Peptidylprolyl isomerase	<i>rot</i> , a rotomase; peptidylprolyl- <i>cis-trans</i> -isomerase A	31121	1670, 2252, 2579, 3214
<i>ppiB</i>	11.9	Peptidylprolyl isomerase	A rotomase; peptidylprolyl- <i>cis-trans</i> -isomerase B	31117	1670
<i>ppiC</i>	85.3	Peptidylprolyl isomerase	<i>parvA</i> ; peptidylprolyl- <i>cis-trans</i> isomerase C	35829	3764
<i>ppk</i>	56.5	Polyphosphate kinase	Polyphosphate (linear P _i linked by high-energy bonds) kinase	32894	2323, 37, 873
<i>pps</i>	38.4	PEP synthase	<i>ppsA</i> ; phosphoenolpyruvate synthase	367	3181
<i>ppx</i>	56.5	Exopolyphosphatase	Exopolyphosphatase	32899	2323, 38
<i>pqiA</i>	21.8	Paraquat inducible	Induced by paraquat, regulated by SoxRS	39521	2289, 2290
<i>pqiB</i>	21.8	Paraquat inducible	Induced by paraquat, regulated by SoxRS	39524	2289
<i>pqqL</i>	33.9	Pyrrroloquinoline quinone	Redox cofactor for pyrrroloquinoline quinone synthesis (cryptic in K-12)	35854	364, 4497
<i>pqqM</i>	33.9	Pyrrroloquinoline quinone	Pyrrroloquinoline quinone synthesis (cryptic in K-12)	35857	4497
<i>prc</i>	41.2	PBP protease, C terminal	<i>tsp</i> ; carboxy-terminal protease for penicillin-binding protein, PBP 3	32334	1643, 1644, 179, 2186, 3082, 3970, 4060, 4061
<i>prfA</i>	27.3	Protein release factor	<i>asuA?</i> , <i>sueB</i> , <i>uar</i> , <i>ups?</i> peptide chain release factor 1	14922	1880, 2460, 2808, 3782, 3283, 4273, 650
<i>prfB</i>	65.4	Protein release factor	<i>supK</i> ; peptide chain release factor 2	17635	1880, 2174, 2178, 2460
<i>prfC</i>	99.3	Protein release factor	<i>tos</i> ; release factor 3	34633	1515, 1739, 2808, 2930, 4873
<i>priA</i>	88.9	Primosome	<i>srqA</i> ; primosome factor Y, also called protein n'	27611	2462, 3227, 3228, 3314, 3846, 59
<i>priB</i>	95.3	Primosome	Primosomal protein n	29153	4920, 68
<i>priC</i>	10.6	Primosome	Primosomal protein n'	29161	4920
<i>prlC</i>	78.5	Protein localization	<i>opdA</i> in <i>Salmonella</i> ; oligopeptidase A	18031	1153, 4471, 4472, 820, 821
<i>prlZ</i>	71.4	Protein localization	Suppresses export defects in signal sequence mutations	36421	4688
<i>prmA</i>	73.4	Posttranslation ribosomal protein modification	Methyltransferase for 50s subunit L11	366	4565
<i>prmB</i>	53.0	Posttranslation ribosomal protein modification	Methylation of 50s subunit L3	365	815
<i>proA</i>	5.6	Proline	<i>pro</i> ₁ ; γ -glutamyl phosphate reductase (EC 1.2.1.41)	364	1026, 1214, 1597, 1676, 1677, 1768, 2721, 315, 3153, 4562, 1722
<i>proB</i>	5.6	Proline	<i>pro</i> ₂ ; γ -glutamyl kinase (EC 2.7.2.11)	363	1026, 1214, 1597, 1676, 1677, 1768, 2721, 315, 3153, 3612, 4562, 878
<i>proC</i>	8.7	Proline	<i>pro</i> ₂ , <i>pro</i> ₃ ; pyrroline-5-carboxylate reductase (EC 1.5.1.2)	362	1025, 1597, 2839, 415, 999
<i>proK</i>	79.8	Proline	<i>proV</i> ; proline tRNA ₁	17632	1285, 2313, 2351, 4128
<i>proL</i>	49.2	Proline	<i>proW</i> ; proline tRNA ₂	17629	2313
<i>proM</i>	85.8	Proline	<i>proU</i> ; proline tRNA ₃	17626	2313, 926
<i>proP</i>	93.3	Proline	Low-affinity transport; proline permease, minor	361	1475, 1476, 2827, 2877, 2899, 3613, 4186, 4814, 884
<i>proQ</i>	41.4	Proline	Sensitivity to toxic proline analogs and positive regulator of proline porter II	36840	2947
<i>proS</i>	4.7	Proline	<i>drp</i> ; prolyl-tRNA synthetase (EC 1.1.1.15)	360	2453, 414
<i>proT</i>	83.8	Proline	Proline transport carrier protein, putative	359	3020
<i>proU</i>	60.4	Proline	<i>osrA</i> ; operon <i>proVWX</i> for high-affinity transport for glycine; see also <i>proM</i>	18025	1477, 1478, 1535, 2826, 3537, 4297, 951, 3599
<i>proV</i>	60.4	Proline	<i>proU</i> ; high-affinity transport for glycine; glycine betaine-binding protein; see also <i>proK</i>	18022	1191, 1285, 1477, 1481, 1535, 2826, 4228, 4297, 951
<i>proW</i>	60.4	Proline	<i>proU</i> ; high-affinity transport for glycine, betaine, and proline; see also <i>proL</i>	18019	1535, 1590, 4228
<i>proX</i>	60.5	Proline	<i>proU</i> ; high-affinity transport for glycine, betaine, and proline	35653	1535, 4228
<i>prpA</i>	97.0	Propionate	Growth on propionate	358	2180, 4158

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>prpB-E</i>	7.5	Propionate	Propionate catabolism operon, <i>Salmonella</i> homology and some expression information	55452	4389a
<i>prpR</i>	7.5	Propionate	Regulator, propionate catabolism operon, <i>Salmonella</i> homology	55455	4389a
<i>prr</i>	31.2	Pyrroline	γ -Aminobutyraldehyde (pyrroline) dehydrogenase activity	18016	3984
<i>prs</i>	27.1	PRPP synthetase	<i>dnaR</i> ; phosphoribosylpyrophosphate synthetase (EC 2.7.6.1)	357	103, 1819, 1820, 1821, 1823, 3808, 3495
<i>psd</i>	94.6	Phosphatidylserine decarboxylase	Phosphatidylserine decarboxylase	356	2531, 4020
<i>psiF</i>	8.7	P starvation induced	<i>pho</i> regulon member, requiring PhoRB system	18013	2909, 4668, 674
<i>pspA</i>	29.4	Phage shock protein	Negative regulatory gene for stress σ^{54} dependent phage-shock-protein operon	32009	2250, 2253, 2276, 2987, 320, 4697, 4698, 506, 507
<i>pspB</i>	29.5	Phage shock protein	Regulatory gene, with PspC activates expression of <i>psp</i> operon	32012	2987, 4697, 4698, 506
<i>pspC</i>	29.5	Phage shock protein	Positive regulatory gene, cooperatively with PspB	32015	2987, 4697, 4698, 506
<i>pspE</i>	29.5	Phage shock protein	Expressed in response to stress as part of <i>psp</i> operon, but also transcribed independently	32018	4697, 506
<i>pspF</i>	29.4	Phage shock protein	Transcriptional σ^{54} -dependent activator of <i>psp</i>	50349	1105, 2063, 2064, 2065, 2066
<i>pssA</i>	58.6	Phosphatidylserine synthase	Phosphatidylserine synthase (EC 2.7.8.8)	355	2806, 3269, 4020, 766, 995
<i>pssR</i>	85.0	Phosphatidylserine synthase	Regulatory gene	18010	4145, 832
<i>pstA</i>	84.2	P-specific transport	<i>R2pho</i> , <i>phoR2b</i> , <i>phoT</i> ; high-affinity P-specific transport	18007	3734, 4196, 4296, 79, 80
<i>pstB</i>	84.2	P-specific transport	<i>phoT</i> ; high-affinity P-specific transport; cytoplasmic ATP-binding protein	18004	2514, 3734, 4196, 4296, 672, 79, 80
<i>pstC</i>	84.2	P-specific transport	<i>phoW</i> ; high-affinity P-specific transport; cytoplasmic membrane component	18001	3734, 4196, 4296, 79, 80
<i>pstS</i>	84.2	P-specific transport	<i>phoR2</i> , <i>nmpA</i> , <i>phoR2a</i> , <i>phoS</i> , <i>R2pho</i> ; high-affinity P-specific transport; periplasmic P binding	17998	1112, 1963, 2513, 2515, 2714, 3004, 3734, 4152, 4196, 4295, 4296, 4611, 4667, 4753, 4818, 4967, 536, 79, 80, 857
<i>psu</i>	1.5	Pleiotropic suppressor	Temporary designation for pleiotropic suppressor gene; oxolinic acid resistance	37018	1160
<i>pta</i>	52.0	Phosphotransacetylase	Phosphotransacetylase (EC 2.3.1.8)	353	1548, 1573, 2094, 2512, 2813, 530
<i>pth</i>	27.1	Peptidyl tRNA hydrolase	<i>rap</i> ; peptidyl-tRNA hydrolase; required for phage λ growth	352	1342, 1364, 1544, 1739, 1820, 3064, 976, 4269a
<i>ptrA</i>	63.7	Protease III	Protease III	351	1106, 1107, 1253, 220, 718, 775
<i>ptrB</i>	41.5	Protease III	Protease II	32339	2112
<i>ptsG</i>	24.9	Phosphotransferase system	<i>CR</i> , <i>car</i> , <i>cat</i> , <i>gpt</i> , <i>umg</i> ; glucosephosphotransferase enzyme II	349	1170, 2233, 2925, 3765, 4095, 459, 461, 557, 890
<i>ptsH</i>	54.6	Phosphotransferase system	<i>Hpr</i> , <i>ctr</i> , <i>hpr</i> ; phosphohistidinoprotein-hexose phosphotransferase (EC 2.7.1.69)	348	9836, 2031, 2679, 3369, 3793, 4391, 508, 509, 510, 982, 983
<i>ptsI</i>	54.6	Phosphotransferase system	<i>ctr</i> ; phosphotransferase system enzyme I	347	3369, 983, 983a, 983b, 1163, 1168, 2491, 3793, 4571, 508, 509, 510, 85, 982
<i>ptsN</i>	72.1	Phosphotransferase system	<i>pts</i> in the <i>rpoN</i> operon	38380	3517
<i>ptsP</i>	63.9	Phosphotransferase system	PEP-protein phosphotransferase (reuse of <i>manY</i> synonym)	53527	1171, 3648
<i>purA</i>	94.9	Purine	Adenylosuccinate synthetase (EC 6.3.4.4)	345	1681, 2788, 304, 4770
<i>purB</i>	25.6	Purine	Adenylosuccinate lyase (EC 4.3.2.2)	344	12, 1503, 2788, 1668, 1682
<i>purC</i>	55.9	Purine	<i>ade_g</i> ; phosphoribosylaminoimidazole-succinocarboxamide synthetase (EC 6.3.2.6)	343	2788, 3364, 4415
<i>purD</i>	90.6	Purine	<i>adth_a</i> ; phosphoribosylglycinamide synthetase (EC 6.3.4.13)	342	1260, 2789, 28, 719
<i>purE</i>	11.9	Purine	<i>Pur2</i> , <i>ade3</i> , <i>adef</i> ; phosphoribosylaminoimidazole carboxylase, catalytic subunit (EC 4.1.1.21)	341	1597, 2103, 4412
<i>purF</i>	52.3	Purine	<i>ade_{ub}</i> , <i>purC</i> ; amidophosphoribosyl transferase (EC 2.4.2.14)	340	2727, 3211, 3719, 3826, 4117, 4483
<i>purH</i>	90.6	Purine	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	338	1260, 2789, 28, 3410
<i>purK</i>	11.9	Purine	<i>purE2</i> ; phosphoribosyl glucinamide formyltransferase	17995	2103, 4412

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>purL</i>	58.0	Purine	<i>purI</i> ; phosphoribosylformylglycinamide synthetase (EC 6.3.5.3)	336	1817, 3827, 3901
<i>purM</i>	56.5	Purine	<i>purG</i> ; phosphoribosylaminoimidazole synthetase (EC 6.3.3.1)	335	1817, 4115, 4116
<i>purN</i>	56.5	Purine	<i>ade_c</i> ; 5'-phosphoribosylglycinamide transformylase 1; see <i>purT</i>	17623	4116
<i>purP</i>	83.9	Purine	High-affinity purine transport	17992	578
<i>purR</i>	37.4	Purine	Purine repressor	17989	1681, 2222, 3718, 741
<i>purT</i>	41.6	Purine	Glycinamide ribonucleotide transformylase 2, non-folate-requiring; see <i>purN</i>	32348	2772, 3230
<i>purU</i>	27.7	Purine	<i>tgs</i> ; formyltetrahydrofolate hydrolase	35231	3088, 3089, 444, 446, 447
<i>pus</i>	20.6	Reverse of <i>sup</i> (amber)	Reverses accentuation effects of amber suppressor on <i>relB</i> mutations	334	1044
<i>putA</i>	23.2	Proline utilization	<i>poaA</i> ; proline dehydrogenase (EC 1.5.99.8)	333	1028, 2743, 2989, 3115, 3612, 4186, 4461, 4771, 4777
<i>putP</i>	23.2	Proline utilization	Proline/Na ⁺ , Li ⁺ symport protein	332	2989, 3115, 3116, 3264, 3612, 4186, 4461, 4775, 4776, 4777, 4849
<i>pykA</i>	41.7	Pyruvate kinase	Pyruvate kinase A (II); (EC 2.7.1.40)	32363	1378, 3477, 4534
<i>pykF</i>	37.8	Pyruvate kinase	Pyruvate kinase I (EC 2.7.1.40); fructose-stimulated	17620	1378, 3255, 3477, 397
<i>pyrB</i>	96.3	Pyrimidine	Aspartate transcarbamylase, catalytic subunit (EC 2.1.3.2)	330	1797, 2275, 2510, 3140, 3383, 3715, 3729, 4499
<i>pyrC</i>	24.2	Pyrimidine	Dihydro-orotase (EC 3.5.2.3)	329	193, 2010, 4754
<i>pyrD</i>	21.6	Pyrimidine	Dihydro-orotate oxidase (EC 1.3.3.1)	328	2010, 2423
<i>pyrE</i>	82.2	Pyrimidine	Orotate phosphoribosyltransferase (EC 2.4.2.10)	327	2009, 3511–3514, 4367, 94
<i>pyrF</i>	28.9	Pyrimidine	Orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	326	1070, 2010, 407, 4498
<i>pyrG</i>	62.6	Pyrimidine	CTP synthetase (EC 6.3.4.2)	325	158, 3426, 4709
<i>pyrH</i>	4.1	Pyrimidine	<i>smbA</i> ; UMP kinase	324	4104, 4843
<i>pyrI</i>	96.3	Pyrimidine	Aspartate transcarbamylase, regulatory subunit (EC 2.1.3.2)	323	1219, 1797, 2510, 3383, 3426, 3715, 3729, 4738
<i>qin</i>	35.1	Q independent	<i>kim</i> ; cryptic lambdaoid phage	17529	1177, 455
<i>qmeC</i>	75.3	Q membrane	Glycine resistance; penicillin sensitivity; membrane defect	321	4735
<i>qmeD</i>	64.4	Q membrane	Glycine resistance; penicillin sensitivity; membrane defect	320	4735
<i>qmeE</i>	37.9	Q membrane	Glycine resistance; penicillin sensitivity; membrane defect	319	4735
<i>qor</i>	91.8	Quinone oxidoreductase	Quinone oxidoreductase, NADPH dependent	36654	2549
<i>qsr'</i>	12.2	QSR replacement	DLP12; defective Q-independent lambdaoid prophage, includes <i>intD</i> and <i>nmpD</i>	19200	115, 1751, 2085, 3059, 390
<i>queA</i>	9.1	Queuosine/queuine	S-Adenosylmethionine:tRNA ribosyltransferase-isomerase	29889	2651, 3654, 4094
<i>rac</i>	30.4	Recombination activation	Defective prophage Rac loci; see <i>recE</i> , <i>oriJ</i> , <i>trkG</i> , <i>sieB</i> , <i>lar</i> , <i>racC</i> , <i>racR</i>	318	1036, 1037, 1181, 2086, 2087, 2643, 355, 4750, 4751, 503, 759a
<i>racC</i>	30.5	Recombination activation	Element of defective prophage Rac	32076	748
<i>racR</i>	30.6	Recombination activation	Element of defective prophage Rac; repressor	37433	748, 759a
<i>radA</i>	99.7	Radiation	<i>sms</i> ; sensitivity to gamma and UV radiation	15905	1059, 3160, 4136
<i>radC</i>	82.1	Radiation	Sensitivity to radiation	13913	1220
<i>ranA</i>	58.3		Affects RNA metabolism	317	121
<i>rarD</i>	86.2	Recombination and repair	Chloramphenicol resistance	34089	3259, 926
<i>ras</i>	9.9	Radiation sensitive	Sensitive to X rays and UV	316	4636, 4637
<i>rbfA</i>	71.4	Ribosome binding factor	Overexpression suppresses cold-sensitive 16S rRNA; ribosome binding factor	36919	2044, 590, 917
<i>rbn</i>	87.8	RNase BN	<i>o290</i> ; RNase BN, tRNA processing enzyme	50482	3850, 618
<i>rbsA</i>	84.7	Ribose	<i>rbsP</i> , <i>rbsT</i> ; D-ribose high-affinity transport system (may have chemotaxis function)	12082	1888, 242, 2630, 291
<i>rbsB</i>	84.8	Ribose	<i>prlB</i> , <i>rbsP</i> ; D-ribose periplasmic binding protein	12092	1153, 1888, 2630
<i>rbsC</i>	84.8	Ribose	<i>rbsP</i> , <i>rbsT</i> ; D-ribose high-affinity transport system	12089	1888, 2630, 291, 4915
<i>rbsD</i>	84.7	Ribose	<i>rbsP</i> ; D-ribose high-affinity transport system	314	291
<i>rbsK</i>	84.8	Ribose	Ribokinase (EC 2.7.1.15)	315	1798, 1888, 2630, 4611
<i>rbsR</i>	84.8	Ribose	Regulatory gene	12086	2630

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>rcaA</i>	43.6	Regulation capsule synthesis	Positive regulatory gene for capsule (colanic acid) synthesis; two regulatory proteins from the same gene	17980	1045, 1471, 4243, 4244, 4441
<i>rcaB</i>	49.9	Regulation capsule synthesis	Positive regulatory gene for capsule (colanic acid) synthesis; when overexpressed, restores <i>ftsZ84</i> growth on low-salt medium	17977	1413, 1471, 2188, 4099, 4243–4245, 504
<i>rcaC</i>	49.9	Regulation capsule synthesis	Negative regulatory gene for capsule (colanic acid) synthesis, controls sliminess; contains TerE; probable histidine kinase	17974	1471, 2188, 3037, 4099, 4245, 504
<i>rcaF</i>	4.7	Regulation capsule synthesis	Overexpression confers mucoid phenotype, increases capsule synthesis; restores colony formation of <i>ftsZ84</i> mutants on low salt	29845	1412
<i>rdgA</i>	16.1	RecA-dependent growth	Dependence of growth upon <i>recA</i> gene product	17971	1317
<i>rdgB</i>	67.0	RecA-dependent growth	Dependence of growth and viability upon <i>recA</i>	17968	784
<i>recA</i>	60.8	Recombination	<i>srf</i> , <i>lexB</i> , <i>umuB</i> , <i>zab</i> ; general recombination and DNA repair; pairing and strand exchange; role in cleavage of LexA repressor, SOS mutagenesis	312	1104, 1123, 1239, 1654, 1803, 2177, 2574, 2575, 3833, 3991, 4395, 4604, 4749, 495, 497, 64, 671, 759
<i>recB</i>	63.6	Recombination	<i>rorA</i> ; recombination and repair; RecBCD enzyme (exonuclease V) subunit	311	1107, 1180, 1249, 1743, 3870, 4365, 690, 759, 4785a, 406a
<i>recC</i>	63.7	Recombination	Recombination and repair; RecBCD enzyme (exonuclease V) subunit	310	1107, 1252, 1262, 1743, 3870, 4365, 690, 759, 4785a
<i>recD</i>	63.6	Recombination	<i>hopE</i> ; recombination and repair; RecBCD enzyme (exonuclease V) α -subunit	4975	1248, 3187, 348, 4365, 759, 87
<i>recE</i>	30.5	Recombination	Recombination and repair; in prophage <i>rac</i> locus; degrades one strand 5'–3' in duplex DNA; exonuclease VIII	309	1181, 1287, 2086, 2087, 362, 4751, 748, 759, 760
<i>recF</i>	83.6	Recombination	<i>uvrF</i> ; recombination and repair	308	10, 11, 132, 1517, 152, 2709, 3626, 3627, 379, 3846, 3847, 3848, 4611, 671, 759
<i>recG</i>	82.4	Recombination	<i>spoV?</i> branch migration of Holliday junctions, junction-specific DNA helicase (see <i>ruvABC</i>)	307	1281, 2100, 2593, 2596, 2597, 2598, 2599, 3086, 4721, 59
<i>recJ</i>	65.4	Recombination	Single-stranded DNA-specific exonuclease, 5'–3'	17965	2638, 2639, 2640, 2641, 2642, 4511, 759
<i>recN</i>	59.3	Recombination	<i>radB</i> ; <i>lexA</i> regulon; recombination and repair	10872	2600, 2924, 3425, 3748, 3861, 3862
<i>recO</i>	58.2	Recombination	Conjugational recombination and repair; DNA-binding protein; RecA-like strand assimilation	17962	2297, 2657
<i>recQ</i>	86.3	Recombination	Conjugational recombination and repair, presynaptic stage of recombination; <i>lexA</i> regulon; RecQ helicase	17959	1923, 2883, 3123, 3124, 58, 926
<i>recR</i>	10.6	Recombination	Recombination and DNA repair	31049	2723
<i>recT</i>	30.4	Recombination	Locus in defective prophage <i>rac</i> ; activated by <i>sbcA</i> mutation; DNA-annealing protein	32070	1612, 2298, 2378, 761
<i>relA</i>	62.7	Relaxed	Required for ppGpp synthesis during stringent response to amino acid starvation; ATP:GTP 3'-pyrophosphotransferase (EC 2.7.6.5)	306	1237, 1441, 1442, 2913, 2914, 2915, 3070, 3606, 3934, 4310, 4807a, 924
<i>relB</i>	35.4	Relaxed	Stringent/relaxed response; regulation of RNA synthesis	305	1042, 266
<i>relE</i>	35.4	Relaxed	Function unknown	17956	1411, 266
<i>relF</i>	35.4	Relaxed	Function unknown; overproduction lethal	17953	1411, 266
<i>relX</i>	62.8	Relaxed	Control of ppGpp synthesis	304	3346
<i>rep</i>	85.3	Replicase	<i>dasC</i> , <i>mbrA</i> , <i>mmrA</i> ; Rep helicase, a single-stranded DNA-dependent ATPase	303	1086, 1428, 257, 2613, 342, 343, 4388, 58, 610, 926
<i>rer</i>	89.9	Resistance to radiation	Resistance to UV and gamma radiation	302	4179
<i>rfaB</i>	81.9	Rough	<i>waaB</i> ; UDP-galactose: (glucosyl)lipopolysaccharide-1,6-galactosyltransferase	17617	3361, 3522, 3726, 3921, 4128, 867
<i>rfaC</i>	81.8	Rough	<i>waaC</i> ; LPS core biosynthesis; proximal hexose; UDB-galactose: (glucosyl)LPS-1,6-galactosyltransferase	300	280, 3362, 3726, 3920, 3921, 4128, 702

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>rfaD</i>	81.7	Rough	<i>htrM</i> ; heat-inducible, LPS; allows high-temperature growth; D-glycero-D-mannoheptose epimerase	299	2269, 2728, 2964, 3392, 3590, 3726, 3920, 3921, 4128, 806, 807, 808
<i>rfaF</i>	81.8	Rough	<i>waaF</i> ; ADP-heptose;LPS heptosyltransferase 1	28434	2269, 3362, 3392, 3726, 3920, 3921, 4079, 4128, 702, 807
<i>rfaG</i>	82.0	Rough	<i>waaG</i> ; LPS core biosynthesis; glucosyltransferase I	15583	172, 3361, 3362, 3522, 3726, 3920, 3921, 4128, 867
<i>rfaH</i>	86.7	Rough	<i>sfrB</i> ; regulates LPS core biosynthesis, transcriptional activator	164	200, 201, 2959, 333, 3641, 3921, 867
<i>rfaI</i>	81.9	Rough	UDP-D-galactose: (glucosyl)lipopolysaccharide-1,3-D-galactosyltransferase	17614	3361, 3523, 3726, 3920, 3921, 4128, 867
<i>rfaJ</i>	81.9	Rough	UDP-D-glucose: (galactosyl)lipopolysaccharide glucosyltransferase	17611	3361, 3522, 3523, 3726, 3920, 3921, 4128, 867
<i>rfaK</i>	81.8	Rough	<i>waaK</i> ; not similar to <i>Salmonella rfaK</i> ; adds terminal GlcNac side branch to the lipopolysaccharide core prior to attachment of the O antigen	33791	1698a, 2269, 2271, 3726, 3920, 3921, 4128
<i>rfaL</i>	81.8	Rough	LPS core biosynthesis; O-antigen ligase	28438	2269, 2271, 3726, 3920, 3921, 4128, 1698a
<i>rfaP</i>	82.0	Rough	LPS core biosynthesis; phosphorylation of core	298	280, 3361, 3362, 3522, 3726, 3920, 3921, 4128
<i>rfaQ</i>	82.0	Rough	Heptose region of LPS core	33801	2268, 2271, 3361, 3362, 3435, 3522, 3523, 3726, 3920, 3921, 4128, 779
<i>rfaS</i>	81.9	Rough	LPS core, not affecting attachment of O antigen	28949	172, 2268, 2270, 2271, 3523, 3726, 3920, 3921
<i>rfaY</i>	81.9	Rough	LPS core biosynthesis	33828	2269, 3920, 3921, 4128
<i>rfaZ</i>	81.8	Rough	LPS core biosynthesis	33824	2269, 2271, 3920, 3921
<i>rfbA</i>	45.4	Rough	<i>som</i> ; TDP-glucose pyrophosphorylase	297	2267, 2728, 4208, 4875
<i>rfbB</i>	45.4	Rough	<i>som</i> ; TDP-glucose oxidoreductase-4,6 dehydratase	296	2267, 2728, 4208, 4875
<i>rfbC</i>	45.4	Rough	<i>rfbD</i> ; dTDP-4-deoxyrhamnose-3,5-epimerase	38129	4875
<i>rfbD</i>	45.5	Rough	<i>rfbC</i> ; TDP-rhamnose synthetase	295	2267, 4208, 4875
<i>rfbX</i>	45.4	Rough	Hydrophobic protein, O-antigen	37353	2267, 4875
<i>rfc</i>	45.4	Rough	O-antigen polymerase	53474	2658, 4875
<i>rfe</i>	85.5	Rough	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-P transferase; common and O-antigen synthesis, tunicamycin sensitivity	294	2866, 2867, 2868, 3268, 926
<i>rffA</i>	85.6	Rough	Lipid III biosynthesis in common antigen synthesis	33935	241, 2867
<i>rffC</i>	85.6	Rough	Synthesis of enterobacterial common antigen and chain elongation	33938	241, 2867
<i>rffD</i>	85.5	Rough	Synthesis of enterobacterial common antigen; UDP-ManNAcA dehydrogenase	293	2866, 2867, 2868, 3268
<i>rffE</i>	85.5	Rough	<i>nfrC</i> , <i>wecB</i> ; synthesis of enterobacterial common antigen; UDP-GlcNAc-2-epimerase	33925	2770, 2867, 2868, 926
<i>rffG</i>	85.6	Rough	<i>rffE</i> ? dehydratase activity	40941	2770, 926
<i>rffH</i>	85.6	Rough	Hypothetical protein in <i>rffE</i> operon	52957	394
<i>rffM</i>	85.7	Rough	UDP-ManNAcA transferase	33948	2867, 2868
<i>rffT</i>	85.7	Rough	Synthesis of enterobacterial common antigen; Fuc4NAc transferase	33930	2867, 2868
<i>rhaA</i>	88.2	Rhamnose	L-Rhamnose isomerase (EC 5.3.1.14)	292	2999, 3465, 4421
<i>rhaB</i>	88.2	Rhamnose	Rhamnulokinase (EC 2.7.1.5)	291	3465, 4421
<i>rhaD</i>	88.2	Rhamnose	Rhamnulosephosphate aldolase D (EC 4.1.2.19)	289	3465, 4421
<i>rhaR</i>	88.3	Rhamnose	<i>rhaC</i> ; positive regulatory gene	290	3465, 4421, 4580
<i>rhaS</i>	88.3	Rhamnose	<i>rhaC</i> ; positive regulatory gene	17950	3465, 4421, 4580
<i>rhaT</i>	88.3	Rhamnose	Rhamnose permease; L-rhamnose-H ⁺ symporter, membrane protein	34185	1362, 211, 4358, 4359, 4580
<i>rhlB</i>	85.4	RNA helicase like	Same as <i>mmrA</i> ? protein with RNA helicase-like motif	36971	2099, 926
<i>rhlE</i>	17.9	RNA helicase like	DEAD-box protein family; ATP-dependent RNA helicase-like protein	33907	3260
<i>rho</i>	85.4	Rho termination factor	<i>nitA</i> , <i>nusD</i> , <i>psuA</i> , <i>msC</i> , <i>sun</i> , <i>tsu</i> ; transcription termination factor Rho	288	1914, 2550, 257, 2717, 2807, 2969, 3436, 3663, 4229, 4240, 4388, 4524, 533, 58, 614, 926, 940

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>RhsA</i>	81.0	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	17947	1232, 2557, 3790, 4596, 4950
<i>RhsB</i>	78.0	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	17944	2557, 3790, 4950
<i>RhsC</i>	15.7	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	17941	3790, 4950
<i>RhsD</i>	11.3	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	17938	3790, 3791, 4950
<i>RhsE</i>	32.9	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	33720	3791, 4950
<i>ribA</i>	28.8	Riboflavin	Riboflavin biosynthesis; GTP-cyclohydrolase II (EC 3.5.4.20)	287	216, 217, 2288, 3670, 4387
<i>ribB</i>	68.6	Riboflavin	<i>htrP</i> ; <i>luxH</i> -like; riboflavin biosynthesis; 3,4-dihydroxy-2-butanone 4-phosphate synthase	286	216, 217, 3594, 3672, 4387
<i>ribC</i>	37.5	Riboflavin	Riboflavin synthase α chain; see <i>ribE</i>	11923	1110, 217, 4387
<i>ribD</i>	9.3	Riboflavin	<i>ribG</i> ; riboflavin biosynthesis; a deaminase	35685	3671, 4361
<i>ribE</i>	9.3	Riboflavin	<i>ribH</i> ; riboflavin synthase β chain; see <i>ribC</i>	35688	4361
<i>ribF</i>	0.5	Riboflavin	Flavokinase and FAD synthetase	35833	185, E
<i>ridA</i>	73.1	Rifampin dependence	Rifampin resistance and dependence	285	898
<i>ridB</i>	85.5	Rifampin dependence	Transcription and translation; rifampin (rifamycin) sensitivity	17935	895
<i>rimB</i>	38.9	Ribosomal modification	50S ribosomal subunit maturation	284	546
<i>rimC</i>	26.2	Ribosomal modification	50S ribosomal subunit maturation	283	546
<i>rimD</i>	87.7	Ribosomal modification	50S ribosomal subunit maturation	282	546
<i>rimE</i>	74.1	Ribosomal modification	Ribosomal protein modification	281	2865
<i>rimF?</i>	0.8	Ribosomal modification	<i>res</i> ; ribosomal modification; may be same as <i>rimG</i>	280	1379
<i>rimG</i>	0.7	Ribosomal modification	<i>ramB</i> ; modification of 30S ribosomal subunit protein S4; probably same as <i>rimF</i> (<i>res</i>) in <i>E. coli</i> B	279	1379, 4961
<i>rimH</i>	13.6	Ribosomal modification	<i>stsB</i> ; ribosomal modification	278	
<i>rimI</i>	99.3	Ribosomal modification	Modification of 30S ribosomal subunit protein S18; acetylation of N-terminal alanine	277	1939, 4895
<i>rimJ</i>	24.2	Ribosomal modification	<i>tcp</i> ; modification of 30S ribosomal subunit protein S5; acetylation of N-terminal alanine	276	1988, 4728, 4729, 4895
<i>rimK</i>	19.2	Ribosomal modification	<i>nek</i> ; modification of 30S ribosomal subunit protein S6 by addition of glutamic acid residues	31682	122, 1860, 2123
<i>rimL</i>	32.3	Ribosomal modification	Modification of 50S ribosomal subunit protein L7/L12; acetylation of N-terminal serine	275	1940, 4348
<i>rimM</i>	59.1	Ribosomal modification	<i>yjfA</i> ; 21-kDa protein essential for 16S RNA processing	51908	589, 590
<i>rit</i>	89.2	Ribosomal thermostability	Affects thermostability of 50S ribosomal subunit	274	3298
<i>rlpA</i>	14.3	Rare lipoprotein	Minor lipoprotein	17932	4332
<i>rlpB</i>	14.5	Rare lipoprotein	Minor lipoprotein	17929	4332
<i>rluA</i>	1.3	rRNA, large, uridine modification	Dual specificity pseudouridine synthase for 23S rRNA and tRNA ^{phe}	36966	1578, 2106, 4787
<i>rluC</i>	24.66 ^b	Pseudouridine synthase	Responsible for pseudouridine at three positions in 23S RNA (not on map, Fig. 1)	57124	827a
<i>rluD</i>	48.9	Suppressor <i>ftsH</i>	<i>sfhB</i> ; suppresses <i>ftsH</i> (ts) mutants; 23S rRNA pseudouridine synthase (pseudouridines at position 1911, 1915, and 1917)	53497	3079, 689a
<i>rmf</i>	21.9	Ribosome modulation factor	Associated with the 100S dimers of 70S ribosomes observed in stationary phase cells	31760	4622, 4624, 4832
<i>rna</i>	13.9	RNase A	<i>msA</i> ; cleaves phosphodiester bond between two nucleotides; RNase I	273	2858
<i>mb</i>	29.0	RNase B	RNase II; mRNA degradation	272	1069, 4958, 4959, 4960
<i>mc</i>	58.2	RNase C	RNase III; cleaves double-stranded RNA	271	1910, 2753, 2810, 3134, 4679, 708, 4339
<i>md</i>	40.6	RNase D	Rnase D; processes tRNA precursors	270	1336, 4919, 4939, 4938
<i>me</i>	24.6	RNase E	<i>ams</i> ; RNase E; enzyme complex for RNA processing, mRNA turnover and 5S RNA maturation	269	183, 1840, 1983, 2663, 2702, 2843, 2876, 2958, 3031, 3299, 3622, 4354, 621, 648, 673, 691, 774, 833
<i>mhA</i>	5.1	RNase H	<i>cer</i> , <i>dasF</i> , <i>herA</i> , <i>mh</i> , <i>sdrA</i> , <i>sin</i> ; degrades RNA of DNA-RNA hybrids; replication; RNase HI; participates in DNA replication	268	127, 1793, 1804, 2113, 2286, 2287, 2553, 2730, 3092, 3209, 3244, 4442, 633, 634, 636, 855

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<i>mhb</i>	4.4	RNase H	Degrades RNA of DNA-RNA hybrids; RNase HII (EC 3.1.26.4)	30604	1944
<i>mk</i>	13.9	Regulator nucleoside-diP kinase	Regulator of nucleoside diphosphate kinase; suppresses <i>Pseudomonas algR2</i>	36984	3911, 3985
<i>mpA</i>	83.7	RNase P	tRNA, 4.5S RNA-processing; RNase P, protein component	267	1632, 2074, 2293, 3328
<i>mpB</i>	70.4	RNase P	RNase P, RNA component	266	1064, 123, 2293, 2311, 2663, 3019, 3634, 3635, 3811
<i>mr</i>	94.3	RNase R	<i>vacB</i> ; homology with <i>Shigella</i> virulence gene <i>vacB</i> ; exoribonuclease R	34417	569, 719a, 4417a
<i>mt</i>	37.2	RNase T	Degrades tRNA; RNase T (EC 3.1.13-)	32271	1843, 3331, 3656, 649
<i>rob</i>	99.8	Right <i>oriC</i> binding	<i>oriC</i> -binding protein, binds to right border of <i>oriC</i>	34661	131, 2093, 4086
<i>rorB</i>	85.1	Roentgen resistance	Sensitivity to ionizing radiation, mitomycin C	36611	991, 992
<i>rpe</i>	75.7	Ribulose-5-phosphate epimerase	D-Ribulose-5-phosphate epimerase, in <i>dam</i> operon	53572	2681
<i>rph</i>	82.2	RNase PH	RNase PH	33892	2009, 2011, 2192, 3309, 94
<i>rpiA</i>	65.9	Ribose-P isomerase	Ribose phosphate isomerase (constitutive) (EC 5.3.1.6)	264	1822
<i>rpiB</i>	92.9	Ribose-P isomerase	Allose-6-P isomerase; ribose P isomerase?	50228	2223, 4138
<i>rpiR</i>	92.9	Ribose-P isomerase	<i>alsR</i> ; repressor for <i>als</i> operon and <i>rpiB</i>	50233	2223, 4138
<i>rplA</i>	90.0	Ribosomal protein, large	50S ribosomal subunit protein L1	263	1083, 1855, 2567, 2577, 2688, 3499, 3605, 537, 89
<i>rplB</i>	74.3	Ribosomal protein, large	50S ribosomal subunit protein L2	262	4969
<i>rplC</i>	74.4	Ribosomal protein, large	50S ribosomal subunit protein L3	261	4969
<i>rplD</i>	74.4	Ribosomal protein, large	<i>eryA</i> ; 50S ribosomal subunit protein L4; erythromycin sensitivity	260	2538, 2559, 4293, 4762, 4927, 4969, 736
<i>rplE</i>	74.2	Ribosomal protein, large	50S ribosomal subunit protein L5	259	666
<i>rplF</i>	74.2	Ribosomal protein, large	50S ribosomal subunit protein L6; gentamicin sensitivity	258	554, 666
<i>rplI</i>	95.4	Ribosomal protein, large	50S ribosomal subunit protein L9	257	15, 1938, 3928
<i>rplJ</i>	90.0	Ribosomal protein, large	<i>strA</i> ; streptomycin resistance; 50S ribosomal subunit protein L10	256	1083, 1238, 1788, 1855, 243, 244, 2567, 2577, 2688, 3165, 3499, 3605, 4210, 4377, 537, 783, 89
<i>rplK</i>	90.0	Ribosomal protein, large	<i>relC</i> ; 50S ribosomal subunit protein L11; kasugamycin sensitivity	255	1083, 1855, 2567, 2577, 3065, 3165, 3499, 3605, 4210, 4377, 537, 89, 891, 918, 4398
<i>rplL</i>	90.1	Ribosomal protein, large	50S ribosomal subunit protein L7/L12	254	1083, 1788, 1855, 243, 244, 2567, 2577, 2688, 3165, 3605, 4210, 537, 89
<i>rplM</i>	72.8	Ribosomal protein, large	50S ribosomal subunit protein L13	253	1941, 894
<i>rplN</i>	74.3	Ribosomal protein, large	50S ribosomal subunit protein L14	252	666
<i>rplO</i>	74.2	Ribosomal protein, large	50S ribosomal subunit protein L15	251	1945, 666
<i>rplP</i>	74.3	Ribosomal protein, large	50S ribosomal subunit protein L16	250	4969
<i>rplQ</i>	74.1	Ribosomal protein, large	50S ribosomal subunit protein L17	249	275, 2865, 3496, 666
<i>rplR</i>	74.2	Ribosomal protein, large	50S ribosomal subunit protein L18	248	666
<i>rplS</i>	59.1	Ribosomal protein, large	50S ribosomal subunit protein L19	247	3407, 597
<i>rplT</i>	38.7	Ribosomal protein, large	<i>pdzA</i> ; 50S ribosomal subunit protein L20	17608	1213
<i>rplU</i>	71.8	Ribosomal protein, large	50S ribosomal subunit protein L21	246	2013, 2246
<i>rplV</i>	74.3	Ribosomal protein, large	<i>eryB</i> ; erythromycin sensitivity; 50S ribosomal subunit protein L22	245	4762, 4969, 736
<i>rplW</i>	74.3	Ribosomal protein, large	50S ribosomal subunit protein L23	244	4969
<i>rplX</i>	74.3	Ribosomal protein, large	50S ribosomal subunit protein L24	243	666, 896
<i>rplY</i>	49.2	Ribosomal protein, large	50S ribosomal subunit protein L25	242	
<i>rpmA</i>	71.8	Ribosomal protein, large	50S ribosomal subunit protein L27	241	2246
<i>rpmB</i>	82.1	Ribosomal protein, large	50S ribosomal subunit protein L28	240	1936, 2466, 2716, 4154
<i>rpmC</i>	74.3	Ribosomal protein, large	50S ribosomal subunit protein L29	239	4969
<i>rpmD</i>	74.2	Ribosomal protein, large	50S ribosomal subunit protein L30	238	666
<i>rpmE</i>	88.9	Ribosomal protein, large	50S ribosomal subunit protein L31	237	893
<i>rpmF</i>	24.7	Ribosomal protein, large	50S ribosomal subunit protein L32	17605	1988
<i>rpmG</i>	82.1	Ribosomal protein, large	50S ribosomal subunit protein L33	236	1936, 2466, 2716, 4154
<i>rpmH</i>	83.7	Ribosomal protein, large	<i>rimA</i> , <i>ssaF</i> ; 50S ribosomal subunit protein L34	235	1631, 3285, 4611, 546
<i>rpmI</i>	38.8	Ribosomal protein, large	50S ribosomal subunit protein A (L35)	17602	4623
<i>rpmJ</i>	74.2	Ribosomal protein, large	50S ribosomal subunit protein X (L36)	17599	4623, 666

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>rpoA</i>	74.1	RNA polymerase	<i>phs, sez</i> ; phage P2 <i>vir1</i> resistance; RNA polymerase, α -subunit (EC 2.7.7.6)	234	1426, 2236, 275, 2865, 3318, 3496, 3497, 3754, 3755, 4292, 666
<i>rpoB</i>	90.1	RNA polymerase	<i>ftsR, groN, mbrD, nitB, rif, ron, stl, stv, tabD, sdgB</i> ; streptovar., rif., streptolyd. sensitivity; RNA polymerase, β -subunit (EC 2.7.7.6)	233	174, 1013, 1083, 1108, 1190, 1406, 1418, 173, 1788, 1855, 2020, 2092, 2286, 243, 244, 2463, 2567, 2577, 2688, 3165, 3316, 3499, 3605, 3698, 3756, 3906, 4210, 4211, 4523, 4588, 4912, 537, 89
<i>rpoC</i>	90.2	RNA polymerase	<i>tabD</i> ; RNA polymerase, β -subunit (EC 2.7.7.6)	232	1083, 1108, 1788, 2020, 2092, 243, 244, 2567, 2577, 2688, 3165, 3315, 3316, 3605, 4175, 4210, 537, 89
<i>rpoD</i>	69.2	RNA polymerase	<i>alt</i> ; most exponential phase transcription; RNA polymerase, σ -subunit, σ^{70} (EC 2.7.7.6)	231	1367, 1531, 2230, 2542, 2671, 2673, 3113, 3114, 4053, 4070, 4376, 565, 579, 580
<i>rpoE</i>	58.4	RNA polymerase	RNA polymerase σ^E -subunit, high-temperature transcription (heat shock and oxidative stress)	36181	1767, 3592
<i>rpoH</i>	77.5	RNA polymerase	<i>fam, hin, htpR</i> ; heat-shock transcription RNA polymerase σ^{32} -subunit (EC 2.7.7.6)	618	1532, 1533, 2120, 2407, 3145, 4418, 4484, 4913, 612
<i>rpoN</i>	72.0	RNA polymerase	<i>glnF, ntrA</i> ; RNA polymerase σ^{60} -subunit, transcription of N-source-controlled genes	17926	1770, 1864, 1904, 2904, 3517, 656, 657
<i>rpoS</i>	61.7	RNA polymerase	<i>abrD, dpeB, katF, nur, appR</i> ; σ^S ; RNA polymerase σ , stationary phase	18208	1226, 1402, 1925, 2049, 2077, 2411, 2610, 2749, 3044, 3045, 3806, 3825, 3899, 4448, 4488, 4591, 4603, 4447, 3697, 2413a
<i>rpoZ</i>	82.3	RNA polymerase	<i>spoS</i> ; RNA polymerase, ω subunit	28445	1400, 2597
<i>rpsA</i>	20.7	Ribosomal protein, small	<i>ssyF</i> ; 30S ribosomal subunit protein S1	230	1099, 2247, 2248, 3390, 3926, 3927, 4027, 746
<i>rpsB</i>	4.1	Ribosomal protein, small	30S ribosomal subunit protein S2	229	2428, 296, 3133, 418, 88
<i>rpsC</i>	74.3	Ribosomal protein, small	30S ribosomal subunit protein S3	228	4969
<i>rpsD</i>	74.1	Ribosomal protein, small	<i>ramA, sud₂</i> ; 30S ribosomal subunit protein S4	227	1662, 275, 3496, 3497, 666
<i>rpsE</i>	74.2	Ribosomal protein, small	<i>eps, spc, spcA</i> ; 30S ribosomal subunit protein S5	226	1662, 2975, 666, 956
<i>rpsF</i>	95.3	Ribosomal protein, small	<i>sdgH</i> ; 30S ribosomal subunit protein S6	225	1937, 3928
<i>rpsG</i>	74.8	Ribosomal protein, small	<i>K12</i> ; 30S ribosomal subunit protein S7	224	3498
<i>rpsH</i>	74.2	Ribosomal protein, small	30S ribosomal subunit protein S8	223	666, 4784
<i>rpsI</i>	72.8	Ribosomal protein, small	30S ribosomal subunit protein S9	17596	1941, 897
<i>rpsJ</i>	74.4	Ribosomal protein, small	<i>nusE</i> ; 30S ribosomal subunit protein S10	222	1012, 2559, 4927, 851
<i>rpsK</i>	74.1	Ribosomal protein, small	30S ribosomal subunit protein S11	221	275, 3496, 666
<i>rpsL</i>	74.8	Ribosomal protein, small	<i>asuB, strA</i> ; 30S ribosomal subunit protein S12	220	489, 3498
<i>rpsM</i>	74.1	Ribosomal protein, small	30S ribosomal subunit protein S13	219	1212, 275, 3496, 666
<i>rpsN</i>	74.2	Ribosomal protein, small	30S ribosomal subunit protein S14	218	666
<i>rpsO</i>	71.3	Ribosomal protein, small	<i>secC</i> ; 30S ribosomal subunit protein S15	217	1126, 1182, 1231, 2246, 2457, 3459, 3492, 3494, 3638, 3850, 4333, 4334
<i>rpsP</i>	59.1	Ribosomal protein, small	30S ribosomal subunit protein S16	216	1935, 3235, 3407, 599
<i>rpsQ</i>	74.3	Ribosomal protein, small	<i>neaA</i> ; 30S ribosomal subunit protein S17	215	4969, 630
<i>rpsR</i>	95.3	Ribosomal protein, small	30S ribosomal subunit protein S18	214	1938, 3928, 891
<i>rpsS</i>	74.3	Ribosomal protein, small	30S ribosomal subunit protein S19	213	1935, 4969
<i>rpsT</i>	0.4	Ribosomal protein, small	<i>sup₂₀</i> ; 30S ribosomal subunit protein S20	212	2700, 2701, 4830
<i>rpsU</i>	69.2	Ribosomal protein, small	30S ribosomal subunit protein S21	211	2671, 2673, 3148, 579, 892
<i>rfA</i>	87.0	Ribosomal RNA, 5S	5S rRNA of <i>rna</i> operon	210	1146, 4044, 439
<i>rfB</i>	89.9	Ribosomal RNA, 5S	5S rRNA of <i>rnB</i> operon	209	4044, 522, 523
<i>rfC</i>	85.0	Ribosomal RNA, 5S	5S rRNA of <i>rnC</i> operon	208	4044, 4904
<i>rfD</i>	73.7	Ribosomal RNA, 5S	5S rRNA of <i>rnD</i> operon	207	1096, 4044
<i>rfE</i>	90.8	Ribosomal RNA, 5S	5S rRNA of <i>rnE</i> operon	206	1146, 2543, 4044, 439
<i>rfF</i>	73.7	Ribosomal RNA, 5S	<i>rfDβ, rrvD</i> ; 5S rRNA of <i>rnD</i> operon	33643	394
<i>rfG</i>	58.7	Ribosomal RNA, 5S	5S rRNA of <i>rnG</i> operon	205	1146, 4044
<i>rfH</i>	4.8	Ribosomal RNA, 5S	5S rRNA of <i>rnH</i> operon	204	1146

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>r1A</i>	87.0	Ribosomal RNA, 23S	23S rRNA of <i>r1A</i> operon	203	1146, 1502, 3236, 4383, 439, 915, 926
<i>r1B</i>	89.8	Ribosomal RNA, 23S	23S rRNA of <i>r1B</i> operon	202	1502, 3063, 3236, 3785, 4383, 522, 523, 524, 915
<i>r1C</i>	85.0	Ribosomal RNA, 23S	23S rRNA of <i>r1C</i> operon	201	1502, 3236, 4383, 915
<i>r1D</i>	73.8	Ribosomal RNA, 23S	23S rRNA of <i>r1D</i> operon	200	1096, 1502, 3236, 4383, 915
<i>r1E</i>	90.7	Ribosomal RNA, 23S	23S rRNA of <i>r1E</i> operon	199	1146, 1502, 2543, 3236, 4383, 439, 915
<i>r1G</i>	58.7	Ribosomal RNA, 23S	23S rRNA of <i>r1G</i> operon	198	1146, 1502, 3236, 4383, 915
<i>r1H</i>	4.8	Ribosomal RNA, 23S	23S rRNA of <i>r1H</i> operon	197	1146, 1502, 3236, 4383, 4384, 915
<i>r1A</i>	41.1	Ribosomal RNA modification	23S rRNA <i>m1G745</i> methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance	56816	1576
<i>r1A</i>	96.9	Ribosomal RNA (operon)	See Fig. 1	23593	
<i>r1B</i>	89.8	Ribosomal RNA (operon)	<i>cqsE</i> , <i>r1B1</i> ; see Fig. 1	195	1661, 248
<i>r1C</i>	84.9	Ribosomal RNA (operon)	<i>cqsB</i> ; see Fig. 1	19503	2056
<i>r1D</i>	73.7	Ribosomal RNA (operon)	<i>cqsD</i> ; see Fig. 1	193	1752
<i>r1E</i>	90.7	Ribosomal RNA (operon)	<i>r1D1</i> ; see Fig. 1	192	1752, 2543
<i>r1G</i>	58.7	Ribosomal RNA (operon)	See Fig. 1	10891	1661, 53
<i>r1H</i>	4.8	Ribosomal RNA (operon)	See Fig. 1	190	
<i>r1A</i>	86.9	Ribosomal RNA, 16S	16S RNA of <i>r1A</i> operon	189	4458, 926
<i>r1B</i>	89.8	Ribosomal RNA, 16S	16S RNA of <i>r1B</i> operon	188	3063, 318, 3341, 3535, 440, 4458, 522, 523, 879
<i>r1C</i>	84.9	Ribosomal RNA, 16S	16S RNA of <i>r1C</i> operon	187	4458
<i>r1D</i>	73.8	Ribosomal RNA, 16S	16S RNA of <i>r1D</i> operon	186	4458
<i>r1E</i>	90.7	Ribosomal RNA, 16S	16S RNA of <i>r1E</i> operon	185	2543, 4458
<i>r1G</i>	58.8	Ribosomal RNA, 16S	16S RNA of <i>r1G</i> operon	184	1146, 4015, 4458
<i>r1H</i>	4.8	Ribosomal RNA, 16S	16S RNA of <i>r1H</i> operon	183	1146, 4058, 4458
<i>r1D</i>	94.4	Regulation of σ^D	Stationary phase protein, binds major σ -subunit	54664	2023
<i>r1E</i>	58.3	Regulation of σ^E	<i>m1A</i> ; membrane protein, negative regulator of σ^E	37241	2965, 977
<i>r1E</i>	58.3	Regulation of σ^E	Binds <i>r1E</i> , negative regulation of σ^E	37244	2965, 977
<i>r1E</i>	58.3	Regulation of σ^E	Deletion does not affect σ^E activity	37247	2965, 977
<i>r1A</i>	35.5	Repressor of σ^S production	Prevents homoserine lactone-induced synthesis of σ^S , starvation induced	36959	1856
<i>r1B</i>	35.5	Repressor of σ^S production	Function unknown, transcribed with <i>r1A</i> , starvation induced	36962	1856
<i>r1A</i>	27.8	Regulation of σ^S	Two-component response regulator, affecting σ^S -dependent proteins	37468	1718
<i>r1B</i>	27.8	Regulation of σ^S	<i>m1A</i> , <i>sprE</i> , two-component response regulator, affecting σ^S -dependent proteins	37471	1718, 3034, 3532, 4952
<i>r1A</i>	49.1	rRNA, small pseudouridine	16S RNA pseudouridine 516 synthase	36034	4786
<i>r1A</i>	76.6	RNA terminal phosphate cyclase	Cyclase activity similar to human enzyme; RNA 3'-terminal phosphate cyclase	56879	1399a
<i>r1B</i>	76.6	RNA terminal phosphate cyclase		56882	1399a
<i>r1C</i>	76.6	RNA terminal phosphate cyclase		56885	1399a
<i>r1N</i>	48.9	Resistance to N4	Probable membrane protein; resistance to phages lambda and N4	54796	1605
<i>r1S</i>	12.3	<i>r1S</i> suppressor	Resolvase; resolves Holliday structures	32471	2722, 2745, 4003
<i>r1A</i>	41.9	Repair UV?	<i>lexA</i> regulon; Holliday junction recognition	17923	1281, 13, 163, 1966, 305, 306, 3373, 4049, 4478, 4479, 4712
<i>r1B</i>	41.9	Repair UV?	<i>lexA</i> regulon; branch migration of Holliday structures	17920	1281, 13, 305, 306, 3373, 4712
<i>r1C</i>	41.9	Repair UV?	Not SOS regulated; resolves Holliday structures; RuvC endonuclease	32474	1101, 151, 1965, 2593, 299, 307, 3999, 4001, 4002, 4328, 4364, 4712, 4713, 4714, 824
<i>sad</i>	34.3	Succinate-semialdehyde deHase	Succinate-semialdehyde dehydrogenase, NAD dependent (EC 1.2.1.24)	180	2759, 4088
<i>sanA</i>	48.1	Sensitivity vancomycin	Amplification abolishes vancomycin-sensitive permeability defects of mutants	50224	3673
<i>sapA</i>	29.2	Sensitivity to antimicrobial peptides	Peptide transport system periplasmic protein	51886	3371, 322a, 4792a
<i>sapB</i>	29.2	Sensitivity to antimicrobial peptides	Peptide transport system permease	51883	322a, 4792a

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>sapC</i>	29.1	Sensitivity to antimicrobial peptides	Peptide transport system permease	51880	I, H
<i>sapD</i>	29.1	Sensitivity to antimicrobial peptides	<i>trkE</i> ; affects potassium transport; peptide transport system ATP-binding protein	35326	1161, 3371, 3372, 3914
<i>sapF</i>	29.1	Sensitivity to antimicrobial peptides	Peptide transport system ATP-binding protein	35323	3372
<i>sbaA</i>	96.5	Serine, branched-chain amino acids	Regulation of serine and branched-chain amino acid metabolism	179	919
<i>sbcB</i>	44.9	Suppression of <i>recBC</i>	<i>xonA</i> ; suppresses <i>recB recC</i> mutations; exonuclease I	178	3156, 3417, 3418, 3529, 3845, 4291, 4834
<i>sbcC</i>	8.9	Suppression of <i>recBC</i>	Cosuppressor with <i>sbcB</i> of <i>recB recC</i> mutations	17917	2451, 2594, 2595, 3128, 4834, 676, 823
<i>sbcD</i>	8.9	Suppression of <i>recBC</i>	Cosuppressor with <i>sbcB</i> of <i>recB recC</i> mutations	30972	1423, 2451, 823
<i>sbmA</i>	8.5	Sensitivity B17 microcin	Methylmalonyl-CoA mutase (<i>mcm</i>)	17914	2435
<i>sbmC</i>	44.8	Sensitivity B17 microcin	<i>gyrI</i> ; DNA gyrase inhibitor; in high copy protects cells from replication inhibitor MccB17; SOS induced; blocks MccB17 export	50396	222, 3114a
<i>sbp</i>	88.5	Sulfate binding protein	Periplasmic sulfate-binding protein	17911	1710
<i>sdaA</i>	40.8	Serine deaminase	L-Serine deaminase	32312	3987, 4258, 4260
<i>sdaB</i>	63.1	Serine deaminase	L-Serine deaminase, L-SD2	33324	3988, 4259
<i>sdaC</i>	63.1	Serine deaminase	<i>dcrA</i> ; regulator of L-SD2; putative serine transporter	33329	2546, 3988, 4259
<i>sdhA</i>	16.3	Succinate dehydrogenase	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	17908	4741, 4773, 615, 866, 934, 3354
<i>sdhB</i>	16.3	Succinate dehydrogenase	Succinate dehydrogenase iron-sulfur protein	17905	4741, 4773, 615, 934, 3354
<i>sdhC</i>	16.3	Succinate dehydrogenase	<i>cybA</i> ; succinate dehydrogenase membrane anchor subunit, cytochrome <i>b</i> ₅₅₆ (EC 1.3.99.1)	17902	3052, 3053, 615, 3354
<i>sdhD</i>	16.3	Succinate dehydrogenase	Succinate dehydrogenase hydrophobic subunit (EC 1.3.99.1)	17899	4741, 4773, 615, 3354
<i>sdjA</i>	43.0	Suppress division inhibitors	Suppresses inhibitory effect of the MinC/MinD division inhibitor, positive regulator <i>ftsQAZ</i>	30919	1361, 4659
<i>sds</i>	30.4	Suppresses disulfide bond	Motility defects		4792a
<i>secA</i>	2.3	Secretory	<i>azi</i> , <i>pea</i> , <i>prlD</i> ; translocation ATPase for protein export	176	1079, 1241, 1279, 2329, 3286, 3287, 3358, 349, 3818, 3919, 598, 751, 921
<i>secB</i>	81.5	Secretory	Protein export; chaperone SecB	17896	1293, 2227, 2234, 2361, 2362, 2363, 2454, 260, 3519, 3919, 4675, 4676
<i>secD</i>	9.2	Secretory	Membrane component of protein export complex	17893	1366, 2329, 2651, 3469, 921
<i>secE</i>	90.0	Secretory	<i>prlG</i> ; inner membrane protein involved in protein secretion (with SecY)	34108	1079, 1080, 1084, 1267, 181, 2035, 2814, 3067, 3068, 3200, 3468, 3470, 349, 350, 3553, 36, 3675, 3893, 3894, 395, 4182, 4264, 4362, 540, 921, 2329
<i>secF</i>	9.2	Secretory	Membrane protein with protein secretion function	29893	1198, 1365, 2329, 2651, 2817, 3467, 3469, 3794, 4264, 921
<i>secG</i>	71.6	Secretory	<i>prlH</i> ; p12 cytoplasmic membrane protein involved with protein export	33484	1079, 1622, 3199, 3201, 450, 451, 4733
<i>secY</i>	74.2	Secretory	<i>prlA</i> ; multispanning membrane protein, translocator of proteins (with SecE)	18037	1079, 1153, 1267, 1293, 180, 1945, 1947, 3218, 3292, 3307, 3470, 349, 350, 3553, 40, 4028, 4037, 4048, 42, 43, 46, 4868, 666, 921, 1949, 2329
<i>selA</i>	81.0	Selenium	<i>fdhA</i> (formate dehydrogenase activity); with SelD, converts serine residue to selenocysteine on tRNA	785	1276, 2480, 3887
<i>selB</i>	81.0	Selenium	<i>fdhA</i> ; novel elongation factor promoting selenocysteine incorporation (specific for selenocysteyl tRNA)	17890	1274, 2480, 345, 3887
<i>selC</i>	82.6	Selenium	<i>fdhC</i> ; selenocysteyl tRNA _{UCA} (converted from serine tRNA)	17887	2313, 237, 2478, 2480, 3887
<i>selD</i>	39.8	Selenium	Selenophosphate synthase; reduced selenium donor for selenocysteyl tRNA and protein	32292	1125, 1275, 2226, 2479, 3887, 4184

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>semA</i>	40.5	Sensitivity to microcin	Sensitivity to microcin E492	17884	3552
<i>seqA</i>	15.4	Sequestration	<i>hobH</i> ; DNA biosynthesis; negative modulator of replication initiation	31506	208, 2646, 4096, 4608, 471
<i>serA</i>	65.9	Serine	Phosphoglycerate dehydrogenase (EC 1.1.1.95)	173	3239, 4420, 4444, 4949, 73
<i>serB</i>	99.6	Serine	Phosphoserine phosphatase (EC 3.1.3.3)	172	3705
<i>serC</i>	20.6	Serine	<i>pdxC</i> , <i>pdxF</i> ; phosphoserine aminotransferase (EC 2.6.1.52)	171	1019, 1020, 1099, 1370, 3161, 4034a
<i>serR</i>	2.3	Serine	Regulates level of seryl-tRNA synthetase		4392
<i>serS</i>	20.2	Serine	Serine hydroxamate resistance; seryl-tRNA synthetase (EC 6.1.1.11)	169	1659, 4444
<i>serT</i>	22.2	Serine	<i>divE</i> ; serine tRNA ₁	168	2313, 34, 4345
<i>serU</i>	44.0	Serine	<i>su</i> ₁ , <i>Su-1</i> , <i>ftsM</i> , <i>supD</i> , <i>supH</i> (amber suppressor); serine tRNA ₂	167	2313, 2455, 3324, 4197, 4407, 1122a
<i>serV</i>	60.7	Serine	<i>supD</i> (ochre suppressor); serine tRNA ₃	166	2313, 1122a
<i>serW</i>	19.9	Serine	<i>serW</i> _α ; <i>serWX</i> duplicate genes; serine tRNA ₅	17881	2313, 3849, 1122a
<i>serX</i>	23.6	Serine	<i>serW</i> _β ; <i>serWX</i> duplicate genes; serine tRNA ₅	17878	2313, 1122a
<i>sfa</i>	22.7	Suppressor of <i>fabA</i>	Suppresses <i>fabA6</i>	46624	3696
<i>sfcA</i>	33.5	<i>sbc</i> fusion C-terminal	Probably <i>maeA</i> , malic enzyme, NAD linked (EC 1.1.1.38)	32176	2719
<i>sfiC</i>	25.8	Septum formation inhibition	Element of <i>e14</i> , inhibitor of cell division	17875	1858, 1978, 2715, 933
<i>sfsA</i>	3.5	Sugar fermentation stimulation	<i>sfsI</i> ; regulatory for maltose metabolism; overexpression increases amyloamylase	30524	2176
<i>sfsB</i>	71.8	Sugar fermentation stimulation	<i>nlp</i> , <i>sfs7</i> ; Ner-like regulatory protein	35693	175, 2176, 744
<i>shiA</i>	44.1	Shikimate	Shikimate and dehydroshikimate permease	163	1185
<i>sipC</i>	82.6	Suppressor of increased permeability	Mutations reverse the susceptibility to vancomycin and other hydrophobic antibiotics caused by TraT plasmid gene	51306	3563
<i>sipD</i>	82.7	Suppressor of increased permeability	Same phenotype as that produced by <i>sipC</i>	36869	3563
<i>sir</i>	61.2	SOS-independent repair	SOS-independent repair of mitomycin C-induced DNA damage	36505	2366
<i>sixA</i>	52.9		Phosphohistidine phosphatase affecting His-Asp phosphorelay of ArcB, etc.	54917	3248
<i>sloB</i>	75.0	Slow growth	Tolerance for amidinopenicillin and nalidixic acid; slow growth rate	162	4716
<i>slp</i>	78.7	Stationary-phase lipoprotein	C starvation and stationary phase inducible; outer membrane lipoprotein	33726	3971, 63
<i>slr</i>	14.7	Selenolipoic acid resistant	Suppresses lipoate requirement of <i>lipA</i> ; functions in lipoic acid synthesis	36705	3633
<i>sly</i>	99.8	Soluble lytic transglycosylase	Lytic transglycosylase, major autolysin	34819	1155, 332
<i>slyD</i>	74.9	Sensitivity to lysis	FK-506-BP-like lysis protein for ϕ X174; metal ion-regulated peptidyl-prolyl <i>cis/trans</i> -isomerase, filamentation if overexpressed	35441	1809, 1814, 3730, 3731, 4804
<i>slyX</i>	74.9	Sensitivity to lysis	Required for ϕ X174 lysis	54726	3731
<i>smp</i>	99.6	Serine B-contraposed membrane protein	Transcribed divergently from <i>serB</i> , overlapping promoter; membrane protein	34649	3162, 3163
<i>smtA</i>	21.0	SAM-dependent methyltransferase	Putative methyltransferase, SAM-dependent	50317	4844
<i>sodA</i>	88.3	SOD	Member of SoxRS regulon; superoxide dismutase, Mn	17593	1217, 301, 3178, 3540, 3541, 4338, 4445, 638, 819, 4355
<i>sodB</i>	37.4	SOD	Superoxide dismutase, Fe	15256	1217, 1529, 2204, 301, 3155, 3178, 3904, 638, 639
<i>sodC</i>	37.1	SOD	Superoxide dismutase, Cu, Zn	50310	1908, 302, 303
<i>sohA</i>	70.6	Suppressor of <i>htr</i>	<i>prIF</i> ; suppressor of <i>htrA</i> ; putative protease	35411	204, 2212, 4123
<i>sohB</i>	28.6	Suppressor of <i>htr</i>	Suppressor of <i>htr</i> ; homology with inner membrane protease IV, which digests cleaved signal peptides	31951	203
<i>solA</i>	24.1	Sarcosine oxidase-like	Homology with sarcosine oxidases, but stronger activity with methyltryptophan than with sarcosine	50669	2332
<i>soxR</i>	92.2	Superoxide	Regulatory protein of <i>soxRS</i> regulon; induces nine-protein <i>sox</i> regulon when superoxide levels increase	27798	1384, 1748, 3223, 3224, 4480, 4793, 78
<i>soxS</i>	92.1	Superoxide	Regulatory protein of <i>soxRS</i> regulon; induces nine-protein <i>sox</i> regulon when superoxide levels increase	27801	1211, 1985, 2539, 3223, 3224, 4793, 4794, 78

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>speA</i>	66.4	Spermidine	Biosynthetic decarboxylase (EC 4.1.1.19)	161	2996, 3877, 472
<i>speB</i>	66.4	Spermidine	Agmatinase (EC 3.5.3.11)	160	3877, 472, 4318
<i>speC</i>	66.9	Spermidine	Ornithine decarboxylase (EC 4.1.1.17)	159	3877, 472
<i>speD</i>	2.9	Spermidine	S-Adenosylmethionine decarboxylase (EC 4.1.1.50)	158	4323, 4324
<i>speE</i>	2.9	Spermidine	Spermidine synthase	17590	4323, 4324
<i>speF</i>	15.5	Spermidine	Ornithine decarboxylase, inducible (EC 4.1.1.17)	31559	2149, 2153
<i>speG</i>	35.7	Spermidine	Spermidine acetyltransferase	53446	1334
<i>spf</i>	87.2	Spot 42	Spot 42 RNA	157	2067, 3473, 3661
<i>spoT</i>	82.3	Spot (magic spot)	Guanosine 5'-diphosphate, 3'-diphosphate pyrophosphatase, ppGpp synthetase II activity	156	2913, 3070, 3868, 3869, 4807a
<i>sppA</i>	39.8	Signal peptide peptidase	Protease IV; signal peptide peptidase	13763	1877, 4308
<i>spr</i>	48.9	Suppressor of <i>prc</i>	Suppresses thermosensitivity of <i>prc</i> mutants at low osmolality; in turn suppressed by multicopy expression of PBP 7	54675	1641
<i>srlA</i>	60.9	Sorbitol	<i>gutA</i> , <i>sbl</i> ; D-glucitol-specific enzyme II of phosphotransferase system	155	3644, 437, 4749, 4822, 4823
<i>srlB</i>	60.9	Sorbitol	<i>gutB</i> , <i>sbl</i> ; D-glucitol (sorbitol)-specific enzyme III of the phosphotransferase system	11886	4822, 4823
<i>srlD</i>	60.9	Sorbitol	<i>gutD</i> , <i>sbl</i> ; sorbitol-6-phosphate dehydrogenase (EC 1.1.1.140)	153	4749, 4822, 4823
<i>srlE</i>	60.9	Sorbitol	<i>gutE</i> ; protein encoded by reading frame adjacent to <i>srlA</i>	56893	3644a
<i>srlR</i>	60.9	Sorbitol	<i>gutR</i> ; regulatory gene for <i>srl</i>	152	4749
<i>srnB</i>	58.4	Suppressor ribosomal mutant	<i>rbaB</i> , <i>rhlA</i> ; ATP-dependent RNA helicase	32859	3191
<i>srnA</i>	9.4	Stable RNA	Degradation of stable RNA	151	3263
<i>ssaE</i>	52.5	Suppression <i>secA</i>	Suppresses <i>secA</i> mutations	17869	3285
<i>ssaG</i>	41.8	Suppression <i>secA</i>	Suppresses <i>secA</i> mutations	17866	3285
<i>ssaH</i>	94.1	Suppression <i>secA</i>	Suppresses <i>secA</i> mutations	17863	3285
<i>ssb</i>	92.1	Single-strand binding	<i>exrB</i> , <i>lexC</i> ; single-strand DNA-binding protein; member of <i>lex</i> regulon	150	1435, 2237, 2393, 2916, 3568, 3835, 3837, 3917
<i>sseA</i>	57.1	Sensitivity to serine	Enhances serine sensitivity (inhibits homoserine deHase) on lactate; rhodanese-like protein	33023	1617
<i>sseB</i>	57.2	Sensitivity to serine	Enhances serine sensitivity (inhibits homoserine deHase) on lactate; weaker than <i>sseA</i>	33026	1617
<i>sspA</i>	72.7	Stringent starvation protein	<i>pog</i> ; stress response protein	17860	1333, 1335, 3979, 3985, 4742
<i>sspB</i>	72.7	Stringent starvation protein	Stress response protein	33594	4742
<i>ssrA</i>	59.3	Small stable RNA	<i>sipB</i> ; 10Sa RNA (nonribosomal); role in modulating DNA-binding proteins	35783	103, 1218, 2310, 2312, 3074, 3251, 3252, 3652, 3653, 692
<i>ssrS</i>	65.8	Small stable RNA	6S RNA	17857	1833, 2459
<i>ssyA</i>	57.1	Suppression of <i>secY</i>	Suppressor of <i>secY</i> mutation	17854	4026
<i>ssyD</i>	3.0	Suppression of <i>secY</i>	Suppressor of <i>secY</i> mutation	17848	4027
<i>stfZ</i>	2.3	<i>fts</i> in reverse	Antisense RNA blocks <i>ftsZ</i> mRNA translation, inhibits cell division	36124	1032
<i>stkA</i>	77.5	Suppressor of transposase killing	Suppresses cell aberrations and death caused by Tn5 transposase overexpression	36083	4699
<i>stkB</i>	86.1	Suppressor of transposase killing	Suppresses cell aberrations and death caused by Tn5 transposase overexpression	36093	4699
<i>stkC</i>	98.5	Suppressor of transposase killing	Suppresses cell aberrations and death caused by Tn5 transposase overexpression	36087	4699
<i>stkD</i>	28.6	Suppressor of transposase killing	Suppresses cell aberrations and death caused by Tn5 transposase overexpression	36090	4699
<i>stpA</i>	60.3	Suppressor of td mutant	<i>hnsB</i> ; <i>hns</i> -like protein, suppresses T4 td mutant	34492	1300, 4024, 4133, 4933–4935
<i>strC</i>	7.0	Streptomycin	<i>strB</i> ; low-level streptomycin resistance; modifies ribosome structure	149	3688
<i>strM</i>	78.3	Streptomycin	<i>asuF</i> ?; control of ribosomal ambiguity	148	4272
<i>stsA</i>	84.7	Streptomycin	Altered RNase activity	147	2493
<i>sucA</i>	16.3	Succinate	<i>lys</i> , <i>met</i> ; α -ketoglutarate dehydrogenase (decarboxylase component)	146	3355, 4149, 4741, 4773, 553, 934, 935
<i>sucB</i>	16.4	Succinate	<i>lys</i> , <i>met</i> ; dihydrolipoamide succinyltransferase component of α -ketoglutarate deHase (EC 2.3.1.61)	145	4149, 4150, 4151, 553
<i>sucC</i>	16.4	Succinate	Succinyl-CoA synthetase β -subunit	17845	4150, 4151, 552, 553
<i>sucD</i>	16.5	Succinate	Succinyl-CoA synthetase α -subunit	17842	552, 553
<i>stfI</i>	68.1	Suppressor of <i>ftsI</i>	<i>sui</i> ; suppressor of <i>ftsI</i>	33437	2164

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>sugE</i>	94.3	Suppressor of <i>gro</i>	Suppresses <i>groL</i> mutation and mimics effects of <i>gro</i> overexpression	34460	1512
<i>suhA</i>	78.4	Suppressor heat-shock proteins	Induction of heat shock genes	17839	4419
<i>suhB</i>	57.4	Suppressor heat-shock proteins	Inositol monophosphate (EC 3.1.3.25)	32968	1910, 1911, 2804, 4870, 675
<i>sulA</i>	22.0	Suppressor of <i>lon</i>	<i>sfiA</i> ; inhibits cell division and <i>ftsZ</i> ring formation	144	1391, 1857, 1978, 2027, 2984, 794
<i>sup</i>		Suppressor	Various suppressor tRNAs, see Table 2		
<i>supQ</i>	12.5	Suppressor	Uncharacterized suppressor	129	3780
<i>surA</i>	1.2	Survival	Affects stationary-phase survival	30326	2446, 2964, 3752, 4440
<i>surE</i>	61.8	Survival	<i>ygbC</i> ; required for stationary-phase survival	33215	2523
<i>syd</i>	63.0	<i>secY-dl</i> suppression	Interacts with <i>secY</i>	36980	4036
<i>tabC</i>	86.3	T4 abortion	Mutants fail to support growth of T4	125	4329
<i>tag</i>	80.0	3-Methyl adenine glycosylase	3-Methyladenine DNA glycosylase I, constitutive	124	1184, 2144, 365, 3816, 3957, 4201, 773
<i>talA</i>	55.5	Transaldolase	Transaldolase A	54690	4164
<i>talB</i>	0.2	Transaldolase	Transaldolase B	36818	4165
<i>tanA</i>	41.6	Trehalose, anaerobic	Anaerobic growth on trehalose	37222	2799
<i>tanB</i>	68.1	Trehalose, anaerobic	Anaerobic growth on trehalose	37910	2799
<i>tap</i>	42.4	Taxis protein	Flagellar regulon; chemotactic membrane receptor for aspartate; methyl-accepting protein IV; peptide receptor	123	2342, 2951, 4101, 4102, 4651, 468
<i>tar</i>	42.4	Taxis, aspartate and repellents	<i>cheM</i> ; chemotactic signal transducer protein II, methyl accepting; aspartate chemoreceptor	122	2206, 2342, 4101, 4102, 4650, 4651, 468
<i>tas</i>	64	Tyrosine auxotrophy suppressor	Suppresses tyrosine requirement of <i>tyrA14</i> O ^b strain	57111	4416a
<i>tauA</i>	8.3	Taurine	Uptake of taurine (probable S source)	51775	4549, 4550
<i>tauB</i>	8.3	Taurine	Taurine transport	51772	4549, 4550
<i>tauC</i>	8.3	Taurine	Taurine transport	51769	4549, 4550
<i>tauD</i>	8.3	Taurine	Taurine dioxygenase	51766	1131, 4549, 4550
<i>thpA</i>	1.6	Thiamin binding protein	Periplasmic thiamin binding protein	34691	1785
<i>tdcA</i>	70.4	Threonine dehydratase, catabolic	Transcriptional activator of <i>tdc</i> operon	29702	1353, 1466, 1600, 3944, 3945, 689
<i>tdcB</i>	70.3	Threonine dehydratase, catabolic	<i>tdc</i> , <i>mukA</i> ; threonine dehydratase (EC 4.2.1.16); LysR family of regulator proteins	17587	1466, 1467, 1468, 3944, 3945, 950
<i>tdcC</i>	70.3	Threonine dehydratase, catabolic	L-Threonine L-serine permease, membrane associated, anaerobically inducible	29709	1466, 3246, 3944, 3945
<i>tdcD</i>	70.3	Threonine dehydratase, catabolic	Propionate kinase, anaerobic	54712	1736, 3944
<i>tdcE</i>	70.2	Threonine dehydratase, catabolic	Pyruvate formate-lyase/ketobutyrate formate-lyase	54717	1736, 3944
<i>tdcF</i>	70.2	Threonine dehydratase, catabolic	Function unknown	54720	1736
<i>tdcG</i>	70.2	Threonine dehydratase, catabolic	Anaerobic pathway, L-serine deaminase, L-serine dehydratase	54723	1736, 3944
<i>tdcR</i>	70.4	Threonine dehydratase, catabolic	Positive regulatory protein for threonine dehydratase, TdcB	29692	3943, 3944
<i>tdh</i>	81.7	Threonine dehydrogenase	Threonine dehydrogenase	17584	141, 3619, 3620, 715
<i>tdi</i>	4.3	Transduction inhibition	Affects transduction, transformation, and rates of mutation	121	4181
<i>tdk</i>	27.9	Thymidine kinase	Deoxythymidine kinase	120	1763, 1887, 369, 405
<i>tehA</i>	32.3	Tellurite resistance	Multidrug resistance; K ⁺ -tellurite ethidium and proflavin transport; membrane protein	32106	4372, 4500, 4501, 4645
<i>tehB</i>	32.3	Tellurite resistance	Multidrug resistance; K ⁺ -tellurite ethidium and proflavin transport	32109	4372, 4500, 4501
<i>TerA</i>	28.8	Terminus	Terminus of DNA replication; replication fork inhibition	17836	1294, 1744, 1754, 1756, 1757, 3395, 979
<i>TerB</i>	36.2	Terminus	<i>psrB</i> ; terminus of DNA replication; replication fork inhibition	17833	1097, 1294, 1744, 1754, 1756, 1757, 281, 3395, 352, 979
<i>TerC</i>	34.6	Terminus	<i>psrA</i> ; terminus of DNA replication; replication fork inhibition	17830	1294, 1744, 297, 298, 454
<i>TerD</i>	27.6	Terminus	Terminus of DNA replication; replication fork inhibition	17827	1294, 1744
<i>TerE</i>	23.3	Terminus	Terminus of DNA replication; replication fork inhibition	29805	1746
<i>TerF</i>	50.0	Terminus	Terminus of DNA replication; replication fork inhibition	29289	3992
<i>tesA</i>	11.2	Thioesterase	<i>apeA</i> ; acyl-CoA thioesterase I; also protease I	31102	1878, 737, 738

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>tesB</i>	10.2	Thioesterase	Thioesterase II	17581	3087, 3130
<i>tgt</i>	9.2	tRNA-guanine transglycosylase	tRNA-guanine transglycosylase	118	1358, 2651, 3205, 3654, 3655
<i>thdA</i>	10.5	Thiophene degradation	Degradation of furans and thiophenes; may be <i>thnA</i> ?	17824	3
<i>thdC</i>	94.2	Thiophene degradation	Degradation of furans and thiophenes	17821	3
<i>thdD</i>	99.8	Thiophene degradation	Degradation of furans and thiophenes	15908	3
<i>thiA</i>	90.3	Thiamin cluster	Hydroxyethylthiazole synthesis, cluster of genes	117	4564
<i>thiB</i>	90.3	Thiamin	Unidentified, not THI-P synthase, thiamine pyrophosphate pyrophosphorylase activity	116	4564
<i>thiC</i>	90.4	Thiamin (and thiazole)	Hydroxymethylpyrimidine synthesis; thiamin pyridine moiety biosynthesis	115	4564
<i>thiD</i>	47.2	Thiamin (and thiazole)	Phosphomethylpyrimidine kinase	114	1905
<i>thiE</i>	90.3	Thiamin (and thiazole)	<i>thiA</i> ; thiamin-thiazole moiety synthesis	34301	4564
<i>thiF</i>	90.3	Thiamin (and thiazole)	<i>thiA</i> ; thiamin-thiazole moiety synthesis	34298	4564
<i>thiG</i>	90.3	Thiamin (and thiazole)	<i>thiA</i> ; thiamin-thiazole moiety synthesis	34295	4564
<i>thiH</i>	90.3	Thiamin (and thiazole)	<i>thiA</i> ; thiamin-thiazole moiety synthesis	342952	4564
<i>thiI</i>	9.5	Thiamin (and thiazole)	Thiamin biosynthesis; also 4-thiouridine generation in tRNAs	56890	3032, 4681a
<i>thiJ</i>	47.1	Thiamin (and thiazole)	<i>thiA</i> , <i>thiN</i> ; hydroxymethylpyrimidine kinase	37230	2977, 3122
<i>thiK</i>	25.1	Thiamin (and thiazole)	Thiamin kinase	113	1906, 2425
<i>thiL</i>	9.4	Thiamin (and thiazole)	<i>thiJ</i> ; thiaminmonophosphate kinase	112	1906, 4681a
<i>thiM</i>	47.2	Thiamin (and thiazole)	Hydroxyethylthiazole kinase (EC 2.7.1.50)	34309	2976
<i>thrA</i>	0.0	Threonine	<i>thrD</i> , <i>Hs</i> ; aspartokinase I-homoserine dehydrogenase I (EC 1.1.1.3 and EC 2.7.2.4)	111	1568, 2162, 2682, 4859, 845, 925
<i>thrB</i>	0.1	Threonine	Homoserine kinase (EC 2.7.1.39)	110	1568, 3801, 4948, 845, 846
<i>thrC</i>	0.1	Threonine	Threonine synthase (EC 4.2.99.2)	109	1568, 3375, 845, 846
<i>thrS</i>	38.8	Threonine	Autogenously regulated threonyl-tRNA synthetase (EC 6.1.1.3)	108	1318, 2743, 2829, 3136, 3333, 3461, 3463, 3527, 4168, 4170, 4710, 4801
<i>thrT</i>	90.0	Threonine	Threonine tRNA ₃	107	1849, 2313, 2467, 3743, 90
<i>thrU</i>	89.9	Threonine	Threonine tRNA ₄	106	1849, 2313, 2467, 3743, 90
<i>thrV</i>	73.7	Threonine	Threonine tRNA ₁ , in <i>rmd</i>	105	1096, 1146, 2313, 3814, 818
<i>thrW</i>	5.6	Threonine	Threonine tRNA ₂	10363	2313, 818, 914
<i>thyA</i>	63.9	Thymine	Aminopterin, trimethoprim resistance; thymidylate synthetase (EC 2.1.1.45)	104	1107, 1730, 1742, 286, 328, 3762, 3870, 658
<i>tig</i>	9.8	Trigger factor	Trigger factor; chaperone	35681	1583, 1737, 1738, 2119, 4236, 4525, 619
<i>tktA</i>	66.3	Transketolase	Transketolase (EC 2.2.1.1)	103	2059, 4161, 4162, 4947
<i>tktB</i>	55.6	Transketolase	Transketolase (EC 2.2.1.1)	29992	1889, 4947
<i>tldD</i>	73.0	Tolerance for <i>letD</i>	Tolerance for effects on DNA gyrase by sex factor F gene <i>letD</i>	50304	3061
<i>thnA</i>	10.5	Thiolutin	<i>thnI</i> ; resistance or sensitivity to thiolutin; may be <i>thdA</i> ?	102	4083
<i>tmk</i>	24.9	Thymidine kinase	Deoxythymidine kinase	17578	357, 3657, 967, 405
<i>tnaA</i>	83.8	Tryptophanase	<i>ind</i> , <i>tnaR</i> ; tryptophanase (EC 4.1.99.1)	101	2927, 3170, 3171, 4222, 4611, 4677, 4911, 568, 996
<i>tnaB</i>	83.8	Tryptophanase	<i>trpP</i> ; low-affinity Trp permease	69	1119, 2102, 3865, 4218, 568, 996
<i>tnm</i>	92.0	Tn migration	Transposition of Tn9 and other transposons, development of phage Mu	100	1901, 1902, 4107, 4725
<i>tolA</i>	16.7	Tolerance	<i>cim</i> , <i>excC</i> , <i>lky</i> , <i>tol-2</i> ; tolerance to group A colicins, single-stranded filamentous DNA phage; required for OM integrity; membrane protein; bacteriocin tolerant	99	1023, 1270, 1284, 2506, 2507, 3039, 4281, 4282, 4397, 4686, 482, 484, 635, 957
<i>tolB</i>	16.7	Tolerance	<i>lkyA</i> (leakage of periplasmic proteins), <i>tol-3</i> ; azaleucine resistant; tolerance to colicins E2, E, A, and K	98	1270, 1284, 2447, 2449, 2506, 3039, 4281, 4282, 484, 635, 957, 99
<i>tolC</i>	68.5	Tolerance	<i>colE1-i</i> , <i>mtcB</i> , <i>refI</i> , <i>weeA</i> , <i>toc</i> (topoisomerase compensation), <i>mukA</i> ; specific tolerance to ColE1; affects chromosome segregation; OM porin	97	1284, 1291, 1593, 1594, 1762, 3007, 3009, 3186, 3311, 4648, 484, 4863, 4864, 635, 957, 975
<i>tolD</i>	22.9	Tolerance	Bacteriocin tolerant; tolerance to colicins E2, E3, and ampicillin	96	1284, 484, 572, 957
<i>tolE</i>	22.9	Tolerance	Bacteriocin tolerant; tolerance to colicins E2, E3, and ampicillin	95	1284, 484, 635, 957
<i>tolI</i>	0.1	Tolerance	Bacteriocin tolerant; sensitivity to colicins Ia and Ib	94	484, 635, 957

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>tolJ</i>	0.1	Tolerance	Bacteriocin tolerant; sensitivity to L, A, S4, E, and K	93	1284, 484, 635, 957
<i>tolM</i>	74.8	Tolerance	<i>cmt</i> ; high-level tolerance to colicin M	92	1284, 1618, 1650, 2865, 3892, 484, 635, 957
<i>tolQ</i>	16.7	Tolerance	<i>fii</i> , <i>tolP</i> ? tolerance to group A colicins, single-stranded DNA filamentous phage; cell envelope integrity; inner membrane protein	17815	2108, 3038, 3039, 4281, 4282, 4397, 4582, 4686, 481, 482
<i>tolR</i>	16.7	Tolerance	Tolerance to group A colicins, single-stranded DNA filamentous phage; cell envelope integrity; inner membrane protein	17812	1721, 2108, 3039, 4282, 4397, 4686, 482
<i>tonB</i>	28.2	T-one	<i>Tlrec</i> , <i>exbA</i> ; sensitivity to T1, ϕ 80, and colicins; uptake of chelated Fe and cyanocobalamin; energy transducer	90	1254, 1470, 1488, 2080, 2135, 2136, 2221, 2502, 251, 3500, 3501, 3502, 4059, 4451, 4452, 482, 484
<i>topA</i>	28.6	Topoisomerase	<i>supX</i> ; topoisomerase I, omega protein I	89	1091, 2494, 2680, 2762, 3301, 3310, 4206, 4466, 4467, 4482, 4654
<i>topB</i>	39.7	Topoisomerase	<i>mutR</i> ; topoisomerase III; <i>mutR</i> phenotype is decreased deletion formation between short repeats	29988	1048, 3931, 4653, 4730, 4937
<i>torA</i>	22.8	Trimethylamine oxide reductase	Molybdoprotein trimethylamine N-oxide reductase	17575	2874, 3377
<i>torC</i>	22.8	Trimethylamine oxide reductase	c-Type cytochrome	29977	2874
<i>torD</i>	22.9	Trimethylamine oxide reductase	Transcribed with <i>tor</i> ; no similarity with other proteins in database	29980	2874
<i>torR</i>	22.8	Trimethylamine oxide reductase	Regulatory gene	36408	4071, 4072
<i>torS</i>	22.7	Trimethylamine oxide reductase	Sensor partner of TorRT, two-component system for trimethylamine N-oxide induction	50902	2061
<i>torT</i>	22.8	Trimethylamine oxide reductase	TorRT system	50188	2062
<i>tpiA</i>	88.6	Triose P isomerase	Triosephosphate isomerase	88	1710, 3423
<i>tpr</i>	27.7	<i>tyrT</i> region protamine	Protamine-like protein, apparently transcribed with <i>tyrT</i>	87	75
<i>tpx</i>	29.9	Thiol peroxidase	Thioredoxin-linked thiol peroxidase	46706	2225, 668
<i>treA</i>	26.8	Trehalose	<i>tre</i> ; trehalase, periplasmic	17572	2865, 3651, 430
<i>treB</i>	96.2	Trehalose	IITre, translocation system, Tre-specific PTS enzyme II	34601	4253, 431
<i>treC</i>	96.2	Trehalose	Trehalose-6-phosphate hydrolase, osmoprotectant	34597	3677, 4253, 431
<i>treF</i>	79.0	Trehalose	Cytoplasmic trehalase	35861	1807
<i>treR</i>	96.2	Trehalose	Repressor	51427	1807, 1808, 2258
<i>trg</i>	32.1	Taxis to ribose and galactose	Methyl-accepting chemotaxis protein III, ribose acceptor, flagellar regulon	85	1646, 1678, 2865, 2991, 362, 363, 419
<i>trkA</i>	74.0	Transport K ⁺	Major constitutive K ⁺ transport system; potassium transport inner membrane protein subunit	84	1161, 1162, 1618, 2865, 3914, 448
<i>trkD</i>	84.7	Transport K ⁺	<i>kup</i> ; major constitutive K ⁺ transport system	81	1161, 3910, 449, 4611
<i>trkG</i>	30.6	Transport K ⁺	Major constitutive K ⁺ transport system; membrane protein, perhaps inactive during anaerobic growth	29963	1074, 1162, 3915, 3916, 4453
<i>trkH</i>	86.9	Transport K ⁺	Potassium transport membrane protein subunit; binding of TrkA to membrane; mutants require high K ⁺	34066	1074, 1162, 3915, 448
<i>trmA</i>	89.7	tRNA methyltransferase	<i>rT</i> ; tRNA (uracil-5)-methyltransferase (EC 2.1.1.35)	79	1577, 256, 2564, 3229, 3405
<i>trmB</i>	7.1	tRNA methyltransferase	tRNA (guanine-7)-methyltransferase (EC 2.1.1.33)	78	2763
<i>trmC</i>	52.6	tRNA methyltransferase	5-Methylaminoethyl-2-thiouridine in tRNA	77	1599, 366
<i>trmD</i>	59.1	tRNA methyltransferase	tRNA (guanine-7)-methyltransferase (EC 2.1.1.33)	76	1599, 3407, 594–596
<i>trmE</i>	83.7	tRNA methyltransferase	<i>thdF</i> (thiophene oxidation?); tRNA base modification, 5-methyl-aminoethyl, 2-thiouridine synthesis	17806	1147, 49, 568
<i>trmF</i>	84.8	tRNA methyltransferase	5-Methyl aminoethyl-2-thiouridine biosynthesis	17803	1147
<i>trmH</i>	82.4	tRNA methyltransferase	<i>spoU</i> ; tRNA (Gm18) 2'-O-methyltransferase	33877	2319, 3406
<i>trmU</i>	25.7	tRNA methyltransferase	<i>asuE</i> ; antisuppressor; tRNA base-modifying enzyme; 2-thiouridine synthesis	37613	1503, 3708, 4272

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Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>trnA</i>	63.1	tRNA	Level of several tRNAs	75	724
<i>trpA</i>	28.3	Tryptophan	Tryptophan synthase subunit A (EC 4.2.1.20)	74	1157, 1470, 1551, 1760, 2819, 3173, 4314, 4788, 4789, 4871
<i>trpB</i>	28.4	Tryptophan	Tryptophan synthase subunit B (EC 4.2.1.20)	73	1157, 1470, 1760, 2819, 4871, 865
<i>trpC</i>	28.4	Tryptophan	Bifunctional enzyme <i>N</i> -(5-phosphoribosyl)anthranilate isomerase, indole-3-glycerolphosphate synthetase (EC 4.1.1.48)	72	1157, 1470, 1760, 1812, 2819, 4871, 747
<i>trpD</i>	28.4	Tryptophan	Bifunctional enzyme anthranilate synthase component II, phosphoribosyl anthranilate transferase; (EC 4.1.3.27 and EC 2.4.2.18)	71	1157, 1470, 1760, 1810, 1812, 2819, 3174, 4871
<i>trpE</i>	28.4	Tryptophan	<i>anth</i> , <i>tryD</i> , <i>tryp-4</i> ; anthranilate synthase component I (EC 4.1.3.27)	70	1157, 1470, 1703, 1760, 2819, 3026, 3174, 3175, 3321, 4871
<i>trpR</i>	99.8	Tryptophan	5-Methyltryptophan resistance; regulator of <i>trp</i> operon and <i>aroH</i> ; autogenously regulated tryptophan repressor protein	68	1567, 1568, 210, 3705, 4078, 4872, 288
<i>trpS</i>	75.7	Tryptophan	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	67	1608, 1609, 410
<i>trpT</i>	85.0	Tryptophan	<i>su7</i> (UGA suppression), <i>supU</i> (UAG suppression), <i>su8</i> , <i>supV</i> (UAA suppression) ^f ; tryptophan tRNA	66	2313, 3324, 4904, 926, 1122a
<i>truA</i>	52.4	tRNA uridine (modification to pseudouridine)	<i>asuC</i> , <i>hisT</i> , <i>leuK</i> ; pseudouridine synthase, anticodon stem and loop specific	623	142, 143, 144, 2784, 3211, 3226, 3363, 3955, 4523, 543
<i>truB</i>	71.3	tRNA uridine (modification to pseudouridine)	Pseudouridine synthase, ψ 55 specific	35528	3226
<i>trxA</i>	85.4	Thioredoxin	<i>fipA</i> , <i>tsnC</i> ; thioredoxin	65	1865, 2550, 2551, 2764, 2807, 3850, 3772, 3773, 3775, 3778, 3784, 4641, 58, 926
<i>trxB</i>	20.1	Thioredoxin	Thioredoxin reductase	17569	1009, 1613, 3774, 3776, 3777
<i>trxC</i>	58.6	Thioredoxin	Thioredoxin 2	54694	2953
<i>tsaA</i>	4.8	t6AtRNA-SAM-methyltransferase	N ⁶ -threonylcarbamoyladenosine(t6A) modification of tRNA ^{Thr} , adenosine A37 to threonylated adenosine; tRNA(m6t6A37) methyltransferase	53741	3564
<i>tsf</i>	4.1	Ts elongation factor	EF-Ts, elongation factor for transcription, stable	64	2428, 296, 418, 88
<i>tsmA</i>	40.1	Thymine suppression modifier	Affects suppression efficiency for nonsense and frameshift mutations of Thy ⁻ strains	36603	1731
<i>tsr</i>	98.9	Taxis to serine and repellents	<i>cheD</i> ; serine chemoreceptor; methyl accepting chemotaxis protein II, membrane receptor	63	1693, 2206, 3367, 4650, 467, 469, 617, 84
<i>tsx</i>	9.3	T-six	<i>T6rec</i> , <i>nupA</i> ; T6, colicin K resistance; nucleoside channel	62	1635, 2651, 492, 494
<i>tttA</i>	69.1	Tartrate dehydratase	L-Tartrate dehydratase subunit (EC 4.2.1.32)	33459	3628
<i>tttB</i>	69.1	Tartrate dehydratase	L-Tartrate dehydratase subunit (EC 4.2.1.32)	33462	3628
<i>ttk</i>	82.2		Function unknown, TetR, AcrR family of regulators	52724	1144, 568
<i>tufA</i>	74.7	Tu elongation factor	<i>kirT</i> , <i>pulT</i> ; duplicate gene for EF-Tu subunit; elongation factor, unstable	61	1561, 2042, 2334, 2379, 2433, 4342, 4543, 4548, 4732, 4887, 4928, 91
<i>tufB</i>	90.0	Tu elongation factor	<i>kirT</i> , <i>pulT</i> ; duplicate gene for EF-Tu subunit; elongation factor, unstable	60	1561, 1849, 2334, 2433, 2467, 2567, 2972, 4336, 4342, 4377, 4543, 4546, 4548, 4732, 89, 90
<i>tus</i>	36.3	Terminus utilization substance	<i>tau</i> ; inhibits replication at Ter; Ter DNA-binding protein, blocking replication forks; DNA sequence-specific contrahelicase	17800	1745, 1756, 1758, 2207, 2279, 2355, 2473, 3395, 3704, 941
<i>tynA</i>	31.2	Tyramine	<i>feaA</i> , <i>maoA</i> ; tyramine oxidase (EC 1.4.3.4)	59	178, 3066, 4200, 4848
<i>tyrA</i>	59.0	Tyrosine	Chorismate mutase T-prephenate dehydrogenase (EC 5.4.99.5 and EC 1.3.1.12) bifunctional; TyrR regulon	58	1847, 2819
<i>tyrB</i>	91.9	Tyrosine	Tyrosine aminotransferase (EC 2.6.1.5); TyrR regulon	57	1283, 2372, 4856
<i>tyrP</i>	42.8	Tyrosine	Tyrosine-specific transport system, TyrR regulon	56	2154, 2155, 4720, 4781, 4782

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^c
<i>tyrR</i>	29.8	Tyrosine	TyrR regulon repressor; regulates <i>aroF</i> , <i>aroG</i> , <i>tyrA</i> , and aromatic amino acid transport; autoregulation of <i>tyrR</i> not mediated by tyrosine	55	2436, 2819, 3441, 4640, 4740, 4855, 4857, 531, 623, 734, 785, 837, 838, 881, 882
<i>tyrS</i>	36.9	Tyrosine	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	54	1043, 236, 2398, 2938
<i>tyrT</i>	27.7	Tyrosine	<i>tyrT</i> α, <i>su</i> _{III} , <i>Su-3</i> , <i>Su-4</i> , <i>supC</i> (ochre suppressor ^f), <i>supF</i> (amber suppressor), <i>supO</i> ? tandemly duplicated tyrosine tRNA ₁ (<i>tyrTV</i>)	53	2313, 3743, 3744, 445, 446, 447
<i>tyrU</i>	90.0	Tyrosine	<i>sup15B</i> , <i>supM</i> (ochre suppressor), <i>supZ</i> (amber suppressor ^f); tyrosine tRNA ₂	52	1122a, 1849, 2313, 2467, 3743, 90
<i>tyrV</i>	27.7	Tyrosine	<i>tyrT</i> β; tandemly duplicated, tyrosine tRNA ₁	51	3743, 1122a
<i>ubiA</i>	91.6	Ubiquinone	4-Hydroxybenzoate polyprenyltransferase	50	2549, 2576, 3195, 725
<i>ubiB</i>	86.7	Ubiquinone	<i>fadI</i> , <i>fre</i> , <i>fsrC</i> ; 2-octaprenylphenol→2-octaprenyl-6-methoxyphenol; flavin reductase (EC 1.6.99.-)?	49	1273, 1385, 4174, 926
<i>ubiC</i>	91.6	Ubiquinone	Chorismate lyase	48	2549, 3176, 4124
<i>ubiD</i>	86.7	Ubiquinone	Reaction: 3-octaprenyl-4-hydroxybenzoate to 2-octaprenylphenol	47	858
<i>ubiE</i>	86.7	Ubiquinone	Reaction: 2-octaprenyl-6-methoxy-1,4-benzoquinone to 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	46	4902
<i>ubiF</i>	14.8	Ubiquinone	Reaction: 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone to 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone	45	811
<i>ubiG</i>	50.4	Ubiquinone	Reaction: 1-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone to ubiquinone 8	44	1421, 1829, 3451
<i>ubiH</i>	65.8	Ubiquinone	<i>visB</i> ; reaction: 2-octaprenyl-6-methoxyphenol to 2-octaprenyl-6-methoxy-1,4-benzoquinone	43	3100, 2974
<i>ubiX</i>	52.3	Ubiquinone	<i>dedF</i> ; sequence homologous to <i>ubiX</i> of <i>S. typhimurium</i> , which codes for 3-octaprenyl 4-hydroxybenzoate carboxy-lyase	17797	3211
<i>ucpA</i>	54.8	Upstream <i>cysP</i>	Temporary name; protein with homology to short-chain dehydrogenases/reductases	51898	4080
<i>udk</i>	46.1	Uridine kinase	Uridine/cytidine kinase (EC 2.7.1.48)	42	2058, 3156, 3157
<i>udp</i>	86.5	Uridine phosphorylase	Uridine phosphorylase (EC 2.4.2.3)	41	1272, 3426, 3539, 58, 66, 926, 4646
<i>ugpA</i>	77.3	Uptake glycerol phosphate	<i>psiB</i> , <i>psiC</i> ; glycerol P transport system, integral membrane protein	40	2147, 2931, 3320, 3539, 3946, 3948, 3949, 4261
<i>ugpB</i>	77.4	Uptake glycerol phosphate	<i>psiB</i> , <i>psiC</i> ; periplasmic binding protein of <i>sn</i> -glycerol-3-phosphate transport system	39	2147, 2931, 3320, 3946, 3948, 3949, 4261
<i>ugpC</i>	77.3	Uptake glycerol phosphate	<i>sn</i> -Glycerol-3-P transport system; ABC family permease	17794	1701, 2147, 3320, 3948, 3949, 4261
<i>ugpE</i>	77.3	Uptake glycerol phosphate	<i>sn</i> -Glycerol-3-P transport system; membrane protein	17791	2147, 3320, 3948, 3949, 4261
<i>ugpQ</i>	77.3	Uptake glycerol phosphate	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.-); cytosolic	33697	548, 4261, 4428
<i>uhpA</i>	82.9	Utilization hexose phosphate	Response regulator (2-component system) required for <i>uhpT</i> transcription	15437	1316, 1933, 2079, 4006, 4717
<i>uhpB</i>	82.9	Utilization hexose phosphate	Membrane protein controlling UhpA activity, sensor kinase	15448	1316, 1933, 1934, 4717
<i>uhpC</i>	82.9	Utilization hexose phosphate	Membrane protein controlling UhpA activity, in concert with UhpB	15449	1316, 1933, 1934, 2079, 4006, 4717
<i>uhpT</i>	82.8	Utilization hexose phosphate	Fosfomycin sensitivity; sugar P transport system; transport protein for hexose P's	37	1179, 1316, 1581, 2079, 2902, 2931, 4005, 4006, 4545, 4571, 4717
<i>uidA</i>	36.5	HexUronIDes	<i>gurA</i> , <i>gusA</i> ; β-D-glucuronidase (EC 3.2.1.31)	36	2000, 386, 387, 3905
<i>uidB</i>	36.5	HexUronIDes	<i>gusB</i> , <i>uidP</i> ; glucuronide permease	53467	33, 394
<i>uidR</i>	36.5	HexUronIDes	<i>gusR</i> ; regulatory gene	35	384, 386, 387, 388
<i>umuC</i>	26.5	UV mutator	<i>umv</i> ; UV induction of mutations, error-prone repair; forms complex with UmuD and UmuD'	34	1068, 1145, 1297, 2245, 2776, 3404, 4041, 4778, 4779, 2284
<i>umuD</i>	26.5	UV mutator	<i>umv</i> ; inducible mutagenesis; error-prone repair; processed to UmuD'; UmuDC single-stranded binding protein with RecA-coated DNA; SOS	17788	1068, 1145, 1297, 2245, 2281, 2776, 3404, 3960, 4041, 2284
<i>ung</i>	58.5	Uracil nucleic acid glycosylase	Uracil-DNA-glycosylase	25	4567

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>upp</i>	56.4	Uracil PRTase	<i>uraP</i> ; uracil phosphoribosyltransferase (EC 2.4.2.9)	24	1621, 1799, 97
<i>ups</i>	27.1	Up-suppression?	Efficiency of nonsense suppressors; see <i>prfA</i>	23	3782, 854
<i>uraA</i>	56.4	Uracil	Uracil concentration dependence of <i>pyr</i> mutants; Ura ABC transporter	33043	96
<i>uro</i>	85.9	Uroporphyrinogen	<i>hemC-Y</i> operon	37849	3871, 60
<i>usgI</i>	52.5	Upstream gene, temporary	Temporary name for gene in <i>pdxB</i> operon, unknown function	32746	144
<i>ushA</i>	10.9	UDP sugar hydrolase	UDP-glucose hydrolase (5'-nucleotidase)	22	574, 854
<i>uspA</i>	78.4	Universal stress protein	Global regulatory gene for stress response	28127	1046, 1302, 3232, 3233
<i>uup</i>	21.7		Precise excision of insertion elements	17785	1799, 3631
<i>uvh</i>	90.2	UV hyperresistant to UVC	Resistance to UVC, peroxide and antibiotics; may affect SOS repair	51073	21
<i>uvrA</i>	92.0	Ultraviolet resistant	<i>dar</i> ; <i>lex</i> regulon; repair of UV damage to DNA; excision nuclease subunit A	21	1867, 2201, 3831, 3834, 3837, 3838, 3479
<i>uvrB</i>	17.5	UV resistant	<i>dar-1</i> , <i>dar-6</i> ; DNA repair; excision nuclease subunit B, ATPase I and helicase II	20	1268, 128, 191, 3345, 1831, 3836, 3838, 3839, 4319, 4547
<i>uvrC</i>	42.9	UV resistant	DNA repair; multicopy causes mucoidy; excision nuclease subunit C	19	1277, 1278, 2995, 3220, 3831, 3832, 3838, 3840, 3994, 3995, 3996, 4493, 4559, 4886
<i>uvrD</i>	86.1	UV resistant	<i>dar-2</i> , <i>dda</i> , <i>mutU</i> , <i>pdeB</i> , <i>rad</i> , <i>recL</i> , <i>srjC</i> , <i>uvr502</i> , <i>uvrE</i> ; DNA-dependent ATPase I-DNA helicase II; increased rates of spontaneous mutagenesis	18	1109, 1250, 1251, 146, 1741, 2368, 2642, 2750, 2883, 2885, 3242, 3243, 4051, 4360, 4672, 4673, 4838, 4936, 521, 58, 926
<i>uvs</i>	91.1	UV sensitivity	UV-sensitive mutants, locus linked to <i>uvr</i>	51076	21
<i>uxaA</i>	69.8	Utilization hexuronate galacturonate	Altronate hydrolase (EC 4.2.1.7)	17	1851, 3489, 3682, 892
<i>uxaB</i>	34.6	Utilization hexuronate galacturonate	Altronate oxidoreductase (EC 1.1.1.58); <i>exu</i> regulon	16	1854, 2796, 381, 383, 394
<i>uxaC</i>	69.9	Utilization hexuronate galacturonate	Uronate isomerase (EC 5.3.1.12)	15	1851, 2795, 2796, 3489, 3682, 382, 892
<i>uxuA</i>	98.1	Utilization hexuronide glucuronate	Mannonate hydrolase (EC 4.2.1.8)	14	1305, 3681, 3687, 385
<i>uxuB</i>	98.1	Utilization hexuronide glucuronate	Mannonate oxidoreductase (EC 1.1.1.57)	13	1304, 3681, 3687, 385
<i>uxuR</i>	98.1	Utilization hexuronide glucuronate	Regulatory gene for <i>uxuBA</i> operon	12	3680, 3681, 3687
<i>valS</i>	96.5	Valine	<i>val-act</i> ; valyl-tRNA synthetase (EC 6.1.1.9)	11	1660, 1691, 1692, 197, 4091
<i>valT</i>	16.8	Valine	<i>valT</i> α ; duplicate gene with triplicated <i>valUXY</i> ; valine tRNA ₁	10	2313, 3324, 4898
<i>valU</i>	54.3	Valine	<i>valU</i> α , <i>valU</i> γ ; tandemly triplicate <i>valUXY</i> ; valine tRNA ₁	17782	2313, 3238, 538, 539
<i>valV</i>	37.6	Valine	Valine tRNA _{2B}	17563	2313
<i>valW</i>	37.6	Valine	Valine tRNA _{2A}	17560	2313
<i>valX</i>	54.3	Valine	<i>valU</i> γ ; tandemly triplicate <i>valUXY</i> ; valine tRNA ₁	28696	3238, 539
<i>valY</i>	54.3	Valine	<i>valU</i> γ ; tandemly triplicate <i>valUXY</i> ; valine tRNA ₁	28699	3238, 539
<i>valZ</i>	16.8	Valine	<i>valT</i> β ; valine tRNA ₁	51028	394
<i>vsr</i>	43.7	Very short (patch) repair	Repairs mismatches; minimizes effects of C methylation	28927	1282, 2540, 2541, 2697, 336, 4130, 1720
<i>wrbA</i>	23.0	W(Trp) repressor binding	Affects association between Trp repressor and operators in stationary phase	31836	4865
<i>xapA</i>	54.4	Xanthosine P	<i>pnxA</i> ; xanthosine phosphorylase	41105	539
<i>xapB</i>	54.3	Xanthosine P	Xanthosine transport protein, NupG-like	41101	3962
<i>xapR</i>	54.3	Xanthosine P	<i>pnxR</i> ; regulatory gene for <i>xapA</i>	8	2282, 3962, 539, 586
<i>xasA</i>	33.8	Extreme acid survival	Glutamate-dependent enzyme, may function in protection against cytoplasmic acidification	36518	1732
<i>xerC</i>	86.1	<i>cer</i> -specific recombination	Recombinase, site specific	30184	2841, 376, 377, 378, 812
<i>xerD</i>	41.7	<i>cer</i> -specific recombination	<i>xprB</i> ; recombinase, site specific	30201	2639, 2641, 376, 377
<i>xni</i>	63.1	Exonuclease nine	<i>exo</i> ; exonuclease IX, a 3'-5' exonuclease acting preferentially on single-stranded DNA, probable excision repair function	56869	3983a
<i>xseA</i>	56.7	Exonuclease VII	Exonuclease VII, large subunit	6	4535, 687
<i>xseB</i>	9.5	Exonuclease VII	Exonuclease VII, small subunit	17557	4535, 4536
<i>xthA</i>	39.4	Exonuclease III	Exonuclease III	7	3711, 3858, 4030

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TABLE 1—Continued

Gene symbol	Map location (min)	Mnemonic for symbol	Synonyms and gene product—enzyme, RNA, or phenotype affected	CGSC no. ^d	References ^e
<i>xylA</i>	80.3	Xylose	D-Xylose isomerase (EC 5.3.1.5)	5	2377, 2437, 2741, 3735, 3896, 4128, 502
<i>xylB</i>	80.3	Xylose	Xylulokinase (EC 2.7.1.17)	4	2741, 3735, 4128, 502
<i>xylE</i>	91.4	Xylose	Xylose-proton symport	17776	1295, 2376, 4277, 961, 962
<i>xylF</i>	80.4	Xylose	<i>xylT</i> ; xylose-binding protein, transport system	17773	2377, 3735, 4128, 4277, 961
<i>xylG</i>	80.4	Xylose	Xylose transport gene	33780	4128
<i>xylH</i>	80.4	Xylose	Xylose permease protein	33783	4128
<i>xylR</i>	80.5	Xylose	Regulatory gene	3	2741, 3735, 4128
<i>yhhP</i>	77.7	Temporary name	<i>sirA</i> ; provisional name for small protein required for cell growth	55460	4847
<i>yihG</i>	87.1	Temporary name	Poly(A) polymerase II; see also <i>pcnB</i>	50490	631
<i>yjaB</i>	90.8	Temporary name	<i>fl47</i> ; temporary names for protein transcribed divergently from a promoter that overlaps the <i>metA</i> promoter, divergent from <i>metA</i>	51779	1414
<i>yohF</i>	47.9	Temporary name	RpoS regulon, acid sensitive, induced by ALS inhibition, similarity to insect-type ADH	55069	4552
<i>zipA</i>	54.5	<i>ftsZ</i> -interacting protein	Essential gene, affects cell division and growth; septal ring structural protein	51069	1602
<i>zntA</i>	77.7	Zn translocation	Zn ²⁺ translocating P-type ATPase; hypersensitive to Zn and Cd salts	53884	3650
<i>znuA</i>	41.8	Zn uptake	High-affinity ABC transport system for zinc	52879	3381
<i>znuB</i>	41.8	Zn uptake	High-affinity ABC transport system for zinc	52882	3381
<i>znuC</i>	41.8	Zn uptake	High-affinity ABC transport system for zinc	52886	3381
<i>zur</i>	91.8	Zn uptake regulation	Regulatory gene for high-affinity transport of zinc	52889	3381
<i>zwf</i>	41.7	Zwischenferment	Glucose 6-phosphate dehydrogenase (EC 1.1.1.49)	2	1211, 3756a, 643a, 828a

^a The following abbreviations are used in the table: ACP, acyl carrier protein; ad, adenine; PFL, pyruvate-formate lyase; PRPP, phosphoribosyl pyrophosphate; DAHP, 3-deoxy-D-arabinoheptulosonic acid 7-phosphate; BPC, binding protein carriers; FHL, formate hydrogen lyase; EPEC, enteropathogenic *E. coli*; ABC, ATP binding cassette; PEP, phosphoenolpyruvate; CMP, cytidine monophosphate; PTS, phosphotransferase system; cAMP, cyclic AMP; ORF, open reading frame; DMSO, dimethyl sulfoxide; PDI, protein disulfide isomerase; DTT, dithiothreitol; SDS, sodium dodecyl sulfate; CoA, coenzyme A; SRP, signal recognition particle; Me, methyl; OMP, outer membrane protein; RNAP, RNA polymerase; *B. subtilis*, *Bacillus subtilis*; GABA, γ -aminobutyric acid; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; FPA, fluorophenyl alanine; QOR, quinone oxidoreductase; PNP, purine nucleoside phosphorylase; GS, glutamine synthetase; GSH, glutathione; HCA, hydrocinnamic acid; IGP, imidazole glycerol phosphate; FMN, flavin mononucleotide; MPT, molybdopterin; QSR, phage QSR; LPS, lipopolysaccharide; FAD, flavin adenine dinucleotide; SAM, S-adenosylmethionine; SOD, superoxide dismutase; streptovar., streptovarycin; rif., rifampin (rifamycin); streptolyd., streptolydigin; NAL, nalidixic acid; TET, tetracycline; AMP, ampicillin.

^b Not shown on map since characterization was published very recently.

^c Letters used as references are identified as follows: A, Table 1 of reference 187; B, Table 1 of reference 189; C, Table 1 of reference 190; D, Table 1 of reference 190a; E, Table 1 of reference 323.

^d These are the unique identifiers of this site in the CGSC database. Although the database is easily queried by name or synonym, this unchanging identifier is useful in tracking gene name changes that may have resulted in homonyms among the alternative names or in following a complicated history of name changes.

^e Also used for "antisuppressor" phenotype for alleles at various known (or subsequently renamed) loci.

^f Only single-mutation suppression is indicated; double and triple mutations suppress other nonsense triplets. See reference 1122a.

TABLE 2. Alternate gene symbols

Synonym ^a	Gene symbol from Table 1	Synonym	Gene symbol from Table 1
<i>abrD</i>	<i>rpoS</i>	<i>air</i>	<i>aer</i> , <i>aegA</i> ?
<i>acpS</i>	<i>acpX</i>	<i>ala-act</i>	<i>alaS</i>
<i>acrB</i>	<i>gyrB</i>	<i>alaWβ</i>	<i>alaX</i>
<i>acrE</i>	<i>acrB</i>	<i>alaWα</i>	<i>alaW</i>
<i>acrS</i>	<i>envR</i>	<i>ald</i>	<i>fbA</i> , <i>aldA</i>
<i>act</i>	<i>alaS</i> , <i>glyS</i> , <i>pflA</i>	<i>alnA</i>	<i>dadB</i>
<i>ade_c</i>	<i>purN</i>	<i>alnR</i>	<i>dadQ</i>
<i>ade3</i>	<i>purE</i>	<i>alt</i>	<i>rpoD</i>
<i>ade_f</i>	<i>purE</i>	<i>alu</i>	<i>dpp</i>
<i>ade_g</i>	<i>purC</i>	<i>ampA</i>	<i>ampC</i>
<i>ade_{ub}</i>	<i>purF</i>	<i>ams</i>	<i>rne</i>
<i>adhC</i>	<i>adhE</i>	<i>amt</i> , <i>amtA</i>	<i>cysQ</i>
<i>adi</i>	<i>adiA</i>	<i>ana</i>	<i>adhE</i>
<i>ads</i>	<i>folD</i>	<i>anr</i>	<i>osmE</i>
<i>adh_a</i>	<i>purD</i>	<i>ant</i>	<i>nhaA</i> , <i>mutS</i>
<i>aeg-46.5</i>	<i>ccm-nap</i> operon	<i>anth</i>	<i>trpE</i>
<i>aidA</i>	<i>alkA</i>	<i>apbC</i>	<i>mrp</i>
<i>aidC</i>	<i>nrfA</i> , <i>nrfG</i>	<i>apeA</i>	<i>tesA</i>
<i>aidD</i>	<i>alkB</i>	<i>apk</i>	<i>lysC</i>

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TABLE 2—Continued

Synonym	Gene symbol from Table 1	Synonym	Gene symbol from Table 1
<i>appR</i>	<i>rpoS</i>	<i>chbF</i>	<i>celF</i>
<i>arg+ura</i>	<i>carA, carB</i>	<i>chbR</i>	<i>celD</i>
<i>Arg1</i>	<i>argA, argD</i>	<i>cheC</i>	<i>fliM</i>
<i>Arg2</i>	<i>argA, argC</i>	<i>cheD</i>	<i>tsr</i>
<i>Arg4</i>	<i>argE</i>	<i>cheM</i>	<i>tar</i>
<i>Arg5</i>	<i>argF</i>	<i>cheX</i>	<i>cheR</i>
<i>Arg6</i>	<i>rargG</i>	<i>chl</i>	<i>moe</i>
<i>argA</i>	<i>argE</i>	<i>chlA</i>	<i>moaA</i>
<i>argB</i>	<i>argA</i>	<i>chlB</i>	<i>mobA</i>
<i>argD</i>	<i>argF</i>	<i>chlC</i>	<i>narG, H</i>
<i>argE</i>	<i>argG</i>	<i>chlD</i>	<i>modC, E, F</i>
<i>argG</i>	<i>argD</i>	<i>chlE</i>	<i>moeA</i>
<i>argH</i>	<i>argC</i>	<i>chlF</i>	<i>fdhF</i>
<i>argVα</i>	<i>argV</i>	<i>chlG</i>	<i>mog</i>
<i>argVβ</i>	<i>argY</i>	<i>chlI</i>	<i>narI</i>
<i>argVγ</i>	<i>argZ</i>	<i>chlJ</i>	<i>modB</i>
<i>aroR</i>	<i>aroT</i>	<i>chlM</i>	<i>moaD</i>
<i>arsE</i>	<i>arsR</i>	<i>chlN</i>	<i>moeB</i>
<i>arsF</i>	<i>arsB</i>	<i>chpAI</i>	<i>chpR</i>
<i>arsG</i>	<i>arsC</i>	<i>chpAK</i>	<i>chpA</i>
<i>asmB</i>	<i>lpxC</i>	<i>chpBI</i>	<i>chpS</i>
<i>asp</i>	<i>ppc</i>	<i>chpBK</i>	<i>chpB</i>
<i>aspB</i>	<i>gltB, D</i>	<i>cim</i>	<i>tolA</i>
<i>astC</i>	<i>cstC</i>	<i>clpY</i>	<i>hslU</i>
<i>asuA</i>	<i>prfA?</i>	<i>cmlA</i>	<i>cmr?</i>
<i>asuB</i>	<i>rpsL</i>	<i>cmlB</i>	<i>ompF</i>
<i>asuC</i>	<i>truA</i>	<i>cmt</i>	<i>tolM</i>
<i>asuD</i>	<i>lysS</i>	<i>coa</i>	<i>ompF</i>
<i>asuE</i>	<i>trmU</i>	<i>colE1-i</i>	<i>tolC</i>
<i>asuF</i>	<i>strM?</i>	<i>con</i>	<i>ompA</i>
<i>ata</i>	<i>attP22</i>	<i>cop</i>	<i>het</i>
<i>avr</i>	<i>ileR</i>	<i>corB</i>	<i>mgtA</i>
<i>Az</i>	<i>atoC</i>	<i>cou</i>	<i>gyrB</i>
<i>azi</i>	<i>secA</i>	<i>cqsB</i>	<i>rrnC</i>
<i>bfe</i>	<i>btuB</i>	<i>cqsD</i>	<i>rrmD</i>
<i>bglC</i>	<i>bglF, G</i>	<i>cqsE</i>	<i>rrmB</i>
<i>bglD</i>	<i>bglA</i>	<i>CR</i>	<i>ptsG</i>
<i>bglE</i>	<i>bglT</i>	<i>cra</i>	<i>fruR</i>
<i>bglS</i>	<i>bglG</i>	<i>cru</i>	<i>nupC</i>
<i>bglY</i>	<i>hns</i>	<i>cry</i>	<i>ompF, R</i>
<i>bicA, bicR</i>	<i>bcr</i>	<i>csdA</i>	<i>deaD</i>
<i>bioB</i>	<i>bioH</i>	<i>csi-5</i>	<i>osmY</i>
<i>bioR</i>	<i>birA</i>	<i>csm</i>	<i>crp</i>
<i>bir, birB</i>	<i>bioP</i>	<i>ctr</i>	<i>ptsH, I</i>
<i>bisA</i>	<i>moaA</i>	<i>cur</i>	<i>hns</i>
<i>bisB</i>	<i>moeA</i>	<i>cutA1</i>	<i>cutA</i>
<i>bisD</i>	<i>mog</i>	<i>cutA2</i>	<i>dipZ</i>
<i>blgA</i>	<i>bglB</i>	<i>cvc</i>	<i>fabF</i>
<i>blgB</i>	<i>bglF</i>	<i>cxr</i>	<i>cxm</i>
<i>blu</i>	<i>malP, pgl, pgm</i>	<i>cybA</i>	<i>sdhC</i>
<i>brnP</i>	<i>ilvH</i>	<i>cycY</i>	<i>cutA</i>
<i>bypA1</i>	<i>infA?</i>	<i>cycZ</i>	<i>dipZ</i>
<i>cadR</i>	<i>lysP</i>	<i>cysZ</i>	<i>cysK</i>
<i>cap</i>	<i>crp, carA, carB</i>	<i>cyxA</i>	<i>appC</i>
<i>capR</i>	<i>lon</i>	<i>cyxB</i>	<i>appB</i>
<i>car</i>	<i>ptsG</i>	<i>dadR</i>	<i>dadA</i>
<i>carP</i>	<i>pepA</i>	<i>dagA</i>	<i>cycA</i>
<i>cat</i>	<i>ptsG</i>	<i>dap</i>	<i>asd</i>
<i>cbr</i>	<i>fepA</i>	<i>dar</i>	<i>uvrA</i>
<i>cbt</i>	<i>fepA</i>	<i>dar-1</i>	<i>uvrB</i>
<i>cdFA</i>	<i>cfa</i>	<i>dar-2</i>	<i>uvrD</i>
<i>cfxB</i>	<i>marA? R</i>	<i>dar-6</i>	<i>uvrB</i>
<i>cel</i>	<i>ispB</i>	<i>dasC</i>	<i>rep</i>
<i>cer</i>	<i>btuB, rnhA</i>	<i>dasF</i>	<i>rnhA</i>
<i>cet</i>	<i>creD</i>	<i>dcrA</i>	<i>sdaC</i>
<i>cfxB</i>	<i>marR, marA</i>	<i>dda</i>	<i>uvrD</i>
<i>chbA</i>	<i>celC</i>	<i>ddl</i>	<i>ddlB</i>
<i>chbB</i>	<i>celA</i>	<i>dec</i>	<i>fadR</i>

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TABLE 2—Continued

Synonym	Gene symbol from Table 1	Synonym	Gene symbol from Table 1
<i>dedB</i>	<i>accD</i>	<i>fdp</i>	<i>fbp</i>
<i>dedE</i>	<i>cvpA</i>	<i>fdv</i>	<i>mutS</i>
<i>dedF</i>	<i>ubiX</i>	<i>feaA</i>	<i>tynA</i>
<i>deg</i>	<i>lon</i>	<i>feeB</i>	<i>leuW</i>
<i>dga</i>	<i>murI</i>	<i>feuA</i>	<i>cirA</i>
<i>dhbB</i>	<i>birA</i>	<i>fexA</i>	<i>arcA</i>
<i>dhl</i>	<i>lpd</i>	<i>fii</i>	<i>tolQ</i>
<i>dhnA</i>	<i>fbaB</i>	<i>fimD</i>	<i>fimA</i>
<i>dig</i>	<i>hca</i>	<i>fimG</i>	<i>hns</i>
<i>dinA</i>	<i>polB</i>	<i>fipA</i>	<i>trxA</i>
<i>dinH</i>	<i>ftsK</i> regulatory region	<i>fir</i>	<i>lpxD</i>
<i>dinP</i>	<i>dinB</i>	<i>firA</i>	<i>hlpA, ileR, lpxD</i>
<i>dir</i>	<i>lon</i>	<i>fii</i>	<i>infC?</i>
<i>div</i>	<i>flk</i>	<i>flaA</i>	<i>fliM</i>
<i>divA</i>	<i>ftsA</i>	<i>flaAI</i>	<i>fliL</i>
<i>divE</i>	<i>serT</i>	<i>flaBI</i>	<i>fliF</i>
DLP ₁₂	<i>qsr'</i>	<i>flaBII</i>	<i>fliG</i>
<i>dnaD</i>	<i>dnaC</i>	<i>flaBIII</i>	<i>fliH</i>
<i>dnaF</i>	<i>nrdA</i>	<i>flaC</i>	<i>fliI</i>
<i>dnaL</i>	<i>ligA</i>	<i>flaD</i>	<i>fliA</i>
<i>dnaP</i>	<i>dnaG</i>	<i>flaE</i>	<i>fliK</i>
<i>dnaR</i>	<i>prs</i>	<i>flaF</i>	<i>fliC</i>
<i>dnaS</i>	<i>dfp, dut</i>	<i>flaG</i>	<i>flhB</i>
<i>dnaW</i>	<i>adk</i>	<i>flaH</i>	<i>flhA</i>
<i>dnaY</i>	<i>argU</i>	<i>flaI</i>	<i>flhC</i>
<i>dnaZ</i>	<i>dnaX</i>	<i>flaJ</i>	<i>motA, B</i>
<i>dniR</i>	<i>mltD</i>	<i>flaK</i>	<i>flgE</i>
<i>dpeA</i>	<i>hupB</i>	<i>flaL</i>	<i>flgG</i>
<i>dpeB</i>	<i>rpoS</i>	<i>flaM</i>	<i>flgI</i>
<i>dpj</i>	<i>acpS</i>	<i>flaN</i>	<i>fliE</i>
<i>dra</i>	<i>deoC</i>	<i>flaO</i>	<i>fliJ</i>
<i>drc</i>	<i>hns</i>	<i>flaP</i>	<i>fliR</i>
<i>drdX</i>	<i>hns</i>	<i>flaQ</i>	<i>fliQ</i>
<i>drm</i>	<i>deoB</i>	<i>flaR</i>	<i>fliP</i>
<i>drp</i>	<i>proS</i>	<i>flaS</i>	<i>flgK</i>
<i>drs</i>	<i>hns</i>	<i>flaT</i>	<i>flgL</i>
<i>dsbD</i>	<i>dipZ</i>	<i>flaU</i>	<i>flgA</i>
<i>dsbE</i>	<i>ccmG</i>	<i>flaV</i>	<i>flgD</i>
<i>dut</i>	<i>dfp</i>	<i>flaW</i>	<i>flgC</i>
<i>dye</i>	<i>arcA</i>	<i>flaX</i>	<i>flgF</i>
<i>ecfB</i>	<i>cpxA</i>	<i>flaY</i>	<i>flgH</i>
<i>efg</i>	<i>nadE</i>	<i>flaZ</i>	<i>flgJ</i>
<i>emrR</i>	<i>mprA</i>	<i>flbA</i>	<i>flgB</i>
<i>envA</i>	<i>lpxC</i>	<i>flbB</i>	<i>flhD</i>
<i>envB</i>	<i>mreB</i>	<i>flbC</i>	<i>fliD</i>
<i>envC</i>	<i>acrE</i>	<i>flbD</i>	<i>fliO</i>
<i>envD</i>	<i>acrF</i>	<i>fr</i>	<i>leuJ</i>
<i>envM</i>	<i>fabI</i>	<i>flrA</i>	<i>ileR</i>
<i>envZ</i>	<i>ompR</i>	<i>fms</i>	<i>def</i>
<i>eps</i>	<i>rpsE</i>	<i>fpg</i>	<i>mutM</i>
<i>eryA</i>	<i>rplD</i>	<i>fpk</i>	<i>fruK</i>
<i>eryB</i>	<i>rplV</i>	<i>frdB</i>	<i>fnr</i>
<i>eup</i>	<i>cpxA</i>	<i>frdR</i>	<i>narL, narX</i>
<i>exbA</i>	<i>tonB</i>	<i>fre</i>	<i>ubiB</i>
<i>excC</i>	<i>pal, toIA</i>	<i>fruC</i>	<i>fruR</i>
<i>exo</i>	<i>xni</i>	<i>fruF</i>	<i>fruB, fruK</i>
<i>exrA</i>	<i>lexA</i>	<i>fsrB</i>	<i>hmp</i>
<i>exrB</i>	<i>ssb</i>	<i>fsrC</i>	<i>ubiB</i>
<i>fabC</i>	<i>fabB</i>	<i>ftsB</i>	<i>nrdB</i>
<i>fabE</i>	<i>accB</i>	<i>ftsH</i>	<i>hflB</i>
<i>fabG</i>	<i>accC</i>	<i>ftsM</i>	<i>serU</i>
<i>fabJ</i>	<i>fabF</i>	<i>ftsR</i>	<i>rpoB</i>
<i>fadI</i>	<i>ubiB</i>	<i>ftsS</i>	<i>ftsX</i>
<i>fam</i>	<i>rpoH</i>	<i>fucC</i>	<i>fucA</i>
<i>far</i>	<i>fusA</i>	<i>gad</i>	<i>gapA, C</i>
<i>fda</i>	<i>fbaA</i>	<i>gadS</i>	<i>gadA?</i>
<i>fdhA</i>	<i>selA, B</i>	<i>galB</i>	<i>galT</i>
<i>fdhC</i>	<i>selC</i>	<i>gapB</i>	<i>epd</i>

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TABLE 2—Continued

Synonym	Gene symbol from Table 1	Synonym	Gene symbol from Table 1
<i>gen-165</i>	<i>fin</i>	<i>Hpr, hpr</i>	<i>ptsH</i>
<i>genA</i>	<i>dcuA</i>	<i>hpr</i>	<i>ptsH</i>
<i>genF</i>	<i>dcuB</i>	<i>hrbA</i>	<i>brnQ</i>
<i>genR</i>	<i>lrhA</i>	<i>hrbB</i>	<i>livG, H, J, K</i>
<i>glcF</i>	<i>glcE</i>	<i>hrbC</i>	<i>livG, H, J, K</i>
<i>glmD</i>	<i>nagB</i>	<i>hrbD</i>	<i>livG, H, J, K</i>
<i>glnF</i>	<i>rpoN</i>	<i>Hs</i>	<i>thrA</i>
<i>glnR</i>	<i>glnL</i>	<i>hs</i>	<i>hsdM, R</i>
<i>glnT</i>	<i>glnG</i>	<i>hsdH</i>	<i>hdhA</i>
<i>glnUα, β</i>	<i>glnU, W</i>	<i>hslF</i>	<i>ldhA</i>
<i>glnVα, β</i>	<i>glnV, X</i>	<i>hslI</i>	<i>ldhA</i>
<i>glr</i>	<i>murI</i>	<i>hslS</i>	<i>ibpB</i>
<i>glu</i>	<i>ppc</i>	<i>hslT</i>	<i>ibpA</i>
<i>glut</i>	<i>gltA</i>	<i>hsm</i>	<i>hsdM</i>
<i>gly</i>	<i>glyS</i>	<i>hsp</i>	<i>hsdM, R</i>
<i>glyD</i>	<i>gpt, glpD</i>	<i>hsr</i>	<i>hsdR</i>
<i>glySα, β</i>	<i>glyQ, S</i>	<i>hss</i>	<i>hsdS</i>
<i>gmhA</i>	<i>lpcA</i>	<i>hipE</i>	<i>ibpB</i>
<i>gntM</i>	<i>gntT</i>	<i>htpG21.0</i>	<i>hslO-R</i>
<i>gpp</i>	<i>gpt</i>	<i>hipH</i>	<i>ldhA</i>
<i>gppB</i>	<i>aslA, B</i>	<i>htpI</i>	<i>hslU</i>
<i>gpt</i>	<i>ptsG</i>	<i>hipN</i>	<i>ibpA</i>
<i>gptB</i>	<i>manX, manZ</i>	<i>htpO</i>	<i>hslV</i>
<i>groEL</i>	<i>groL</i>	<i>hipR</i>	<i>rpoH</i>
<i>groES</i>	<i>groS</i>	<i>htpY</i>	<i>htgA</i>
<i>gro</i>	<i>dnaK</i>	<i>htrA</i>	<i>degP</i>
<i>groN</i>	<i>rpoB</i>	<i>htrH</i>	<i>degS</i>
<i>groNB</i>	<i>nusB</i>	<i>htrM</i>	<i>rfaD</i>
<i>groP</i>	<i>dnaB, J, K</i>	<i>htrP</i>	<i>ribB</i>
<i>groPAB</i>	<i>dnaK</i>	<i>hyd</i>	<i>nik</i>
<i>groPC</i>	<i>dnaK</i>	<i>hydB</i>	<i>hypE</i>
<i>groPF</i>	<i>dnaK</i>	<i>hydC</i>	<i>hybA, nika-D</i>
<i>gpa</i>	<i>dnaB</i>	<i>hydD</i>	<i>nika-E</i>
<i>gpc</i>	<i>dnaJ, K</i>	<i>hydF</i>	<i>hypD</i>
<i>gpd</i>	<i>dnaB</i>	<i>hydL</i>	<i>hybA</i>
<i>gpf</i>	<i>dnaK</i>	<i>iarA</i>	<i>dsbA</i>
<i>gsa</i>	<i>hemL</i>	<i>iarB</i>	<i>dsbB</i>
<i>gsr</i>	<i>crr</i>	<i>icc</i>	<i>cpdA</i>
<i>gts</i>	<i>fabI</i>	<i>icdB</i>	<i>gltA</i>
<i>guaR</i>	<i>guaB</i>	<i>icdE</i>	<i>icd</i>
<i>gura</i>	<i>uidA</i>	<i>iciA</i>	<i>argP</i>
<i>gusA, B, R</i>	<i>uidA, B, R</i>	<i>icl</i>	<i>aceA</i>
<i>gutA-E, R</i>	<i>srhA-E, R</i>	<i>iex</i>	<i>crr</i>
<i>gxu</i>	<i>gpt</i>	<i>ihb</i>	<i>lrp</i>
<i>gyrI</i>	<i>sbmC</i>	<i>ile</i>	<i>ilvA</i>
<i>hag</i>	<i>fliC</i>	<i>ileS</i>	<i>lspA</i>
<i>hdh</i>	<i>groE</i>	<i>ind</i>	<i>tnaA</i>
<i>herA</i>	<i>mhA</i>	<i>ins</i>	<i>glyV, W</i>
<i>herC</i>	<i>lysS</i>	<i>int (qsr')</i>	<i>intD</i>
<i>hga</i>	<i>eda</i>	<i>irk</i>	<i>hns</i>
<i>hhoA</i>	<i>degQ</i>	<i>K12</i>	<i>rpsG</i>
<i>hhoB</i>	<i>degS</i>	<i>kac</i>	<i>kdpA, B, C, D</i>
<i>hid</i>	<i>ihfA</i>	<i>katF</i>	<i>rpoS</i>
<i>himA</i>	<i>ihfA</i>	<i>kdgA</i>	<i>eda</i>
<i>himB</i>	<i>gyrB</i>	<i>kga</i>	<i>eda</i>
<i>himD</i>	<i>ihfB</i>	<i>kim</i>	<i>qin</i>
<i>hin</i>	<i>rpoH</i>	<i>kirT</i>	<i>tufA, B</i>
<i>hip</i>	<i>ihfB</i>	<i>kup</i>	<i>trkD</i>
<i>hisE</i>	<i>hisI</i>	<i>lcs</i>	<i>asnS</i>
<i>hisT</i>	<i>hisR, truA</i>	<i>lct</i>	<i>lldD</i>
<i>hisU</i>	<i>gyrB</i>	<i>lctD</i>	<i>lldD</i>
<i>hisW</i>	<i>gyrA</i>	<i>lctP</i>	<i>lldP</i>
<i>hnsB</i>	<i>stpA</i>	<i>lctR</i>	<i>lldR</i>
<i>hobH</i>	<i>seqA?</i>	<i>ldh</i>	<i>dld</i>
<i>hom</i>	<i>asd</i>	<i>leuK</i>	<i>truA</i>
<i>hopD</i>	<i>hupB, gsp*</i>	<i>leuVα, β, γ</i>	<i>leuV, P, Q</i>
<i>hopE</i>	<i>recD</i>	<i>lexB</i>	<i>recA</i>
<i>hopG</i>	<i>gsp*</i>	<i>lexC</i>	<i>ssb</i>

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TABLE 2—Continued

Synonym	Gene symbol from Table 1	Synonym	Gene symbol from Table 1
<i>lig</i>	<i>ligA</i>	<i>msmC</i>	<i>cspE</i>
<i>lipP</i>	<i>nike?</i>	<i>msp</i>	<i>arcA</i>
<i>lir</i>	<i>acrA</i>	<i>mssA</i>	<i>cmk</i>
<i>livR</i>	<i>lrp</i>	<i>mssB</i>	<i>deadD</i>
<i>lky</i>	<i>tolA, B</i>	<i>msuA</i>	<i>dadX?</i>
<i>lkyA</i>	<i>tolB</i>	<i>msyA</i>	<i>hns</i>
<i>lnt</i>	<i>cutE</i>	<i>mtcA</i>	<i>acrA</i>
<i>lolB</i>	<i>hemM</i>	<i>mtcB</i>	<i>tolC</i>
<i>LopC</i>	<i>clpX</i>	<i>muc</i>	<i>lon</i>
<i>LopP</i>	<i>clpP</i>	<i>mukA</i>	<i>tolC</i>
<i>lov</i>	<i>argS</i>	<i>mukE</i>	<i>kicA</i>
<i>lovB</i>	<i>alaS</i>	<i>mukF</i>	<i>kicB</i>
<i>loxB</i>	<i>attPI, P7</i>	<i>murZ</i>	<i>murA</i>
<i>lrs</i>	<i>lrp</i>	<i>mutA</i>	<i>glyV</i>
<i>lss</i>	<i>lrp</i>	<i>mutC</i>	<i>glyW</i>
<i>lstR</i>	<i>lrp</i>	<i>mutD</i>	<i>dnaQ</i>
<i>luxH-like</i>	<i>ribB</i>	<i>mutH</i>	<i>dnaX</i>
<i>lysTα, β, γ</i>	<i>lysT, W, Y</i>	<i>mutR</i>	<i>topB</i>
<i>mac</i>	<i>maa</i>	<i>mutU</i>	<i>uvrD</i>
<i>malB</i>	<i>malK</i>	<i>mvrA</i>	<i>fpr</i>
<i>maoA</i>	<i>tynA</i>	<i>mvrC</i>	<i>emrE</i>
<i>maoB</i>	<i>feaR</i>	<i>nagR</i>	<i>nagC</i>
<i>mas</i>	<i>aceB</i>	<i>nalA</i>	<i>gyrA</i>
<i>mazE</i>	<i>chpR</i>	<i>nalC</i>	<i>gyrB</i>
<i>mazF</i>	<i>chpA</i>	<i>nalD</i>	<i>gyrB</i>
<i>Mb</i>	<i>acrA</i>	<i>nam</i>	<i>pncA</i>
<i>mbf</i>	<i>lrp</i>	<i>narA</i>	<i>moaA</i>
<i>mbL</i>	<i>acrA</i>	<i>narB</i>	<i>mobA</i>
<i>mbrA</i>	<i>rep</i>	<i>narC</i>	<i>narG</i>
<i>mcb</i>	<i>pmbA</i>	<i>narD</i>	<i>modC, E, F</i>
<i>mclA</i>	<i>rseA</i>	<i>narR</i>	<i>narL, X</i>
<i>mdaA</i>	<i>nfsA</i>	<i>nbp</i>	<i>fis</i>
<i>mdfA</i>	<i>cmr</i>	<i>ncf</i>	<i>hemB</i>
<i>mdrA</i>	<i>cydC</i>	<i>neaA</i>	<i>rpsQ</i>
<i>mdrH</i>	<i>cydC</i>	<i>nek</i>	<i>rimK</i>
<i>mec</i>	<i>dcm</i>	<i>nfrC</i>	<i>rffE</i>
<i>mel-4</i>	<i>melB</i>	<i>nfsB</i>	<i>nfnB</i>
<i>mel-7</i>	<i>melA</i>	<i>nfsI</i>	<i>nfnB</i>
<i>meoA</i>	<i>ompC</i>	<i>nfxA</i>	<i>gyrA</i>
<i>met-1</i>	<i>metB</i>	<i>nfxC</i>	<i>marA</i>
<i>metM</i>	<i>metL</i>	<i>nfxD</i>	<i>parE</i>
<i>metTβ</i>	<i>metU</i>	<i>nic</i>	<i>nadB</i>
<i>metZβ</i>	<i>metV</i>	<i>nirA</i>	<i>fnr</i>
<i>mgID</i>	<i>gals</i>	<i>nirR</i>	<i>fnr</i>
<i>mgIP</i>	<i>mgLA, C</i>	<i>nitA</i>	<i>rho</i>
<i>mhpS</i>	<i>mhpD</i>	<i>nitB</i>	<i>rpoB</i>
<i>micA</i>	<i>mutY</i>	<i>nlp</i>	<i>sfsB</i>
<i>mlc</i>	<i>dgsA</i>	<i>nlpE</i>	<i>cutF</i>
<i>mlpA</i>	<i>lpp</i>	<i>nmpA</i>	<i>pst, pstS</i>
<i>mmrA</i>	<i>rep, rhlB?</i>	<i>nmpB</i>	<i>phoR</i>
<i>mni</i>	<i>manC</i>	<i>norA</i>	<i>gyrA</i>
<i>modR</i>	<i>modE</i>	<i>norB</i>	<i>marA?</i>
<i>molA</i>	<i>malM</i>	<i>nov</i>	<i>cls</i>
<i>momR</i>	<i>oxyR</i>	<i>ntr</i>	<i>nfnB</i>
<i>mon</i>	<i>mreB</i>	<i>ntrA</i>	<i>rpoN</i>
<i>mopA</i>	<i>groS</i>	<i>ntrB</i>	<i>glnL</i>
<i>mopB</i>	<i>groL</i>	<i>ntrC</i>	<i>glnG</i>
<i>mor</i>	<i>oxyR</i>	<i>ntrL</i>	<i>nadE</i>
<i>moiD</i>	<i>ftiN</i>	<i>nucR</i>	<i>deoR</i>
<i>mpt</i>	<i>manX, Z</i>	<i>nupA</i>	<i>tsx</i>
<i>mra</i>	<i>murF</i>	<i>nur</i>	<i>rpoS</i>
<i>mrB</i>	<i>murA</i>	<i>nusD</i>	<i>rho</i>
<i>mrc</i>	<i>lpcB</i>	<i>nusE</i>	<i>rpsJ</i>
<i>mrsA</i>	<i>glmM</i>	<i>oldB</i>	<i>fadB</i>
<i>mrsC</i>	<i>hflB</i>	<i>ole</i>	<i>fadR</i>
<i>msgA</i>	<i>ftsN</i>	<i>ompB</i>	<i>envZ, ompR</i>
<i>msmA</i>	<i>dksA</i>	<i>ompE</i>	<i>phoE</i>
<i>msmB</i>	<i>cspC</i>	<i>ompH</i>	<i>hlpA</i>

Continued on following page

TABLE 2—Continued

Synonym	Gene symbol from Table 1	Synonym	Gene symbol from Table 1
<i>omsA</i>	<i>lpxD</i>	<i>pmi</i>	<i>manA</i>
<i>opdA</i>	<i>prlC</i>	<i>pmsR</i>	<i>msrA</i>
<i>oppI</i>	<i>lrp</i>	<i>pndR</i>	<i>xapR</i>
<i>optA</i>	<i>dgt</i>	<i>poaA</i>	<i>putA</i>
<i>osmZ</i>	<i>hns</i>	<i>pog</i>	<i>sspA</i>
<i>osrA</i>	<i>proU</i>	<i>poh</i>	<i>oriC</i>
<i>ossA</i>	<i>fnr</i>	<i>polC</i>	<i>dnaE</i>
<i>ossB</i>	<i>gltB, D, F</i>	<i>pon</i>	<i>lpcB</i>
<i>ostA</i>	<i>imp</i>	<i>ponA</i>	<i>mrcA</i>
<i>padA</i>	<i>feaB</i>	<i>ponB</i>	<i>mrcB</i>
<i>panK</i>	<i>coaA</i>	<i>popA</i>	<i>hemH</i>
<i>papA</i>	<i>atpA</i>	<i>popB</i>	<i>hemF</i>
<i>papC</i>	<i>atpG</i>	<i>popC</i>	<i>hemL</i>
<i>papD</i>	<i>atpB, D</i>	<i>popE</i>	<i>hemC</i>
<i>papE</i>	<i>atpH</i>	<i>ppfA</i>	<i>dsbA</i>
<i>papF</i>	<i>atpF</i>	<i>ppsA</i>	<i>pps</i>
<i>papG</i>	<i>atpC</i>	<i>prd</i>	<i>fucP</i>
<i>papH</i>	<i>atpE</i>	<i>prlA</i>	<i>secY</i>
<i>par</i>	<i>ompC</i>	<i>prlB</i>	<i>rbsB</i>
<i>parB</i>	<i>dnaG</i>	<i>prlD</i>	<i>secA</i>
<i>parD</i>	<i>gyrA</i>	<i>prlF</i>	<i>sohA</i>
<i>parvA</i>	<i>ppiC</i>	<i>prlG</i>	<i>secE</i>
<i>paxA</i>	<i>dcd</i>	<i>prlH</i>	<i>secG</i>
<i>pbpA</i>	<i>mrda</i>	<i>Pro2</i>	<i>proC</i>
<i>pbpB</i>	<i>ftsI</i>	<i>pro₁</i>	<i>proA</i>
<i>pbpF</i>	<i>mrcB</i>	<i>pro₂</i>	<i>proB</i>
<i>pcbA</i>	<i>gyrB</i>	<i>pro₃</i>	<i>proC</i>
<i>pcsA</i>	<i>dinD</i>	<i>prv</i>	<i>mutH</i>
<i>pdeB</i>	<i>uvrD</i>	<i>psiB</i>	<i>ugpA, B</i>
<i>pdeC</i>	<i>ligA</i>	<i>psiC</i>	<i>ugpA, B</i>
<i>pdxC</i>	<i>serC</i>	<i>psiD</i>	<i>phn, phnD</i>
<i>pdxF</i>	<i>serC</i>	<i>psiH</i>	<i>phoH</i>
<i>pdzA</i>	<i>rplT</i>	<i>psrA, B</i>	<i>TerC, B</i>
<i>pea</i>	<i>secA</i>	<i>psuA</i>	<i>rho</i>
<i>pel</i>	<i>manY</i>	<i>pts</i>	<i>man</i>
<i>perA</i>	<i>envZ</i>	<i>ptsF</i>	<i>fruA</i>
<i>pexB</i>	<i>dps</i>	<i>ptsL</i>	<i>manX</i>
<i>pfv</i>	<i>dacA</i>	<i>ptsM</i>	<i>manX, Y, Z</i>
<i>pgsB</i>	<i>lpxB</i>	<i>ptsN</i>	<i>nagE</i>
<i>phd</i>	<i>hcaA, B</i>	<i>ptsO</i>	<i>npr</i>
<i>phe-act</i>	<i>pheS</i>	<i>ptsP</i>	<i>manY</i>
<i>pheR</i>	<i>pheU</i>	<i>ptsX</i>	<i>manX, Z</i>
<i>pheW</i>	<i>pheU</i>	<i>pulT</i>	<i>tufA, B</i>
<i>phmA</i>	<i>nmpC</i>	<i>pup</i>	<i>deoD</i>
<i>phoM</i>	<i>creC</i>	<i>Pur2</i>	<i>purE</i>
<i>phoM-orf2</i>	<i>creB</i>	<i>purC</i>	<i>purF</i>
<i>phoR1</i>	<i>phoR</i>	<i>purE2</i>	<i>purK</i>
<i>phoR2a</i>	<i>pstS</i>	<i>purG</i>	<i>purM</i>
<i>phoR2b</i>	<i>pstA</i>	<i>purI</i>	<i>purL</i>
<i>phoRc</i>	<i>phoB</i>	<i>pyrA</i>	<i>carA, B</i>
<i>phoS</i>	<i>pstS</i>	<i>qmeA</i>	<i>fabI</i>
<i>phoT</i>	<i>phoB, U, pstA, B</i>	<i>R1pho</i>	<i>phoR</i>
<i>phoW</i>	<i>pstC</i>	<i>R2pho</i>	<i>pstA, S</i>
<i>phrA</i>	<i>modF</i>	<i>rad</i>	<i>uvrD</i>
<i>phs</i>	<i>rpoA</i>	<i>radB</i>	<i>recN</i>
<i>phsE?</i>	<i>dacD</i>	<i>ramA</i>	<i>rpsD</i>
<i>pil</i>	<i>fim, fimB, C, D</i>	<i>ramB</i>	<i>rimG</i>
<i>pilA</i>	<i>fimA</i>	<i>rap</i>	<i>pth</i>
<i>pilB</i>	<i>fimC</i>	<i>rapA</i>	<i>hepA</i>
<i>pilC</i>	<i>fimD</i>	<i>rbaB</i>	<i>smB</i>
<i>pilD</i>	<i>fimF, G</i>	<i>rbIA</i>	<i>lrp</i>
<i>pilE</i>	<i>fimH</i>	<i>rbsP</i>	<i>rbsA, B, C, D</i>
<i>pilG</i>	<i>hns</i>	<i>rbsT</i>	<i>rbsA, C</i>
<i>pilH</i>	<i>fimE</i>	<i>recA</i>	<i>lexA</i>
<i>pin</i>	<i>argU</i>	<i>recL</i>	<i>uvrD</i>
<i>pinO</i>	<i>pioO</i>	<i>refI</i>	<i>tolC</i>
<i>plsA</i>	<i>adk</i>	<i>refII</i>	<i>creD</i>
<i>PMG</i>	<i>mgl</i>	<i>relC</i>	<i>rplK</i>

Continued on following page

TABLE 2—Continued

Synonym	Gene symbol from Table 1	Synonym	Gene symbol from Table 1
<i>res</i>	<i>rimF</i>	<i>spr</i>	<i>lexA</i>
<i>resA</i>	<i>polA</i>	<i>srf</i>	<i>recA</i>
<i>rfbC</i>	<i>rfbD</i>	<i>srgA</i>	<i>priA</i>
<i>rfbD</i>	<i>rfbC</i>	<i>srjA</i>	<i>infC</i>
<i>rffE</i>	<i>rffG?</i>	<i>srjB</i>	<i>hldD</i>
<i>rglA</i>	<i>mcrA</i>	<i>srjC</i>	<i>uvrD</i>
<i>rglB</i>	<i>mcrB</i>	<i>ssaD</i>	<i>nusB</i>
<i>rhaC</i>	<i>rhaR, S</i>	<i>ssaF</i>	<i>rpmH</i>
<i>rhIA</i>	<i>srnB</i>	<i>ssc</i>	<i>lpxD</i>
<i>ribE</i>	<i>ribC</i>	<i>ssd</i>	<i>cpxA</i>
<i>ribG</i>	<i>ribD</i>	<i>ssyB</i>	<i>nusB</i>
<i>ribH</i>	<i>ribE</i>	<i>ssyF</i>	<i>rpsA</i>
<i>rif</i>	<i>rpoB</i>	<i>ssyG</i>	<i>infB</i>
<i>rimA</i>	<i>rpmH</i>	<i>stc</i>	<i>micF</i>
<i>rm</i>	<i>hsdM, R</i>	<i>stl</i>	<i>rpoB</i>
<i>mh</i>	<i>mhA</i>	<i>strA</i>	<i>rpsL</i>
<i>mnsA</i>	<i>ma</i>	<i>strB</i>	<i>strC</i>
<i>mnsC</i>	<i>rho</i>	<i>stsB</i>	<i>rimH</i>
<i>rodA</i>	<i>mrdB</i>	<i>stv</i>	<i>rpoB</i>
<i>rodY</i>	<i>mreB</i>	<i>Su-1</i>	<i>serU</i>
<i>ron</i>	<i>rpoB</i>	<i>Su-2</i>	<i>glnV, X</i>
<i>rorA</i>	<i>recB</i>	<i>Su-3</i>	<i>tyrT</i>
<i>rot</i>	<i>ppiA</i>	<i>Su-4</i>	<i>tyrT</i>
<i>rpoF</i>	<i>ftiA</i>	<i>Su-6</i>	<i>leuX</i>
<i>rfdB</i>	<i>rffF</i>	<i>SuB</i>	<i>lysT</i>
<i>rmBI</i>	<i>rmB</i>	<i>Su_{II}</i>	<i>glnV, X</i>
<i>rmDI</i>	<i>rmE</i>	<i>su_I</i>	<i>serU</i>
<i>rvd</i>	<i>rffF</i>	<i>su_B</i>	<i>glnU</i>
<i>rsgA</i>	<i>ftn</i>	<i>su_{III}</i>	<i>tyrT</i>
<i>rT</i>	<i>trnA</i>	<i>su7</i>	<i>trpT</i>
<i>rts</i>	<i>coaA</i>	<i>su8</i>	<i>trpT</i>
<i>sac</i>	<i>ascB, F</i>	<i>suA36</i>	<i>glyU</i>
<i>sbl</i>	<i>srlA, B, D</i>	<i>sud₂</i>	<i>rpsD</i>
<i>sdgA</i>	<i>dnaG</i>	<i>sueB</i>	<i>prfA</i>
<i>sdgB</i>	<i>rpoB</i>	<i>sufD</i>	<i>glyU</i>
<i>sdgE</i>	<i>era</i>	<i>sui</i>	<i>sufI</i>
<i>sdrA</i>	<i>mhA</i>	<i>suB</i>	<i>ftsZ</i>
<i>sec</i>	<i>hemF</i>	<i>sumA</i>	<i>glyT, U</i>
<i>secC</i>	<i>rpsO</i>	<i>sumB</i>	<i>glyU</i>
<i>sefA</i>	<i>fabZ</i>	<i>sun</i>	<i>rho</i>
<i>seg</i>	<i>arcA, dnaK</i>	<i>sup_{S20}</i>	<i>rpsT</i>
<i>sep</i>	<i>ftsI</i>	<i>sup15B</i>	<i>tyrU</i>
<i>sez</i>	<i>rpoA</i>	<i>supB</i>	<i>glnU, W</i>
<i>sfcA</i>	<i>mae?</i>	<i>supC</i>	<i>tyrT</i>
<i>sfhB</i>	<i>rtuD</i>	<i>supD</i>	<i>serU, V</i>
<i>sfiA</i>	<i>sulA</i>	<i>supE</i>	<i>glnV, X</i>
<i>sfiB</i>	<i>ftsZ</i>	<i>supF</i>	<i>tyrT</i>
<i>sfrA</i>	<i>arcA</i>	<i>supG</i>	<i>lysT</i>
<i>sfrB</i>	<i>rfaH</i>	<i>supH</i>	<i>serU</i>
<i>sfs1</i>	<i>sfsA</i>	<i>supK</i>	<i>prfB</i>
<i>sfs7</i>	<i>sfsB</i>	<i>supL</i>	<i>lysT</i>
<i>shl</i>	<i>fruR</i>	<i>supM</i>	<i>tyrU</i>
<i>sin</i>	<i>mhA</i>	<i>supN</i>	<i>lysV</i>
<i>sipB</i>	<i>acrA, ssrA</i>	<i>supO</i>	<i>tyrT?</i>
<i>sirA</i>	<i>yhhP</i>	<i>supP</i>	<i>leuX</i>
<i>skp</i>	<i>hlpA, lpxD</i>	<i>supT</i>	<i>glyU</i>
<i>slpA</i>	<i>intA</i>	<i>supU</i>	<i>trpT</i>
<i>slr</i>	<i>lplA</i>	<i>supV</i>	<i>trpT</i>
<i>slt</i>	<i>mltB</i>	<i>supX</i>	<i>topA</i>
<i>smbA</i>	<i>pyrH</i>	<i>supZ</i>	<i>tyrU</i>
<i>sms</i>	<i>radA</i>	<i>sur</i>	<i>bcr</i>
<i>sof</i>	<i>dut</i>	<i>surB</i>	<i>cydC</i>
<i>som</i>	<i>rfaA, B</i>	<i>suxA</i>	<i>bcr</i>
<i>soxQ</i>	<i>marA, R</i>	<i>T1</i>	<i>fhuA</i>
<i>spcA</i>	<i>rpsE</i>	<i>T1rec</i>	<i>tonB</i>
<i>spoS</i>	<i>rpoZ</i>	<i>T5rec</i>	<i>fhuA</i>
<i>spoU</i>	<i>trnH</i>	<i>T6rec</i>	<i>tsx</i>
<i>spoV</i>	<i>recG?</i>	<i>tabB</i>	<i>groE</i>

Continued on following page

TABLE 2—Continued

Synonym	Gene symbol from Table 1	Synonym	Gene symbol from Table 1
<i>tabD</i>	<i>rpoB, C</i>	<i>umpA</i>	<i>lgt</i>
<i>talA</i>	<i>alaT</i>	<i>unuA</i>	<i>lexA</i>
<i>talD</i>	<i>alaU</i>	<i>umuB</i>	<i>recA</i>
<i>tasC</i>	<i>aspT</i>	<i>uncA-I</i>	<i>atpA-I</i>
<i>tau</i>	<i>tus</i>	<i>ups?</i>	<i>prfA</i>
<i>tcp</i>	<i>rimJ</i>	<i>ura</i>	<i>car</i>
<i>tdc</i>	<i>tdcB</i>	<i>uraP</i>	<i>upp</i>
<i>tgs</i>	<i>crr, purU</i>	<i>usg</i>	<i>accD</i>
<i>tgtB</i>	<i>gltT</i>	<i>usgA</i>	<i>gntT</i>
<i>tgtC</i>	<i>gltU</i>	<i>uvm</i>	<i>umuC, D</i>
<i>tgtE</i>	<i>gltV</i>	<i>uvr502</i>	<i>uvrD</i>
<i>thdB</i>	<i>fadR</i>	<i>uvrE</i>	<i>uvrD</i>
<i>thdF</i>	<i>trmE</i>	<i>uvrF</i>	<i>recF</i>
<i>thiA</i>	<i>thiE, F, G, H</i>	<i>vacB</i>	<i>mr</i>
<i>thiJ</i>	<i>thiL</i>	<i>val-act</i>	<i>valS</i>
<i>thiN</i>	<i>thiJ</i>	<i>valTα</i>	<i>valT</i>
<i>thrD</i>	<i>thrA</i>	<i>valTβ</i>	<i>valZ</i>
<i>thyR</i>	<i>deoB, C</i>	<i>valUα</i>	<i>valU</i>
<i>tldE</i>	<i>pmbA</i>	<i>valUγ</i>	<i>valY</i>
<i>tlnI</i>	<i>tlnA</i>	<i>virR</i>	<i>hns</i>
<i>thr</i>	<i>deoB, C</i>	<i>visA</i>	<i>hemH</i>
<i>tls</i>	<i>aspS</i>	<i>visB</i>	<i>ubiH</i>
<i>tmrA</i>	<i>folA</i>	<i>vtr</i>	<i>fabF</i>
<i>tnaC, L</i>	<i>tna leader</i>	<i>waaA</i>	<i>kdtA</i>
<i>tnaR</i>	<i>tnaA</i>	<i>waaB</i>	<i>rfaB</i>
<i>toc</i>	<i>tolC</i>	<i>waaC</i>	<i>rfaC</i>
<i>tol-2</i>	<i>tolA</i>	<i>waaE</i>	<i>rfaE</i>
<i>tol-3</i>	<i>tolB</i>	<i>waaF</i>	<i>rfaF</i>
<i>tolF</i>	<i>ompF</i>	<i>waaG</i>	<i>rfaG</i>
<i>tolG</i>	<i>ompA</i>	<i>waaI</i>	<i>rfaI</i>
<i>tolM</i>	<i>cmtB</i>	<i>waaJ</i>	<i>rfaJ</i>
<i>tolP</i>	<i>tolQ?</i>	<i>waaK</i>	<i>rfaK</i>
<i>tolZ</i>	<i>hfbB</i>	<i>waaL</i>	<i>rfaL</i>
<i>tonA</i>	<i>flnA</i>	<i>waaM</i>	<i>htrB</i>
<i>topX</i>	<i>hns</i>	<i>waaN</i>	<i>mltA</i>
<i>tos</i>	<i>prfC</i>	<i>waaP</i>	<i>rfaP</i>
<i>tpo</i>	<i>envZ</i>	<i>waaQ</i>	<i>rfaQ</i>
<i>tpp</i>	<i>dppA?</i>	<i>waaS</i>	<i>rfaS</i>
<i>tpp-75</i>	<i>deoA</i>	<i>waaU</i>	<i>rfaK</i>
<i>tpx</i>	<i>ahpC</i>	<i>waaY</i>	<i>rfaY</i>
<i>tre</i>	<i>treA</i>	<i>waaZ</i>	<i>rfaZ</i>
<i>trkB</i>	<i>kefB</i>	<i>wbbH</i>	<i>rfc</i>
<i>trkC</i>	<i>kefC</i>	<i>wcaN</i>	<i>galF</i>
<i>trkE</i>	<i>sapD</i>	<i>wec</i>	<i>rff</i>
<i>trpP</i>	<i>tnaB</i>	<i>wecA</i>	<i>rfe</i>
<i>trpX</i>	<i>miaA</i>	<i>wecB</i>	<i>rffE</i>
<i>tryD</i>	<i>trpE</i>	<i>weeA</i>	<i>tolC</i>
<i>tryp-4</i>	<i>trpE</i>	<i>witA</i>	<i>kgiP</i>
<i>tsnC</i>	<i>trxA</i>	<i>wzxB</i>	<i>rfbX</i>
<i>tsp</i>	<i>prc</i>	<i>xerA</i>	<i>argR</i>
<i>tss</i>	<i>asnS</i>	<i>xerB</i>	<i>pepA</i>
<i>tsu</i>	<i>rho</i>	<i>xonA</i>	<i>sbcB</i>
<i>ttr</i>	<i>fadL</i>	<i>xprA</i>	<i>dsbC</i>
<i>tut</i>	<i>ompA</i>	<i>xprB</i>	<i>xerD</i>
<i>tyrTα, β</i>	<i>tyrT, V</i>	<i>xyIT</i>	<i>xyIF</i>
<i>uar</i>	<i>prfA</i>	<i>zab</i>	<i>recA</i>
<i>uidP</i>	<i>uidB</i>	<i>zfiA</i>	<i>csrA</i>
<i>ung</i>	<i>ptsG</i>		

^a Temporary names (*y* names, *orfs*) are not included.

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ERRATUM

Linkage Map of *Escherichia coli* K-12, Edition 10: The Traditional Map

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Volume 62, no. 3, p. 814–984, 1998. The following changes should be made to the “References” column in Table 1 (p. 822–881) (rows are indicated by gene symbol in the table): *accB*, add “2536”; *ada*, delete “3078”; *ansA*, add “2014”; *atpA*, add “2115, 2117”; *atpB*, add “2116 A”; *atpC*, add “2118”; *atpD*, add “2117, 2118”; *atpE*, add “2115”; *atpF*, add “2116”; *atpG*, add “2117”; *bglX*, “48154” should read “4858”; *bioA*, add “1085a”; *bioB*, add “1085a”; *bioC*, add “1085a”; *bioD*, add “1085a”; *cobS*, “add 2440”; *cobT*, add “2440”; *cobU*, add “2440”; *crr*, delete “1023”; *cycA*, “3686” should read “842a”; *cyoA*, add “2948”; *cysC*, add “2521”; *cysD*, add “2521”; *cysN*, add “2521”; *cytR*, “4128” should read “4129”; *dicB*, add “971”; *dnaJ*, add “4021”; *dnaK*, add “4021”; *dnaQ*, add “999a” and delete “4052,” “779,” and “856”; *e14*, add “1511”; *eda*, add “643a,” “828a,” “4594,” and “1289” and delete “1154”; *edd*, add “643a” and “828a” and delete “1289”; *emrE*, “300” should read “3003”; *entA*, delete “4180”; *entE*, add “4180”; *exuR*, “3687” should read “3686a”; *fdhE*, “3193” should read “3913”; *flhC*, “40” should read “4038”; *gapC*, add “444”; *glgX*, add “3721”; *glyT*, add “3687”; *grpE*, add “4021”; *hepA*, add “3078”; *hsdM*, add “815”; *hsdR*, add “815”; *hsdS*, add “815”; *hyaA*, add “515”; *ihfA*, add “4700”; *ihfB*, add “4700”; *infB*, add “3789”; *lpcB*, “10241” should read “4344”; *lpxD*, add “4615”; *lysX*, delete “2008”; *mbrB*, add “4470”; *mhpF*, delete “1228”; *mhpR*, delete “1228”; *mmrA*, delete “4508”; *mraA*, add “4508”; *mtlA*, add “2459”; *mutS*, add “3908”; *narJ*, add “4126”; *nfo*, add “3859”; *ompA*, add “3006”; *oxyR*, add “4351”; *pcnB*, “1682” should read “1684”; *pdxH*, “4034” should read “4034a”; *ppiA*, add “3933”; *prmB*, “815” should read “814a”; *prs*, add “1683”; *ptrB*, add “2111”; *ptsH*, add “983a” and “983b”; *purR*, add “1683”; *putA*, add “819a”; *recB*, add “4366”; *recC*, add “4366”; *recD*, add “4366”; *recQ*, add “4514”; *rne*, add “4353”; *rpmA*, add “2013”; *rmG*, add “3976”; *rvvB*, add “4478” and “4479”; *selA*, add “405”; *selB*, add “405”; *selC*, add “405”; *slt*, add “1154”; *speA*, add “1683” and “2691a”; *speB*, add “2691a”; *srlE*, “3644a” should read “3647a”; *tmk*, “405” should read “406”; *tnaA*, add “4873”; *truB*, add “3850”; *ugpA*, add “547”; *ugpB*, add “547”; *ugpC*, add “547”; *ugpE*, add “547”; *uxuA*, “3687” should read “3686a”; *uxuB*, add “3686” and “3687” should read “3686a”; *uxuR*, “3687” should read “3686a”; *zwf*, add “1290.”

The following changes should be made to the “Synonyms. . .” column in Table 1 (rows are indicated by gene symbol in the table): *argR*, add “Rarg”; *argQ*, delete “Rarg”; *atpE*, “DCCD” should read “DCCD binding”; *cydB*, add “htrD”; *dicB*, add “activates MinC”; *dicF*, “Qin” should read “ftsZ”; *htrB*, add “waaM”; *mdoA*, “modGH” should read “mdoGH”; *mesJ*, “cell cycle protein” should read “function unknown”; *rfaI*, add “waaI”; *rfaJ*, add “waaI”; *rfaK*, add “waaI”; *rfaL*, add “waaK”; *rfaM*, add “waaL”; *rfaN*, add “waaM”; *rfaO*, add “waaN”; *rfaP*, add “waaO”; *rfaQ*, add “waaQ”; *rfaS*, add “waaS”; *rfaT*, add “waaT”; *rfaU*, add “waaU”; *rfaV*, add “waaV”; *rfaW*, add “waaW”; *rfaX*, add “waaX”; *rfaY*, add “waaY”; *rfaZ*, add “waaZ”; *rfbX*, add “wzxB”; *rfc*, add “wbbH”; *rfe*, add “wecA.”

The following change should be made to the “Mnemonic for symbol” column in Table 1 (row indicated by gene symbol): *greAB*, “restorer?” should read “regulator.”

The following additions should be made to Table 2 (p. 881–888) (synonym, gene symbol): “*bglR*”, “*bglGo*”; “*ecfB*”, “*ssd*”; “*feuB*”, “*fep*”; “*galB*”, “*galT*”; “*hmpI*”, “*rne*”; “*htrD*”, “*cydB*”; “*hydE*”, “*hypB*”; “*lps*”, “*rfa*”; “*recX*”, “*oraA*”; “*rol*”, “*cld*”; “*rssE*”, “*cpxA*”; “*sbcA*”, “*rac*”; “*sprE*”, “*rasB*.”

The genes *kicA* and *kicB* have been renamed *mukE* and *mukF*, respectively, by their discoverers.

The following references should be changed as indicated: 734, add “F. Casse” as the fourth author; 828a, “5297–5298” should read “5247–5248”; 979, add “J. M. Louarn” as the fourth author; 1022, “Denklau” should read “Denk”; 1027, “A. H. Deutch” should read “C. E. Deutch”; 1290a, “*catC*, and” should read “*cstC*, an” and “U80416” should read “U90416”; 1320, “Froschauer” should read “Froschauer”; 1335, delete “R. Fukuda” as the fourth author; 1634, add “C. C. Brinton, Jr.” as the second author; 1698, “Heinrich” should read “Henrich”; 1769, “1978” should read “1979”; 1810, “E. Christie” should read “G. E. Christie”; 2101, “Kalnis” should read “Kalinis”; 2431, “43–47” should read “43–57”; 2558, “Lin, R. T.” should read “Tuan, L. R.”; 2674, “154:1339–1346” should read “6:22–25”; 2690, “1961” should read “1962”; 2754, “Inoue” should read “Inouye”; 2905, “1978” should read “1979”; 3044, add “P. A. Sorby, B. L. Triggs-Raine, and P. C. Loewen” as additional authors; 3193, “cariolipin” should read “cardiolipin”; 3347, “Triesmann” should read “Treishmann”; 3686, “glucoronate” should read “glucuronate”; 3690, “Robertson” should read “Roberton”; 3915, “Meldrof” should read “Meldorf”; 4034, “*pdxIt*” should read “*pdxH*”; 4034a, “. . . mutants” should read “in *serC* mutants”; 4411, “Thorne-Holst” should read “Throne-Holst”; 4470, “1991” should read “1992”; 4714, “1993” should read “1994.”

The following references should be added:

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