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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.unigiessen.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

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.

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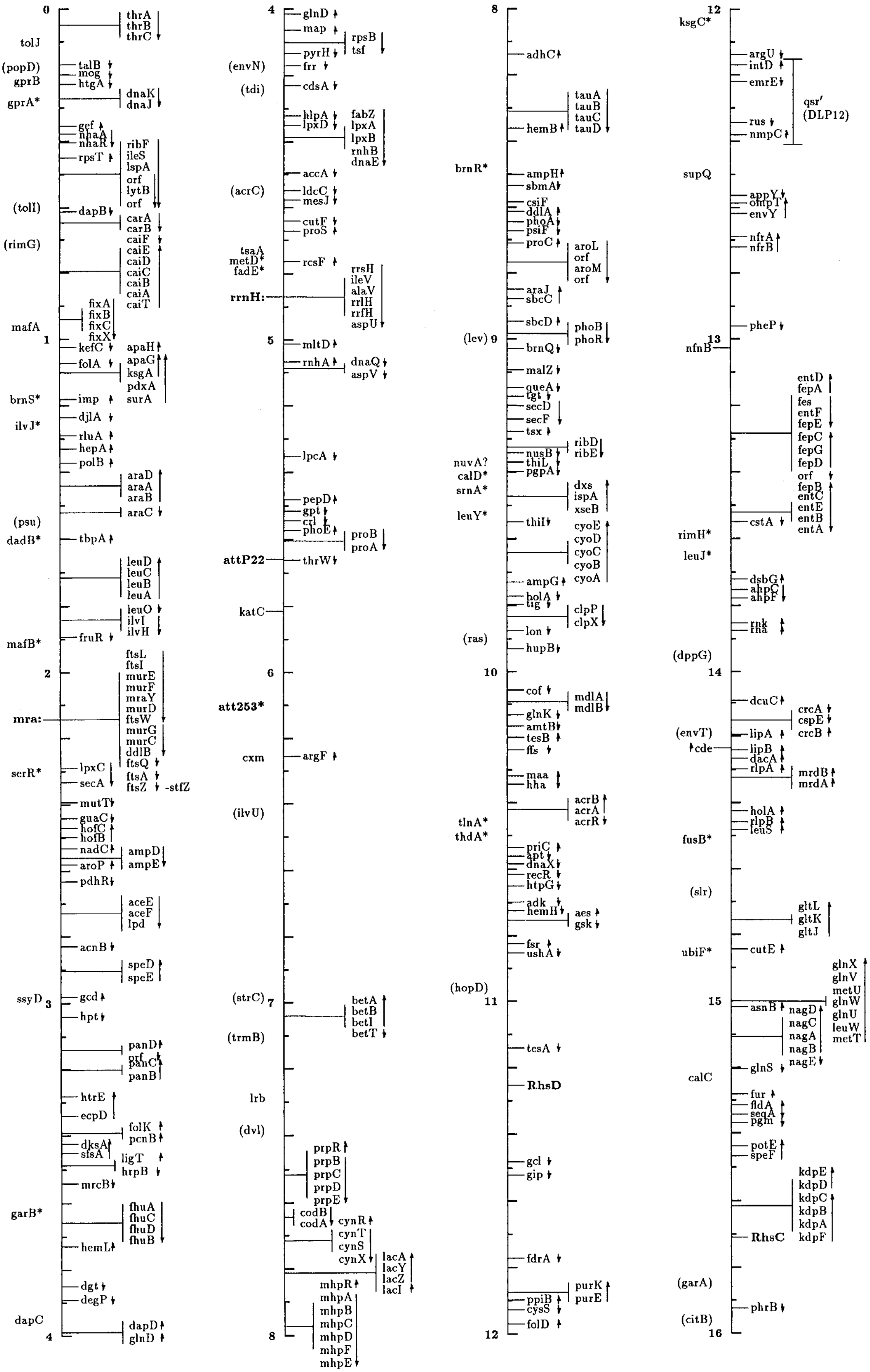
0
tolJ
(popD)
gprB
gprA*
(tolI)
(rimG)
mafA
1
brnS*
ilvJ*
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dadB*
mafB*
2
mra:
serR*
ssyD 3
garB*
dapC
4
thrA
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thrC
talB
mog
htgA
dnaK
dnaJ
gef
nhaA
nhaR
ribF
rpsT
ileS
lspA
orf
lytB
orf
dapB
carA
carB
caiF
caiE
caiD
caiC
caiB
caiA
caiT
fixA
fixB
fixC
fixX
kefC
apaH
apaG
folA
ksgA
pdxA
imp
surA
djlA
rluA
hepA
polB
araD
araA
araB
araC
tbpA
leuD
leuC
leuB
leuA
leuO
ilvI
ilvH
fruR
ftsL
ftsI
murE
murF
mraY
murD
ftsW
murG
murC
ddlB
ftsQ
lpxC
ftsA
secA
ftsZ
-stfZ
mutT
guaC
hofC
hofB
nadC
ampD
aroP
ampE
pdhR
aceE
aceF
lpd
acnB
speD
speE
gcd
hpt
panD
orf
panC
panB
htrE
ecpD
folK
pcnB
dksA
sfsA
ligT
hrpB
mrcB
fhuA
fhuC
fhuD
fhuB
hemL
dgt
degP
dapD
glnD
4
(envN)
(tdi)
(acrC)
tsaA
metD*
fadE*
rrnH:
5
attP22
katC
6
att253*
cxm
(ilvU)
(strC) 7
(trmB)
lrb
(dvl)
8
glnD
map
rpsB
tsf
pyrH
frr
cdsA
hlpA
fabZ
lpxD
lpxA
lpxB
rnhB
dnaE
accA
ldcC
mesJ
cutF
proS
rcsF
rrsH
ileV
alaV
rrlH
rrfH
aspU
mltD
rnhA
dnaQ
aspV
lpcA
pepD
gpt
crl
phoE
proB
proA
thrW
argF
betA
betB
betI
betT
prpR
prpB
prpC
prpD
prpE
codB
codA
cynR
cynT
cynS
cynX
lacA
lacY
lacZ
lacI
mhpR
mhpA
mhpB
mhpC
mhpD
mhpF
mhpE
8
brnR*
(lev) 9
nuvA?
calD*
srnA*
leuY*
(ras)
10
tlnA*
thdA*
(hopD)
11
12
adhC
tauA
tauB
tauC
hemB
tauD
ampH
sbmA
csiF
ddlA
phoA
psiF
proC
aroL
orf
aroM
orf
araJ
sbcC
sbcD
phoB
phoR
brnQ
malZ
queA
tgt
secD
secF
tsx
ribD
nusB
ribE
thiL
pgpA
dxs
ispA
xseB
thiI
cyoE
cyoD
cyoC
cyoB
ampG
cyoA
holA
tig
clpP
clpX
lon
hupB
cof
mdlA
glnK
mdlB
amtB
tesB
ffs
maa
hha
acrB
acrA
acrR
priC
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dnaX
recR
htpG
adk
hemH
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ushA
tesA
RhsD
gcl
gip
fdrA
purK
ppiB
purE
cysS
folD
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ksgC*
supQ
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nfnB
rimH*
leuJ*
(dppG)
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(envT)
cde
fusB*
(slr)
ubiF*
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calC
(garA)
(citB)
16
argU
intD
emrE
qsr′
(DLP12)
rus
nmpC
appY
ompT
envY
nfrA
nfrB
pheP
entD
fepA
fes
entF
fepE
fepC
fepG
fepD
orf
fepB
entC
entE
cstA
entB
entA
dsbG
ahpC
ahpF
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rna
dcuC
crcA
cspE
lipA
crcB
lipB
dacA
rlpA
mrdB
mrdA
holA
rlpB
leuS
gltL
gltK
gltJ
cutE
glnX
glnV
metU
asnB
nagD
glnW
nagC
glnU
nagA
leuW
nagB
metT
glnS
nagE
fur
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RhsC
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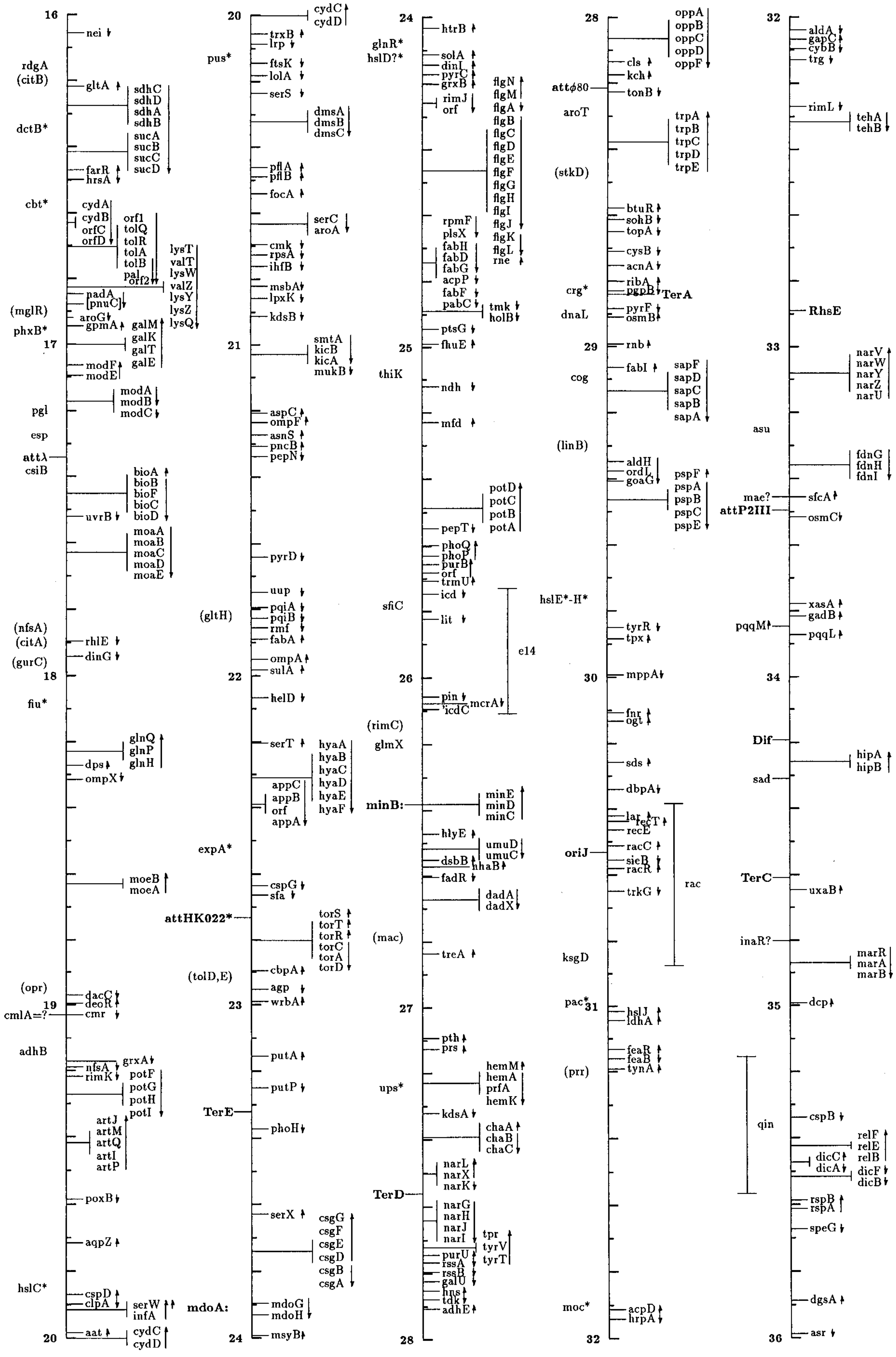


FIG. 1—*Continued.*

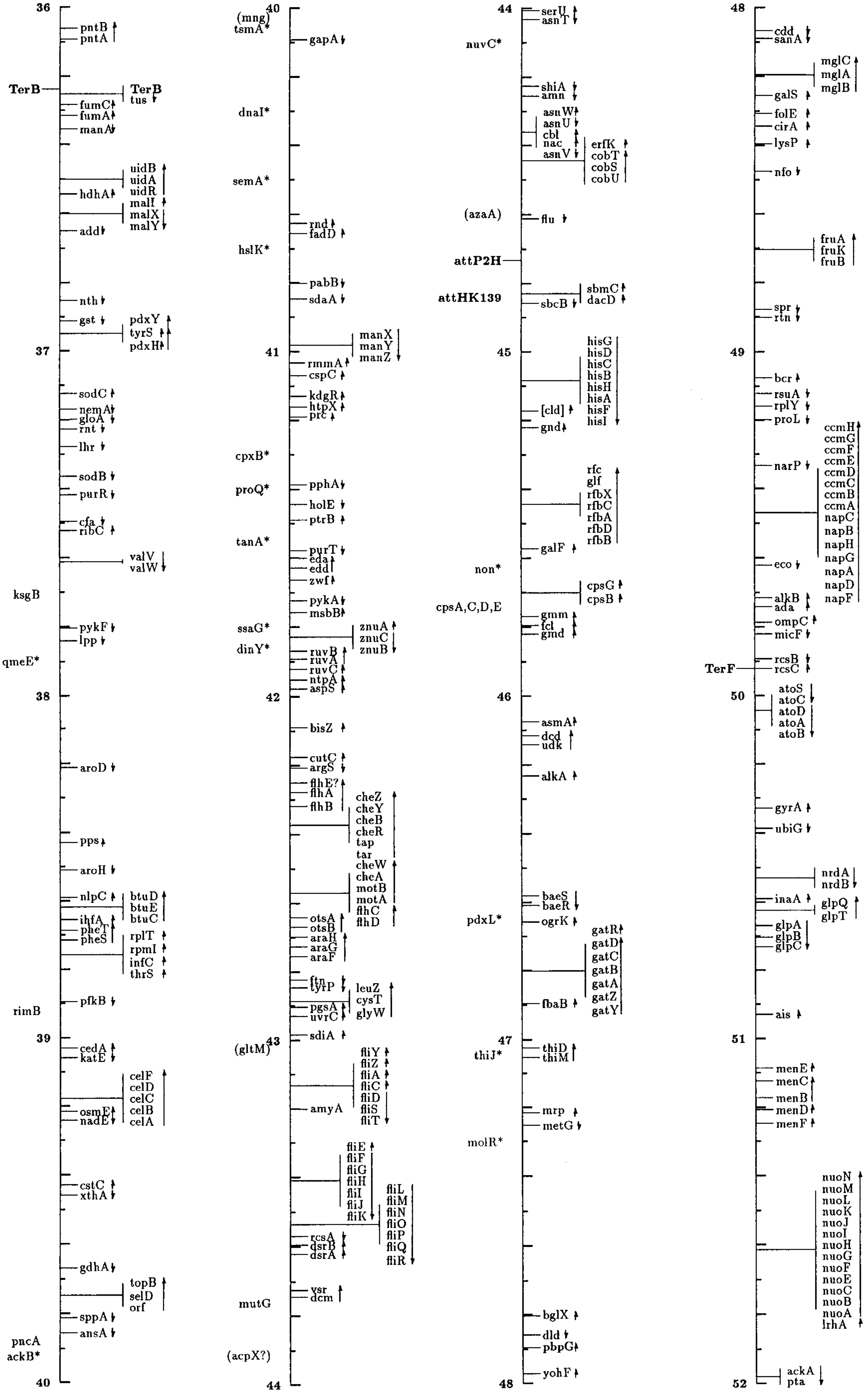
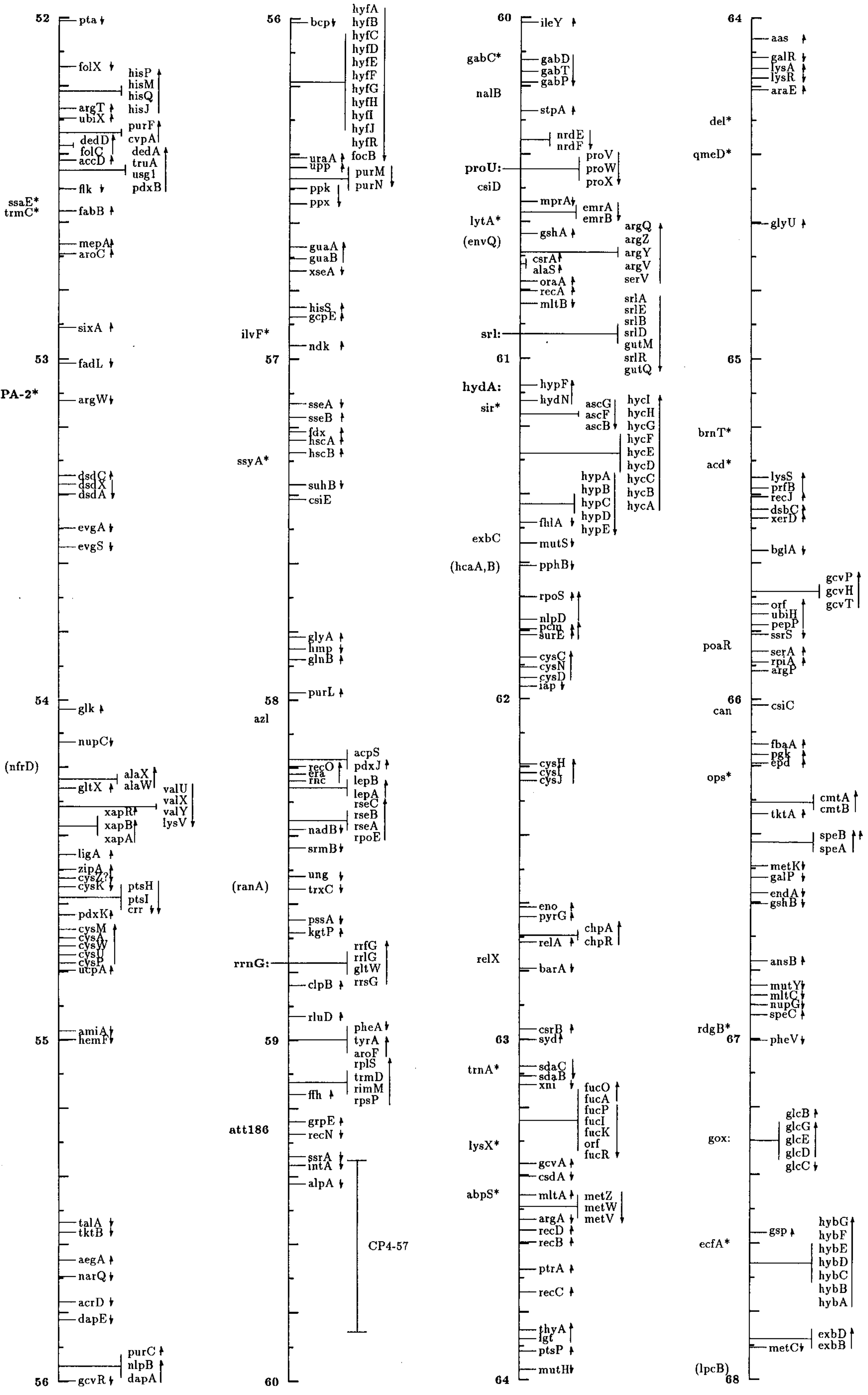


FIG. 1—*Continued.*



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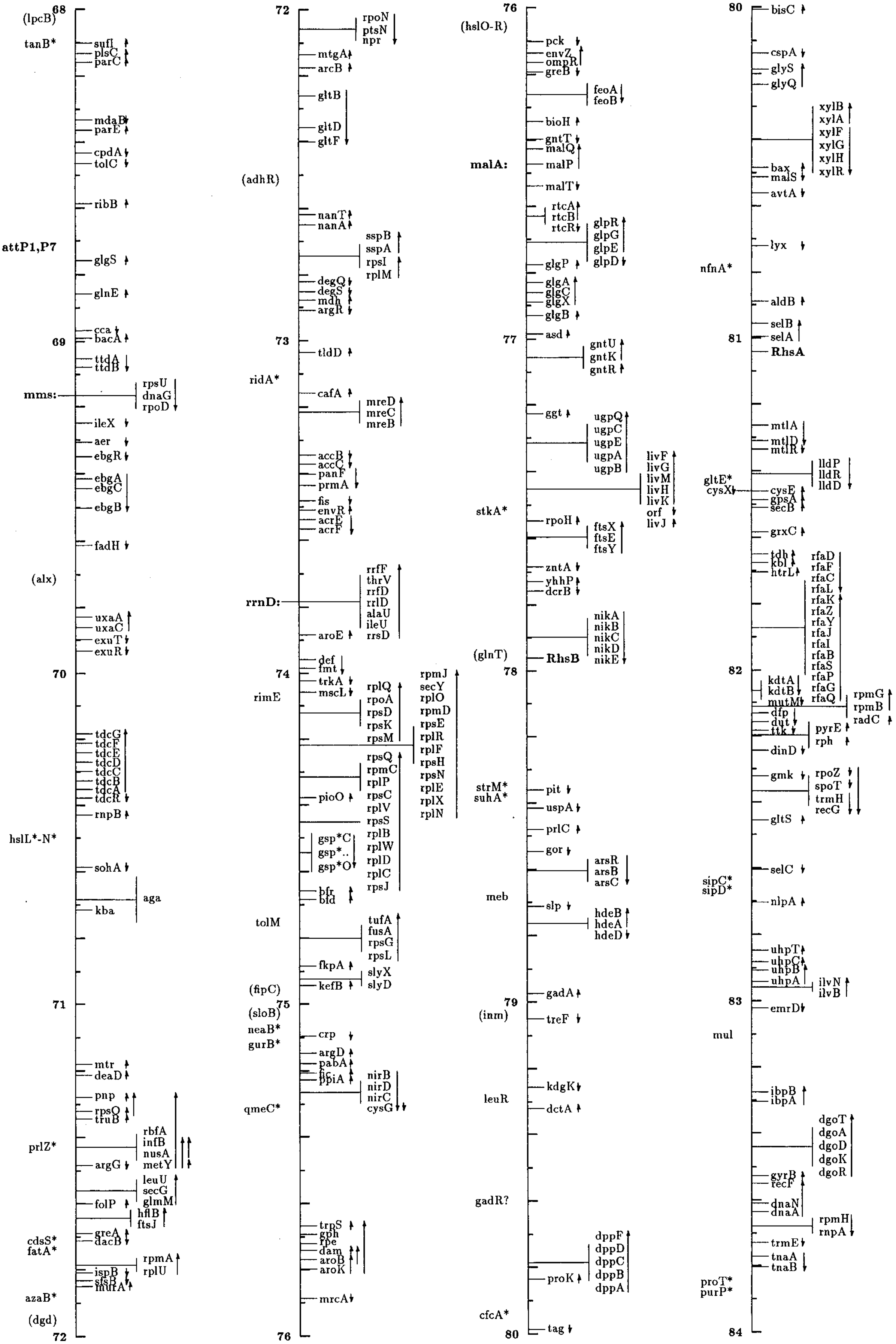

FIG. 1—*Continued.*

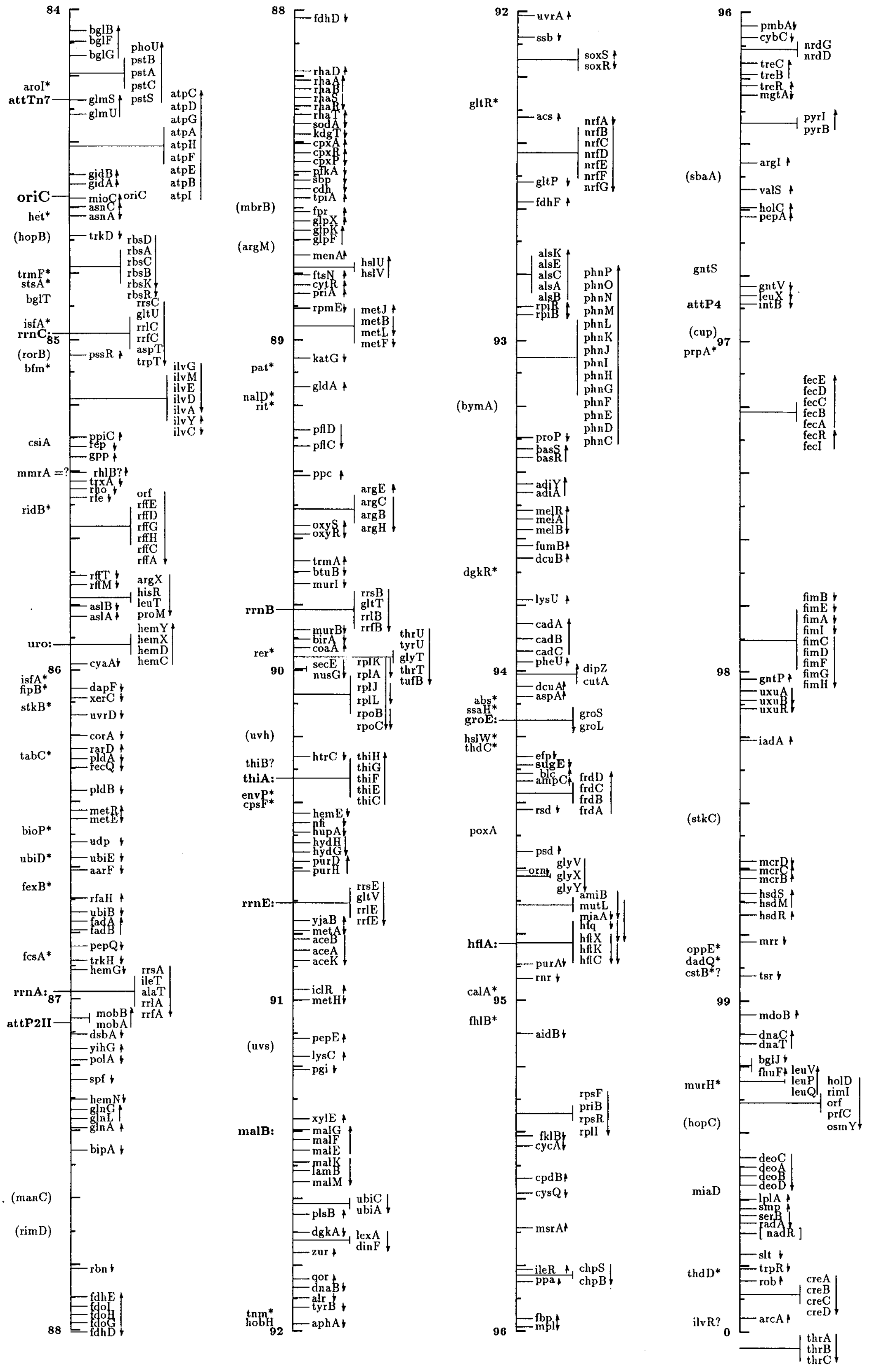

FIG. 1—*Continued.*

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]
aarF	86.6	Aminoglycoside acetyltransferase regulator	*yigQR*; regulator of 2′-*N*-acetyltransferase; involved in respiratory cofactor ubiquinone production	53879	2696
aas	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
aat	20.0	Amino acyl-tRNA-protein transferase	Aminoacyl-tRNA-protein-transferase (EC 2.3.2.6)	1054	4045
abpS	63.5	Arg binding protein	Low-affinity transport system for arginine and ornithine; periplasmic binding protein	18562	664
abs	94.1	Antibiotic sensitivity	Sensitivity and permeability to antibiotics and dyes	18559	763
accA	4.5	Acetyl-CoA carboxylase	Acetyl-CoA carboxylase α-carboxyltransferase subunit; (EC 6.4.1.2)	29829	2536, 2537
accB	73.4	Acetyl-CoA carboxylase	*fabE*; acetyl-CoA carboxylase, biotin carboxyl carrier protein (EC 6.4.1.2)	796	2537, 2712, 3057, 4302, 4616
accC	73.4	Acetyl-CoA carboxylase	*fabG*; acetyl-CoA carboxylase, biotin carboxylase (BC) subunit (EC 6.4.1.2)	29834	2315, 2537, 3253
accD	52.4	Acetyl-CoA carboxylase	*dedB*, *usg*; acetyl-CoA carboxylase β-carboxyltransferase subunit (EC 6.4.1.2)	28570	2534, 2537, 3081
acd	65.1	Acetaldehyde-CoA deHase	Acetaldehyde-CoA dehydrogenase (EC 1.2.1.10)	1053	764
aceA	90.8	Acetate	*icl*; isocitrate lyase (EC 4.1.3.1); acetate utilization	1052	2744, 2811, 3674, 754, 841
aceB	90.8	Acetate	*mas*; malate synthase A (EC 4.1.3.2)	1051	2744, 591, 592, 840, 841
aceE	2.7	Acetate	*aceE1*; pyruvate dehydrogenase (decarboxylase component) E1p; (EC 1.2.4.1); acetate requirement	1050	1553, 1555, 1556, 1558, 2934, 4150, 4204, 655
aceF	2.7	Acetate	*aceE2*; pyruvate dehydrogenase (dihydrolipoyltransacetylase component) E2p (EC 1.6.4.3, EC 2.3.1.12); acetate requirement	26530	1554, 2934, 655
aceK	90.9	Acetate	Isocitrate dehydrogenase kinase/phosphatase	17770	1343, 1897, 2274, 2418, 2419, 753, 842, 754
ackA	52.0	Acetate kinase	Acetate kinase (EC 2.7.2.1); mutants fluoroacetate resistant	1048	1548, 2094, 2512, 2812, 530, 224
ackB	39.9	Acetate kinase	Acetate kinase activity* (EC 2.7.2.1)	1047	3379
acnA	28.8	Aconitase	Aconitase A (EC 4.2.1.2)	28218	3542, 3543
acnB	2.8	Aconitase	Aconitase B (EC 4.2.1.2)	36955	1538, 2141, 474
acpD	31.9	Acyl carrier protein	ACP phosphodiesterase	52896	1256, 394
acpP	24.8	Acyl carrier protein	ACP (acyl carrier protein)	31871	2183, 3621
acpS	58.2	Acyl carrier protein	*dpj*; holo-ACP synthase (EC 2.7.8.7)	32953	2397, 2400, 2401, 3471, 4340
acpX	43.9	Acyl carrier protein	*acpS*; originally thought to be holo-ACP synthase; perhaps cryptic second gene or regulator	1046	3471
acrA	10.4	Acridine	*Mb*, *lir*, *mbl*, *mtcA*, *sipB*; AcrAB efflux system effects Mar multiple resistance	1045	1291, 1726, 2684, 2685, 3282, 3563, 4723, 808
acrB	10.4	Acridine	*acrE*; AcrAB system has major role in Mar multiple resistance to NAL, TET, AMP, etc.; beware renamings of *acrE*, *acrB*, and *envC*	35806	1291, 2684, 2685, 3282, 4723
acrC	4.5	Acridine	Sensitivity to acriflavine; transmembrane protein	1044	3104
acrD	55.7	Acridine	Sensitivity to acriflavine	35697	3188
acrE	73.5	Acridine	*envC*; anomolous cell division; chain formation; splits cross-wall to form new poles; see *acrB*	813	2133, 2255, 2256, 2516, 3702
acrF	73.6	Acridine	*envD*; encodes lipoprotein with signal peptide; osmotically remedial envelope defect	33608	2255, 2256, 2516, 2684
acrR	10.5	Acridine	Regulatory protein for *acrA* and *acrB*	35809	2686
acs	92.3	Acetyl-CoA synthetase	Acetyl CoA synthetase 2 (EC 6.2.1.1)	34317	2367, 395
ada	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
add	36.6	Adenine deaminase	Adenosine deaminase (EC 3.5.4.4.); mutants affect growth on deoxyadenosine in *purA*, *B* mutants	1042	2024, 765

Continued on following page

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]
adhB	19.1	Alcohol dehydrogenase	Alcohol dehydrogenase	36932	E, 763a
adhC	8.1	Alcohol dehydrogenase	Alcohol-acetaldehyde dehydrogenase; *adhC* has also been used for *adhE* control region	52901	2070, 394
adhE	27.9	Alcohol/acetaldehyde dehydrogenase	*ana*; *adhC*; 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
adhR	72.5	Alcohol/acetaldehyde dehydrogenase	Regulatory gene for *acd* and *adhE*	18556	723, 767
adiA	93.5	Arginine decarboxylase, induced	*adi*; arginine decarboxylase, inducible by acid; homology with CadA, SpeC, SpeF	34495	1665, 4022, 4023, 4024, 4223, 4224
adiY	93.4	Arginine decarboxylase, induced	Sequence similarity with XylS/AraC family, including EnvY and AppY regulates *adiA*	35597	4224
adk	10.7	Adenylate kinase	*dnaW*, *plsA*; adenylate kinase (EC 2.7.4.3) pleiotropic effects on glycerol-3-phosphate acyltransferase activity	1040	1176, 1725, 541
aegA	55.6	Anaerobically expressed gene	*air*; induced by anaerobiosis, repressed by NO_3; control mediated by Fnr, NarX, Q, L; nonessential in respiration, N source utilized	50847	662
aer	69.3	Aerotaxis	*air*; possibly flavoprotein, mediates positive aerotactic responses; signal transducer	47273	347
aes	10.7	Acetyl esterase	Esterase affecting maltose system expression	53369	2114, 3393
aga	70.7	Acetylgalactosamine	Cluster of putative *N*-acetylgalactosamine pathway genes, including the *kba* gene, and mannose permease homologs	55305	3649
agp	23.0	Acid glucose-1-phosphatase	Homology with *appA*; periplasmic	31830	3521, 3524, 3525, 3526
ahpC	13.8	Alkyl hydroperoxide	*tpx*; alkyl hydroperoxide reductase small subunit	31190	4106, 4241, 667, 668
ahpF	13.8	Alkyl hydroperoxide	Alkyl hydroperoxide reductase large subunit	31194	4106, 4241, 668
aidB	95.1	Alkylating agent induced	Adaptive response	18553	2408, 2409, 4602, 4603
ais	50.9	Aluminum inducible	An aluminum-inducible protein	53490	1589
alaS	60.7	Alanine	*act*, *ala-act*, *lovB*; alanyl-tRNA synthetase 1B (ligase) (EC 6.1.1.7)	1039	2132, 2317, 3556, 3557, 3558, 458, 4590
alaT	87.0	Alanine	*talA*; alanine tRNA 1B; *rrnA* operon	1038	2313, 926
alaU	73.8	Alanine	*talD*; alanine tRNA 1B; *rrnD* operon	1037	2313
alaV	4.8	Alanine	Alanine tRNA 1B; *rrnH* operon	1036	1146
alaW	54.2	Alanine	*alaW*α; alanine tRNA 2; tandemly duplicated; see *alaX*	32851	539
alaX	54.2	Alanine	*alaW*β; alanine tRNA 2; tandemly duplicated *alaW*	18547	2313, 539
aldA	32.0	Aldehyde dehydrogenase	*ald*; aldehyde dehydrogenase, NAD linked	17767	1749, 3571, 712
aldB	80.9	Aldehyde dehydrogenase	Aldehyde dehydrogenase	35668	4813, 4815
aldH	29.3	Aldehyde dehydrogenase	Putative aldehyde dehydrogenase, by homology; transcribed in operon with *goaG*	35320	1697, 2066
alkA	46.2	Alkylation	*aidA*; 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
alkB	49.7	Alkylation	*aidD*; DNA repair specific for alkylated DNA; mutants extremely sensitive to MMS	18544	2157, 2158, 2316, 4602, 4689, 693
alpA	59.4	Activation of Lon protease	Alp protease; cryptic prophage CP4-57 element; regulates *intA* (*slp* [suppressor of Lon])	33086	2241, 4455
alr	91.9	Alanine racemase	Alanine racemase (EC 5.1.1.1)	1034	2549, 395
alsA	92.8	Allose	Allose transport ABC protein	53362	2223
alsB	92.9	Allose	Allose-binding protein	53365	2223
alsC	92.8	Allose	Allose transport, membrane component	53357	2223
alsE	92.8	Allose	Allulose-6-P 3-epimerase	53353	2223
alsK	92.8	Allose	Allose kinase	53345	2223
alx	70.0	Alkaline-induced expression	pH-regulated locus; induced in alkaline medium	36513	356
amiA	55.0	Amidase	*N*-Acetylmuramyl-L-alanine amidase activity	18541	4425
amiB	94.7	Amidase	Cell wall amidase (EC 3.5.1.28?); overexpression causes lysis, osmotic hypersensitivity, autolysis	34432	4489, 4490
amn	44.3	AMP nucleosidase	AMP nucleosidase (EC 3.2.2.4)	17764	2503, 2504
ampC	94.3	Ampicillin	*ampA*; β-lactamase; penicillin resistance; affects peptidoglycan synthesis; cell morphology	1033	1116, 1117, 1167, 1540, 1541, 1713, 1993–1995, 3213, 796
ampD	2.6	Ampicillin	*ampC* regulation	30478	1794, 2561
ampE	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[c]
ampG	9.7	Ampicillin	Ampicillin resistance; membrane protein	31027	2560
ampH	8.5	Ampicillin	Probable role in peptidoglycan, cell wall synthesis; cell morphology	51873	1713
amtB	10.2	Ammonia transport	Putative ammonia transporter	47403	4557
amyA	43.2	Amylase	α-amylase, cytoplasmic	30745	3581, 3582
ansA	39.9	Asparaginase	L-Asparaginase I; (EC 3.5.1.1)	1030	1005, 4167
ansB	66.8	Asparaginase	L-Asparaginase II; (EC 3.5.1.1)	30045	427, 2008
apaG	1.1	ad-P-ad	Expressed as part of complex *ksgA* operon	30310	3683, 380
apaH	1.1	ad-P-ad	Diadenosine tetraphosphatase; stress response; complex operon	17761	1205, 2034, 2509, 2861, 3683, 380
aphA	92.0	Acid phosphatase	Acid phosphatase/phosphotransferase, class B	45401	4390
appA	22.4	Acid (poly)phosphatase	Acid phosphatase, pH 2.5, exopolyphosphatase (EC 3.1.3.2, 3.6.1.11); *agp* homology; phytase P2	17758	1514, 432, 945, 946, 4446
appB	22.4	Acid (poly)phosphatase	*cyxB*; cytochrome oxidase, putative additional one	31813	161, 947
appC	22.4	Acid (poly)phosphatase	*cyxA*; cytochrome oxidase, putative additional one	31810	161, 947
appY	12.6	Acid (poly)phosphatase	Regulates *hya* and *appA* operons; induced by PO_4 starvation and stationary phase	31146	160, 161, 162, 1786, 2195, 516
apt	10.6	ad-P transferase	Adenine phosphoribosyltransferase (EC 2.4.2.7); adenine salvage, AMP from PRPP + Ad	1029	1733, 1734, 577
aqpZ	19.7	Aquaporin	Aquaporin Z, bacterial water channel	40930	607, 608
araA	1.4	Arabinose	L-Arabinose isomerase (EC 5.3.1.4)	1028	2469
araB	1.5	Arabinose	Ribulokinase (EC 2.7.1.16)	1027	1102, 2169, 2469, 2470, 2970, 3247, 4110
araC	1.5	Arabinose	Regulatory gene: activator and repressor	1026	1102, 1158, 2169, 2300, 2470, 2971, 3247, 4018, 4110, 4237, 4642, 643, 651
araD	1.4	Arabinose	L-Ribulosephosphate 4-epimerase (EC 5.1.3.4)	1025	2469, 2949
araE	64.2	Arabinose	Low-affinity L-arabinose transport; L-arabinose proton symport	1024	2299, 2300, 2708, 2724, 4238
araF	42.7	Arabinose	L-Arabinose-binding protein	1023	2299, 2300, 2328, 3953, 3954, 758
araG	42.7	Arabinose	High-affinity L-arabinose transport	1022	2299, 2300, 2328, 3953
araH	42.7	Arabinose	High-affinity L-arabinose transport, membrane protein	18535	3953
araJ	8.8	Arabinose	Function unknown, arabinose inducible, not affecting Ara transport or utilization	29861	1716, 3636
arcA	100.0	Aerobic pathways control	*dye*, *fexA*, *msp*, *seg*, *sfrA*; negative regulatory gene for aerobic path genes, anaerobic repression; activates *cydAB*	831	1089, 1955, 333, 4069, 587, 588, 689
arcB	72.2	Aerobic pathways control	Activates ArcA in response to anoxia; probable histidine kinase phosphorylating ArcA	29063	1953, 1956, 1958, 3886, 689
argA	63.5	Arginine	*Arg1*, *Arg2*, *argB*; *N*-acetylglutamate synthase (EC 2.3.1.1); growth on acetylornithine; see *argE*	1021	1107, 3152, 3870, 528, 862
argB	89.5	Arginine	Acetylglutamate kinase (EC 2.7.2.8); see *argA*	1020	255, 3000, 3374, 862, 863
argC	89.5	Arginine	*Arg2*, *argH*; *N*-acetyl-γ-glutamyl-phosphate reductase (EC 1.2.1.38)	1019	255, 3000, 311, 3374, 3433, 862, 863
argD	75.2	Arginine	*Arg1*, *argG*; acetylornithine aminotransferase (EC 2.6.1.11); see *argF*	1018	2191, 315, 3676, 862
argE	89.5	Arginine	*Arg4*, *argA*; acetylornithine deacetylase (EC 3.5.1.16); see *argG*	1017	2187, 255, 3000, 311, 3433, 863
argF	6.2	Arginine	*Arg5*, *argD*; ornithine transcarbamylase (EC 2.1.3.3); see duplicate locus, *argI*	1016	1597, 1838, 2015, 2476, 2997, 2998, 3434, 4561, 4892, 863, 1717
argG	71.5	Arginine	*Arg6*, *argE*; argininosuccinate synthetase (EC 6.3.4.5); see *argD*	1015	4560, 1717
argH	89.5	Arginine	Argininosuccinate lyase (EC 4.3.2.1); see *argC*	1014	255, 3000, 863, 1717
argI	96.5	Arginine	Ornithine transcarbamylase (EC 2.1.3.3); see *argF*	1013	295, 3434, 3729
argM	88.7	Arginine	Acetylornithine transaminase; cryptic gene; may be duplicate of *argD*	18532	3676
argP	65.9	Arginine	*iciA* (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]
argQ	60.7	Arginine	*Rarg*; arginine $tRNA_2$ tandem quadruple genes	2313	35604
argR	72.9	Arginine	*xerA*; repressor of Arg regulon; *cer*-mediated site-specific recombination	1011	1114, 2187, 2481, 254, 2552, 2690, 315, 3399, 3427, 4225
argS	42.2	Arginine	*lov*; arginyl-tRNA synthetase (EC 6.1.1.19);	1010	1164, 1772, 3147, 4590
argT	52.3	Arginine	*Salmonella* homolog codes for Lys-, Arg-, and Orn-binding proteins	18529	3211
argU	12.1	Arginine	*dnaY*, *pin*; arginine $tRNA_4$	17755	1285, 1360, 1415, 2313, 2563, 3888, 4140, 505, 696
argV	60.7	Arginine	*argV*α; arginine $tRNA_2$ tandem quadruple genes	2313	11650
argW	53.1	Arginine	Arginine $tRNA_5$	17752	2313
argX	85.8	Arginine	Arginine $tRNA_3$	17749	1832, 2313, 926
argY	60.7	Arginine	*argV*β; arginine $tRNA_2$ tandem quadruple genes	2313	35610
argZ	60.7	Arginine	*argV*γ; arginine $tRNA_2$ tandem quadruple genes	2313	35607
aroA	20.7	Aromatic	3-Enolpyruvylshikimate-5-phosphate synthetase (EC 2.5.1.19)	1008	1098, 1099
aroB	75.8	Aromatic	3-Dehydroquinate synthase (EC 4.6.1.3)	1007	2937
aroC	52.7	Aromatic	Chorismate synthase (EC 4.6.1.4)	1006	683
aroD	38.2	Aromatic	3-Dehydroquinate dehydratase (EC 4.2.1.10)	1005	2240, 433
aroE	73.9	Aromatic	Dehydroshikimate reductase (EC 1.1.1.25)	1004	116, 2865
aroF	59.0	Aromatic	DAHP synthetase (tyrosine repressible) (EC 4.1.2.15)	1003	1371, 1847, 4047
aroG	16.9	Aromatic	DAHP synthetase (phenylalanine repressible) (EC 4.1.2.15); TyrR regulon	1002	1189, 1704, 1903, 2819, 958, 959
aroH	38.5	Aromatic	DAHP synthetase (tryptophan repressible) (EC 4.1.2.15)	1001	1100, 1848, 3030, 433, 4968, 958
aroI	84.2	Aromatic	Function unknown	1000	1422
aroK	75.8	Aromatic	Shikimate kinase I	30224	1516, 2604, 2605, 4586, 4719
aroL	8.7	Aromatic	Shikimate kinase II (EC 2.7.1.71)	999	2436, 2936, 4719, 998, 999
aroM	8.8	Aromatic	Function unknown; regulated by *aroR*	18523	998, 999
aroP	2.6	Aromatic	General aromatic amino acid transport; TyrR regulon	998	1553, 1556, 1558, 1657, 2131, 2415, 2416, 3689, 529, 755, 756, 83, 1795
aroT	28.3	Aromatic	*trpR*; *aroR*; indole acrylic acid resistant mutants; transport	997	4410
arsB	78.6	Arsenate resistance	*arsF*; resistance to arsenate, arsenite, and antimonite	35996	1055, 4128, 600, 637
arsC	78.6	Arsenate resistance	*arsG*; resistance to arsenate, arsenite, and antimonite	35999	1055, 4128, 600, 637
arsR	78.6	Arsenate resistance	*arsE*; resistance to arsenate, arsenite, and antimonite	35993	1055, 4128, 4812, 600, 637
artI	19.4	Arginine transport	Periplasmic binding protein of Arg transport system	31674	4759, 4760
artJ	19.4	Arginine transport	Periplasmic binding protein of Arg transport system	31664	4759
artM	19.4	Arginine transport	Arg periplasmic transport system; similarity to transmembrane proteins, BPC ATPases	31667	4759, 4760
artP	19.4	Arginine transport	Arg periplasmic transport system; similarity to transmembrane proteins, BPC ATPases	31677	4759, 4760
artQ	19.4	Arginine transport	Arg periplasmic transport system; similarity to transmembrane proteins, BPC ATPases	31670	4759, 4760
ascB	61.2	Arbutin, salicin, cellobiose	*sac*; cryptic; paralogous to cryptic *bglFB*; expressed when AscG is mutated	33236	1606, 3365
ascF	61.2	Arbutin, salicin, cellobiose	*sac*; cryptic; paralogous to cryptic *bglFB*; expressed when AscG is mutated	33233	1606, 3365
ascG	61.1	Arbutin, salicin, cellobiose	Repressor of cryptic *asc* operon; *galR* paralog	33230	1606
asd	77.0	Aspartate semialdehyde deHase	*dap*, *hom*; aspartate semialdehyde dehydrogenase (EC 1.2.1.11)	996	1679, 1680, 3281, 3940
aslA	85.8	Arylsulfatase-like	*gppB*; suppresses *gpp* mutants	33957	3069
aslB	85.8	Arylsulfatase-like	*gppB*; suppresses *gpp* mutants	33960	3069
asmA	46.1	Assembly suppressor mutant	Membrane protein; suppressor of *ompF* assembly mutants	41068	1021; 2957, 4811
asnA	84.6	Asparagine	Asparagine synthetase A (EC 6.3.1.1)	995	1769, 1861, 2295, 3111, 4610, 4621, 556
asnB	15.0	Asparagine	Asparagine synthetase B (EC 6.3.1.1)	994	1861, 3454, 3952
asnC	84.6	Asparagine	Regulatory gene for *asnA*, *asnC*, *gidA*	18520	1033, 2294, 556, 729

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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]
asnS	21.3	Asparagine	*lcs*, *tss*; asparaginyl-tRNA synthetase (EC 6.1.1.22)	993	1917, 4433
asnT	44.0	Asparagine	Asparagine tRNA	992	1285, 2313, 3324
asnU	44.4	Asparagine	Asparagine tRNA	17746	2313
asnV	44.4	Asparagine	Asparagine tRNA	17743	2313
asnW	44.3	Asparagine	Asparagine tRNA	51238	2313
aspA	94.1	Aspartate	Aspartate ammonia-lyase (aspartase) (EC 4.3.1.1)	991	1557, 4327
aspC	21.2	Aspartate	Aspartate aminotransferase (EC 2.6.1.1)	990	1283, 2317, 2373, 2740
aspS	42.0	Aspartate	*tls*; aspartyl-tRNA synthetase	32508	1165, 1351, 4000
aspT	85.0	Aspartate	*tasC*; aspartate $tRNA_1$ triplicated gene	989	2313, 2777, 4904, 926
aspU	4.8	Aspartate	Aspartate $tRNA_1$ triplicated gene, in *rrnH* operon	988	1146, 2313, 2777
aspV	5.1	Aspartate	Aspartate $tRNA_1$ triplicated gene	987	1806, 2313, 2777, 3324
asr	35.9	Acid shock RNA	Acid shock RNA; expression controlled by *phoBR*	53672	1986
asu[e]	33.3	Asparagine utilization	Utilizes asparagine as sole nitrogen source	18517	723
atoA	50.1	Acetoacetate	Acetate CoA-transferase (EC 2.8.3.-)	986	2321
atoB	50.1	Acetoacetate	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	985	2005
atoC	50.0	Acetoacetate	Az; positive regulator in two-component system, with AtoS sensor kinase	984	395a, 1949a, 3985a, 2005, 2006, 3382, 3817, 629
atoD	50.0	Acetoacetate	Acetyl-CoA:acetoacetyl-CoA transferase β-subunit	18514	2005
atoS	50.0	Acetoacetate	AtoS sensor kinase, with AtoC response regulator in 2-component system	37061	395a, 1949a, 3985a
atpA	84.4	ATP	*papA*, *uncA*; membrane-bound ATP synthase, F_1 sector, α-subunit (EC 3.6.1.3)	33	1390, 1570, 2275, 4187, 4635
atpB	84.5	ATP	*papD*, *uncB*; membrane-bound ATP synthase, F_0 sector, subunit a (EC 3.6.1.3)	32	1570, 1830, 2993, 3180, 3860, 4609, 4635
atpC	84.3	ATP	*papG*, *uncC*; membrane-bound ATP synthase, F_1 sector, ε-subunit (EC 3.6.1.3)	31	1570, 4635, 4809, 4810
atpD	84.4	ATP	*papB*, *uncD*; membrane-bound ATP synthase, F_1 sector, β-subunit (EC 3.6.1.3)	30	1570, 3296, 4635
atpE	84.5	ATP	*papH*, *uncE*; membrane-bound ATP synthase, F_0 sector, subunit c; $DCCD^-$ (EC 3.6.1.3)	29	1570, 1992, 2836, 2993, 3860, 3900, 4635
atpF	84.5	ATP	*papF*, *uncF*; membrane-bound ATP synthase, F_0 sector, subunit b (EC 3.6.1.3)	28	1570, 2993, 4635
atpG	84.4	ATP	*papC*, *uncG*; membrane-bound ATP synthase, F_1 sector, γ-subunit (EC 3.6.1.3)	27	1570, 2275, 2692, 3860, 4635
atpH	84.4	ATP	*papE*, *uncH*; membrane-bound ATP synthase, F_1 sector, δ-subunit (EC 3.6.1.3)	26	1570, 2994, 3380, 4635
atpI	84.5	ATP	*uncI*; 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
att186	59.3	Attachment	Integration site for phage HK186	972	D
att253	6.1	Attachment	Integration site for phage HK253	18508	3484
attHK139	44.8	Attachment	Attachment site for phage HK139	981	1035
attHK022	22.7	Attachment	*atthtt*; lambdoid prophage HK022 attachment site	982	1034, 2301
*att*λ	17.3	Attachment	*att92*, *att434*; lambda attachment site	980	1470, 18, 1035, 1836, 2940
attP1,P7	68.7	Attachment	*loxB*; attachment site for phage P1 and P7	979	4205, 722
attP22	5.6	Attachment	*ata*; phage P22 attachment site, within *thrW* gene	975	2562
attP2H	44.7	Attachment	Integration site H for phage P2	978	241a, 4291, D
attP2II	87.1	Attachment	Integration site II for phage P2	977	241a, 37, D
attP2III	83.5	Attachment	Integration site III for phage P2	32179	241a
attP4	96.9	Attachment	Integration site for phage P4	976	611, 3431
attPA-2	53.1	Attachment	Integration site for phage PA-2	974	C
*att*φ*80*	28.2	Attachment	Integration site for phage phi80	973	3794a
*att*Tn*7*	84.3	Attachment	Specific site for Tn*7* insertion	37363	1520, 2852
avtA	80.6	Alanine-isoketovalerate transaminase	Alanine-α-ketoisovalerate transaminase, transaminase C	971	1196, 2585, 4656, 4718
azaA	44.6	Azaserine	Mutants azaserine resistant	970	4744
azaB	71.9	Azaserine	Mutants azaserine resistant	969	4744
azl	58.1	Azaleucine	Mutants azaleucine resistant; regulates *ilv* and *leu*	967	3452

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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]
bacA	69.0	Bacitracin resistance	A lipid kinase; may confer resistance by phosphorylation of undecaprenol	29739	606
baeR	46.6	Bacterial adaptive *envZ* regulator	Suppresses *envZ* and *phoR*/*creC* mutations	30764	3083
baeS	46.6	Bacterial adaptive *envZ* regulator	Suppresses *envZ* and *phoR*/*creC* mutations	30761	3083
barA	62.8	Bacterial adaptive response	Has sensory kinase and response regulator domains like OmpR and EnvZ	33320	1924, 3084
basR	93.4	Bacterial adaptive sensor	BasRS two-component regulatory system homologous with OmpR-EnvZ family	28168	3083, 3716
basS	93.3	Bacterial adaptive sensor	BasRS two-component regulatory system homologous with OmpR-EnvZ family	28171	3083
bax	80.5		Gene transcribed divergently from *malS*	54736	3922
bcp	56.0	Bacterioferritin comigratory protein	Probable bacterioferritin	33035	112
bcr	49.1	Bicyclomycin resistance	*bicA*, *bicR*, *sur*, *suxA*; transmembrane; affects sulfathiazole-sulfonamide resistance	32582	309
betA	7.0	Betaine	Choline dehydrogenase	17740	104, 2399, 4257, 470
betB	7.0	Betaine	Betaine aldehyde dehydrogenase (EC 1.2.1.8)	17737	104, 2399, 470
betI	7.1	Betaine	Regulatory gene, perhaps repressor for choline regulation of *bet* genes	30692	2399
betT	7.1	Betaine	High-affinity choline transport	18505	104, 2399
bfd	74.7	Bfr regulating	Regulatory or redox component complexing with Bfr in iron storage and mobility [2Fe-2S]	43017	1369
bfm	85.9	BF23 multiplication	Controls phage BF23 multiplication	966	A, 4041a
bfr	74.7	Bacterioferritin	Bacterioferritin	32528	111
bglA	65.6	β-Glucoside	*bglD*; phospho-β-glucosidase A; growth on arbutin or salicin when activated	965	2076, 3239
bglB	84.1	β-Glucoside	*blgA*; phospho-β-glucosidase B; growth on arbutin or salicin when activated	964	2718, 3528, 3658, 3924, 3925, 4611
bglF	84.1	β-Glucoside	*bglC*, *bglB*; BglG kinase; transport	18502	2718, 3924, 476, 704
bglG	84.1	β-Glucoside	*bglC*, *bglS*; positive regulatory gene, RNA-binding protein; regulated by phosphorylation	963	1818, 2718, 3658, 3659, 3924, 3825, 4077, 4506
bglJ	99.2	β-Glucoside	Mutation *bglJ4* activates silent *bgl* operon, allowing arbutin and salicin transport and utilization	45483	1424, 4506
bglT	84.9	β-Glucoside	*bglE*; regulatory gene for BglA	961	3890
bglX	47.8	β-Glucoside	Periplasmic β-glucosidase (EC 3.2.1.21)	4858	48154
bioA	17.4	Biotin	Diaminopelargonic acid synthetase	959	18, 232, 2331, 235, 3312, 4246, 4319
bioB	17.4	Biotin	Biotin synthetase; dethiobiotin to biotin pathway	958	18, 232, 2331, 235, 3312, 4246, 4319
bioC	17.5	Biotin	Blocked prior to pimeloyl CoA formation	957	18, 2488, 4246, 4319
bioD	17.5	Biotin	Dethiobiotin synthetase	956	18, 2488, 4246, 4319, 4852
bioF	17.5	Biotin	7-Keto-8-aminopelargonic acid synthetase	955	18, 2488, 4246, 4319
bioH	76.3	Biotin	*bioB*; blocked prior to pimeloyl CoA formation	954	232, 2488, 3303, 3940
bioP	86.6	Biotin	*bir*, *birB*; biotin transport	953	1298, 624
bipA	87.4	BPI-induced protein	*yihK*; in EPEC strains, it mediates interactions with epithelial cells; tyrosine-phosphorylated GTPase	37329	1206
birA	89.9	Biotin retention	*bioR*, *dhbB*; biotin-[acetyl-CoA carboxylase] holoenzyme synthetase, and repressor	952	1825, 232–234, 2743, 3337, 4817, 624
bisC	80.0	Biotin sulfoxide	Biotin sulfoxide reductase, structural gene	951	1003, 3430
bisZ	42.1	Biotin sulfoxide	Responsible for background activity of biotin sulfoxide reductase in *bisC* mutants	50496	1004
blc	94.3	Bacterial lipocalin	Membrane protein, first prokaryotic lipocalin; cell division and growth, *rpoS* regulon; shares translation termination codons with *sugE*	40887	361
bolA	9.8	Bolus	Morphogene; overexpression produces osmotically stable spherical cells; FtsZ dependent	31032	2413, 55–57
brnQ	9.0	Branched chain	*hrbA*; mutants valine and *o*-methylthreonine resistant, glycylvaline sensitive; transport system I for Ile, Leu, and Val	950	1542, 1543
brnR	8.5	Branched chain	Mutants valine resistant, glycylvaline sensitive	949	1542
brnS	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
brnT	65.2	Branched chain	Low-affinity transport of Ile	947	1876a
btuB	89.7	B12 uptake	*bfe*, *cer*; 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
btuC	38.6	B12 uptake	Vitamin B_{12} transport	945	1029, 1031, 1315
btuD	38.6	B12 uptake	B_{12} transport, membrane associated	18499	1029, 1031, 1315
btuE	38.6	B12 uptake	Not required for vitamin B_{12} transport, perhaps periplasmic protein	18496	1029, 1315, 3679
btuR	28.6	B12 uptake	Regulatory gene affecting *btuB*	18493	2667
bymA	93.2	Bypass maltose	Growth on maltose in MalT$^-$ cells	944	1781
cadA	93.9	Cadaverine	Lysine decarboxylase (EC 4.1.1.18)	943	168, 169, 2886, 2887, 3144, 4022, 4325, 4680
cadB	93.9	Cadaverine	Arginine/ornithine antiporter, probably	34228	2886, 3144, 4680
cadC	93.9	Cadaverine	Regulatory gene	34231	2887, 3144, 4680
cafA	73.2	Cytoplasmic axial filaments	Cell division and growth, overexpression forms minicells and chains with long axial structures	31358	3278
caiA	0.8	Carnitine inducible	Carnitine metabolism, oxidoreductase	36825	1134, 550
caiB	0.8	Carnitine inducible	Carnitine dehydratase	36800	1135, 550
caiC	0.8	Carnitine inducible	Crotonobetain/carnitine-CoA ligase	36828	1134, 550
caiD	0.8	Carnitine inducible	Putative enoyl hydratase/isomerase with carnitine racemase activity	36831	1134, 550
caiE	0.8	Carnitine inducible	Stimulates carnitine racemase activity of CaiD and CaiB activity	36834	1134, 550
caiF	0.7	Carnitine inducible	Regulatory gene; transcriptional activation of *cai* operon	42995	1133, 550
caiT	0.9	Carnitine inducible	Putative carnitine/betaine transport	36822	1134, 550
calA	95.0	Calcium	Calcium-proton antiport activity	941	4417, 499
calC	15.2	Calcium	Calcium transport; mutants defective in chemotaxis	940	4417, 499
calD	9.4	Calcium	Calcium transport; mutants defective in chemotaxis	939	4417, 499
can	66.0	Canavanine	Resistance to canavanine	938	A, 2691a
carA	0.6	Carbamoyl P	*arg+ura*, *cap*, *pyrA*; carbamoylphosphate synthase (glutamine-hydrolysing) light subunit (EC 6.3.5.5)	936	1427, 3432, 465, 861
carB	0.7	Carbamoyl P	*arg+ura*, *cap*, *pyrA*; carbamoylphosphate synthase (ammonia), heavy subunit (EC 6.3.4.16)	935	1427, 3234, 861
cbl	44.4	*cysB*-like	*cys* regulon member; perhaps an accessory regulatory circuit within the *cys* regulon	50175	1964, 4550
cbpA	22.9	Curved-DNA binding protein	Recognizes a curved DNA sequence; sequence similarity to DnaJ	31822	4505
cbt	16.6	Colicin B (and D) tolerance	Dicarboxylate binding protein production; ColB and ColD tolerance	934	334
cca	69.0	CCA tRNA terminus	tRNA nucleotidyl transferase	933	880
ccmA	49.5	Cytochrome *c* maturation	ABC transporter, ATPase subunit	36574	1537, 4406, 4411, 739, 740
ccmB	49.5	Cytochrome *c* maturation	ABC transporter, ATPase subunit	36577	1537, 4406, 4411, 739, 740
ccmC	49.4	Cytochrome *c* maturation	ABC transporter, heme binding	36581	1537, 4406, 4411, 739, 740
ccmD	49.4	Cytochrome *c* maturation	Cytochrome *c* related	36584	1537, 4406, 739, 740
ccmE	49.4	Cytochrome *c* maturation	Cytochrome *c* related	36587	1537, 4406, 739, 740
ccmF	49.4	Cytochrome *c* maturation	Required for synthesis of *c*-type cytochromes; similarity with NrfE	36590	1536, 1537, 4406, 4411, 739, 740
ccmG	49.4	Cytochrome *c* maturation	*dsbE*; thioredoxin homolog; thiol-disulfide interchange protein	36594	1192, 1537, 4406, 4411, 739, 740
ccmH	49.3	Cytochrome *c* maturation	Required for synthesis of *c*-type cytochromes; similarity with NrfF and NrfG	36597	1536, 1537, 4406, 739, 740
cdd	48.1	Deoxycytidine deaminase	Deoxycytidine deaminase (EC 3.5.4.5); mutants 5-fluorodeoxycytidine resistant	932	1075, 2057, 2058, 2925, 3241, 429, 4325, 4851
cde	14.2	Control of *dam* expression	Affects growth rate control of *dam* expression; near or within *lipB*	37102	3616
cdh	88.5	CDP diglyceride hydrolase	CDP-diglyceride hydrolase	931	1710, 1884, 51, 559, 560
cdsA	4.2	CDP diglyceride synthase	CDP-diglyceride synthase	930	1356, 1886
cdsS	71.7	CDP diglyceride synthase	Stability of CDP diglyceride synthase	18490	1355
cedA	39.1	Cell division	Modulates cell division, affects inhibition after overreplication of chromosome in *dnaAcos* 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[c]
celA	39.2	Cellobiose	*chbB*; member of cryptic *cel* operon	34873	2205, 3366
celB	39.2	Cellobiose	*chbC*; phosphotransferase system enzyme IIcel, PEP dependent; cryptic operon; cellobiose, arbutin, and salicin transport	18487	2205, 2340, 2341, 3366, 3647
celC	39.2	Cellobiose	*chbA*; phosphotransferase system enzyme IIIcel, PEP dependent; cryptic operon; cellobiose, arbutin, and salicin transport	18484	2205, 2340, 2341, 3366, 3547
celD	39.2	Cellobiose	*chbR*; Cel regulatory protein	18481	2205, 2340, 2341, 3366
celF	39.1	Cellobiose	*chbF*; phospho-β-glucosidase B; cryptic operon	17734	2205, 2340, 2341, 3366
cfa	37.5	Cyclopropane fatty acid	*cdfA*; cyclopropane fatty acid synthase	10810	1527, 1528, 1529, 4649
cfcA	79.9	Control frequency of cell division	Controls cell division frequency per round of DNA replication	36615	3194
chaA	27.4	Ca^{2+}/H^+ antiporter	Ca^{2+}/H^+ antiporter	30293	1961, 3271, 3330
chaB	27.4	Ca^{2+}/H^+ antiporter	Accessory and regulatory protein for *chaA*	37193	4792a
chaC	27.4	Ca^{2+}/H^+ antiporter	Accessory and regulatory protein for *chaA*	37196	4792a
cheA	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
cheB	42.4	Chemotaxis	Protein methylesterase; flagellar regulon member	927	2349, 3076, 4101, 4214, 468, 923
cheR	42.4	Chemotaxis	*cheX*; protein methyltransferase (in chemotactic response); flagellar regulon	926	2951, 3076, 4101, 468
cheW	42.5	Chemotaxis	Signal transduction; couples CheA to chemoreceptor control by promoting CheW/CheA/Tsr; flagellar regulon	925	3076, 3757, 4064, 4101
cheY	42.4	Chemotaxis	Response regulator CheY for chemotactic signal transduction; flagellar regulon member	924	2679, 2809, 3076, 3757, 3857, 4046, 4101, 468, 776
cheZ	42.3	Chemotaxis	Chemotactic signal transduction; flagellar regulon member	923	3076, 3856, 3857, 4101, 468
chpA	62.7	Chromosomal homolog of *pem*	*chpAK*, *mazF*; ChpAB growth inhibitor, homology to R100 pemK gene, programmed cell death? toxic protein	33287	2794, 35
chpB	95.8	Chromosomal homolog of *pem*	*chpBK*, *yjfB*; ChpAB growth inhibitor, homology to *pemK*	33290	2793, 2794
chpR	62.7	Chromosomal homolog of *pem*	*chpAI*, *mazE*; homology to R100 *pemI*, which suppresses *pemK*; suppresses ChpA inhibition	33283	2794, 35
chpS	95.8	Chromosomal homolog of *pem*	*chpBI*, *yjfA*; homology to *pemI*; supresses ChpB	33293	2793, 2794
cirA	48.3	Colicin I resistance/receptor	*feuA*; colicin I receptor production	916	1518, 2925, 428, 4783
citA	17.9	Citrate	Cryptic gene for citrate transport system	18469	1604
citB	16.0	Citrate	Cryptic gene for citrate transport system	18466	1604
cld	45.2	Chain length determination	*rol*; regulator of lipopolysaccharide O-chain length; gene studied in *Salmonella* and non-K-12 strains	56819	1061a, 1293a
clpA	19.9	Caseinolytic protease	Clp ATP-dependent protease, ATP-binding subunit	31293	1472, 3972, 3973, 3990
clpB	58.8	Caseinolytic protease	ClpB protease, ATP dependent (EC 1.17.4.–, 3.4.21.–)	32875	1327, 2244, 3359, 3478, 4178, 4772
clpP	9.8	Caseinolytic protease	F21.5, LopP; ClpP ATP-dependent protease proteolytic subunit	31280	2344, 2822, 2824, 3973, 4765
clpX	9.8	Caseinolytic protease	LopC; ClpX protease, which activates ClpP	31287	1297, 1473, 2505, 4765, 4891
cls	28.1	Cardiolipin synthase	*nov*; cardiolipin synthase; mutants dihydroxybutylphosphonate resistant; novobiocin sensitivity	915	1690, 1765, 1766, 1876, 1960, 3193, 3267, 3600, 4462, 4463
cmk	20.7	CMP kinase	*mssA*; multicopy suppressor; CMP kinase	31736	1308, 4843
cmlA	19.0	Chloramphenicol	Probably same as *cmr*; resistance or sensitivity to chloramphenicol, also tetracycline resistance	914	187, 3637, 4043
cmr	19.0	Chloramphenicol resistance	*cmlA*?, *mdfA*; transmembrane multidrug/chloramphenicol efflux transporter	55066	1115, 3189, 3637
cmtA	66.3	Cryptic mannitol	Similar to mannitol phosphotransferase enzymes	33362	4163
cmtB	66.3	Cryptic mannitol	*tolM*; protein-*N*π-phosphohistidine sugar P-transferase; enzyme III of PEP-PTS cryptic mannitol transport	33365	4163
coaA	89.9	CoA	*panK*, *rts*; pantothenate kinase	17731	1259, 4134, 4135, 4538
cobS	44.5	Cobalamin, coenzyme B12	Partial cobalamin biosynthesis pathway present in *E. coli*	40912	2439

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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]
cobT	44.4	Cobalamin, coenzyme B12	Partial cobalamin biosynthesis pathway present in *E. coli*	40908	2439
cobU	44.5	Cobalamin, coenzyme B12	Partial cobalamin biosynthesis pathway present in *E. coli*	40916	2439
codA	7.7	Cytosine deaminase	Cytosine deaminase (EC 3.5.4.1)	913	23, 4562, 927, 95
codB	7.6	Cytosine deaminase	Cytosine transport	912	23, 927, 95
cof	10.1	Complementation of *fur*	Complements deletion mutant for growth on succinate	53227	1640
cog	29.1	Control of *ompG*	Probable repressor of *ompG*	37297	2956
corA	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 *intA* and *alpA*	33089	2241, 3653
cpdA	68.4	Cyclic nucleotide P-diesterase	*icc*; affects cAMP requirement during growth on maltose; 3′,5′ cAMP phosphodiesterase	37437	1907
cpdB	95.5	Cyclic nucleotide P-diesterase	2′,3′-Cyclic nucleotide 2′-phosphodiesterase (EC 3.1.4.16)	909	1996, 2580, 259
cpsA	45.4	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	18463	4460
cpsB	45.7	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis; mannose 1-P guanyltransferase	18460	4460
cpsC	45.8	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	18457	4460
cpsD	45.8	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	18454	4460
cpsE	45.8	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	51241	4460
cpsF	90.2	Capsular polysaccharide synthesis	Colanic acid (CPS) biosynthesis	18448	4460
cpsG	45.7	Capsular polysaccharide synthesis	Phosphomannomutase isozyme; colanic acid biosynthesis	37429	1999
cpxA	88.4	Conjugative plasmid expression	*ecfB*, *eup*, *ssd*; membrane sensor in two-component *cpxAR* 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
cpxB	41.3	Conjugative plasmid expression	Phage Q resistance, membrane protein	907	2844, 2845, 4066
cpxP	88.4	Conjugative plasmid expression	Periplasmic protein, CpxA/R activated, induced in alkaline pH; suppresses toxic envelope protein effects	54751	922
cpxR	88.4	Conjugative plasmid expression	Regulator in two-component *cpxAR*	34166	1065, 3596, 843
crcA	14.1	Camphor resistance and chromosome condensation	High-copy *crc-csp* restores normal chromosome condensation in presence of camphor or *mukB* mutations	41127	1837
crcB	14.2	Camphor resistance and chromosome condensation	See *crcA*	41131	1837
creA	99.9	Catabolite regulation	Function unknown; transcribed with *cre* operon	34809	81
creB	99.9	Catabolite regulation	*phoM-orf2*; structurally homologous to *creC* (*phoM*)	34803	81, 82
creC	99.9	Catabolite regulation	*phoM*; sensor in Pho regulon	395	2654, 2733, 2734, 4431, 4660, 4661, 4664, 4666, 4667, 81
creD	99.9	Catabolite regulation	*cet* (colicin E2 tolerance), *refII*	929	1090, 1284, 1462, 1568, 81
crg	28.8	Cold resistant growth	Allows cold-resistant growth	18445	2175
crl	5.6	Curli	Regulatory protein for curli (cryptic *csgA*)	30625	137, 1722, 3291, 3545
crp	75.1	cAMP receptor protein	*cap*, *csm*; cAMP receptor protein	906	1404, 147, 1559, 2233, 2365, 258, 2627, 32, 3610, 3279, 3559, 3617, 4108, 4394, 500, 8, 844, 924
crr	54.6	Carrier?	*gsr*, *iex*, *tgs*; phosphocarrier protein for glucose of the PTS; IIIglc	905	1023, 2326, 2859, 3150, 3369, 3370, 3793, 508, 539, 557, 562, 982, 983b
csdA	63.4	Cysteine, selenocysteine decomposition	Cysteine sulfinate desulfinase	52073	2926
csgA	23.8	Curlin σ^S-dependent growth	Curlin, σ^S (stationary phase) dependent, cryptic	30620	137, 138, 1619, 2612, 3289–3291, 3725, 4584
csgB	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[c]
csgD	23.7	Curlin σ^S-dependent growth	*csgD* insertions eliminate σ^S-dependent transcription from *csgBA* promoter	50655	1619, 3725
csgE	23.7	Curlin σ^S-dependent growth	Possible secretion or assembly protein for bacterial fibers	50658	1619, 3725
csgF	23.7	Curlin σ^S-dependent growth	Possible assembly or transport protein for curli	50661	1619
csgG	23.7	Curlin σ^S-dependent growth	Possible assembly or transport protein for curli; novel lipoprotein	50664	1619, 2612, 3725
csiA	85.3	Carbon starvation induced	Stationary phase inducible protein	36892	4690
csiB	17.4	Carbon starvation induced	Stationary phase inducible protein	36895	4690
csiC	66.0	Carbon starvation induced	Stationary phase inducible protein	36898	4690
csiD	60.5	Carbon starvation induced	Stationary phase inducible protein	36904	2775, 4690
csiE	57.4	Carbon starvation induced	Stationary phase inducible protein	36901	2774, 4690
csiF	8.6	Carbon starvation induced	Stationary phase inducible protein	36998	4690
cspA	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
cspB	35.3	Cold shock protein	Cold shock protein with similarity to CspA	32231	1200, 2473
cspC	41.1	Cold shock protein	*msmB*; multicopy suppresses *mukB* mutants	35339	2043, 2473, 4842
cspD	19.9	Cold shock protein	Similarity to CspA but not cold shock induced	31688	2473, 4841
cspE	14.2	Cold shock protein	*msmC*; with *crcAB*, high copy promotes or protects chromosome condensation	31528	1837, 4841, 4842
cspG	12.6	Cold shock protein	Cold-induced CspA/B analog	53423	194, 3119
csrA	60.7	Carbon storage regulator	*zfiA*, regulatory gene inhibiting glycogen biosynthesis; global regulatory protein	34504	2586, 3061, 3723, 3724, 3787, 4854
csrB	62.9	Carbon storage regulator	CsrA-binding RNA, antagonizing CsrA regulation		2585a
cstA	13.5	Carbon starvation	Starvation induced stress response protein	31179	1523, 2798, 3937, 403
cstC[b]	39.4	Carbon starvation	*astC*; starvation gene regulated by cAMP and RpoS, T; induced by ornithine; arginine succinyltransferase	54626	1290a, 1290b, 1950a, 3921a
cup	97.0	Carbohydrate uptake	Mutants have defective carbohydrate uptake	18442	2720
cutA	94.0	Cu tolerance	*cycY*, *cutA1*; copper sensitivity; possible role in cytochrome *c* maturation; cytochrome *c*-like	34216	1271, 1921, 875
cutC	42.2	Cu tolerance	Copper sensitivity	36974	1574
cutE	14.8	Cu tolerance	*lnt*; copper sensitivity; apolipoprotein *N*-acetyltransferase	31471	3710
cutF	4.6	Cu tolerance	*nlpE*; copper sensitivity	35748	1574, 4122
cvpA	52.3	Colicin V production	*dedE*; member of *purF* operon; affects Col V production	32727	1207
cxm	6.3	Carbon-xylose metabolism	*cxr*; methyl glyoxal synthesis; D-xylose utilization	903	8
cyaA	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
cybB	32.1	Cytochrome *b*	Cytochrome b_{561}	17728	3052, 3054, 3105
cybC	96.1	Cytochrome *b*	Cytochrome b_{562}	34583	4465
cycA	95.4	Cycloserine	*dagA*; D-alanine, D-serine, glycine permease	900	3685, 3686, 3939, 4671, 569
cydA	16.6	Cytochrome *d*	Cytochrome *d* terminal oxidase, polypeptide subunit I	10369	1060, 1447, 1491, 1492, 1493, 1494, 3039, 3611, 615, 847
cydB	16.6	Cytochrome *d*	Cytochrome *d* terminal oxidase, polypeptide subunit II	9469	1009, 1010, 1011, 1060, 1447, 1491, 1492, 1494, 1495, 3039, 3611, 4638, 615, 847
cydC	20.0	Cytochrome *d*	*mdrA*, *mdrH*, *surB*; cytochrome *d* terminal oxidase, possibly heme d component	17725	1009, 1405, 1447, 3763, 4054, 4055
cydD	20.0	Cytochrome *d*	ATP-binding cassette membrane transporter; bd-type oxidase	31720	1009, 1447, 262, 3479–3481
cynR	7.7	Cyanase; cyanate metabolism	Transcriptional activator of *cyn* operon	31255	102, 2403, 4288
cynS	7.7	Cyanase; cyanate metabolism	Cyanate aminohydrolase (EC 3.5.5.3)	15267	102, 1564, 1565, 2403, 4286, 4288, 4289
cynT	7.7	Cyanase; cyanate metabolism	Carbonic anhydrase	31258	102, 1564, 1566, 2333, 4286, 4287, 4289
cynX	7.7	Cyanase; cyanate metabolism	Apparent hydrophobic protein, member of *cyn* operon	31261	102, 1564
cyoA	9.7	Cytochrome *o* oxidase	Cytochrome *o* oxidase subunit II; cytochrome bo_3 ubiquinol oxidase subunit II	18439	164, 165, 2687, 615
cyoB	9.7	Cytochrome *o* oxidase	Cytochrome *o* 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]
cyoC	9.6	Cytochrome *o* oxidase	Cytochrome *o* oxidase subunit III	31005	164, 615, 720, 721
cyoD	9.6	Cytochrome *o* oxidase	Cytochrome *o* oxidase subunit IV	31008	164, 615, 720
cyoE	9.6	Cytochrome *o* oxidase	Cytochrome *o* oxidase subunit, protoheme IX farnesyltransferase	31014	164, 3799, 615, 720, 721
cysA	54.7	Cysteine	Sulfate permease; chromate resistance	898	3793, 4082, 4172, 47, 539
cysB	28.7	Cysteine	Positive regulator for *cys* regulon	897	1980, 3310, 4382
cysC	61.9	Cysteine	Adenylylsulfate kinase (EC 2.7.1.25)	896	2520, 3879, 4380
cysD	61.9	Cysteine	Sulfate adenylyltransferase (EC 2.7.7.4)	895	1862, 2742, 4380
cysE	81.5	Cysteine	Serine acetyltransferase (EC 2.3.1.30)	894	1021, 4381
cysG	75.3	Cysteine	Uroporphyrinogen III methyltransferase; transcribed from *nirB* operon and *cysG* promoters	893	1647, 1973, 2693, 2694, 3386, 3387, 4148, 4380, 792
cysH	62.2	Cysteine	Adenylylsulfate reductase (EC 1.8.99.2)	892	1862, 2345, 2346, 2522, 4380
cysI	62.2	Cysteine	*cysQ*; sulfite reductase, α-subunit (EC 1.8.1.2)	891	1175, 1862, 2522, 4380, 4795
cysJ	62.3	Cysteine	*cysP*; sulfite reductase, β-subunit (EC 1.8.1.2)	890	1175, 1862, 2522, 2637, 4380, 4795
cysK	54.5	Cysteine	*cysZ*; cysteine synthase (EC 4.2.99.8); homodimer; selenate resistance, azaserine resistance	889	1247, 3370, 3793, 4082, 438, 47, 4731, 508, 539
cysM	54.7	Cysteine	*o*-Acetylserine sulfhydrolase B (EC 4.2.99.8)	17722	3793, 4082, 47, 539
cysN	61.9	Cysteine	ATP sulfurylase (ATP:sulfate adenylyltransferase)	18436	2520
cysP	54.8	Cysteine	Periplasmic sulfate binding protein; see *cysJ*	27367	1828, 4081
cysQ	95.6	Cysteine	*amt*, *amtA*; requirement for sulfite or cysteine during aerobic growth; see also *cysI*	34409	1193, 1996, 1997, 3159
cysS	11.9	Cysteine	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	888	176, 413, 1816
cysT	42.9	Cysteine	Cysteine tRNA; see also *cysU*	17719	1285, 2313
cysU	54.7	Cysteine	Cysteine transport system; may also transport molybdate (see *mod*)	37093	4081
cysW	54.7	Cysteine	Membrane-bound sulfate transport protein; may also transport molybdate (see *mod*)	27371	4081
cysX	81.5	Cysteine	Reading frame in opposite orientation within *cysE* gene; polypeptide synthesized in maxicells	55332	4381
cysZ	54.5	Cysteine	putative; ORF upstream of *cysK* may be *cysZ*	33018	593
cytR	88.8	Cytosine resistant?	Regulatory gene for *deo*, *udp*, and *cdd*; mutants show improved growth on uridine	887	226, 3048, 3617, 4128, 4529
dacA	14.3	D-Alanine carboxypeptidase	*pfv*; D-alanine carboxypeptidase IA (EC 3.4.12.11); penicillin-binding protein; deletion suppresses *ftsK* mutant block	886	2801, 2802, 3198, 3360, 4157, 4232, 520
dacB	71.7	D-Alanine carboxypeptidase	D-Alanine carboxypeptidase IB; penicillin-binding protein (EC 3.4.12.11)	885	2322, 2803, 3021, 3022, 4075, 4337
dacC	19.0	D-Alanine carboxypeptidase	Penicillin-binding protein 6 (EC 3.4.17.8)	34706	276, 3421, 520
dacD	44.8	D-Alanine carboxypeptidase	*phsE*? Penicillin-binding protein 6b	50486	223
dadA	26.7	D-Amino acid dehydrogenase	*dadR*; D-amino acid dehydrogenase subunit	884	2357, 2607, 2797, 4736, 4737, 4739, 4740
dadB	1.6	D-Amino acid dehydrogenase	*alnA*; D-amino acid dehydrogenase subunit	883	1298
dadQ	98.9	D-Amino acid dehydrogenase	*alnR*; regulator of *dad* regulon	882	1298
dadX	26.7	D-Amino acid dehydrogenase	*msuA*? alanine racemase (EC 5.1.1.1)	17716	1526, 2607, 2797, 4739
dam	75.7	DNA adenine methylase	DNA adenine methylase	881	145, 1609, 2851, 3411, 518
dapA	56.0	Diaminopimelate (lysine path)	Dihydrodipicolinate synthase (EC 4.2.1.52)	880	3667
dapB	0.6	Diaminopimelate (lysine path)	Dihydrodipicolinate reductase (EC 1.3.1.26); see *dapE* and *lspA*	879	2699, 464
dapC	3.9	Diaminopimelate (lysine path)	Tetrahydropicolinate succinylase	878	1359, 558
dapD	4.0	Diaminopimelate (lysine path)	Succinyl-diaminopimelate aminotransferase	877	1000, 1359, 296, 3665
dapE	55.8	Diaminopimelate (lysine path)	*dapB*; *N*-succinyl-diaminopimelate deacylase	876	3364, 3667
dapF	86.1	Diaminopimelate (lysine path)	Diaminopimelate epimerase	17713	3664, 3666, 926
dbpA	30.3	DNA binding protein	Binds DNA, RNA, only hydrolyses ATP in presence of 23S rRNA	32058	1337, 3177
dcd	46.1	dCTP deaminase	*paxA*; dCTP deaminase (EC 3.5.4.13); mutants suppress lethal *dut* mutants	875	1180, 3156, 4655
dcm	43.7	DNA cytosine methylation	*mec*; DNA cytosine methylase; internal cytosine methylated	874	1314, 1625, 337
dcp	35.0	Dipeptidyl carboxypeptidase	Dipeptidyl carboxypeptidase II (EC 3.4.15.1)	873	1027, 1723, 269
dcrB	77.8	C resistance	Resistant to lytic phage C1; periplasmic protein perhaps anchored to inner membrane	46606	2546

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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
dctA	79.3	Dicarboxylic acid transport	Uptake of C-4 dicarboxylic acids; 3-fluoromalate resistance, D-tartrate resistant	872	206, 2181, 2602, 3897
dctB	16.4	Dicarboxylic acid transport	Uptake of C-4 dicarboxylic acids; 3-fluoromalate resistance, D-tartrate resistant	871	2181, 3897
dcuA	94.0	Dicarboxylate uptake	*genA*; C4-dicarboxylate transporter, anaerobic	34476	4084
dcuB	93.7	Dicarboxylate uptake	*genF*; C4-dicarboxylate transporter, anaerobic	34479	4084
dcuC	14.1	Dicarboxylate uptake	C4-dicarboxylate carrier, anaerobic; W3110 has an IS*5* insertion	50968	4956
ddlA	8.6	D-Alanine ligase	D-Alanine:D-alanine ligase, ADP-forming	30966	3350, 4921
ddlB	2.2	D-Alanine ligase	*ddl*; D-Alanine:D-alanine ligase	870	1893, 2071, 2675, 2676, 3350, 3692
deaD	71.2	Dead-box protein	*csdA*, *mssB*; gene dosage-dependent suppressor of *rpsB*(ts) mutations; putative RNA helicase	33472	1200, 2045, 4437, 4843
dedA	52.4	Downstream, expressed?	Temporary designation for genes in *pdxB* and *folC* operons; unknown function	32742	3211
dedD	52.4	Downstream, expressed?	Temporary designation for genes in *pdxB* and *folC* operons; unknown function	32739	3211
def	74.0	Deformylase	*fms*; peptide deformylase, *N*-formylmethionylaminoacyl-tRNA deformylase (EC 3.4.11.–, EC 3.5.1.27)	33619	2830, 2869, 2871, 2872, 2873, 3597
degP	3.9	Degradative protease	*htrA*; 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
degQ	72.8	Degradative protease	*hhoA*; periplasmic serineendoprotease	36675	2296, 250, 4643
degS	72.8	Degradative protease	*htrH*, *hhoB*; periplasmic serineendoprotease	36678	250, 4643
del	64.3	Deletion	Affects frequency of IS*1*-mediated deletions; 1,000-fold reduction in deletion frequency	869	3164
deoA	99.5	Deoxyribose	*tpp-75*; thymidine phosphorylase (EC 2.4.2.4)	868	1255, 22, 4270, 4528, 4530, 4531, 4532
deoB	99.5	Deoxyribose	*drm*, *thyR*, *tlr*; deoxyribouratase (EC 2.7.5.6), phosphopentomutase	867	1255, 22, 2616, 3705, 4527, 4530, 4532
deoC	99.5	Deoxyribose	*dra*, *thyR*, *tlr*; deoxyribose-phosphate aldolase (EC 4.1.2.4)	866	1255, 2616, 3705, 4526, 4527, 4528, 4532, 54, 920
deoD	99.6	Deoxyribose	*pup*; purine-nucleoside phosphorylase PNP (EC 2.4.2.1)	865	1255, 22, 2282, 2422, 3705, 4528, 4532
deoR	19.0	Deoxyribose	*nucR*, *nupG*, *tse*; regulatory gene for *deo* operon	864	3017, 3048, 4533
dfp	82.1	DNA synthesis flavoprotein	*dnaS*, *dut*; flavoprotein affecting DNA synthesis and pantothenate metabolism	18430	4154, 4155
dgd	72.0	D-Galactose dehydrogenase	D-Galactose dehydrogenase production	863	4803
dgkA	91.7	Diglyceride kinase	Diglyceride kinase	862	2544, 2545
dgkR	93.7	Diglyceride kinase	Regulatory	861	3578
dgoA	83.4	D-Galactonate	2-Oxo-3-deoxygalactonate 6-phosphate aldolase (EC 4.1.2.21)	36891	182
dgoD	83.4	D-Galactonate	Galactonate dehydratase (EC 4.2.1.6)	859	182
dgoK	83.5	D-Galactonate	2-Oxo-3-deoxygalactonate kinase (EC 2.7.1.58)	858	182
dgoR	83.5	D-Galactonate	Regulatory; growth on 2-keto-3-deoxygalactonate, *dgoR*^{c}	857	830
dgoT	83.4	D-Galactonate	Galactonate transport	856	182
dgsA	35.9	D-Glucosamine	*mlc* (makes large colonies); affects function of phosphotransferase system enzyme IIA/IIB, anaerobic growth on glucosamine; binds NagC promoters; regulates *manX*	855	1813, 3012, 3453, 3707
dgt	3.9	dGTP triphosphohydrolase	*optA*; deoxyguanosine 5′-triphosphate triphosphohydrolase (EC 3.1.5.1)	30546	261, 3572, 3573, 4806
dicA	35.5	Division control	Regulatory for *dicB*	18427	282, 283
dicB	35.5	Division control	Control of cell division	18424	282, 283, 622
dicC	35.5	Division control	Regulatory for *dicB*	18421	282, 283
dicF	35.5	Division control	DicF antisense RNA; inhibits Qin	32240	1208, 1209, 4389, 453
dif	34.2	Deletion-induced filamentation	Recombination site in terminus, *recA* independent	30208	1675, 2354, 2356, 376, 378, 835, 836, 4378
dinB	5.4	Damage inducible	*dinP*; increased mutagenesis, apparently independent of *umuDC*; SOS related	53389	2232, 526
dinD	82.2	Damage inducible	*orfY*, *pcsA*, *yicD*; mutant cs phenotype filamentous with large nucleoid	33582	2200, 2352, 2353, 2664, 3262, 4877
dinF	91.7	Damage inducible	Induced by UV and mitomycin C; SOS, *lexA* 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[c]
dinG	17.9	Damage inducible	LexA regulated (SOS) repair enzyme	31247	2318, 2518, 2519
dinI	24.1	Damage inducible	Multicopy suppresses phenotype of cold-sensitive *dinD* filamentous mutation	53428	4877
dinY	41.9	Damage inducible	Repair gene	36880	3412
dipZ	94.0	Disulfide isomerase	*cycZ*, *dsbD*, *cutA2*; may be involved in cytochrome maturation, see *ccm* genes; affects disulfide binding	34213	1921, 268, 2910, 874, 875
djlA	1.2	DnaJ-like	Proposed to dock and interact with variety of membrane proteins; mutants rapidly accumulate suppressors	51192	2188, 769, 770
dksA	3.5	*dnaK* suppressor	*msmA*; high copy suppresses *muk* and TS growth and filamentation of *dnaK* mutant	30521	2122, 4842
dld	47.9	D-Lactate dehydrogenase	*ldh*; D-lactate dehydrogenase (EC 1.1.1.28); vinylglycolate resistance, FAD enzyme	852	2058, 3768, 4012, 626
dmsA	20.3	DMSO reductase	DMSO reductase subunit A, anaerobic	17710	353, 354, 3749
dmsB	20.3	DMSO reductase	DMSO reductase subunit B; apparent Fe-S binding domain; anaerobic	31724	354, 3749
dmsC	20.3	DMSO reductase	DMSO reductase subunit C, membrane bound	31727	354, 3749
dnaA	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
dnaB	91.9	DNA	*groP*, *grpA*, *grpD*; DNA biosynthesis; chain elongation	850	1406, 2259, 2545, 3126, 3333, 3804, 3951, 4449, 561
dnaC	99.1	DNA	*dnaD*; DNA biosynthesis; initiation and chain elongation	849	2786, 3125, 3753
dnaE	4.4	DNA	*polC*, *sdgC* (suppressor of *dnaG* mutation); DNA polymerase III, α-subunit	373	1239, 1240, 2194, 296, 3889, 4016, 4424, 4708, 4761
dnaG	69.2	DNA	*dnaP*, *parB*, *sdgA*; 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
dnaI	40.3	DNA	DNA biosynthesis	846	334a
dnaJ	0.3	DNA	*groP*, *grpC*; 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
dnaK	0.3	DNA	*gro*, *groP*, *groPAB*, *groPC*, *groPF*, *grpC*, *grpF*, *seg*; 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
dnaL	28.9	DNA	DNA biosynthesis	843	3982
dnaN	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
dnaQ	5.1	DNA	*mutD*; DNA polymerase III ε-subunit; streptomycin, azaserine resistant; 3′ to 5′ proofreading, *lexA* regulon	840	1047, 1113, 1239, 1706, 1804, 2194, 2730, 2783, 3209, 3568, 3903, 4052, 779, 855, 856, 4331
dnaT	99.1	DNA	Primasomal protein i	839	2786, 2787, 3125
dnaX	10.6	DNA	*mutH*, *dnaZ*; 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
dppA	79.8	Dipeptide permease	*alu*, *tpp*?; uptake of dipeptides	35111	3294, 4, 4576
dppB	79.8	Dipeptide permease	Uptake of dipeptides	33771	4, 4118, 4576
dppC	79.8	Dipeptide permease	Uptake of dipeptides	33768	4, 4118, 4576
dppD	79.8	Dipeptide permease	Uptake of dipeptides	33765	4, 4118, 4576
dppF	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]
dppG	14.0	Dipeptide permease	Uptake of dipeptides; dipeptide permease	835	1453, 3384, 997
dps	18.3	DNA-binding protein, stationary phase	*pexB*; stress response DNA-binding protein; starvation induced resistance to H_2O_2	31650	1226, 2620, 71
dsbA	87.1	Disulfide bond	*iarA*, *ppfA*; disulfide oxidoreductase, periplasmic protein disulfide-isomerase; role in cytochrome *c* synthesis (EC 5.3.4.1)	34063	1560, 2243, 229, 230, 2778, 287, 2910, 3549, 3550, 3823, 45, 4805, 4840, 67, 904
dsbB	26.6	Disulfide bond	*iarB*; PDI or PDI-like protein; DTT-sensitive phenotype; periplasm/inner membrane	31933	1560, 1989, 2243, 229, 288, 2960, 3823, 67
dsbC	65.4	Disulfide bond	*xprA*; periplasmic disulfide oxidoreductase, protein disulfide isomerase	33355	2639, 2641, 2962, 4019
dsbG	13.8	Disulfide bond	Thiol-disulphide oxidase; multicopy resistance to DTT; mutants accumulate reduced proteins, corrected by DsbA/B overexpression	53792	92
dsdA	53.4	D-Serine deaminase	D-Serine deaminase	834	2751, 2846, 2847, 3215, 3339, 436, 48, 642
dsdC	53.3	D-Serine deaminase	LysR-type transcriptional regulator; previously cited as D-serine permease; *dsdC/X* order reversed in different sequence entries	833	2847, 3215, 3339, 436, 48, 642
dsdX	53.4	D-Serine deaminase	Homology with gluconate permease; D-serine tolerance; *dsdC/A* order reversed in different sequence entries	35717	3215
dsrA	43.6	Small RNA	Regulatory RNA; positive regulation of promoters sensitive to HNS negative regulation	48173	2249, 4098
dsrB	43.6	Small RNA	Regulatory RNA; regulated by DsrA and HNS, under control of RpoS	48176	4099
dut	82.2	dUTPase	*dnaS*, *sof*; deoxyuridinetriphosphatase (EC 3.6.1.23)	832	2661, 2662, 4154, 4367
dvl	7.4	Dye-visible light?	Sensitivity to SDS and toluidine blue plus light	18418	4632
dxs	9.4	Deoxy-xylulose-P synthase	DXP synthase; DXP is precursor to isoprenoids, thiamin, pyridoxol	52930	2615, 4166
e14	25.7	Prophage element 14	Defective prophage element; includes loci *sfiC*, *lit*, *pin*, *mcrA*	18409	2128, 2715, 3447, 3448, 3604, 4544, 511, 512, 625
ebgA	69.4	Evolved β-galactosidase	Cryptic β-galactoside utilization	830	1607, 4234, 4235, 627
ebgB	69.5	Evolved β-galactosidase	Cryptic β-galactoside utilization, possible paralog of *lacY*	18415	1607, 4234
ebgC	69.5	Evolved β-galactosidase	Phospho-β-D-galactosidase, β-subunit; cryptic gene	18412	1607
ebgR	69.4	Evolved β-galactosidase	Regulatory gene from *ebg* cryptic operon	829	1607, 4234
ecfA	67.6	Energy coupling factor	With *metC* mutation, *ecf* mutation abolishes coupling of energy with active transport	828	4434
eco	49.6	Ecotin	Ecotin, serine protease inhibitor	32630	1173
ecpD	3.4	*E. coli papD* homolog	Possible pilin chaperone	30513	3593
eda	41.6	Entner-Douderoff aldolase	*hga*, *kdgA*, *kga*; 2-keto-3-deoxygluconate 6-phosphate aldolase (EC 4.1.2.14); 2-keto-4-hydroxyglutarate aldolase	826	1154, 1290
edd	41.6	Entner-Douderoff dehydratase	Phosphogluconate dehydratase (EC 4.2.1.12); growth on gluconate	825	1121, 1289, 1290, 4594
efp	94.3	Elongation factor P	Elongation factors P and EF-P; prokaryotic	34470	118, 119, 1357
emrA	60.6	E-multidrug resistance	Multidrug resistance pump family	33259	2619, 2621
emrB	60.6	E-multidrug resistance	Hydrophobic, inner membrane-spanning domains; multidrug resistance pump family	33262	2619, 2621
emrD	83.0	E-multidrug resistance	Multidrug resistance pump family	36938	3132
emrE	12.2	E-multidrug resistance	*envB*, *mvrC*, *mon*, *rodY*; multidrug resistance pump family; cell shape; methylviologen sensitivity	36935	2452, 4879, 4880, 300
endA	66.6	Endonuclease	DNA-specific endonuclease I; extensive DNA breakdown	824	2002, 4785
eno	62.6	Enolase	Enolase (EC 4.2.1.11)	823	158, 2257, 4709
entA	13.5	Enterochelin	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase	822	1262, 1777, 2394, 2395, 2581, 3090, 3091, 3424, 4180
entB	13.5	Enterochelin	2,3-Dihydro-2,3-dihydroxybenzoate synthetase	821	1262, 2394, 2395, 3090, 3091, 3326, 5424
entC	13.5	Enterochelin	Isochorismate synthetase	820	1262, 2394, 2395, 2582, 3090, 3091, 3325, 3326, 3424, 4644

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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]
entD	13.1	Enterochelin	Enterochelin synthetase, component D; facilitates secretion of enterobactin peptide	819	1261, 133, 1534, 2394, 2395, 2400, 786, 787
entE	13.5	Enterochelin	Enterochelin synthetase, component E	818	1262, 2394, 2395, 3090, 3091, 3424
entF	13.2	Enterochelin	Enterochelin synthetase, component F	817	1262, 2394, 2395, 3415, 3770, 286
envN	4.2	Envelope	Affects envelope; defects osmotically remedied	811	1120
envP	90.4	Envelope	Affects envelope; defects osmotically remedied	810	1120
envQ	60.7	Envelope	Affects envelope; defects osmotically remedied	809	1120
envR	73.5	Envelope	*acrS*; regulatory gene for *envCD* (*acrEF*)	33605	2516, 2684
envT	14.2	Envelope	Affects envelope; defects osmotically remedied	808	1120
envY	12.6	Envelope	Envelope protein involved with thermoregulation of porin	18406	2666, 2668
envZ	76.1	Envelope	*ompB*, *perA*, *tpo*; 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
epd	66.2	Erythrose-4-P dehydrogenase	*gapB*; erythrose-4-P dehydrogenase	32089	1071, 3980, 444, 4946, 61
epp		E-pentapeptide	Minigene within 23S rRNA encoding functional pentapeptide; erythromycin resistance	51135	4383
era	58.2	*E. coli ras*-like	*sdgE*; GTP-binding protein, essential gene	29010	2498, 25, 4137, 708
esp	17.3	Efficiency site for phage	Site for efficient packaging of phage T1	805	1085a
evgA	53.5	*E. coli* homolog of virulence gene	Multicopy on plasmid in *envZ*-deleted strain induces *ompC* expression; see *evgS*	32763	4519
evgS	53.5	*E. coli* homolog of virulence gene	With *evgA*, two-component regulatory system, environmentally responsive	32766	4519
exbB	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
exbC	61.5	Export	Uptake of enterochelin; resistance or sensitivity to colicins	803	1580, 3554
exbD	67.9	Export	Uptake of enterochelin; resistance or sensitivity to colicins; similarity with TolR	33384	1137, 1254, 1721, 2221, 24, 482
expA	22.2	Export	Expression of a group of export proteins	802	944
exuR	69.9	Hexuronate	Negative regulatory gene for *exu* regulon (*exu*, *uxu*, *uxa*)	801	1852, 1853, 2795, 3489, 3490, 3682, 3687
exuT	69.9	Hexuronate	Transport of hexuronates	800	1852, 2795, 2796, 3489, 3490, 3682, 382
fabA	21.9	Fatty acid biosynthesis	β-hydroxydecanoylthioester dehydrase (EC 4.2.1.60)	799	870, 872
fabB	52.6	Fatty acid biosynthesis	*fabC*; β-ketoacyl-acyl carrier protein synthase I (EC 2.3.1.41)	798	1380, 1381, 4056
fabD	24.8	Fatty acid biosynthesis	Malonyl-CoA-acyl carrier protein transacylase (EC 2.3.1.39)	797	1381, 2713, 4579
fabF	24.8	Fatty acid biosynthesis	*cvc*, *fabJ*, *vtr*; β-ketoacyl-acyl carrier protein synthase II (EC 2.3.1.41)	795	1380, 1381, 3621, 4057, 4512
fabG	24.8	Fatty acid biosynthesis	3-Ketoacyl-ACP reductase (EC 1.1.1.100); reuse of *fabG* synonym for *accC*	31865	2315, 3253, 3621
fabH	24.7	Fatty acid biosynthesis	ACP synthase III	31860	3253, 3466, 4481
fabI	29.1	Fatty acid biosynthesis	*gts*, *envM*, *qmeA*; enoyl-ACP reductase, NADH dependent (EC 1.3.1.9)	812	1687, 2251, 321, 322, 4502, 4734, 4735
fabZ	4.4	Fatty acid biosynthesis	*sefA*; 3R-hydroxymyristoyl acyl carrier protein dehydrase	30597	2990, 3212
fadA	86.8	Fatty acid degradation	Thiolase I (EC 2.3.1.16)	794	1057, 3099, 4160, 4860, 4862, 762, 926
fadB	86.8	Fatty acid degradation	*oldB*; 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
fadD	40.7	Fatty acid degradation	Acyl-CoA synthetase (EC 6.2.1.3)	792	1336, 371
fadE	4.8	Fatty acid degradation	Electron transport flavoprotein of β-oxidation	791	762
fadH	69.6	Fatty acid degradation	2,4-Dienoyl CoA reductase	54705	1686
fadL	53.0	Fatty acid degradation	*ttr*; 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]
fadR	26.6	Fatty acid degradation	*dec*, *ole*, *thdB*; negative regulatory gene for *fad* regulon, positive regulator of *fabA*; regulates *aceBAK*, glyoxylate shunt	789	1056, 1058, 1204, 1729, 2744, 3, 4073, 4074, 4739, 762
farR	16.5	Fatty acyl responsive	Fatty acyl responsive regulator	36837	3566, 551
fatA	71.7	Fatty acid	Utilization of *trans* unsaturated fatty acids	18403	1030
fbaA	66.1	Fructose bis-P aldolase	*ald*, *fda*; fructose-bisphosphate aldolase	786	326, 3560, 4076, 62
fbaB	46.9	Fructose bis-P aldolase	*dhnA*; fructose 1,6-bisphosphate aldolase	54836	4404, 4076
fbp	96.0	Fructose-bisphosphatase	*fdp*; fructose-bisphosphatase (EC 3.1.3.11)	784	2275, 3961
fcl	45.8	Fucose, FX-like	Colanic acid gene cluster, fucose synthetase	55074	113
fcsA	86.9	Filamentous, cold sensitive	Cold-sensitive cell division mutant	787	2352
fdhD	88.0	Formate dehydrogenase	Homologous to *fdnC* and *-B* of *Salmonella* spp.	33972	2746, 3465, 3912, 4221
fdhE	87.9	Formate dehydrogenase	Homologous to *fdnC* and *-B* of *Salmonella* spp.	33978	2746, 3193, 3465, 3912, 4221
fdhF	92.6	Formate dehydrogenase	*chlF*, *fdh*; 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
fdnG	33.3	Formate dehydrogenase-N	Formate dehydrogenase-N major subunit	32160	2527, 312, 313, 314, 3575, 3678, 4221
fdnH	33.4	Formate dehydrogenase-N	Formate dehydrogenase-N Fe-S subunit	32164	2527, 312, 313, 314, 3575, 3678, 4221, 859
fdnI	33.4	Formate dehydrogenase-N	Formate dehydrogenase-N cytochrome subunit	32168	2527, 312, 313, 314, 3575, 3678, 4221
fdoG	88.0	Formate dehydrogenase-O	Formate dehydrogenase-O subunit, major	33985	2, 3465
fdoH	87.9	Formate dehydrogenase-O	Formate dehydrogenase-O subunit, Fe-S	33988	2, 3465
fdoI	87.9	Formate dehydrogenase-O	Formate dehydrogenase-O subunit cytochrome b_{556}	33991	2, 3465
fdrA	11.8	*ftsH* dominant rescue	In multicopy, suppresses negative *ftsH* mutations	40877	44
fdx	57.2	Ferredoxin	Ferredoxin, cotranscribed with *hscBA*, presumably cold inducible	32984	2484, 4320, 4321
feaB	31.2	Phenylethylamine	*padA*; catabolism of phenylethylamine	50925	1230, 1629
feaR	31.1	Phenylethylamine	*maoB*; regulates expression of *tynA* and *padA*	50928	1230, 1629
fecA	97.3	Iron (citrate dependent)	Citrate-dependent iron transport, outer membrane receptor	783	114, 1870, 3536, 4558, 4569, 4629, 4962
fecB	97.2	Iron (citrate dependent)	Citrate-dependent iron transport, periplasmic protein	782	1870, 3536, 4190, 4569, 4962
fecC	97.2	Iron (citrate dependent)	Transport gene	35620	4190, 4569, 4558
fecD	97.2	Iron (citrate dependent)	Citrate-dependent iron transport, membrane bound	18394	3536, 4190, 4569, 4558
fecE	97.2	Iron (citrate dependent)	Transport gene	35617	4190, 4569, 4558
fecI	97.3	Iron (citrate dependent)	Transport gene mediating induction by iron	35630	114, 4569, 4558
fecR	97.3	Iron (citrate dependent)	Regulatory gene mediating induction by iron	35627	4558, 4569
feoA	76.3	Ferrous iron	Ferrous iron uptake system	28964	1638, 2107
feoB	76.3	Ferrous iron	Membrane protein of ferrous iron uptake system	28967	1638, 2107
fepA	13.1	Ferrienterobactin permease	*cbr*, *cbt*; outer membrane component of ferribactin transport system	18388	1261, 1863, 2669, 3325, 3416, 3429, 3554, 4013, 4780, 786
fepB	13.4	Ferrienterobactin permease	Periplasmic component of ferrienterobactin transport system	18385	3325, 3428, 3429, 4013, 4202, 4780, 486, 501
fepC	13.3	Ferrienterobactin permease	Cytoplasmic membrane component of ferrienterobactin transport	4987	3325, 3326, 3428, 4013
fepD	13.4	Ferrienterobactin permease	Ferrienterobactin permease, membrane-bound subunit	18382	1863, 3325, 4013
fepE	13.3	Ferrienterobactin permease	Ferric enterobactin uptake	18379	3325, 4013
fepG	13.4	Ferrienterobactin permease	Ferrienterobactin permease, membrane-bound subunit	31162	717, 4013
fes	13.2	Iron	Enterochelin esterase	780	1261, 1777, 1863, 2394, 2395, 3415, 3416, 786
fexB	86.7	F exclusion	Affects ArcA phenotype	778	2499
ffh	59.2	54-kDa homolog (4.5S particle)	4.5S-RNP protein; RNP has mammalian protein-targeting counterpart: SRP	33006	2695, 325, 3407, 3419, 3488, 3520
ffs	10.2	4.5S	4.5S rRNA; mammalian counterpart, SRP, includes 4.5S RNA; cotranslational integration of proteins into membrane	18373	1064, 1834, 2695, 534
fhlA	61.5	Formate hydrogen-lyase	Transcription factor, formate hydrogen lyase system activator, global regulator, *hyc*, *hyp*	18370	1800, 1801, 1957, 3745, 3852, 3853, 3907, 3909
fhlB	95.1	Formate hydrogen-lyase	Formate hydrogen-lyase; activated by fhlA	36851	2821
fhuA	3.6	Ferric hydroxamate uptake	*T1*, *T5rec*, *tonA*; OMP receptor for ferrichrome, colicin M, and phages T1, T5, and ϕ80; energy-coupled transport of Fe^{3+} via ferrichrome; mutants albomycin resistant	777	1216, 2081, 2219, 2221, 2220, 2652, 2653, 457, 483, 485, 486, 849, 850

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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]
fhuB	3.7	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component; mutants albomycin resistant	776	1216, 2081, 2330, 3544, 486
fhuC	3.7	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component; mutants albomycin resistant	11187	1216, 486, 566, 848
fhuD	3.7	Ferric hydroxamate uptake	Hydroxamate-dependent iron uptake, cytoplasmic membrane component; mutants albomycin resistant	11184	1216, 3712, 486, 566, 848
fhuE	25.0	Ferric hydroxamate uptake	Outer membrane receptor for ferric-rhodotorulic acid	18367	1636, 3881, 3882
fhuF	99.2	Ferric hydroxamate uptake	Ferric hydroxamate transport	18364	1639, 3033
fic	75.2	Filamentation-cAMP	Filamentation in presence of cyclic AMP, in mutants	18361	2302, 4521
fimA	97.9	Fimbriae	*fimD*, *pilA*; fimbrin type 1, major structural subunit; phase variation	18358	1142, 1304, 1305, 1634, 2261, 2264, 5
fimB	97.8	Fimbriae	*pil*; recombinase? regulatory gene for *fimA*	18355	1072, 1142, 1347, 1348, 2262, 2264, 2838
fimC	97.9	Fimbriae	*pil*, *pilB*; biosynthesis of fimbriae; periplasmic chaperone for type 1 fimbriae	18352	2038, 2263, 2264
fimD	97.9	Fimbriae	*pil*, *pilC*; export and assembly of type 1 fimbrial outer membrane protein	18349	2264
fimE	97.9	Fimbriae	*pilH*; recombinase? regulatory gene for expression of *fimA*	18346	1072, 1142, 1347, 1348, 2262, 2838
fimF	98.0	Fimbriae	*pilD*; fimbrin type 1 minor component; fimbrial morphology, assembly	18343	2265, 3779
fimG	98.0	Fimbriae	*pilD*; fimbrin type 1 minor component; pilus length; perhaps inhibits polymerization in pilus assembly	18340	2265, 3779
fimH	98.0	Fimbriae	*pilE*; membrane-specific adhesin (lectin); major fimbrial subunit; mediates mannose-binding	18337	1634, 1655, 2265, 2343, 6
fimI	97.9	Fimbriae	Fimbria related	35633	2261
fipB	86.0	F1 phage	Morphogenesis of phage F1	18334	2629
fipC	75.0	F1 phage	Morphogenesis of phage F1	18331	2629
fis	73.5	Factor for inversion stimulation	*nbp*; 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
fiu	18.1	Ferric iron uptake	Outer membrane protein, ferric iron uptake	18325	1636
fixA	0.9	Sequence similar to those of N-fixation genes	Related to carnitine metabolism; amino acid similarity to *Rhizobium fix* gene	53111	1132, 550
fixB	0.9	Sequence similar to those of N-fixation genes	Related to carnitine metabolism; amino acid similarity to *Rhizobium fix* gene	53114	1132, 550
fixC	1.0	Sequence similar to those of N-fixation genes	Related to carnitine metabolism; amino acid similarity to *Rhizobium fix* gene	53117	1132, 550
fixX	1.0	Sequence similar to those of N-fixation genes	Related to carnitine metabolism; amino acid similarity to *Rhizobium fix* gene	53121	1132, 550
flkB	95.4	FKBP-like	Periplasmic PPIase, of FK506-binding protein type (EC 5.2.1.8); contains pipecolic acid residue	48137	3584
fkpA	74.9	FK506-binding protein	Protein that binds immunosuppressive drug FK506, a peptidomacrolide, MIP-like	36042	1809, 2964
fldA	15.3	Flavodoxin	Flavodoxin	31496	3306
flgA	24.3	Flagella	*flaU*; flagellar synthesis; flagellar regulon member	756	1892, 2305
flgB	24.4	Flagella	*flbA*; flagellar synthesis; flagellar regulon member	750	2309
flgC	24.4	Flagella	*flaW*; flagellar synthesis; flagellar regulon member; basal body protein	754	2309
flgD	24.4	Flagella	*flaV*; flagellar synthesis; flagellar regulon member; basal body rod modification	755	2309, 2307
flgE	24.4	Flagella	*flaK*; flagellar hook subunit protein; flagellar regulon member	766	2308, 2309, 2307
flgF	24.4	Flagella	*flaX*; flagellar synthesis; flagellar regulon member; basal body rod protein	753	2309
flgG	24.4	Flagella	*flaL*; flagellar synthesis; flagellar regulon member; basal body rod protein	765	2307, 2309
flgH	24.5	Flagella	*flaY*; flagellar synthesis, basal body L-ring protein	752	2039, 2309

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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]
flgI	24.5	Flagella	*flaM*; flagellar regulon member; basal body P-ring protein	764	2039, 2307, 2309
flgJ	24.5	Flagella	*flaZ*; flagellar synthesis; flagellar regulon member	751	2704
flgK	24.5	Flagella	*flaS*; flagellar synthesis; flagellar regulon member; hook-associated protein I	758	2307
flgL	24.6	Flagella	*flaT*; flagellar synthesis; flagellar regulon member; hook-associated protein	757	2307
flgM	24.3	Flagella	*anti*-σ factor regulator of FlhD	53436	532
flgN	24.3	Flagella	FlgN flagellar synthesis protein	53440	532
flhA	42.3	Flagella	*flaH*; flagellar synthesis; flagellar regulon member	768	2704
flhB	42.3	Flagella	*flaG*; flagellar synthesis; flagellar regulon member	769	2704, 86
flhC	42.6	Flagella	*flaI*; flagellar synthesis; regulatory gene	767	246, 2589, 2590, 40
flhD	42.6	Flagella	*flbB*; regulatory gene, flagellum-specific σ factor, transcriptional activator of Fla class II operons	749	246, 2589, 2590, 3547
fliA	43.1	Flagella	*flaD*, *rpoF*; regulation of late gene expression; σ transcription factor for class 3a and 3b operons	771	1925, 2083, 2305, 2369, 2591, 2623, 2704
fliC	43.1	Flagella	*flaF*, *hag*; flagellin, structural gene; flagellar regulon member	649	1623, 2382, 4316
fliD	43.2	Flagella	*flbC*; hook-associated protein 2, axial family; flagellar regulon member	748	2172
fliE	43.3	Flagella	*flaN*; flagellar synthesis; basal body component	763	2704, 3041
fliF	43.4	Flagella	*flaBI*; flagellar basal body M-ring protein	17707	1891, 2304, 2306, 247, 4065
fliG	43.4	Flagella	*flaBII*; motor switching and energizing	18322	1891, 2304, 2306, 247, 2601, 2785, 3720, 4065
fliH	43.4	Flagella	*flaBIII*; flagellar biosynthesis	18319	1891, 2304, 2306, 247, 4065
fliI	43.4	Flagella	*flaC*; flagellar biosynthesis	772	247
fliJ	43.5	Flagella	*flaO*; flagellar biosynthesis	762	247
fliK	43.5	Flagella	*flaE*; hook filament junction; controls hook length	770	2171, 2172, 247, 2704
fliL	43.5	Flagella	*flaAI*; flagellar biosynthesis	18316	2370, 247, 2739, 3580
fliM	43.5	Flagella	*cheC*, *flaA*; flagellar synthesis, motor switching and energizing	774	2370, 2785, 777
fliN	43.5	Flagella	*motD*; flagellar switch protein	18313	2739
fliO	43.5	Flagella	*flbD*; flagellar synthesis; flagellar regulon member	17510	2704, 2738, 2739
fliP	43.5	Flagella	*flaR*; flagellar synthesis; flagellar regulon member	759	2738, 2739
fliQ	43.6	Flagella	*flaQ*; flagellar synthesis; flagellar regulon member	760	2739
fliR	43.6	Flagella	*flaP*; flagellar synthesis; flagellar regulon member	761	2738, 2739
fliS	43.2	Flagella	Flagellar synthesis; flagellar regulon member	30736	2172
fliT	43.2	Flagella	Flagellar synthesis; flagellar regulon member	30739	2172
fliY	43.1	Flagella	Not required for motility; may regulate FliA (σ^F)	49936	3080
fliZ	43.1	Flagella	Not required for motility; may regulate FliA (σ^F)	49933	3080
flk	52.5	Flagella	*div*; transcribed divergently from *pdxB*, promoters overlapping, *Salmonella* homolog functions in sensing flagellar assembly stage	32751	2134, 3930
flu	44.6	Flagella	Antigen 43, phase-variable bipartite outer membrane protein; affects surface properties, piliation, colonial morphology; unstable gene	746	1712, 1712a, 2704
fmt	74.0	fMet-tRNA formyltransferase	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	33616	1562, 1563, 2748, 2830, 2870, 3609
fnr	30.1	Fumarate-nitrate-reductase	*frdB*, *nirA*, *nirR*, *ossA*; regulatory gene for nitrite and nitrate reductases, hydrogenase, fumarate reductase	745	2878, 3611, 3863, 4008, 4009, 4010, 4153, 4216
focA	20.5	Formate channel	Membrane protein	31732	2088, 4294
focB	56.3	Formate channel	Membrane protein, formate transporter of *hyf* operon	55723	108a

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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]
folA	1.1	Folate	*tmrA*; trimethoprim resistance; dihydrofolate reductase (EC 1.5.1.3)	744	106, 1962, 3437, 3728, 380, 4014, 4112, 4113, 4114
folC	52.4	Folate	Dihydrofolate:folylpolyglutamate synthetase (EC 6.3.2.12)	17704	1228, 3211, 409
folD	12.0	Folate	*ads*; methenyltetrahydrofolate dehydrogenase/cyclohydrolase (EC 1.5.1.5, EC 3.5.4.9)	31127	1052, 932
folE	48.3	Folate	GTP cyclohydrolase I	32718	2170
folK	3.4	Folate	Dihydro-hydroxymethylpterin pyrophosphokinase	29572	4341
folP	71.6	Folate	Dihydropteroate synthase (EC 2.5.1.15)	29566	4312, 910, 911
folX	52.1	Folate	Dihydroneopterin triphosphate epimerase	54773	1668
fpr	88.6	Ferredoxin NADP$^+$ reductase	*mvrA*; ferredoxin NADP$^+$ reductase; anaerobic	18127	3002, 344, 4474
frdA	94.4	Fumarate reductase	Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	742	1116, 1540, 2041, 2614, 396, 793, 796, 797, 798, 801
frdB	94.4	Fumarate reductase	Fumarate reductase iron-sulfur protein subunit (EC 1.3.99.1)	741	1540, 2041, 2614, 663, 796, 797, 801
frdC	94.3	Fumarate reductase	Fumarate reductase membrane anchor polypeptide (EC 1.3.99.1)	740	1540, 2041, 2486, 663, 796
frdD	94.3	Fumarate reductase	Fumarate reductase membrane anchor polypeptide (EC 1.3.99.1)	739	1540, 2041, 2486, 663, 796
frr	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
fruA	48.7	Fructose	*ptsF*; fructosephosphotransferase enzyme II	350	1396, 3538
fruB	48.7	Fructose	*fruF*; fructosephosphotransferase enzyme III	17515	1396, 3646
fruK	48.7	Fructose	*fpk*, *fruF*; fructose-1-phosphate kinase (EC 2.7.1.3)	743	1061, 1396, 2925, 428
fruR	1.9	Fructose	*fruC*, *shl*, *cra*; regulatory gene for *fru* operon, other catabolite-regulated genes	18304	1396, 1982, 2324, 3611, 3797, 397
fsr	10.8	Fosmidomycin resistance	Amplification confers fosmidomycin resistance	49279	1329
ftn	42.8	Ferritin	*gen-165*, *rsgA*; ferritin	32521	1846, 1970
ftsA	2.2	Filamentation, temperature sensitive	*divA*; cell division, septation	738	1024, 17, 2036, 2675, 2676, 2689, 279, 3691, 3693, 4274, 4589, 4882, 57, 621
ftsE	77.6	Filamentation, temperature sensitive	Cell division; ATP-binding protein	736	1429, 3821
ftsI	2.0	Filamentation, temperature sensitive	*pbpB*, *sep*; peptidoglycan synthetase; penicillin-binding protein 3	423	1439, 1642, 2071, 279, 2889, 3107
ftsJ	71.7	Filamentation, temperature sensitive	Cell division and growth; heat inducible	33511	3250
ftsK	20.1	Filamentation, temperature sensitive	Cell division and growth, septation; NA-binding membrane protein; homology with *B. subtilis* SpoIIIE protein; filamentous growth mutants, suppressed by *dacA* deletion; promoter region *dinH*	40896	1046, 2519, 278, 4908
ftsL	2.0	Filamentation, temperature sensitive	Cell division and growth; essential gene; cytoplasmic membrane protein	30402	1588, 1929, 2071, 238
ftsN	88.8	Filamentation, temperature sensitive	*msgA*; essential gene; cell division and growth; multicopy suppresses *ftsA12*	34153	16, 903
ftsQ	2.2	Filamentation, temperature sensitive	Cell division and growth of wall at septum	734	1024, 2071, 277, 279, 3691, 3692, 4240, 4882, 57
ftsW	2.1	Filamentation, temperature sensitive	Cytoplasmic membrane required for PBP 2 expression; homology to *rodA*	30409	1896, 2071, 2209, 2210
ftsX	77.6	Filamentation, temperature sensitive	*ftsS*; cell division	18298	1429
ftsY	77.6	Filamentation, temperature sensitive	Cell division	18295	1429, 2381, 2656, 3520
ftsZ	2.3	Filamentation, temperature sensitive	*sfiB*, *sulB*; 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
fucA	63.2	Fucose	*fucC*; L-fuculose-1-phosphate aldolase	17701	2650, 4089, 4955, 669, 713, 714
fucI	63.2	Fucose	L-Fucose isomerase	10878	2650, 4955, 713, 714
fucK	63.3	Fucose	L-Fuculose kinase (EC 2.7.1.51)	10881	2650, 4955, 713, 714
fucO	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]
fucP	63.2	Fucose	*prd*; fucose permease	10875	2650, 4089, 4955, 669, 713, 714
fucR	63.3	Fucose	Positive regulatory protein for *fuc* regulon	10884	2650, 4090, 4955, 713, 714
fumA	36.3	Fumarate	Fumarase A, aerobic	18292	1555, 2932, 2933, 3357
fumB	93.6	Fumarate	Fumarase B, anaerobic; regulatory gene?	18289	1552, 1555, 292
fumC	36.3	Fumarate	Fumarase C, aerobic; member of *soxRS* regulon	15273	1552, 2568, 3357
fur	15.3	Ferric uptake regulation	Ferric iron uptake, negative regulatory gene	18286	1637, 1777, 198, 199, 3178, 3891, 978
fusA	74.8	Fusidic acid	*far*; fusidic acid resistance; protein chain elongation factor G	732	1815, 2383, 3498, 4929
fusB	14.5	Fusidic acid	Fusidic acid resistance; pleiotropic effects on RNA synthesis and ribosomes, ribosomal protein S6	731	1923a, 4332a
gabC	60.1	γ-Aminobutyrate	Utilization of GABA as N source; regulatory for *gab*?	730	1082, 2911, 2912
gabD	60.1	γ-Aminobutyrate	Succinate-semialdehyde dehydrogenase; NADP dependent (EC 1.2.1.16)	729	2911, 2912, 3179
gabP	60.2	γ-Aminobutyrate	GABA permease, membrane protein	728	2239, 2911, 2912
gabT	60.2	γ-Aminobutyrate	Aminobutyrate aminotransferase (EC 2.6.1.19)	727	249, 2911, 2912
gadA	79.0	Glutamate deCase	*gadS*? glutamate decarboxylase (EC 4.1.1.15)	32191	4111
gadB	33.8	Glutamate deCase	Glutamate decarboxylase (EC 4.1.1.15)	32194	4111
gadR	79.6	Glutamate deCase	Regulatory gene for *gat*?	726	2670, 2758
galE	17.0	Galactose	UDP-galactose 4-epimerase; hexose-1-phosphate uridylyltransferase (EC 2.7.7.12)	724	2456, 2485, 31, 4678, 4693, 581
galF	45.5	Galactose	*wcaN*; not required for colanic acid synthesis; putative UTP-glucose-P-uridylyltransferase (*galU*) regulatory subunit	53092	2771, 4209
galK	17.0	Galactose	Galactose resistance; galactokinase (EC 2.7.1.6)	723	225, 2456, 3792, 4285, 4693, 4876, 993, 994
galM	17.0	Galactose	Aldose-1-epimerase (mutarotease)	35171	456
galP	66.5	Galactose	D-Galactose/H^+ symporter	722	4693
galR	64.1	Galactose	Repressor of *galETK* operon; regulates low-affinity transport; Gal repressor	721	1395, 2491, 2708, 3792, 4613, 4691, 4692, 4693, 4953, 584
galS	48.3	Methyl-galactoside	*mglD*? utilization of methylgalactoside; negative regulation of high-affinity transport; Gal isorepressor; represses *mgl*	499	1395, 3684, 3751, 4693
galT	17.0	Galactose	*galB*; galactose-1-phosphate uridylyltransferase; (EC 2.7.7.10)	720	2095, 2371, 2456, 2485, 2491, 4693, 839
galU	27.8	Galactose	Glucose-1-P uridylyltransferase (UDP-glucose pyrophosphorylase) (EC 2.7.7.9), regulatory	719	1168, 1299, 1547, 3989, 4678, 4704
gapA	40.1	Glyceraldehyde phosphate dehydrogenase	*gad*; glyceraldehyde 3-P dehydrogenase A (EC 1.2.1.12); horizontal transfer? similar to eukaryotic GAPDH	718	1071, 2438, 3149, 3980, 480
gapC	32.1	Glyceraldehyde phosphate dehydrogenase	*gad*; glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12)	53105	1747
garA	15.8	Glucarate	D-Glucarate utilization	717	3690
garB	3.6	Glucarate	D-Glucarate utilization	716	3690
gatA	46.8	Galactitol	Galactitol-specific enzyme IIA of phosphotransferase system (PTS)	715	1015, 2058, 2565, 2925, 3202, 3644, 429
gatB	46.8	Galactitol	Galactitol-specific enzyme IIB of PTS	32559	3202
gatC	46.8	Galactitol	Galactitol-specific enzyme IIC of PTS	714	2058, 2565, 2925, 3202, 429
gatD	46.8	Galactitol	Galactitol-1-phosphate dehydrogenase	713	2058, 2565, 2925, 3202, 429
gatR	46.7	Galactitol	Regulatory gene for *gat*	32562	3202
gatY	46.8	Galactitol	D-Tagatose-1,6-bisphosphate aldolase	53142	3202
gatZ	46.8	Galactitol	Function unknown	53139	3202
gcd	3.0	Glucose dehydrogenase	Glucose dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.17); inner membrane	30502	4825, 782
gcl	11.5	Glyoxylate carboligase	Glyoxylate carboligase (EC 4.1.1.47)	31107	677
gcpE	56.9	Gene coding for protein E	Apparently essential gene	32909	205
gcvA	63.4	Glycine cleavage	*trans*-Acting protein, responsible for glycine-induced activation of *gcv*, perhaps repression in the presence of inosine	28676	4756, 4757, 4758
gcvH	65.7	Glycine cleavage	Glycine cleavage, carrier of aminomethyl group	28664	4192, 4194
gcvP	65.6	Glycine cleavage	Glycine dehydrogenase (decarboxylating) (EC 1.4.4.2)	28661	3280

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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]
gcvR	56.0	Glycine cleavage	Regulatory gene	40204	1416, 1417
gcvT	65.7	Glycine cleavage	Aminomethyl transferase, tetrahydrofolate dependent (EC 2.1.2.10)	28667	3280, 4192, 4193
gdhA	39.7	Glutamate dehydrogenase	Glutamate dehydrogenase	712	1707, 265, 2857, 3844, 4539, 4540, 853, 968
gef	0.4	Gene expression fatal	Small toxic membrane polypeptide; multimeric	30252	2012, 3507, 3508, 3509, 3510
ggt	77.2	γ-Glutamyltranspeptidase	γ-Glutamyltranspeptidase (EC 2.3.2.2)	18280	1663, 4303, 4304, 4305, 4306
gidA	84.5	Glucose-inhibited division	Glucose effects on cell division, perhaps replication	18277	2275, 3245, 4635, 556
gidB	84.5	Glucose-inhibited division	Glucose effects on cell division, perhaps replication	18274	2275, 3180, 3245, 4635
gip	11.5	Glyoxylate-induced protein	Induced by glyoxylate, downstream of *gcl*	49283	677
glcB	67.2	Glycolate	Malate synthase G (EC 4.1.3.2)	711	3396
glcC	67.4	Glycolate	Regulatory gene	49985	3396
glcD	67.3	Glycolate	Regulatory protein, transcriptional activator	49982	3396
glcE	67.3	Glycolate	*glcF* (frameshifted segment of *glcE*); glycolate oxidase subunit, FeS protein	49979	3396
glcG	67.3	Glycolate	Unknown function	49974	3396
gldA	89.1	Glycerol dehydrogenase	Glycerol dehydrogenase, NAD^+ dependent	34147	395, 4473
glf	45.4	Galactofuranose	UDP-galactopyranose mutase (EC 5.4.99.9)	54669	3137
glgA	76.8	Glycogen	Glycogen synthase (EC 2.4.1.21)	710	2084, 2364, 2432, 3281, 3721, 3722, 4854
glgB	76.9	Glycogen	1,4-α-Glucan branching enzyme (EC 2.4.1.18)	709	196, 2432, 3721, 3722, 3820
glgC	76.9	Glycogen	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)	708	195, 2432, 3721, 3722, 3281
glgP	76.8	Glycogen	α-Glucan phosphorylase (EC 2.4.1.1)	33653	4907, 742
glgS	68.8	Glycogen	Glycogen synthesis protein, controlled by σ^S (stationary phase) and cAMP	29727	1719, 4854
glgX	76.9	Glycogen	Glycogen debranching enzyme	53576	4854
glk	54.0	Glucokinase	Glucokinase; (EC 2.7.1.2)	707	539, 890
glmM	71.6	Glucosamine	*mrsA*; phosphoglucosamine mutase; essential gene; UDP-GlcNAc path, peptidoglycan, lipopolysaccharide synthesis; mRNA stability effects	47201	2893, 4658
glmS	84.3	Glucosamine	Glucosamine-6-phosphate synthase (EC 2.6.1.16)	706	3464, 4611, 4635
glmU	84.3	Glucosamine	Bifunctional glucosamine-1-phosphate acetyltransferase and *N*-acetylglucosamine-1-P uridyltransferase	29106	2891, 2892
glmX	26.2	Glucosamine	Affects suppression of *glmS* mutations by *nagB*	36538	4601
glnA	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
glnB	57.9	Glutamine	PII regulatory protein for glutamine synthetase	32933	1683, 2578, 4132, 4555, 555
glnD	4.0	Glutamine	Uridylyltransferase	704	1359, 4556
glnE	68.9	Glutamine	GS adenylyl transferase (EC 2.7.7.42)	33468	4555
glnG	87.3	Glutamine	*glnT*, *ntrC*; nitrogen regulator I	702	192, 2705, 2706, 2707, 2710, 2849, 2952, 3335, 3336
glnH	18.2	Glutamine	Periplasmic glutamine-binding protein	18271	3206, 3207
glnK	10.2	Glutamine	Regulated through NRI/NRII two-component regulatory system	38502	4554, 4557
glnL	87.4	Glutamine	*glnR*, *ntrB*; bifunctional protein kinase/phosphatase nitrogen regulator II, NRII	701	159, 192, 2706, 2707, 2710, 2848, 2849, 2952, 3207, 3336, 3645, 3695, 4510, 711
glnP	18.2	Glutamine	L-Glutamate periplasmic binding protein; transport; methionine sulfoximine resistance	700	2792, 3207, 4695, 4696
glnQ	18.2	Glutamine	Glutamine high-affinity transport system	18268	3207
glnR	24.1	Glutamine	Glutamine transport	699	724
glnS	15.2	Glutamine	Glutaminyl-tRNA synthetase (EC 6.1.1.18)	698	136, 3454, 3709, 4846, 1776
glnT	78.0	Glutamine	Levels of glutamine $tRNA_1$ and glutamine synthetase	697	3001
glnU	15.0	Glutamine	*glnU*α; su_B, *supB* (ochre [UAA] suppression); glutamine $tRNA_1$, tandem duplication	696	1285, 1915, 2313, 3102, 3103, 3454
glnV	15.0	Glutamine	*glnV*α; Su_{II}, *Su2*, *supE* (amber suppression); glutamine $tRNA_2$, tandem duplication (VX)	695	1122a, 1285, 1915, 1916, 2313, 3102, 3103, 3454

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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]
glnW	15.0	Glutamine	*glnU*β; *su*$_B$, *supB* (ochre [UAA] suppression); glutamine tRNA$_1$, tandem duplication (UW)	37440	1122a, 3001
glnX	15.0	Glutamine	*glnV*β; *Su*$_{II}$, *Su2*, *supE* (amber suppression); glutamine tRNA$_2$, tandem duplication (VX)	37443	1122a, 1285, 1915, 1916, 2313, 3102, 3103, 3454
gloA	37.2	Glyoxalase	Glyoxalase I	39135	2703, 952
glpA	50.7	Glycerol phosphate	Glycerol-3-phosphate dehydrogenase (anaerobic) large subunit (EC 1.1.99.5)	694	1130, 2424, 3936, 799
glpB	50.7	Glycerol phosphate	*sn*-Glycerol-3-phosphate dehydrogenase (anaerobic) subunit (EC 1.1.99.5); membrane anchor	17692	1130, 4566, 799
glpC	50.7	Glycerol phosphate	*sn*-Glycerol-3-phosphate dehydrogenase (anaerobic) small subunit (EC 1.1.99.5)	17695	1130, 799
glpD	76.7	Glycerol phosphate	*glyD*; glycerol-3-phosphate dehydrogenase (aerobic) (EC 1.1.99.5)	693	171, 2491, 3940, 3942, 3947
glpE	76.7	Glycerol phosphate	Gene of *glp* regulon	18265	3942, 4926
glpF	88.7	Glycerol phosphate	Glycerol facilitator	692	4313
glpG	76.7	Glycerol phosphate	Gene of *glp* regulon	18262	3942, 4926
glpK	88.7	Glycerol phosphate	Glycerol kinase (EC 2.7.1.30)	691	324, 3413, 3414, 3798, 3940, 827
glpQ	50.6	Glycerol phosphate	Glycerol-3-phosphate diesterase, periplasmic	690	2424, 2426, 4428
glpR	76.7	Glycerol phosphate	Repressor of *glp* operon	688	3940, 3942, 3950, 4926, 743
glpT	50.6	Glycerol phosphate	*sn*-Glycerol-3-phosphate permease	689	1130, 1138, 1581, 1620, 2424, 2477, 2931, 334, 3936, 4571, 4753, 4827
glpX	88.6	Glycerol phosphate	May be involved in glycerol metabolism but not required for growth on glycerol	30884	4474
gltA	16.2	Glutamate	*glut*, *icdB*; citrate synthase (EC 4.1.3.7)	687	1549, 1708, 1859, 2396, 3151, 3356, 402, 4149, 4741, 4773
gltB	72.3	Glutamate	*aspB*, *ossB*; glutamate synthase, large subunit (EC 1.4.1.13)	686	1172, 1363, 2644, 3288, 3863, 657, 853
gltD	72.4	Glutamate	*aspB*, *ossB*; glutamate synthase, small subunit	17689	1363, 3288, 3863, 657
gltE	81.4	Glutamate	Glutamyl-tRNA synthetase; possible regulatory subunit	685	3062
gltF	72.4	Glutamate	*ossB*; regulatory gene?	18259	657
gltH	21.8	Glutamate	Growth on glutamate	684	2757, 2758, 3897
gltJ	14.8	Glutamate	Membrane protein, transport gene	49541	2659, 3308
gltK	14.8	Glutamate	Membrane protein, transport gene	49537	2659, 3308
gltL	14.7	Glutamate	Membrane protein, transport gene	49528	2659, 3308
gltM	43.0	Glutamate	Affects glutamyl-tRNA synthetase level or activity?	683	3062
gltP	92.5	Glutamate	Proton-glutamate-aspartate transport protein	34330	1001, 2660, 4423, 4639
gltR	92.3	Glutamate	Growth on glutamate at 42°C	682	2758
gltS	82.5	Glutamate	Glutamate permease	681	1001, 1002, 1078, 1178, 2098, 2655, 2757, 2758, 2950, 3897
gltT	89.8	Glutamate	*tgtB*; glutamate tRNA$_2$	680	2313, 3446, 3579, 522, 523
gltU	85.0	Glutamate	*tgtC*; glutamate tRNA$_2$	679	2313
gltV	90.7	Glutamate	*tgtE*; glutamate tRNA$_2$	678	2313
gltW	58.8	Glutamate	Glutamate tRNA$_2$	677	1146, 2313
gltX	54.3	Glutamate	Glutamyl-tRNA synthetase (EC 6.1.1.17)	676	2336, 3851, 498, 539
glyA	57.8	Glycine	Serine hydroxymethyltransferase (EC 2.1.2.1)	675	2633, 3444, 3445, 4191, 4522
glyQ	80.2	Glycine	*glyS*α; glycyl-tRNA synthetase, α-subunit (EC 6.1.1.14)	33775	4127
glyS	80.2	Glycine	*act*, *gly*, *glyS*β; glycyl-tRNA synthetase, β-subunit (EC 6.1.1.14)	674	2196, 4127, 502
glyT	90.0	Glycine	*sumA*; glycine tRNA$_2$, UGA suppression[f]	673	1849, 2313, 2467, 3743, 90
glyU	64.6	Glycine	*suA36*, *sufD*, *sumA*, *sumB*, *supT*; glycine tRNA$_1$	672	1122a, 2313
glyV	94.6	Glycine	*ins*, *mutA*; glycine tRNA$_3$ (VXY)	35636	1122a, 2921, 2313
glyW	42.9	Glycine	*ins*, *mutC*; glycine tRNA$_3$	670	2313, 2921, 4493, 4494
glyX	94.6	Glycine	Glycine tRNA$_3$ (VXY)	35639	2313
glyY	94.6	Glycine	Glycine tRNA$_3$ (VXY)	35642	2313
gmd	45.8	GDP-D-mannose dehydratase	Fucose biosynthesis; GDP-D-mannose 4,6-dehydratase	51902	4256
gmk	82.3	GMP kinase	Guanylate kinase (EC 2.7.4.8)	33871	1401
gmm	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[c]
gnd	45.2	Gluconate-P dehydrogenase	Gluconate-6-phosphate dehydrogenase (EC 1.1.1.43)	669	3135, 3138, 3156, 4291, 4768
gntK	77.1	Gluconate	Gluconokinase, thermoresistant	35465	1969, 4436, 980
gntP	98.0	Gluconate	Membrane protein, homologous to *B. subtilis* gluconate permease	50203	2266
gntR	77.1	Gluconate	Controls *gntKU* induction, also *edd* and *eda*; gluconate transport and P′n	667	1194, 186, 1969, 3391, 3940, 4436, 4970
gntS	96.8	Gluconate	Secondary gluconate transport system; putative regulator of GntV	666	186, 1943, 569
gntT	76.4	Gluconate	*gntM*, *usgA*; high-affinity gluconate transport	668	1942, 3391, 3487, 4826, 981
gntU	77.0	Gluconate	Low-affinity gluconate transport protein, membrane protein	35461	1969, 4436, 4826, 980
gntV	96.8	Gluconate	Glucokinase, thermosensitive	17686	1942, 569
goaG	29.4		GABA aminotransferase (EC 2.6.1.19)	51935	2066
gor	78.5	GSH oxidoreductase	Glutathione oxidoreductase (EC 1.6.4.2)	665	1150, 1513, 270, 964
gph	75.7	Glycolate phosphatase	Phosphoglycolate phosphatase activity, in *dam* operon	53568	2681
gpmA	16.9	Glycerol P mutase	Phosphoglycerate mutase 1	35790	456, 958
gpp	85.4	Guanosine pentaphosphatase	Guanosine pentaphosphatase activity; exopolyphosphatase	664	289, 58, 926
gprA	0.3	Growth of phage, replication	Replication of certain lambdoid phage	15896	3240, 3829
gprB	0.2	Growth of phage, replication	Replication of certain lambdoid phage	15890	3240
gpsA	81.5	Glycerol phosphate	*sn*-Glycerol-3-phosphate dehydrogenase [NAD(P)$^+$] (EC 1.1.1.94)	663	3700, 3701, 4032
gpt	5.5	Guanine-xanthine phosphotransferase	*glyD*, *gpp*, *gxu*; guanine-xanthine phosphoribosyltransferase (EC 2.4.2.22)	662	1469, 1722, 1979, 3221, 3531, 3662, 535
greA	71.7	Growth restorer?	Transcription elongation factor	33506	1166, 1835, 4141, 4142, 4195, 441, 442, 76
greB	76.2	Growth restorer?	Transcription elongation factor	35448	1835, 442, 76
groE	94.2	Growth of phage	*hdh*, *mop*, *tabB*, *groS*; operon	13587	See *groE*, *groL*
groL	94.2	Growth of phage	*groEL*, *mopB*; *hdh*; *tabB*; chaperone for assembly of enzyme complexes; phage morphogenesis; large subunit	492	1068, 1215, 1407, 1409, 2119, 2393, 2454, 3146, 4416, 573
groS	94.2	Growth of phage	*groES*, *mopA*; *hdh*, *tabB*; small subunit of GroE chaperone	493	1068, 1409, 2119, 2393, 2475, 3146, 4416
grpE	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
grxA	19.2	Glutaredoxin	Glutaredoxin 1	17683	1796, 2337, 3771, 3778, 4350
grxB	24.2	Glutaredoxin	Glutaredoxin 2	52078	154, 4595
grxC	81.6	Glutaredoxin	Glutaredoxin 3	42921	154, 155
gshA	60.6	GSH, glutathione	γ-Glutamyl-cysteine synthetase; (EC 6.3.2.2)	659	1368, 1504, 1613, 2853, 3060, 4674
gshB	66.6	GSH, glutathione	Glutathione synthetase (EC 6.3.2.3)	33370	966
gsk	10.8	Guanosine kinase	Guanosine kinase	658	1653, 1824
gsp	67.6	Glutathionylspermidine	Glutathionylspermidine synthetase/amidase; bifunctional protein	36859	420
*gsp**	74.6	General secretory pathway operon	*hopD*, *hopG*; *gsp* previously used for glutathionylspermidine (see above), cryptic general secretory pathway; *pul* in *Klebsiella* spp.	55310	1292
gst	36.9	GSH *S*-transferase	Glutathione *S*-transferase	37217	3192
guaA	56.7	Guanine	GMP synthetase (EC 6.3.4.1)	657	4414, 4503, 955, 4386
guaB	56.7	Guanine	*guaR*; IMP dehydrogenase (EC 1.2.1.14)	656	4399, 4400, 4413, 4503, 955, 4386
guaC	2.4	Guanine	GMP reductase (EC 1.6.6.8)	655	110, 2988, 3689
gurB	75.1	Glucuronide	Utilization of glucuronides	654	3219
gurC	18.0	Glucuronide	Utilization of glucuronides	653	3219
gutM	60.9	Glucitol (sorbitol)	Part of *srl* operon	33198	4824
gutQ	61.0	Glucitol (sorbitol)	Part of *srl* operon; putative ATP-binding protein	33206	4828, 757
gyrA	50.3	Gyrase	*hisW*, *nalA*, *parD*, *nfxA*, *norA*; 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]
gyrB	83.5	Gyrase	*cou*, *acrB*, *himB*, *hisU*, *nalC*, *nalD*, *pcbA*, *parA*; novobiocin, coumermycin resistance; DNA gyrase, subunit B	650	10, 1053, 11, 1397, 2159, 2900, 2901, 2944, 3112, 3304, 4607, 4611, 4831, 9, 4438
hcaA	61.6	HCA, hydrocinnamic acid	*dig*, *phd*; 3-phenylpropionate dioxygenase	35007	570, 571
hcaB	61.7	HCA, hydrocinnamic acid	*dig*, *phd*; 3-phenylpropionate-2′,3′-dihydrodiol deHase	35010	570, 571
hdeA	78.8	H-NS-determined expression	Periplasmic, unknown function, has σ^S-dependent promoter	33734	138, 4894
hdeB	78.8	H-NS-determined expression	Periplasmic, unknown function, has σ^S-dependent promoter	33731	138, 4894
hdeD	78.8	H-NS-determined expression	Periplasmic, unknown function, has σ^S-dependent promoter	33737	4894
hdhA	36.5	Hydroxysteroid dehydrogenase	*hsdH*; 7-α-hydroxysteroid dehydrogenase (EC 1.1.1.159)	32248	4897
helD	22.1	Helicase	*srjB*; helicase IV	31769	2642, 2883, 2884, 2885, 4774
hemA	27.2	Hemin	Neomycin sensitivity; hemin biosynthesis; glutamyl tRNA dehydrogenase	648	1087, 177, 1898, 2528, 4573, 709, 4575
hemB	8.4	Hemin	*ncf*; 5-aminolevulinate dehydratase (EC 4.2.1.24)	647	1111, 19, 2517, 2529, 2530, 2839, 2840, 3297
hemC	86.0	Hemin	*popE*; porphobilinogen deaminase (EC 4.3.1.8); neomycin sensitivity	646	1596, 2052, 2054, 2055, 2405, 2645, 2840, 3870, 3871, 4042, 4401, 60, 926
hemD	85.9	Hemin	Uroporphyrinogen III cosynthase; neomycin sensitivity	645	2052, 2053, 3870, 3871, 4042, 926
hemE	90.4	Hemin	Uroporphyrinogen decarboxylase (EC 4.1.1.37)	644	1912, 3196, 3874
hemF	55.0	Hemin	*popB*, *sec*; coproporphyrinogen III oxidase (EC 1.3.3.3)	643	2840, 3037, 4464
hemG	86.9	Hemin	Protoporphyrinogen oxidase activity; neomycin sensitivity	642	3197, 3872, 3873, 4853
hemH	10.7	Hemin	*popA*, *visA*; ferrochelatase (EC 4.99.1.1)	641	1323, 3100, 3101, 2974
hemK	27.3	Hemin	Heme biosynthesis	36992	3127
hemL	3.7	Hemin	*gsa*, *popC*; glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)	372	1519, 1899, 1900
hemM	27.2	Hemin	*lolB*; glutamyl-tRNA dehydrogenase? novel outer membrane lipoprotein?	31940	1898, 1981, 2815, 2816, 4573, 709
hemX	85.9	Hemin	Uroporphyrinogen III methylase	33965	3875, 926
hemY	85.9	Hemin	Member of *uro* (*hemC*) operon	33969	926
hepA	1.3	Helicase-like protein	*rapA*; sequence similarity to helicases, downstream of *polB*, not under *lexA* control	29491	1139, 2519, 4269a, 435
het	84.6	Heterogeneous size	*cop*; possibly structural gene for DNA-binding protein; near *ori*	640	3249, 4610, 4771
hflA	94.8	High frequency lysogeny	Operon including *hfq*, *hflX*, -K, -C; part of complex *mutL-hflC* transcription unit	34429	4487
hflB	71.6	High-frequency lysogenization	*ftsH*, *mrsC*, *tolZ*; 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
hflC	94.9	High-frequency lysogenization	HflA complex cleaves lambda cII; protease	17520	220, 285
hflK	94.8	High frequency lysogenization	HflA complex cleaves lambda cII; protease	639	220, 285
hflX	94.8	High frequency lysogenization	HflX GTPase, putative	34423	220, 3203
hfq	94.8	Host factor for Q β	HF-I, host factor for phage Qβ	34450	2090, 2091, 4024, 4487–4490
hha	10.3	High hemolysin activity	Histone-like; downregulates gene expression, stimulates transposition events	31084	1438, 2929, 3182
hipA	34.2	High persistence	Probable role in cell division	18244	2882, 3028, 3029, 367, 368, 3902
hipB	34.3	High persistence	Probable role in cell division	32207	2882, 367, 368
hisA	45.1	Histidine	*N*-(5′-phospho-L-ribosylformimino)-5-amino-1-(5′-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	636	1202, 65
hisB	45.1	Histidine	Bifunctional enzyme imidazoleglycerolphosphate (IGP) dehydratase, histidinol phosphatase (EC 3.1.3.15, EC 4.2.1.19)	635	1521, 730
hisC	45.1	Histidine	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	634	1521, 1522
hisD	45.0	Histidine	Histidinol dehydrogenase (EC 1.1.1.23)	633	542, 65, 731
hisF	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]
hisG	45.0	Histidine	ATP phosphoribosyltransferase (EC 2.4.2.17)	630	1322, 3027, 4572, 542
hisH	45.1	Histidine	Amidotransferase component of IGP synthase	629	1263, 1296, 1376, 1451, 2260, 65
hisI	45.2	Histidine	Formerly *hisE* and *hisI*; bifunctional enzyme PR-ATP pyrophosphatase PR-AMP cyclohydrolase (EC 3.5.4.19, EC 3.6.1.31)	628	65, 731
hisJ	52.3	Histidine	Histidine-binding protein of high-affinity histidine transport system	627	126, 2512
hisM	52.2	Histidine	Histidine transport membrane protein M	25879	2335
hisP	52.2	Histidine	Histidine permease	626	126, 2335, 2512
hisQ	52.2	Histidine	Histidine transport gene	32721	126
hisR	85.8	Histidine	*hisT*; histidine tRNA	625	1832, 2313, 2535, 926
hisS	56.8	Histidine	Histidyl-tRNA synthetase (EC 6.1.1.21)	624	1140, 1141, 1301
hlpA	4.3	Histone-like protein	*ompH*; *firA*, *orf* (*skp*), *skp*; histone-like protein HLP-I (cytoplasmic?); early confusion with adjacent *lpxD* gene	18241	1, 1040, 1773, 1775, 1784, 2429, 2964, 4402, 4403, 706, 804, 1702
hlyE	26.5	Hemolysin (latent)	Latent hemolysin expressed in presence of *Actinobacillus glyX* or *fnr* mutant	53859	1498
hmp	57.9	Hemoglobin-like	*fsrB*; hemoglobin-like flavoprotein	32917	109, 2879, 2880, 2881, 3482, 3483, 4068
hns	27.8	Histone-like protein, H-NS	*bglY*, *cur*, *drc*, *drdX*, *drs*, *fimG*, *irk*, *msyA*, *osmZ*, *pilG*, *topX*, *virR*; 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
hofB	2.5	Homologous to *fim*	*hopB*; homologous to PilB of *Pseudomonas aeruginosa*; function not established, insertion mutation gives no phenotype	33679	4722
hofC	2.5	Homologous to *fim*	*hopC*; homologous to PilC of *P. aeruginosa*; function not established, insertion mutation gives no phenotype	33676	4722
holA	14.4	Holoenzyme	DNA polymerase III, δ-subunit	31431	1067, 2194, 3300, 645
holB	24.9	Holoenzyme	DNA polymerase III, δ′-subunit	31447	1067, 2194, 3300
holC	96.6	Holoenzyme	DNA polymerase III, χ-subunit	31456	2194, 3295, 4808, 644
holD	99.3	Holoenzyme	DNA polymerase, ψ-subunit	31460	2194, 3295, 4808, 646
holE	41.5	Holoenzyme	DNA polymerase III, θ-subunit	31439	2194, 2224, 4097, 4254, 647
hopB	84.7	Host plasmid maintenance	*hop*; also used for *hof* loci (homologous to Pil genes in *Pseudomonas*); required for mini-F	37343	3184
hopC	99.4	Host plasmid maintenance	Required for maintenance of stable mini-F plasmid; see also *hofC*	37346	3184
hopD	11	Host plasmid maintenance	Required for maintenance of stable mini-F plasmid	37349	3184
hpt	3.0	HGPRT	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	622	2024, 535
hrpA	31.9	Helicase-related protein	RNA helicase-like; similarity to eukaryotic DEAH family	36987	3005
hrpB	3.5	Helicase-related protein	RNA helicase-like; similarity to eukaryotic DEAH family and *araC*	36926	3005, 1331
hrsA	16.5	Heat-responsive suppressor	Suppresses *ompC* mutation's defective thermoresponse	53146	4520
hscA	57.2	Heat shock cognate	Stress response gene; Hsp70 family	32977	2179, 2484, 3956, 4583
hscB	57.3	Heat shock cognate	Stress response gene; heat shock regulon	40196	2484, 4583
hsdM	98.7	Host specificity	*hs*, *hsm*, *hsp*, *rm*; host DNA modification; DNA methylase M	621	1014, 2608, 3800, 4909
hsdR	98.7	Host specificity	*hs*, *hsp*, *hsr*, *rm*; host DNA restriction; endonuclease R	620	1014, 2608, 3800, 4909
hsdS	98.7	Host specificity	*hss*; specificity determinant for *hsdM* and *hsdR*	619	1474, 2608, 3071, 3800, 4909
hslC	19.9	Heat shock locus	Protein expressed as heat shock regulon member	36762	749
hslD	24.1	Heat shock locus	Protein expressed as heat shock regulon member	36765	749
hslE-H	29.7	Heat shock loci	Protein expressed as heat shock regulon member	37190	749
hslJ	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]
hslK	40.7	Heat shock locus	Protein expressed as heat shock regulon member	36945	749
hslL-N	70.5	Heat shock loci	Protein expressed as heat shock regulon member	37449	749
hslO-R	76.0	Heat shock loci	Heat shock proteins; HslO is HspG21.0	36769	749
hslU	88.8	Heat shock locus	*htpI*, *clpY*; 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
hslV	88.8	Heat-shock locus	*htpO*; heat shock regulon	34160	1341, 2121, 2208, 2963, 3713, 4889, 4890, 749, 750
hslW	94.2	Heat shock locus	Heat-inducible; regulatory gene, near *groE*	41190	749
htgA	0.2	High-temperature growth	*htpY*; heat inducible	30233	1987, 2961, 984
htpG	10.7	Heat shock protein	Heat shock protein C62.5; chaperone	17680	228
htpX	41.2	Heat shock protein	Protein expressed as heat shock regulon member	32320	2327
htrB	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
htrC	90.3	High temperature (requirement)	Essential for growth at high temperature, under σ^{32} (heat shock) regulation	34265	2141, 3589
htrE	3.3	High temperature (requirement)	Sequence homology with pilin protein PapC	30510	3593
htrL	81.7	High temperature (requirement)	RfaH-regulated high-temperature gene	54740	3591
hupA	90.5	HU protein	HU-β, HU-2, histone-like protein	34243	1977, 2125, 2126, 2292, 2391, 422
hupB	9.9	HU protein	*dpeA*, *hopD*; HU-α, HU-1, histone-like protein	18235	1463, 1977, 2124, 2127, 2292, 2391, 2749, 4239
hyaA	22.2	Hydrogenase 1	Hydrogenase 1 small subunit [NiFe]	31781	2897, 2898
hyaB	22.3	Hydrogenase 1	Hydrogenase 1 large subunit [NiFe]	31784	2897, 2898
hyaC	22.3	Hydrogenase 1	Possible membrane-spanning protein of *hya* operon	31788	2897, 2898
hyaD	22.3	Hydrogenase 1	Processing of HyaA and HyaB	31791	2897, 2898
hyaE	22.3	Hydrogenase 1	Processing of HyaA and HyaB	31794	2897, 2898
hyaF	22.3	Hydrogenase 1	Nickel incorporation in hydrogenase 1 proteins	31797	2897, 2898
hybA	67.7	Hydrogenase 2	*hydL*, *hydC*; hydrogenase 2 [Ni, Fe], small subunit, probably	33407	2896
hybB	67.7	Hydrogenase 2	HYD2 cytochrome *b* type component, probably	33414	2896
hybC	67.7	Hydrogenase 2	Hydrogenase 2 [Ni Fe] large subunit, probably	33418	2896
hybD	67.7	Hydrogenase 2	Processing element for hydrogenase 2, probably	33421	2896
hybE	67.6	Hydrogenase 2	Function undefined	33424	2896
hybF	67.6	Hydrogenase 2	Regulatory gene	33427	2896
hybG	67.6	Hydrogenase 2	May affect maturation of hydrogenase 2 large subunit	33403	2896
hycA	61.4	Hydrogenase 3	Regulatory gene for *hyc* and *hyp*; counteracts activation by FhlA	33143	1801, 2554, 3883, 412, 4294
hycB	61.4	Hydrogenase 3	Formate-hydrogenlyase system, formate regulon, small subunit of hydrogenase 3?	33169	3883, 2554
hycC	61.3	Hydrogenase 3	Formate-hydrogenlyase system, formate regulon, small subunit of hydrogenase 3?	33166	3883, 2554
hycD	61.3	Hydrogenase 3	Hydrogenase 3 subunit	33162	3883, 2554
hycE	61.3	Hydrogenase 3	Hydrogenase 3 subunit, large, precursor	33159	3746, 3883
hycF	61.3	Hydrogenase 3	Hydrogenase 3 subunit	33154	3883
hycG	61.2	Hydrogenase 3	Hydrogenase 3 subunit	33151	3883
hycH	61.2	Hydrogenase 3	Required for converting HycE precursor to Hyd-3 subunit	33140	2678, 3883
hycI	61.2	Hydrogenase 3	Maturation protease for Ni-containing Hyd-3	50402	3747
hydA	61.1	Hydrogenase	*hydNF* operon	18232	2145, 2465, 2726, 3376, 3852, 4835
hydG	90.6	Hydrogenase	Two-component regulation of Hyd-3 activity	34252	3410, 4231
hydH	90.5	Hydrogenase	Two-component regulation of Hyd-3 activity, sensor kinase	34249	4231
hydN	61.1	Hydrogenase	Iron-sulfur protein required for Hyd-3 activity	33521	2726
hyfA-J	56.2	Hydrogenase 4	Part of 12-cistron operon encoding putative proton-translocating formate hydrogenlyase system	55682	108a
hyfR	56.3	Hydrogenase 4	Formate-sensing regulator for *hyf* 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]
hypA	61.4	Hydrogenase	Formate-hydrogenlyase system; guanine-nucleotide-binding protein, Ni donor for Hyd-3 large subunit	33104	1801, 1976, 2678, 3745
hypB	61.4	Hydrogenase	*hydE*; formate-hydrogenlyase system; formate regulon	33110	1801, 1976, 2678, 2725, 3745
hypC	61.4	Hydrogenase	Formate-hydrogenlyase system: formate regulon	33113	1801, 1976, 2678, 3745
hypD	61.4	Hydrogenase	*hydF*; formate-hydrogenlyase system: formate regulon	33116	1801, 1976, 2678, 3745, 3855
hypE	61.5	Hydrogenase	*hydB*; formate-hydrogenlyase system: formate regulon	33119	1801, 1976, 2678, 3745, 3854
hypF	61.1	Hydrogenase	Mutation results in loss of hydrogenase activity; affects maturation of all hydrogenases, formate regulon	50120	2726
iadA	98.2	Isoaspartyl dipeptidase	Isoaspartyl dipeptidase	53593	1382
iap	62.0	Isozymic alkaline P′ase	Aminopeptidase, presumably, that generates alkaline phosphatase isozyme	616	1931, 3120
ibpA	83.3	Inclusion body protein	*hslT*, *htpN*; chaperone, heat-inducible protein of HSP20 family	33847	2427, 69, 750
ibpB	83.3	Inclusion body protein	*hslS*, *htpE*; chaperone, heat-inducible protein of HSP20 family	33843	2427, 69, 750
icd	25.7	Isocitrate dehydrogenase	*icdE*; isocitrate dehydrogenase, NADP$^+$-specific (EC 1.1.1.42)	615	124, 1709, 1729, 1753, 625
iclR	91.0	Isocitrate lyase	Isocitrate lyase (EC 4.1.3.1)	614	1331, 2744, 3382, 4290, 840
ihfA	38.7	Integration, host factor	*himA*, *hid*; 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
ihfB	20.8	Integration, host factor	*himD*, *hip*; see *ihfA*, β subunit	637	1156, 1258, 1603, 2216, 2461, 2941, 2943, 2944, 4687
ileR	95.8	Isoleucine	*avr*, *flrA*; Ile repressor; regulation of *thr* and *ilv* operons; originally placed at 99.9 min; sequence puts it at 95.8 min	15914	2028, 2029, 4702, 569
ileS	0.5	Isoleucine	Isoleucyl-tRNA synthetase (EC 1.1.1.5)	613	2104, 2945, 3640, 4317, 4422, 4820, 4830
ileT	87.0	Isoleucine	Isoleucine tRNA$_1$, triplicate (T, U, V)	612	2313, 926
ileU	73.8	Isoleucine	Isoleucine tRNA$_1$, triplicate (T, U, V)	611	2313
ileV	4.8	Isoleucine	Isoleucine tRNA$_1$, triplicate (T, U, V)	610	1146, 2313
ileX	69.2	Isoleucine	Isoleucine tRNA$_2$	17677	3058
ileY	60.0	Isoleucine	Isoleucine tRNA$_2$ variant	53508	4837
ilvA	85.2	Isoleucine-valine (requirement)	*ile*; threonine deaminase (EC 4.2.1.16)	609	1086, 1490, 1839, 2445, 3824, 4614, 58, 860, 926
ilvB	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
ilvC	85.3	Isoleucine-valine (requirement)	*ilvA*; ketol-acid reductoisomerase (EC 1.1.1.86)	607	257, 351, 4707, 58, 926
ilvD	85.2	Isoleucine-valine (requirement)	Dihydroxyacid dehydrase (EC 4.2.1.9)	606	1086, 1490, 1839, 2445, 317, 58, 860, 926
ilvE	85.1	Isoleucine-valine (requirement)	*ilvC*, *ilvJ*; 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
ilvF	57.0	Isoleucine-valine (requirement)	Production of valine-resistant acetolactate synthase activity	604	3452, 960
ilvG	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
ilvH	1.9	Isoleucine-valine (requirement)	*brnP*; acetolactate synthase II, valine sensitive (EC 4.1.3.18)	602	1437, 1453, 184, 1982, 3450, 3607, 4176, 4177, 4299, 4513, 960
ilvI	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
ilvJ	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]
ilvM	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
ilvN	83.0	Isoleucine-valine (requirement)	Acetohydroxy acid synthase I, small subunit (EC 4.1.3.18); valine sensitive small subunit; positive regulator for *thr* and *ilv*	15441	1310, 4705, 681
ilvR	99.9	Isoleucine-valine		15917	2029
ilvU	6.4	Isoleucine-valine (requirement)	Regulation of *ileS* and modification of Ile tRNA$_2$ and Val tRNA$_2$	599	1214
ilvY	85.2	Isoleucine-valine (requirement)	Positive regulator for *ilvC*	598	351, 3824, 4707, 58, 926
imp	1.2	Increased membrane permeability	*ostA*; permeability of outer membrane to large maltodextrins; antibiotic and detergent sensitivity, stress induced	36754	3828
inaA	50.6	Inducible by acid	Protein induced by acid, independent of SoxRS regulation	32692	3737, 4727
inaR	34.8	Inducible by acid	Regulates *inaA* (may be *marA* or *soxZ*?)	32696	4727
infA	19.9	Initiation factor	*hypA1*? protein chain initiation factor IF1	17674	3475, 3849, 885, 886, 899
infB	71.4	Initiation factor	*ssyG*; protein chain initiation factor 2, IF2	597	1561, 1928, 2748, 3016, 3108, 3459, 3462, 4026, 4027, 4029
infC	38.8	Initiation factor	*fit*?, *srjA*; protein chain initiation factor 3, IF3	596	1148, 1601, 2500, 2592, 2829, 3056, 3463, 3527, 3788, 4168, 4710, 4801, 514, 582, 583, 732, 942
inm	79.0	Insensitive NG mutagenesis	Susceptibility to mutagenesis by nitrosoguanidine	595	3767
intA	59.4	Integrase	*slpA*; from defective prophage CP4-57	33082	2241, 4455
intB	96.9	Integrase	Prophage P4 integrase, defective prophage derivative	53585	394
intD	12.2	Integrase	*int* (*qsr′*); integrase locus within defective prophage derivative *qsr′*	31133	3059
isfA	86.0	Inhibits SOS function	Regulatory gene; SOS-related	41044	263, 264
ispA	9.5	Isoprenoid synthesis	Farnesyl diphosphate synthase (EC 2.5.1.1)	30978	1328, 1330
ispB	71.8	Isoprenoid synthesis	*cel*; octaprenyl diphosphate synthase	35712	150, 3277
katC	6.0	Catalase	IS1B and IS20B insertions sensitize to peroxide; deletion or Tn insertion increases resistance	594	4605
katE	39.1	Catalase	Catalase hydroperoxidase III	593	2609, 2611, 3898, 3899, 4612
katG	89.1	Catalase	Catalase hydrogen peroxidase I	14983	2611, 3036, 3898, 4457, 4592, 4456
kba	71.8	Ketose-bis-phosphate aldolase	Ketose-bis-phosphate aldolase, tagatose-bis-phosphate aldolase; part of *aga* cluster for K$^+$ transport	592	2490, 3649
kbl	81.7	Ketobutyrate ligase	2-Amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29)	18205	140, 3620
kch	28.2	Potassium (K$^+$) channel	Homology to potassium channel proteins	35309	2026, 2935
kdgK	79.3	Ketodeoxygluconate	Ketodeoxygluconokinase (EC 2.7.1.45)	591	3515
kdgR	41.1	Ketodeoxygluconate	Regulator of *kdgK*, *kdgT*, and *eda*	590	2047, 3515
kdgT	88.4	Ketodeoxygluconate	Ketodeoxygluconate transport system, structural gene	589	2047, 2747, 3465, 3515
kdpA	15.7	Potassium dependence	*kac*; K$^+$-translocating ATPase Kdp subunit	588	1225, 4266, 74
kdpB	15.6	Potassium dependence	*kac*; high-affinity potassium transport	587	4266, 74
kdpC	15.6	Potassium dependence	*kac*; high-affinity potassium transport	586	4266, 74
kdpD	15.5	Potassium dependence	*kac*; sensor kinase for K$^+$-*kdp* system	585	153, 3117, 3118, 3472, 3555, 4266, 4597, 4633
kdpE	15.5	Potassium dependence	Transcriptional effector of *kdp* operon	31571	153, 3117, 3118, 3472, 4266, 4597, 4633
kdpF	15.7	Potassium dependence	Inner membrane protein for K$^+$ transport	35751	1735, 74
kdsA	27.3	KDO synthesis	3-Deoxy-D-*manno*-octulosonic acid 8-P synthetase	17671	4763, 4764
kdsB	20.9	KDO synthesis	CMP-3-deoxy-D-*manno*-octulosonate cytidylyltransferase	18202	1449, 1450, 3420
kdtA	82.0	KDO transfer (to lipid A)	*waaA*; 3-deoxy-D-*manno*-octulosonate-lipid A transferase (EC 2.4.99.–)	33819	293, 3921, 779, 780
kdtB	82.1	KDO transfer (to lipid A)	CMP-deoxy-D-*manno*-octulosonate-lipid A transferase (EC 2.4.99.–)	33900	3726, 4128
kefB	74.9	K efflux	*trkB*; NEM-activatable K$^+$/H$^+$ antiporter	83	1226, 209
kefC	1.0	K efflux	*trkC*; NEM-activatable K$^+$/H$^+$ antiporter	82	1226, 209, 2946, 3050
kgtP	58.7	Ketoglutarate	*witA*; 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]
kicA	21.0	Kill cell	*mukE*; killing protein	31751	1223, 4844, 4845
kicB	21.0	Kill cell	*mukF*; Suppressor of killing protein	31748	1223, 4845
ksgA	1.1	Kasugamycin	*S*-Adenosylmethionine-6-*N*′,*N*′-adenosyl (rRNA) dimethyltransferase	583	105, 106, 107, 1711, 380, 4542
ksgB	37.7	Kasugamycin	High-level resistance to kasugamycin	582	1042, 1286, 1529, 4144
ksgC	12.0	Kasugamycin	Resistance to kasugamycin; affects ribosomal protein S2	581	4896
ksgD	30.9	Kasugamycin	Resistance to kasugamycin	580	1286
lacA	7.8	Lactose	Thiogalactoside acetyltransferase; (EC 2.3.1.18)	579	1696, 1805
lacI	7.9	Lactose	Repressor protein of *lac* operon	578	1203, 1461, 1811, 2202, 2417, 2492, 2501, 2625, 2626, 2767, 3042, 3217, 331, 335, 3798, 4121, 620
lacY	7.8	Lactose	Galactoside permease (M protein)	577	1127, 1685, 1805, 2033, 3042, 3293, 346, 404, 4121, 4647, 549
lacZ	7.8	Lactose	β-D-Galactosidase (EC 3.2.1.23)	576	1597, 1805, 2033, 2101, 2417, 2781, 4021, 4630
lamB	91.5	Lambda	Phage lambda receptor protein; maltose high-affinity uptake system; in *malB* cluster	575	1152, 1695, 1778, 1779, 1780, 3941, 4394, 488, 778, 814, 987
lar	30.4	Ral inverse	*rac* locus; restriction alleviation	37053	2238, 4439
ldcC	4.5	Lysine decarboxylase	Lysine decarboxylase	49257	2217, 4836, 4839
ldhA	31.0	Lactate dehydrogenase	*hslF*, *hslI*, *htpH*; lactate dehydrogenase	37446	2800, 749, 561a
lepA	58.3	Leader peptidase	GTP binding membrane protein, function unknown; *lep*	18199	1039, 2754, 2755, 4062
lepB	58.3	Leader peptidase	Signal peptidase I (for nonlipoproteins)	573	2754, 4769, 906, 4062
leuA	1.8	Leucine (biosynthesis)	α-Isopropylmalate synthase (EC 4.1.3.12)	572	1399, 4711, 963, 245
leuB	1.7	Leucine (biosynthesis)	β-Isopropylmalate dehydrogenase (EC 1.1.1.85)	571	963
leuC	1.7	Leucine (biosynthesis)	α-Isopropylmalate isomerase subunit	570	963
leuD	1.7	Leucine (biosynthesis)	α-Isopropylmalate isomerase subunit	569	963
leuJ	13.7	Leucine (biosynthesis)	*flr*; regulation of *leu* and *ilv* operons	18196	2028
leuO	1.8	Leucine (biosynthesis)	Affects expression of small regulatory Dsr-RNA, translational regulation of *rpoS*, relieves *bgl* silencing	35918	2249, 4025, 4506
leuP	99.2	Leucine	*leuV*β tandemly triplicate *leuVPQ*, duplicate with *leuT*; leucine tRNA$_1$	38293	2313
leuQ	99.2	Leucine	*leuV*γ tandemly triplicate, and duplicate with *leuT*; leucine tRNA$_1$	38296	2313
leuR	79.3	Leucine	Regulates level of leucyl-tRNA synthetase	567	4392
leuS	14.5	Leucine	Leucyl-tRNA synthetase (EC 6.1.1.4)	566	1658, 4157
leuT	85.8	Leucine	Leucine tRNA$_1$, duplicate with *leuVPQ*	565	1832, 2313, 926
leuU	71.6	Leucine	Leucine *tRNA*$_2$	564	2313, 4631
leuV	99.2	Leucine	*leuV*α leucine tRNA$_1$, tandemly triplicate *leuV*PQ, duplicate with *leuT*	563	1095, 1285, 2313
leuW	15.0	Leucine	*feeB*; leucine tRNA$_3$	562	2313, 3102, 3103, 3454, 460, 703
leuX	96.9	Leucine	*Su-6*, *supP*; leucine tRNA$_5$ (amber [UAG] suppressor)	561	1122a, 135, 2313, 3210, 4407, 4409, 4899
leuY	9.5	Leucine	Regulates level of leucyl-tRNA synthetase	560	2420
leuZ	42.9	Leucine	Leucine tRNA$_4$	17668	2313
lev	9.0	Levallorphan	Resistance to levallorphan	559	916
lexA	91.7	Lambda excision	*exrA*, *recA*, *spr*, *umuA*; global regulator for SOS regulon (represses ca. 20 genes)	558	1654, 1755, 1802, 2575, 2576, 2765, 2928, 4017, 479, 496, 497
lgt	63.9	(Pro)lipoprotein glyceryl transferase	*umpA*; phosphatidylglycerol:prolipoprotein diacylglycerol transferase	33350	1352, 3561, 3562, 4743
lhr	37.2	Long helicase related protein	Probable ATP-dependent helicase	35720	3656
ligA	54.5	Ligase	*lig*, *dnaL*, *pdeC*; DNA ligase	557	1398, 1932, 1959
ligT	3.5	Ligase tRNA	Name temporary, not published; 2′-5′ RNA ligase	50132	134
linB	29.3	Lincomycin	High-level lincomycin resistance	556	120
lipA	14.2	Lipoate	Lipoate biosynthesis	31534	1672, 1673, 3632, 4563
lipB	14.2	Lipoate	Lipoyl-protein ligase	555	3014, 3632, 4157, 4563, 681
lit	25.8	Late induced T4	Locus within defective prophage e14; 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]
livF	77.4	Leucine, isoleucine, valine (transport)	Membrane protein	33713	14
livG	77.4	Leucine, isoleucine, valine (transport)	*hrbB*, *hrbC*, *hrbD*; high-affinity branched-chain amino acid transport system; membrane component	553	14, 1657, 3141, 3323, 4850
livH	77.5	Leucine, isoleucine, valine (transport)	*hrbB*, *hrbC*, *hrbD*; high-affinity branched-chain amino acid transport system; membrane component	552	14, 3142, 3323, 4850, 98
livJ	77.5	Leucine, isoleucine, valine (transport)	*hrbB*, *hrbC*, *hrbD*; binding protein, high-affinity branched-chain amino acid transport system	551	14, 2406, 3317, 3323, 4418, 4850, 98
livK	77.5	Leucine, isoleucine, valine (transport)	*hrbB*, *hrbC*, *hrbD*; leucine-specific periplasmic binding protein, high-affinity branched-chain amino acid transport	550	14, 2406, 3141, 3142, 332, 3323, 4418, 4850, 98
livM	77.4	Leucine, isoleucine, valine (transport)	High-affinity transport system	18190	14, 3141, 3142
lldD	81.4	L-Lactose dehydrogenase	*lct*, *lctD*; L-lactate dehydrogenase, FMN dependent (EC 1.1.1.27); Arc regulon	574	1066, 1951, 2556, 4012
lldP	81.4	L-Lactose dehydrogenase	*lctP*; L-lactate permease	35161	1066, 1951, 2556, 4012, 4128
lldR	81.4	L-Lactose dehydrogenase	*lctR*; regulatory gene	35164	1066, 2556, 4012, 4128
lolA	20.2	Localization OM lipoproteins	Periplasmic protein responsible for sorting and transporting lipoproteins to outer membrane	53417	2815, 2816
lon	9.9	Long form	*capR*, *deg*, *dir*, *muc*; DNA-binding, ATP-dependent protease LA; *lon* mutants form long cells	547	1063, 1297, 1324, 1392, 20, 2768, 2769, 2823, 2992, 3929, 4924, 4925, 682, 733, 752, 4396
lpcA	5.4	Lipopolysaccharide core	*gmhA*; phosphoheptose isomerase, T-phage resistance	546	1698, 4562, 517
lpcB	68.0	Lipopolysaccharide core	*mrc*, *pon*; T-phage resistance, novobiocin sensitivity	545	10241
lpd	2.8	Lipoamide dehydrogenase	*dhl*; lipoamide dehydrogenase (NADH) (EC 1.8.1.4)	544	1553, 1556, 1558, 2415, 2416, 4199, 4150, 4203, 655, 866
lplA	99.6	Lipoprotein ligase	*slr*; lipoate-protein ligase A; selenolipoate resistant	33052	3013, 3014, 3633
lpp	37.8	Lipoprotein	*mlpA*; murein lipoprotein structural gene	543	1420, 1529, 1671, 3109, 3110, 4792, 4819, 487, 4971, 3748a
lpxA	4.4	Lipid A expression	UDP-*N*-acetylglucosamine acetyltransferase	17665	1346, 4747, 804, 876, 877
lpxB	4.4	Lipid A expression	*pgsB*; lipid A disaccharide synthase	404	4424, 804, 876, 877
lpxC	2.3	Lipid A expression	*asmA*; *envA*; essential gene; cell envelope and cell separation	815	2071, 2273, 260, 2675, 2676, 2911, 3091, 3921, 4139, 4275, 4903
lpxD	4.3	Lipid A expression	*fir*, *firA*, *hlpA*, *omsA*, *skp*, *ssc*; UDP-3-O-(R-3-hydroxymyristoyl)-glucosamine *N*-acyltransferase	775	1, 1040, 1773, 1775, 2193, 3761, 3921, 804, 1702
lpxK	20.9	Lipid A expression	Lipid A 4′ kinase	51784	1375
lrb	7.3	L-Ribose (utilization)	Affects NADPH-linked L-ribose reductase activity	36791	4459
lrhA	51.8	LysR homolog	*genR*; regulatory protein, similar to LysR family	32685	421
lrp	20.1	Leucine regulatory protein	*mbf*, *ihb*, *livR*, *lrs*, *lss*, *lstR*, *oppI*, *rblA*; 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
lspA	0.5	Lipoprotein signal peptidase	*dapB*, *ileS*; prolipoprotein signal peptidase (EC 3.4.99.–)	11326	1913, 2104, 2945, 3640, 4422, 466, 4820, 4829, 4830, 4905
lysA	64.1	Lysine	Diaminopimelate decarboxylase (EC 4.1.1.20)	540	4247, 4249, 716
lysC	91.2	Lysine	*apk*; aspartokinase III (EC 1.1.1.3)	539	467, 652, 653
lysP	48.4	Lysine	*cadR*; lysine permease	942	3143, 3485, 4198, 4325
lysQ	16.8	Lysine	Lysine tRNA (multiple loci, see *lysT*)	51037	2313
lysR	64.2	Lysine	LysR, prototype of family of global transcriptional regulators	18187	4248
lysS	65.3	Lysine	*asuD herC*; lysyl tRNA synthetase, constitutive	17662	1122a, 1151, 1351, 1383, 1771, 1946, 2173, 686, 768
lysT	16.8	Lysine	*Su*β, *lysT*α, *supG*, *supL* (ochre suppression); lysine tRNA (multiple loci, *lysQTVWYZ*)	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]
lysU	93.8	Lysine	Lysyl tRNA synthetase, inducible	16693	1394, 1946, 1948, 2508, 4541, 686, 268
lysV	54.3	Lysine	*supN*; lysine tRNA (multiple loci, see *lysT*)	132	1122a, 2313, 3238, 4509, 539
lysW	16.8	Lysine	*lysT*β; lysine tRNA (multiple loci, see *lysT*)	28352	2313
lysX	63.3	Lysine	Lysine excretion	536	2007, 2008
lysY	16.8	Lysine	*lysT*γ; lysine tRNA (multiple loci, see *lysT*)	51031	2313
lysZ	16.8	Lysine	lysine tRNA (multiple loci, see *lysT*)	51034	2313
lytA	60.6	Lytic	Tolerance to β-lactams; autolysis	18184	1649, 1651, 2380, 4035
lytB	0.6	Lytic	Penicillin tolerance and stringent response effects	34696	1575, 1651, 2380, 3506, 466
lyx	80.7	Lyxose	Novel pathway for utilization of lyxose via xylulose through rhamnose and pentose pathways; xylulose kinase	36908	2437, 3843
maa	10.3	Maltose acetylase	*mac*; maltose transacetylase	36808	477
mac	26.5	Macrolide	Macrolide resistance, erythromycin resistance; see also *maa*	535	4143
mae	33.5	Malic enzyme	May be *sfcA*; malic enzyme, NAD linked (EC 1.1.1.38)	36710	2719
mafA	0.9	Maintenance of F	Maintenance of F-like plasmids	534	3249, 3313, 4625–4628
mafB	1.9	Maintenance of F	Maintenance of F-like plasmids	533	4625
malA	76.4	Maltose	*malQPT* cluster	23561	1781
malB	91.5	Maltose	*malG-M* cluster	18924	
malE	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
malF	91.4	Maltose	Maltose transport complex, inner membrane-spanning subunit	531	1128, 1320, 2850, 3798
malG	91.4	Maltose	Maltose/maltodextrin transport complex, inner membrane-spanning subunit	530	1224, 1295, 3798, 943
malI	36.6	Maltose	Regulatory gene whose product has homology to repressors LacI, GalR, CytR	18181	1129, 3642
malK	91.5	Maltose	*malB*; maltose transport complex, ATP-binding subunit	529	1224, 1431, 1701, 271, 272, 274, 3265, 3798, 4394, 814
malM	91.5	Maltose	*molA*; periplasmic protein	18178	1432
malP	76.5	Maltose	*blu*; maltodextrin phosphorylase (EC 2.4.1.1)	528	1778, 1779, 1781, 3340, 3588, 3706, 3940, 990
malQ	76.4	Maltose	Amylomaltase (EC 2.4.1.25)	527	1778, 1779, 1781, 3551, 3940
malS	80.5	Maltose	α-Amylase, periplasmic, MalT dependent	17659	1306, 3922
malT	76.5	Maltose	Lambda sensitivity; positive regulator for *mal* regulon	526	1224, 1778, 1779, 1780, 1781, 3587, 3588, 3669, 800, 928, 931, 988, 989, 990
malX	36.6	Maltose	PTS enzyme II homolog; *malI* regulated	32254	3643
malY	36.6	Maltose	Affects induction of maltose system	32257	3643, 4922
malZ	9.1	Maltose	Maltodextrin glucosidase	29868	2651, 3394, 4352
manA	36.4	Mannose	*pmi*; mannosephosphate isomerase (EC 5.3.1.8)	525	2024, 2491, 2932, 2933, 3207, 386
manC	87.6	Mannose	*mni*; D-mannose isomerase	524	4207
manX	41.0	Mannose	*gptB*, *mpt*, *ptsL*, *ptsM*, *ptsX*; mannose phosphotransferase system, protein II-A (III)	17656	1169, 1171, 3344, 4745
manY	41.0	Mannose	*pel*, *ptsM*, *ptsP*	18175	1169, 1171, 1844, 3344, 4745
manZ	41.0	Mannose	*gptB*, *mpt*, *ptsM*, *ptsX*; mannosephosphotransferase enzyme IIB	346	1844, 3344, 4745, 890
map	4.1		Methionine aminopeptidase (EC 3.4.11.18)	30569	294, 676
marA	34.9	Multiple antibiotic resistance	*soxQ*, *cfxB*? *nfxC*, *norB*? 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
marB	34.9	Multiple antibiotic resistance	Regulatory gene for *mar*	32217	130, 1448, 3737, 790
marR	34.9	Multiple antibiotic resistance	*cfxB*, *soxQ*; repressor of *mar* operon	30935	130, 1448, 2780, 3737, 4271, 790
mbrB	88.6	Mothball resistant	Resistance to camphor vapors; coupling of cell division and replication, growth rate and partitioning	36929	4468, 4469
mcrA	26.1	Methylcytosine restriction	*rglA*; 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]
mcrB	98.6	Methylcytosine restriction	*rglB*; restriction of DNA at 5-methylcytosine residues	4978	1050, 2350, 3602, 3603, 3604, 3739, 3740, 3741
mcrC	98.6	Methylcytosine restriction	Modifies specificity of McrB restriction	34613	1050, 2350, 3603, 3740
mcrD	98.6	Methylcytosine restriction	Inhibits McrE restriction resistance to DMP840, adriamycin, etoposide; possibly modulates Topo IV activity	34616	3603, 3740
mdaB	68.3	Modulator of drug activity		53544	688
mdh	72.9	MDH	Malate dehydrogenase (EC 1.1.1.37)	523	1227, 2831, 4298, 4598
mdoA	23.9	Membrane-derived oligosaccharide	*modGH* operon	4970	
mdoB	99.0	Membrane-derived oligosaccharide	Phosphoglycerol transferase I activity	18169	1234, 1974, 569
mdoG	23.9	Membrane-derived oligosaccharide	*mdoA*; periplasmic oligosaccharide synthesis	31849	1235, 2387, 2388, 2636, 411
mdoH	23.9	Membrane-derived oligosaccharide	*mdoA*; membrane glycosyltransferase	31852	1235, 2387, 2388, 2636, 411
meb	78.7	*malE* bypass	Suppressor of *malE secB*-defective transport of *mal*-binding protein	28194	1293
melA	93.5	Melibiose	*mel-7*; α-galactosidase (EC 3.2.1.22)	522	1624, 2185, 2501, 2548, 4031, 4685
melB	93.6	Melibiose	*mel-4*; thiomethylgalactoside permease II	521	1624, 2185, 2501, 252, 4878
melR	93.5	Melibiose	Regulatory	18166	2501, 462, 4685, 659
menA	88.7	Menaquinone (vitamin K_2)	Dimethylmenaquinone formation in vitamin K_2 biosynthesis	520	3465, E
menB	51.2	Menaquinone	1,4-Dihydroxy-2-naphthoate synthase	519	1548, 1550, 3997, 4007, 4011
menC	51.2	Menaquinone	*o*-Succinylbenzoate synthase II	518	1548, 1550, 310, 4007, 4011
menD	51.2	Menaquinone	*o*-Succinylbenzoate synthase I (EC 4.1.3.-)	517	1548, 1550, 3338, 3486, 4007, 4011
menE	51.1	Menaquinone	*o*-Succinylbenzoate-CoA synthase	17653	2384, 3998, 4011
menF	51.2	Menaquinone	Menaquinone pathway-specific isochorismate synthase	35955	3040, 310, 936
mepA	52.7	Murein peptidase	Murein DD-endopeptidase	17650	1890, 2184
mesJ	4.6		Cell cycle protein	49262	3423a
metA	90.8	Methionine	Homoserine transsuccinylase (EC 2.3.1.46)	516	1094, 2919, 2920, 358, 35
metB	88.9	Methionine	met_1, *met-1*; cystathionine γ-synthase (EC 4.2.99.9)	515	1093, 1508, 1509, 2242, 2347, 2547, 3802, 4917
metC	67.9	Methionine	Cystathionine β-lyase; (EC 4.4.1.8)	514	284, 2918
metD	4.8	Methionine	Methionine sulfoximine sensitivity, D-methionine transport	513	2078
metE	86.5	Methionine	Tetrahydropteroyltriglutamate methyltransferase (EC 2.1.1.14)	512	3284, 58, 66, 926
metF	89.0	Methionine	5,10-Methylenetetrahydrofolate reductase (EC 1.1.1.68)	511	1509, 2242, 2347, 3802, 3803, 4454, 4917
metG	47.3	Methionine	Methionyl-tRNA synthetase; ethionine effects	510	125, 929, 930
metH	91.0	Methionine	B_{12}-dependent homocysteine-N^5-methyltetrahydrofolate transmethylase	509	218, 2756, 3283, 3284
metJ	88.9	Methionine	Methionine sulfoximine plus methylmethionine sensitivity; repressor	508	1509, 2078, 2242, 2336, 2347, 2547, 3802, 4109, 4917
metK	66.5	Methionine	Methionine adenosyltransferase (EC 2.5.1.6); ethionine sensitivity	507	1510, 1598, 2336, 2766, 3878, 472
metL	89.0	Methionine	*metM*; aspartokinase II-homoserine dehydrogenase II	506	1093, 1508, 1509, 2242, 2347, 3802, 3877, 4916, 4917, 789, 953
metR	86.4	Methionine	Positive regulatory gene for *metE* and *metH* and autogenous regulation	18163	2825, 4515, 4703, 601, 926, 4515
metT	15.0	Methionine	*metT*α; duplicate gene; methionine $tRNA_m$; see *metU*	505	1285, 1915, 2313, 3102, 3103, 3454
metU	15.0	Methionine	*metT*β; duplicate gene; methionine $tRNA_m$	28349	2313
metV	63.5	Methionine	*metZ*β; triplicate gene; initiator methionine $tRNA_{f1}$ (*metVWZ*)	35659	2198, 2199, 2313
metW	63.5	Methionine	Triplicate gene; methionine $tRNA_{f1}$	35656	2313, 2198
metY	71.5	Methionine	Methionine $tRNA_{f2}$	504	1487, 1927, 1928, 2197, 2313
metZ	63.5	Methionine	*metZ*α; triplicate gene; initiator methionine $tRNA_{f1}$; *metVWZ*	503	2198, 2199, 2313, 3085
mfd	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[c]
mglA	48.2	Methyl-galactoside	*mglP*; PMG; methyl-galactoside transport and galactose taxis; cytoplasmic membrane protein	502	1158, 1645, 1783, 2925, 3156, 3302, 3751, 3932, 428, 429, 758
mglB	48.2	Methyl-galactoside	PMG; galactose-binding protein; receptor for galactose taxis	501	1158, 1645, 1783, 2925, 3156, 3302, 3751, 3932, 3938, 3954, 758
mglC	48.2	Methyl-galactoside	*mglP*; PMG; methyl-galactoside transport and galactose taxis	500	1158, 1645, 1783, 2925, 3156, 3302, 3751, 758
mglR	16.9	Methyl-galactoside	R-MG; regulatory gene	498	1354
mgsA	22.1[b]	Methylglyoxal synthase	Methylglyoxal synthase (not shown on map)	57077	4444a
mgtA	96.2	Magnesium transport	*corB*; cobalt resistance, magnesium transport	497	3353, 569
mhpA	7.9	*m*-Hydroxyphenylpropionic acid	3-(3-Hydroxyphenyl)propionate 2-hydroxylase; utilizes MHP	29024	1229, 570, 571
mhpB	8.0	*m*-Hydroxyphenylpropionic acid	3-(2,3-Dihydroxyphenyl)propionate dioxygenase; utilizes MHP	29027	1229, 4147, 570, 571
mhpC	8.0	*m*-Hydroxyphenylpropionic acid	Dihydroxyphenylpropionate-ring-fission-product hydrolase; utilizes MHP	29030	1229, 570, 571
mhpD	8.0	*m*-Hydroxyphenylpropionic acid	*mhpS*; 2-keto-4-pentenoate hydratase; utilizes MHP	29033	1229, 570, 571
mhpE	8.0	*m*-Hydroxyphenylpropionic acid	4-Hydroxy-2-oxovalerate aldolase; utilizes MHP	51197	1229
mhpF	8.0	*m*-Hydroxyphenylpropionic acid	Acetaldehyde dehydrogenase, acylating; utilizes MHP	53814	1228, 1229
mhpR	7.9	*m*-Hydroxyphenylpropionic acid	Regulatory gene for MHP utilization	29021	1228, 1229, 570, 571
miaA	94.8	Me-isopentyl-adenine	*trpX*; 2-methylthio-N^6-isopentyladenosine tRNA hypermodification	18160	1345, 4487, 4489, 4490, 563, 605, 825, 826
miaD	99.6	Me-isopentyl-adenine	Suppresses leaky *miaA*(Oc) mutation	35254	826
micF	49.8	mRNA interfering cRNA	*stc*; regulatory antisense RNA affecting *ompF*; member of *soxRS* regulon	18157	2955, 2982, 3008, 3608, 3918, 4309, 4520, 93, 4335
minB	26.4	Minicell	*min* operon; formation of minicells containing no DNA; positioning division septum	495	3895, 954, 971a
minC	26.4	Minicell	Inhibition of FtsZ ring at division site	31329	340, 3614, 970, 971, 971a
minD	26.4	Minicell	Affects cell division and growth; membrane ATPase that activates MinC	31326	2386, 340, 3614, 948, 969, 970, 971a
minE	26.4	Minicell	Reverses inhibition by MinC of FtsZ ring	31317	3614, 948, 970, 993, 971a
mioC	84.6	Minimal origin	Initiation of replication; transcription of 16-kDa protein proceeds through *oriC*	18154	2603, 2606, 3245, 408
mltA	63.5	Membrane-bound lytic transglycosylase	*waaN*; lipoprotein lytic transglycosylase; membrane-bound murein hydrolase, affecting sacculus maturation	53524	1789, 2618, 4517
mltB	60.8	Membrane-bound lytic transglycosylase	*slt*; murein hydrolase lipoprotein; Slt35, soluble lytic transglycosylase	41040	1124, 1154, 1789, 1048a
mltC	66.9	Membrane-bound lytic transglycosylase	Peptidoglycan hydrolase activity, lytic transglycosylase family	54700	1049
mltD	5.0	Membrane-bound lytic transglycosylase	*dniR* (dissimilatory nitrite reductase); reduced amounts of hexaheme nitrite reductase; membrane transglycosylase	1575	2089
mmrA	85.4	Minimal medium recovery	Same as *rhlB*? RNA helicase motif	18151	2099, 3993, 926, 4508
mms	69.2	Macromolecular synthesis	Complex operon, macromolecular synthesis	36863	3154
mng	40.0	Manganese	Manganese resistance	494	4063
moaA	17.6	Molybdenate	*bisA*, *chlA*, *narA*; MPT synthesis; chlorate resistance protein A	922	1003, 1245, 1434, 18, 187, 2030, 207, 2402, 3534, 3986, 4570, 72
moaB	17.6	Molybdenate	MPT synthesis; chlorate resistance protein B	31222	3986
moaC	17.6	Molybdenate	MPT synthesis; chlorate resistance protein C	31225	3986
moaD	17.6	Molybdenate	*chlM*; MPT synthesis; chlorate resistance	18475	2030, 3986, 4373
moaE	17.6	Molybdenate	MPT synthesis; chlorate resistance	31228	3986
mobA	87.1	Molybdenum	*chlB*, *narB*; MPT guanine dinucleotide synthesis; chlorate resistance	921	1003, 1245, 1434, 18, 187, 1922, 2402, 3342, 3343, 3465, 3534, 3749, 3986, 654
mobB	87.0	Molybdenum	Molybdenum cofactor biosynthesis, putative nucleotide binding site	43961	1922, 3343
moc	31.9	Modification of CCA	Modification of CCA at 3′ end of tRNA	36923	3237
modA	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[c]
modB	17.1	Molybdenum	*chlJ*; molybdate uptake; chlorate resistance; membrane-spanning ABC protein	18478	2025, 2060, 2820, 2973, 3630, 3986, 4634
modC	17.2	Molybdenum	*chlD*, *narD*; molybdate uptake; chlorate resistance	920	1003, 1245, 1434, 18, 187, 2025, 2060, 2820, 2973, 3630, 3986, 4634
modE	17.1	Molybdenum	*chlD*, *modR*, *narD*; molybdate uptake	37366	1539, 2855, 4634
modF	17.1	Molybdenum	*chlD*, *narD*, *phrA*; molybdate uptake	37369	1539, 4634
moeA	18.6	Molybdenum	*bisB*, *chlE*; MPT synthesis; chlorate resistance	919	1003, 1245, 1434, 1664, 18, 187, 2030, 2402, 3208, 3378, 3534, 3986, 4219
moeB	18.6	Molybdenum	*chlN*; MPT synthesis; chlorate resistance	18472	2030, 3208, 3986, 4373
mog	0.2	Molybdenum	*bisD*, *chlG*; unknown function; chlorate resistance	917	1003, 1245, 1434, 18, 187, 2003, 2004, 2060, 3986, 4219
molR	47.3	Molybdate	Unknown function, probably related to molybdate transport	32567	2464, 3736
motA	42.6	Motility	*flaJ*; flagellar-regulon member; flagellar rotation	491	374, 375, 4064, 4101, 985
motB	42.5	Motility	*flaJ*; flagellar-regulon member; flagellar rotation	490	373, 4064, 4101, 4183
mpl	96.0	*meso*-Diaminopimelate ligase	UDP-*N*-acetylmuramate:L-alanyl-γ-D-glutamyl-*meso*-diaminopimelate ligase; recycles cell wall peptidoglycan (EC 6.3.2.13)	46610	2894
mppA	30.0	Murein peptide permease	Murein tripeptide (L-Ala-γ-D-Glut-*m*-DAP) permease	53908	3352
mprA	60.5	Microcin peptide regulation	*emrR*; controls level of microcin synthesis; negative regulation of EmrAB	33255	1006, 1007, 2622
mraA	2.0	Murein cluster a	D-Alanine carboxypeptidase	489	
mraY	2.1	Murein cluster a	UDP-*N*-acetylmuramoyl-pentapeptide:undecaprenyl-PO_4 phosphatase (EC 2.7.8.13)	30466	1894, 1895
mrcA	75.9	Murein cluster c	*ponA*; penicillin-binding protein 1A	484	1930, 4337, 519
mrcB	3.6	Murein cluster c	*pbpF*, *ponB*; peptidoglycan synthetase; penicillin-binding protein 1Bs	483	2166, 3096, 3097, 3601, 3714, 4307, 4337, 4346, 4957, 519
mrdA	14.3	Murein cluster d	*pbpA*; penicillin-binding protein PBP 2, mecillinam resistance	18148	156, 157, 279, 4157, 4232, 4233, 4343, 4587, 545
mrdB	14.3	Murein cluster d	*rodA*; affects cell shape; mecillinam sensitivity	18145	156, 157, 279, 2818, 4232, 4233
mreB	73.2	Murein cluster e; mecillinam resistance	*envB*, *mon*, *rodY*; mecillinam resistance; cell shape, affects division versus elongation	31343	1062, 1968, 2624, 434, 4616, 4617, 4619, 4716
mreC	73.2	Mecillinam resistance	Cell division and growth; mecillinam resistance; rod shape-determining protein	31348	4617, 4618
mreD	73.2	Mecillinam resistance	Mecillinam resistance; rod shape-determining protein	31351	4617, 4618
mrp	47.2	Methionine-related protein	Putative ATPase; in *Salmonella*, homolog is part of alternative pyrimidine pathway to Thi (*apbC*)	32572	3409, 930
mrr	98.8	Methyl-purine restriction	Restriction of methylated adenine	18139	1700, 3603
msbA	20.8	Multicopy suppressor of *htrB*	ABC transporter homology; biogenesis of outer membrane	31743	2139, 3474
msbB	41.8	Multicopy suppressor of *htrB*	Role in outer membrane structure or function	32359	2138
mscL	74.1	Mechanosensitive channel	Cytoplasmic membrane channel protein, opens large pore in response to mechanical stress	35417	400, 401, 4267, 4268, 4269
msrA	95.7	Methionine sulfoxide reductase	*pmsR*; methionine sulfoxide reductase	34400	3018, 3585, 3586, 525
msyB	24.0	Multicopy suppressor of secY	In multicopy restores growth and protein export functions of *secY* and *secA* mutants	34718	4504
mtgA	72.1	Monofunctional transglycolase	Monofunctional biosynthetic peptidoglycan transglycosylase	54732	4159
mtlA	81.3	Mannitol	*mtlC* (promoter/operator); mannitol-specific enzyme II of PTS	481	2018, 2459, 2468, 965
mtlD	81.3	Mannitol	Mannitol-1-phosphate dehydrogenase (EC 1.1.1.17)	479	2018, 2347, 965
mtlR	81.3	Mannitol	Mannitol repressor	36774	1236
mtr	71.2	Methyltryptophan	High-affinity Trp permease; TyR regulon	478	1689, 1764, 1688, 3864
mukB	21.0	Mukaku (anucleate)	Required for chromosome partitioning; DNA binding; kinesin-like motor protein?	31516	1188, 1761, 1977, 3183, 1185, 3819, 4589
mul	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]
murA	71.8	Murein	*mrbA*, *murZ*; UDP-*N*-acetylglucosamine enoylpyruvyl transferase (EC 2.5.1.7); phosphomycin resistance	33518	2773, 3548, 4571, 527
murB	89.9	Murein	UDP-*N*-acetylglucosaminyl-3-enolpyruvate reductase (EC 1.1.1.158)	34141	308, 3548, 395
murC	2.2	Murein	L-Alanine adding enzyme	476	1183, 1893, 2021, 2071, 2675, 2676
murD	2.1	Murein	UDP-*N*-acetylmuramoyl-L-alanine:D-glutamate ligase (EC 6.3.2.9)	30450	1894, 2889, 2890, 3533
murE	2.0	Murein	*meso*-Diaminopimelate adding enzyme	475	1183, 2071, 2889, 2923, 4349
murF	2.0	Murein	*mra*; D-alanyl:D-alanine adding enzyme	474	101, 1183, 2071, 2889, 3368
murG	2.1	Murein	UDP-NAc-glucosamine: NAc-muramyl-(pentapeptide) pyrophosphoryl-undecaprenol NAc-glucosamine transferase	473	1893, 2071, 2889, 2895, 3820
murH	99.3	Murein	Terminal stage in peptidoglycan synthesis, incorporating disaccharide peptide units into wall	18136	3204, 900
murI	89.7	Murein	*mbrC*, *dga*, *glr*; glutamate racemase (EC 5.1.1.3); D-glutamate synthesis, essential for peptidoglycan	29401	1076, 1077, 1078, 212, 2584, 4900, 523
mutG	43.7	Mutator	Mutation causes high C-to-T mutation in second C of CCAGG; near but distinct from *vsr*; provisionally termed *mutG*	28933	3766
mutH	64.0	Mutator	*mutR*, *prv*; methyl-directed mismatch repair; see also *dnaX*	471	1222, 1484, 1485, 1706, 4052, 4488, 856
mutL	94.7	Mutator	Methyl-directed mismatch repair	470	1088, 1222, 139, 1706, 4052, 4487, 4489, 4490, 856
mutM	82.1	Mutator	*fpg*; repair; GC to TA; formamidopyrimidine-DNA glycosylase	18133	1221, 1489, 1706, 2434, 3717, 4052, 4128, 416, 417, 568, 599, 805, 856
mutS	61.5	Mutator	*ant*? *fdv* (formate dehydrogenase 2?); methyl-directed mismatch repair	469	1222, 1706, 2587, 3615, 3853, 4052, 4488, 4802, 856
mutT	2.4	Mutator	AT to GC transversions	468	1288, 1706, 2729, 338, 39, 4052, 856
mutY	66.8	Mutator	*micA*; GC to TA transversions; adenine glycosylase, G-A repair	18130	1706, 2922, 3172, 3576, 4052, 856, 4476, 4477
nac	44.4	Nitrogen assimilation control	Regulatory gene, binding *ntrC*	50182	3073
nadA	16.8	Nicotinamide adenine dinucleotide	Quinolinate synthetase, A protein	467	1257, 2819, 4246
nadB	58.4	Nicotinamide adenine dinucleotide	Quinolinate synthetase, B protein	466	1257, 3015, 4379, 3963
nadC	2.5	Nicotinamide adenine dinucleotide	*nic*; quinolinate phosphoribosyl transferase	465	1553, 1556, 1558, 2415, 2416, 3689
nadE	39.2	Nicotinamide adenine dinucleotide	*efg*, *ntrL*; NAD synthetase, ammonia dependent	28576	4752, 70
nagA	15.1	*N*-Acetylglucosamine	*N*-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	464	2491, 3402, 3454–3456, 4599, 4726
nagB	15.1	*N*-Acetylglucosamine	*glmD*; glucosamine-6-phosphate deaminase (EC 5.3.1.10)	463	3402, 3454, 3455, 3456, 3464, 3709, 4601, 4726
nagC	15.1	*N*-Acetylglucosamine	*nagR*; transcriptional regulator of *nag* operon	31479	3402, 3455, 3456, 3457, 4593, 3458
nagD	15.1	*N*-Acetylglucosamine	Function unknown, expressed as part of *nag* operon	36240	3455
nagE	15.2	*N*-Acetylglucosamine	*pstN*; *N*-acetylglucosamine-specific enzyme II of phosphotransferase system	462	2048, 2491, 3401, 3402, 3454, 3709, 4599, 4726, 4600
nalB	60.2	Nalidixic acid	Sensitivity to nalidixic acid (NAL)	460	1626
nalD	89.2	Nalidixic acid	NAL sensitivity; NAL and glycerol penetration	18124	1827
nanA	72.6	*N*-Acetylneuraminate	*N*-Acetylneuraminate lyase (aldolase) (EC 4.1.3.3)	17647	2782, 3270, 4585
nanT	72.6	*N*-Acetylneuraminate	Sialic acid transport	18121	2782, 4585
napA	49.5	NitrAte reductase, periplasmic	Nitrate reductase homolog	36550	1537, 739, 740
napB	49.5	NitrAte reductase, periplasmic	Cytochrome *c* homolog	36560	1537, 739, 740
napC	49.5	NitrAte reductase, periplasmic	Cytochrome *c* homolog	36566	1537, 739, 740
napD	49.6	NitrAte reductase, periplasmic	Unknown function, *nap* operon	36547	1537, 739, 740

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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]
napF	49.6	NitrAte reductase, periplasmic	Ferredoxin homolog	36544	1537, 739, 740
napG	49.5	NitrAte reductase, periplasmic	Ferredoxin homolog	36553	1537, 739, 740
napH	49.5	Nitrate reductase, periplasmic	Ferredoxin homolog	36556	1537, 739, 740
narG	27.6	Nitrate reductase, nitrate regulation	*chlC*, *narC*; nitrate reductase α-subunit (EC 1.7.99.4)	459	1118, 1595, 240, 2495, 2532, 2533, 2856, 3727, 391, 4125
narH	27.7	Nitrate reductase, nitrate regulation	*chlC*; nitrate reductase β-subunit	18118	1118, 1246, 1433, 240, 2495, 392, 4125
narI	27.7	Nitrate reductase, nitrate regulation	*chlI*; cytochrome b_{NR}, structural gene; γ subunit	458	1595, 2495, 3305, 3727, 4125, 4126, 4219, 425, 735
narJ	27.7	Nitrate reductase, nitrate regulation	Nitrate reductase δ-subunit; chaperone	18115	1092, 2495, 2588, 3343, 392, 4125
narK	27.5	Nitrate reductase, nitrate regulation	Nitrate/nitrite antiporter (probably)	18112	1017, 2495, 391, 4220
narL	27.5	Nitrate reductase, nitrate regulation	*frdR*, *narR*; regulatory protein	18109	1122, 1569, 1954, 2096, 2097, 2495, 4008, 4215, 4220
narP	49.3	Nitrate reductase, nitrate regulation	Regulatory protein	32598	3575, 4217
narQ	55.7	Nitrate reductase, nitrate regulation	Nitrate sensor-transmitter protein, anaerobic respiratory path; function redundant with *narX*	36333	3574, 3575, 3935, 726–728
narU	33.2	Nitrate reductase, nitrate regulation	Nitrate sensor-trasmitter protein, anaerobic respiratory path	52770	423
narV	33.1	Nitrate reductase, nitrate regulation	Cryptic nitrate reductase II, γ-subunit	32136	391, 393
narW	33.1	Nitrate reductase, nitrate regulation	Cryptic nitrate reductase II, δ-subunit	32139	391, 393, 423
narX	27.5	Nitrate reductase, nitrate regulation	*frdR*, *narR*; nitrate sensor-transmitter protein; functional redundance with *narQ*	18106	2096, 2097, 2495, 4215, 4220, 4746, 728
narY	33.1	Nitrate reductase, nitrate regulation	Cryptic NR II, β-subunit	32142	391, 393, 423
narZ	33.1	Nitrate reductase, nitrate regulation	Cryptic NR II, α-subunit	18103	391, 393, 424
ndh	25.1	NADH dehydrogenase	Respiratory NADH dehydrogenase	457	1497, 2888, 4901, 615
ndk	57.0	Nucleoside diphosphate kinase	Nucleoside diphosphate kinase (EC 2.7.4.6)	32926	1615, 1616, 2649, 3985
neaB	75.0	Neamine	Neamine sensitivity	456	630
nei	16.0	Endonuclease VIII	DNA glycosylase/apurinic lyase, deoxyinosine-specific; endonuclease VIII	53314	1656, 2016, 2017, 2875, 3805
nemA	37.2	*N*-Ethylmaleimide	*N*-Ethylmaleimide reductase	52714	2968
nfi	90.5	Endonuclease V	Endonuclease V, specific for single-stranded DNA or duplex DNA with damaged U	45426	1018, 1571, 1572, 4874
nfnA	80.8	Nitrofurantoin	Nitrofurantoin sensitivity	18100	3876
nfnB	13.0	Nitrofurantoin	*nfsI*, *nfsB*; resistance to nitrofurantoin; a nitroreductase	18097	2832, 2917, 3876, 490, 4931, 4932
nfo	48.5	Endonuclease IV	Endonuclease IV; member of *soxRS* regulon	14161	889
nfrA	12.7	N4 (phage) resistant	Outer membrane protein, putative structural receptor for N4 adsorption	31154	2213, 2214
nfrB	12.7	N4 (phage) resistant	Phage N4 susceptibility; membrane protein	31157	2213, 2214
nfrD	54.2	N4 (phage) resistant	Phage N4 susceptibility	36113	2215
nfsA	21.9	Nitrofurazone sensitivity	*mdaA*; nitrofuran reductase I activity B; overexpression results in resistance to cytotoxic drugs	454	688, 2832, 490, 4930
nhaA	0.4	Na$^+$/H$^+$ antiporter	*ant*; Na$^+$/H$^+$ antiporter; stress response to high salinity and pH	15893	1081, 1410, 1440, 1909, 2142, 2143, 3272, 3329, 3330, 3583, 4326, 4393, 4577
nhaB	26.6	Na$^+$/H$^+$ antiporter	Regulator of intracellular pH	30269	2182, 3272, 3329, 3330, 3438, 3439, 4393, 4577
nhaR	0.4	Na$^+$/H$^+$ antiporter	Positive regulator of Na$^+$-dependent transcription of *nhaA*; DNA-binding; LysR family of regulatory proteins	30281	3330, 3583, 641
nikA	77.8	Nickel	*hydC*, *hydD*; affects formate hydrogen-lyase activity, hydrogenase, and hydrogenase-related fumarase	18226	1340, 3139, 4230, 4796, 4797, 4800
nikB	77.9	Nickel	*hydC*, *hydD*; activity as *nikA*	33180	3139, 4796

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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]
nikC	77.9	Nickel	*hydC*, *hydD*; activity as *nikA*	33183	3139, 4796
nikD	77.9	Nickel	*hydC*, *hydD*; activity as *nikA*	33186	3139, 4796
nikE	77.9	Nickel	*hydD*, *lipP*? formate hydrogen-lyase activity	18223	3139, 4796, 4797
nirB	75.3	Nitrite reductase	Nitrite reductase [NAD(P)H] subunit (EC 1.6.6.4)	451	1647, 1973, 1998, 2693, 2694, 3386
nirC	75.3	Nitrite reductase	Membrane protein affecting nitrite reductase [NAD(P)H] activity	452	1647, 3386
nirD	75.3	Nitrite reductase	Nitrite reductase [NAD(P)H] subunit (EC 1.6.6.4)	35425	1647, 3386
nlpA	82.7	New lipoprotein	Lipoprotein in outer membrane vesicles	35704	2022, 3563, 4833, 4906
nlpB	56.0	New lipoprotein	Nonessential lipoprotein in outer membrane vesicles	33030	463
nlpC	38.6	New lipoprotein	Lipoprotein	35802	4792a
nlpD	61.8	New lipoprotein	May function in cell wall formation	33225	1879, 2414
nmpC	12.4	New membrane protein	*phmA*; locus of defective phage *qsr′*; porin, outer membrane, not expressed in K-12 due to IS*5* insertion	447	1751, 389, 390, 809
non	45.7	Nonmucoid	Affects capsule formation	446	3577
npr	72.1	N-regulated protein	*ptsO*; NPr, N-regulated HPr-like protein	43864	3517
nrdA	50.5	Nucleotide reductase	*dnaF*; 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
nrdB	50.6	Nucleotide reductase	*ftsB*; 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
nrdD	96.1	Nucleotide reductase	Ribonucleotide reductase, class III, anaerobic	34589	4284
nrdE	60.3	Nucleotide reductase	Nonessential ribonucleoside-diP reductase 2, subunit α, class I, function unknown	53512	2050, 2051
nrdF	60.3	Nucleotide reductase	Nonessential ribonucleoside-diP reductase 2, subunit β, class I, function unknown	53515	2050, 2051
nrdG	96.1	Nucleotide reductase	NrdD activating enzyme, generating glycyl radical	54766	4283
nrfA	92.4	Nitrite reductase, formate-dependent	*aidC*; formate-dependent nitrite reduction; tetraheme cytochrome c_{552}; *aidC* mutation complemented by *nrfG*	34336	1868, 1921, 3334, 937, 11a, 4602
nrfB	92.4	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; pentaheme cytochrome *c*	34364	1868, 938
nrfC	92.4	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; nonheme FE-S protein, probably transmembrane	34352	1868, 938
nrfD	92.4	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; transmembrane protein similar to QOR	34355	1868, 938
nrfE	92.5	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; membrane protein	34358	1536, 1868, 938
nrfF	92.5	Nitrite reductase, formate-dependent	Formate-dependent nitrite reduction; periplasmic protein; NrfA/B synthesis?	34361	1536, 1868, 938
nrfG	92.5	Nitrite reductase, formate-dependent	*aidC*; function unknown, required for Nrf pathway; *aidC* mutation complemented by *nrfG*	34345	1536, 1868, 3334, 11a, 4602
nth	36.9	Endonuclease III	DNA glycosylase/apyrimidinic (AP) lyase, specific for damaged pyrimidine sites, particularly Thy; endonuclease III	13070	1656, 202, 2434, 3717, 3805, 4701, 888
ntpA	42.0	Nucleoside triphosphatase	dATP-preferring nucleoside tri-P pyrophosphohydrolase	46700	1950, 3254
nuoA	51.8	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32679	1197, 4694, 4918, 616
nuoB	51.8	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32676	1197, 4694, 4918, 616
nuoC	51.7	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32673	1197, 4694, 616
nuoE	51.7	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32667	4694, 616
nuoF	51.7	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32664	1197, 3546, 4694, 616
nuoG	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]
nuoH	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32658	1197, 3546, 4694, 616
nuoI	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32655	1197, 3546, 4694, 616
nuoJ	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32652	3546, 4694, 616
nuoK	51.6	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32649	3546, 4694, 616
nuoL	51.5	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32646	3117, 3546, 616
nuoM	51.5	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	32639	1197, 4694, 616
nuoN	51.5	NADH:ubiquinone oxidoreductase	NADH dehydrogenase I subunit (EC 1.6.99.–)	29354	1197, 4694, 616
nupC	54.1	Nucleoside permease	*cru*; transport of nucleosides, except guanosine	443	2303, 3046, 3047, 4944, 539, 586, 864
nupG	66.9	Nucleoside permease	Transport of nucleosides	442	3046, 3047, 3172, 4715
nusA	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
nusB	9.4	N (λ protein) utilization substance	*groNB*, *ssaD*, *ssyB*; survives prophage induction; transcription termination L factor	440	1313, 1366, 1408, 1926, 3285, 3598, 4004, 4315, 4361, 4670, 851
nusG	90.0	N (λ protein) utilization substance	Stabilizes λ-N-NusA-RNAP antitermination complex	31308	2525, 2526, 2566, 4276, 576, 939
nuvA	9.4	Near UV (sensitivity)	Uridine thiolation factor A activity	439	1210, 2573, 3606, 609
nuvC	44.1	Near UV (sensitivity)	Uridine thiolation factor C activity	438	3781
ogrK	46.7	P2 *ogr* gene	Positive regulator of P2 growth (insertion of P2 *ogr* gene)	53483	4100
ogt	30.1	O-methylguanine transferase	O^6-methylguanine-DNA methyltransferase, constitutive	31984	1990, 2698, 2761, 3006, 3503, 3504, 3505, 3629, 7
ompA	21.9	Outer membrane protein	*con*, *tolG*, *tut*; outer membrane protein 3a (II*; G;d) structural gene	437	1501, 1694, 267, 280, 3023, 3024, 3025, 493, 707, 795, 949, 986
ompC	49.8	Outer membrane protein	*meoA*, *par*; outer membrane protein 1b (Ib, c)	436	2954, 2980, 2981, 3880, 4520, 4574, 4811
ompF	21.2	Outer membrane protein	*cmlB*, *coa*, *cry*, *tolF*; 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
ompG	29.7	Outer membrane protein	Novel porin; not shown in Fig. 1; see EcoMap10 (3763a) at 29.75 min	57349	2987, 1194a
ompR	76.2	Outer membrane protein	*cry*, *envZ*, *ompB*; 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
ompT	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
ompX	18.3	Outer membrane protein	Outer membrane protein, with role in inducing RNAP-σ^E production	35913	2863
oppA	28.0	Oligopeptide permease	Oligopeptide permease	18094	108, 1782, 2494, 3351, 4188
oppB	28.0	Oligopeptide permease	Oligopeptide transport	18091	108, 1782, 2494
oppC	28.1	Oligopeptide permease	Oligopeptide transport	18088	108, 1782
oppD	28.1	Oligopeptide permease	Oligopeptide transport	18085	108, 1782
oppE	98.9	Oligopeptide permease	Oligopeptide transport	18082	108
oppF	28.1	Oligopeptide permease	Oligopeptide transport; ATP hydrolysis	35799	1344
opr	19.0	*rpo* reversed	Rate of degradation of aberrant RNAP-subunit proteins	18079	3983
ops	66.1	Overproduction of polysaccharide	Level of exopolysaccharide production	18076	4963
oraA	60.8	*orf-recA*	Putative RecX regulatory protein	33246	4914
ordL	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[c]
oriC	84.6	Origin of replication	*poh*; 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
oriJ	30.5	Origin of replication	Locus in defective prophage rac	430	1037, 1038, 2086
orn	94.6	Oligoribonuclease	3′ to 5′ oligoribonuclease	54868	4942
osmB	28.9	Osmotically inducible	OsmB lipoprotein	31965	1054, 2072, 2073
osmC	33.5	Osmotically inducible	Nonessential gene	32184	1460, 1584
osmE	39.2	Osmotically inducible	*anr*; promoter overlaps *nadE* promoter; regulated by growth phase as well as osmotic pressure	36628	1585, 828
osmY	99.3	Osmotically inducible	*csi-5*; periplasmic, σ^S dependent protein (stationary phase)	34640	1054, 2412, 4883, 4884
otsA	42.6	Osmoregulated trehalose synthesis	Trehalose phosphate synthase (EC 2.4.1.15)	18073	1419, 2077
otsB	42.7	Osmoregulated trehalose synthesis	Trehalose phosphate phosphatase (EC 3.1.3.12)	18070	1419, 2077
oxyR	89.6	Oxygen	*mor*, *momR*; bifunctional regulatory protein sensor for oxidative stress	28841	1455, 1712, 2358, 2359, 4242, 4951, 4356
oxyS	89.6	Oxygen	Regulatory RNA; activator for genes that detoxify oxidative damage; small RNA	28844	77
pabA	75.2	*para*-Aminobenzoate	Sulfonamide resistance; *p*-aminobenzoate biosynthesis	429	2130, 4593, 535, 4450
pabB	40.8	*para*-Aminobenzoate	Sulfonamide resistance; *p*-aminobenzoate biosynthesis	428	1454, 3624, 4593, 535
pabC	24.8	*para*-Aminobenzoate	Sulfonamide resistance; aminodeoxychorismate lyase	31889	1499, 1500
pac	31.0	Phenylacetate	Phenylacetate degradation	18067	831
pal	16.8	Peptidoglycan-associated lipoprotein	*excC*; essential lipoprotein associated with peptidoglycan	35129	1270, 2448, 2450, 4581, 705
panB	3.2	Pantothenate	Ketopantoate hydroxymethyltransferase (EC 4.1.2.12)	427	2037, 2903, 871
panC	3.2	Pantothenate	Pantothenate synthetase (EC 6.3.2.1)	426	2903, 871
panD	3.2	Pantothenate	Aspartate 1-decarboxylase (EC 4.1.1.11)	425	2903, 871
panF	73.4	Pantothenate	Pantothenate permease (symporter)	10818	1971, 4537, 4565
parC	68.2	Partition	Cell partitioning; topoisomerase IV subunit A	33440	1699, 2163, 2164, 2165, 2211, 2360, 3397, 3398, 4923, 695, 4213
parE	68.4	Partition	*nfxD*; topoisomerase IV subunit B	33451	2163, 2165, 2211, 2511, 3397, 3398, 491, 4923
pat	89.1	Putrescine aminotransferase	Putrescine aminotransferase	18064	3984
pbpG	47.9	Penicillin-binding protein	Penicillin-binding protein 7 (PBP7)	36349	1714
pck	76.1	PEP carboxykinase	Phosphoenolpyruvate carboxykinase (ATP); (EC 4.1.1.49)	422	1444, 1445, 1446, 2864
pcm	61.8	Protein carboxyl methyltransferase	L-Isoaspartyl protein carboxyl methyltransferase (EC 2.1.1.77); repair of isoaspartyl residues	33221	1325, 2524, 4591
pcnB	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
pdhR	2.6	Pyruvate-dehydrogenase	Pyruvate-dehydrogenase repressor	30488	1674, 3567, 655
pdxA	1.1	Pyridoxine	Isoniazid resistance; pyridoxine biosynthesis	420	1020, 105, 106
pdxB	52.5	Pyridoxine	Isoniazid resistance; erythronate-4-phosphate dehydrogenase? pyridoxine biosynthesis	419	1020, 143, 144, 3930
pdxH	37.0	Pyridoxine	Isoniazid resistance; pyridoxine-phosphate oxidase	417	1020, 1526, 1529, 2398, 4034
pdxJ	58.2	Pyridoxine	Codon overlap with *recO*; complex operon	416	2397, 4340
pdxK	54.6	Pyridoxine	Vitamin B_6 kinase	51757	4866
pdxL	46.6	Pyridoxine	Pyridoxine kinase	50836	2977
pdxY	37	Pyridoxine	Pyridoxal kinase	53757	4867
pepA	96.6	Peptidase	*xerB*, *carP*; amino-exopeptidase A	30215	2842, 3732, 4226, 4227, 684
pepD	5.5	Peptidase	Peptidase D, a dipeptidase	415	1698, 1722, 2254, 2938, 3384, 724
pepE	91.1	Peptidase	α-Aspartyl dipeptidase (EC 3.4.11.–)	34261	822
pepN	21.3	Peptidase	Aminopeptidase N	414	1233, 1269, 213, 214, 215, 2431, 2833, 2834, 2835, 3384

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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]
pepP	65.8	Peptidase	Proline aminopeptidase II	28682	4897a, 3100
pepQ	86.8	Peptidase	Proline dipeptidase (EC 3.4.13.9)	34071	3098, 926
pepT	25.5	Peptidase	Putative peptidase T	31914	2617
pfkA	88.5	Phosphofructokinase	6-Phosphofructokinase I (EC 2.7.1.11)	413	1710, 3706, 907
pfkB	38.9	Phosphofructokinase	Suppresses *pfkA* mutations; phosphofructokinase, Pfk-2	412	817, 908, 909
pflA	20.5	Pyruvate formate-lyase	*act*; pyruvate formate lyase I activase	35839	1085, 3699
pflB	20.5	Pyruvate formate-lyase	Pyruvate formate lyase I; induced anaerobically	410	3389, 3699, 3884, 3885, 3886
pflC	89.3	Pyruvate formate-lyase	Pyruvate formate lyase II activase	35847	395, 396
pflD	89.3	Pyruvate formate-lyase	Pyruvate formate lyase II	35843	395, 396
pfs	3.8	PNP similarity	5′-Methylthioadenosine/*S*-adenosylhomocysteine nucleosidase	54950	834
pgi	91.2	Phosphoglucose isomerase	Glucosephosphate isomerase (EC 5.3.1.9)	409	1311, 1319, 3706, 4678
pgk	66.2	Phosphoglycerate kinase	Phosphoglycerate kinase (EC 2.7.2.3)	408	3148
pgl	17.2	Phosphogluconolactonase	*blu*; 6-phosphogluconolactonase (EC 3.1.1.31)	407	3706
pgm	15.4	Phophoglucomutase	*blu*; phosphoglucomutase (EC 5.4.4.2)	406	2647, 3706
pgpA	9.5	Phosphatidylglycerophosphate phosphatase	Phosphatidylglycerophosphate phosphatase, membrane bound, nonessential	17644	1338, 1882, 1885
pgpB	28.8	Phosphatidylglycerophosphate phosphatase	Phosphatidylglycerophosphate phosphatase, membrane bound, nonessential	17641	1051, 1338, 1883, 1885
pgsA	42.9	Phosphotidylglycerophosphate synthase	Phosphatidylglycerophosphate synthetase (EC 2.7.8.5)	405	1459, 3266, 4493, 4518
pheA	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
pheP	13.0	Phenylalanine	Phenylalanine-specific permease	402	3422, 4720
pheS	38.7	Phenylalanine	*phe-act*; phenylalanyl-tRNA synthetase α-subunit (EC 6.1.1.20)	400	1148, 1201, 1213, 2132, 2860, 2862, 3460, 3461, 3463, 4168, 4169, 4171, 4801
pheT	38.7	Phenylalanine	Phenylalanyl-tRNA synthetase β-subunit (EC 6.1.1.20)	399	1148, 1213, 2860, 2862, 3460, 3461, 3463, 4168, 4169, 4801
pheU	94.0	Phenylalanine	*pheR*, *pheW*; phenylalanine tRNA	18061	1345, 1387, 1388, 2313, 3938, 4755, 603, 3442
pheV	67.0	Phenylalanine	Phenylalanine tRNA	18058	2313, 4755, 602, 604, 3442
phnC	93.2	Phosphonate	Phosphonate transporter subunit I (cryptic in K-12); member Pho regulon	34553	2737, 2906, 2908, 4669, 694
phnD	93.1	Phosphonate	*psiD*; phosphonate transporter subunit, periplasmic (cryptic in K-12)	17638	2737, 2906, 2907, 2908, 2909, 4621, 4665, 4669, 694
phnE	93.1	Phosphonate	Phosphonate transporter subunit, integral membrane component (cryptic in K-12)	34550	2737, 2906, 2908, 4669, 694
phnF	93.1	Phosphonate	Phosphonate utilization (cryptic in K-12); putative regulatory gene, member of *pho* regulon	34547	2737, 2906, 2908, 4669, 694
phnG	93.1	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34544	2737, 2906, 2908, 4669, 694
phnH	93.1	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34541	2737, 2906, 2908, 4669, 694
phnI	93.1	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34538	2737, 2906, 2908, 4669, 694
phnJ	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34535	2737, 2906, 2908, 4669, 694
phnK	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34532	2737, 2906, 2908, 4669, 694
phnL	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34529	2737, 2906, 2908, 4669, 694
phnM	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34526	2737, 2906, 2908, 4669, 694
phnN	93.0	Phosphonate	Carbon-phosphorus lyase complex subunit (phosphonate utilization cryptic in K-12)	34523	2737, 2906, 2908, 4669, 694
phnO	93.0	Phosphonate	Probably regulatory for C-P lyase complex (phosphonate utilization cryptic in K-12)	34520	2737, 2906, 2908, 4669, 694
phnP	92.9	Phosphonate	Carbon-phosphorus lyase complex membrane-bound subunit (utilization cryptic in K-12)	34514	2737, 2906, 2908, 4669, 694
phoA	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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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]
phoB	9.0	Phosphate	*phoRc*, *phoT*; positive response regulator for *pho* regulon, two-component system	397	1597, 2230, 2732, 2734, 2735, 4040, 415, 4426, 4430, 4661, 4663, 4667, 4668
phoE	5.6	Phosphate	*ompE*; outer membrane porin protein E	396	1676, 1722, 3221, 3319, 4426, 4429, 4432, 4433, 4553
phoH	23.4	Phosphate	*psiH*; member of *pho* regulon, P starvation induced	31841	2231, 2320, 2909, 4661
phoP	25.6	Phosphate	In *Salmonella*, a sensor in the two-component regulatory system, with *phoQ*	31919	1530, 2146
phoQ	25.6	Phosphate	In *Salmonella* two-component regulatory system with *phoP*	31922	2146
phoR	9.0	Phosphate	*nmpB*, *phoR1*, *R1pho*; positive and negative regulatory gene for *pho* regulon; sensor of two-component system for *pho* regulon	394	1112, 2734, 2736, 4040, 4427, 4430, 4661, 4663, 4667, 4753
phoU	84.2	Phosphate	*phoT*; P uptake, high-affinity P-specific transport system, regulatory gene	18055	3121, 4196, 4295, 79, 80
phrB	15.9	Photoreactivation	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	391	1073, 1826, 1866, 2632, 2683, 3327, 3841, 3842
phxB	17.0	Phage ϕX	Adsorption of ϕX154	389	3049
pin	26.1	Prophage-derived inversion	Locus in defective prophage e14; calcium-binding protein required for initiation of replication	18049	1159, 2168, 3447, 3448, 4544
pioO	74.4	Protein, initiation?	*pinO*; calcium-binding protein, may have a role in initiation of replication	53557	1586, 1587
pit	78.4	P_i transport	Low-affinity P_i transport	385	1149, 1150, 300, 4156
pldA	86.3	Phospholipase, detergent resistant	Detergent-resistant phospholipase A activity	384	1648, 1791, 1792, 2277, 4606, 513, 58, 926, 973, 974
pldB	86.4	Phospholipase, detergent resistant	Lysophospholipase L2	5001	1792, 2277, 2278, 58, 926
plsB	91.6	Phospholipid synthesis	Glycerolphosphate acyltransferase activity	382	2544, 2545
plsC	68.1	Phospholipid synthesis	1-Acyl-*sn*-glycerol-3-phosphate acyltransferase (EC 2.3.1.51); affects partitioning	33443	802, 803
plsX	24.7	Phospholipid synthesis	Glycerol P auxotrophy in *plsB* background	18046	2425
pmbA	96.0	Peptide MccB17	*mcb*, *tldE*; antibiotic peptide MccB17	34577	2619, 3061, 3703
pncA	39.9	Pyridine nucleotide cycle	*nam*; nicotinamide deamidase (EC 3.5.1.19)	381	1321, 2487, 3347
pncB	21.3	Pyridine nucleotide cycle	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	380	2487
pnp	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
pntA	36.1	Pyridine nucleotide transhydrogenase	Pyridine nucleotide transhydrogenase α subunit (EC 1.6.1.1)	18043	771, 772
pntB	36.1	Pyridine nucleotide transhydrogenase	Pyridine nucleotide transhydrogenase β subunit (EC 1.6.1.1)	18040	1436, 771, 772
pnuC	16.9	Putative NMN uptake	Nicotinamide mononucleotide transporter, putative, by homology with *Salmonella*	53409	1280, 4954
poaR	65.9	Proline oxidase	Regulation of proline oxidase production	377	819a
polA	87.2	Polymerase	*resA*; DNA polymerase I (EC 2.7.7.7)	375	2068, 2189, 2190, 3072, 4869, 4941, 4966
polB	1.4	Polymerase	*dinA*; DNA polymerase II (EC 2.7.7.7)	374	1174, 1967, 2519, 3385, 4039, 426, 698, 699
popD	0.2	Porphyrin	5-Aminolevulinate dehydratase (EC 4.2.1.24)	371	2839, 3518
potA	25.5	Putrescine-ornithine transporter	ATP-binding membrane protein; putrescine/spermidine-ornithine transporter	31899	1339, 2148, 2150, 2617
potB	25.5	Putrescine-ornithine transporter	Membrane protein, channel-forming, for spermidine uptake	31902	1339, 2150, 2617
potC	25.5	Putrescine-ornithine transporter	Membrane protein, channel-forming, for spermidine uptake	31905	1339, 2150, 2617
potD	25.5	Putrescine-ornithine transporter	Spermidine-binding membrane protein	31908	1339, 2150, 2617
potE	15.4	Putrescine-ornithine transporter	Putrescine-lyase antiporter	31552	2149, 2151, 2152
potF	19.2	Putrescine-ornithine transporter	Apparent periplasmic putrescine-specific binding protein	31694	3440
potG	19.3	Putrescine-ornithine transporter	Apparent nucleotide-binding subunit of putrescine-ornithine transporter	31697	3440
potH	19.3	Putrescine-ornithine transporter	Transmembrane-spanning subunit	31700	3440
potI	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]
poxA	94.5	Pyruvate oxidase	Regulator of *poxB*	370	679
poxB	19.6	Pyruvate oxidase	Pyruvate oxidase (EC 1.2.2.2)	369	1482, 1483, 678, 680, 681
ppa	95.8	Pyrophosphatase	Inorganic pyrophosphatase (EC 3.6.1.1)	34394	2389, 2390, 700
ppc	89.4	PEP carboxylase	*asp*, *glu*; phosphoenolpyruvate carboxylase (EC 4.1.1.31)	368	1332, 3000, 3786
pphA	41.4	Phosphoprotein phosphatase	Phosphoprotein phosphatase involved in signalling protein misfolding; heat shock regulon	54632	2966
pphB	61.5	Phosphoprotein phosphatase	As above; heat shock regulon	54636	2966
ppiA	75.2	Peptidylprolyl isomerase	*rot*, a rotomase; peptidylprolyl-*cis-trans*-isomerase A	31121	1670, 2252, 2579, 3214
ppiB	11.9	Peptidylprolyl isomerase	A rotomase; peptidylprolyl-*cis-trans*-isomerase B	31117	1670
ppiC	85.3	Peptidylprolyl isomerase	*parvA*; peptidylprolyl-*cis-trans* isomerase C	35829	3764
ppk	56.5	Polyphosphate kinase	Polyphosphate (linear P_i linked by high-energy bonds) kinase	32894	2323, 37, 873
pps	38.4	PEP synthase	*ppsA*; phosphoenolpyruvate synthase	367	3181
ppx	56.5	Exopolyphosphatase	Exopolyphosphatase	32899	2323, 38
pqiA	21.8	Paraquat inducible	Induced by paraquat, regulated by SoxRS	39521	2289, 2290
pqiB	21.8	Paraquat inducible	Induced by paraquat, regulated by SoxRS	39524	2289
pqqL	33.9	Pyrroloquinoline quinone	Redox cofactor for pyrroloquinoline quinone synthesis (cryptic in K-12)	35854	364, 4497
pqqM	33.9	Pyrroloquinoline quinone	Pyrroloquinoline quinone synthesis (cryptic in K-12)	35857	4497
prc	41.2	PBP protease, C terminal	*tsp*; carboxy-terminal protease for penicillin-binding protein, PBP 3	32334	1643, 1644, 179, 2186, 3082, 3970, 4060, 4061
prfA	27.3	Protein release factor	*asuA*?, *sueB*, *uar*, *ups*? peptide chain release factor 1	14922	1880, 2460, 2808, 3782, 3283, 4273, 650
prfB	65.4	Protein release factor	*supK*; peptide chain release factor 2	17635	1880, 2174, 2178, 2460
prfC	99.3	Protein release factor	*tos*; release factor 3	34633	1515, 1739, 2808, 2930, 4873
priA	88.9	Primosome	*srgA*; primosome factor Y, also called protein n′	27611	2462, 3227, 3228, 3314, 3846, 59
priB	95.3	Primosome	Primosomal protein n	29153	4920, 68
priC	10.6	Primosome	Primosomal protein n″	29161	4920
prlC	78.5	Protein localization	*opdA* in *Salmonella*; oligopeptidase A	18031	1153, 4471, 4472, 820, 821
prlZ	71.4	Protein localization	Suppresses export defects in signal sequence mutations	36421	4688
prmA	73.4	Posttranslation ribosomal protein modification	Methyltransferase for 50s subunit L11	366	4565
prmB	53.0	Posttranslation ribosomal protein modification	Methylation of 50s subunit L3	365	815
proA	5.6	Proline	pro_1; γ-glutamyl phosphate reductase (EC 1.2.1.41)	364	1026, 1214, 1597, 1676, 1677, 1768, 2721, 315, 3153, 4562, 1722
proB	5.6	Proline	pro_2; γ-glutamyl kinase (EC 2.7.2.11)	363	1026, 1214, 1597, 1676, 1677, 1768, 2721, 315, 3153, 3612, 4562, 878
proC	8.7	Proline	pro_2, pro_3; pyrroline-5-carboxylate reductase (EC 1.5.1.2)	362	1025, 1597, 2839, 415, 999
proK	79.8	Proline	*proV*; proline tRNA_1	17632	1285, 2313, 2351, 4128
proL	49.2	Proline	*proW*; proline tRNA_2	17629	2313
proM	85.8	Proline	*proU*; proline tRNA_3	17626	2313, 926
proP	93.3	Proline	Low-affinity transport; proline permease, minor	361	1475, 1476, 2827, 2877, 2899, 3613, 4186, 4814, 884
proQ	41.4	Proline	Sensitivity to toxic proline analogs and positive regulator of proline porter II	36840	2947
proS	4.7	Proline	*drp*; prolyl-tRNA synthetase (EC 1.1.1.15)	360	2453, 414
proT	83.8	Proline	Proline transport carrier protein, putative	359	3020
proU	60.4	Proline	*osrA*; operon *proVWX* for high-affinity transport for glycine; see also *proM*	18025	1477, 1478, 1535, 2826, 3537, 4297, 951, 3599
proV	60.4	Proline	*proU*; high-affinity transport for glycine; glycine betaine-binding protein; see also *proK*	18022	1191, 1285, 1477, 1481, 1535, 2826, 4228, 4297, 951
proW	60.4	Proline	*proU*; high-affinity transport for glycine, betaine, and proline; see also *proL*	18019	1535, 1590, 4228
proX	60.5	Proline	*proU*; high-affinity transport for glycine, betaine, and proline	35653	1535, 4228
prpA	97.0	Propionate	Growth on propionate	358	2180, 4158

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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]
prpB-E	7.5	Propionate	Propionate catabolism operon, *Salmonella* homology and some expression information	55452	4389a
prpR	7.5	Propionate	Regulator, propionate catabolism operon, *Salmonella* homology	55455	4389a
prr	31.2	Pyrroline	γ-Aminobutyraldehyde (pyrroline) dehydrogenase activity	18016	3984
prs	27.1	PRPP synthetase	*dnaR*; phosphoribosylpyrophosphate synthetase (EC 2.7.6.1)	357	103, 1819, 1820, 1821, 1823, 3808, 3495
psd	94.6	Phosphatidylserine decarboxylase	Phosphatidylserine decarboxylase	356	2531, 4020
psiF	8.7	P starvation induced	*pho* regulon member, requiring PhoRB system	18013	2909, 4668, 674
pspA	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
pspB	29.5	Phage shock protein	Regulatory gene, with PspC activates expression of *psp* operon	32012	2987, 4697, 4698, 506
pspC	29.5	Phage shock protein	Positive regulatory gene, cooperatively with PspB	32015	2987, 4697, 4698, 506
pspE	29.5	Phage shock protein	Expressed in response to stress as part of *psp* operon, but also transcribed independently	32018	4697, 506
pspF	29.4	Phage shock protein	Transcriptional σ^{54}-dependent activator of *psp*	50349	1105, 2063, 2064, 2065, 2066
pssA	58.6	Phosphatidylserine synthase	Phosphatidylserine synthase (EC 2.7.8.8)	355	2806, 3269, 4020, 766, 995
pssR	85.0	Phosphatidylserine synthase	Regulatory gene	18010	4145, 832
pstA	84.2	P-specific transport	*R2pho*, *phoR2b*, *phoT*; high-affinity P-specific transport	18007	3734, 4196, 4296, 79, 80
pstB	84.2	P-specific transport	*phoT*; high-affinity P-specific transport; cytoplasmic ATP-binding protein	18004	2514, 3734, 4196, 4296, 672, 79, 80
pstC	84.2	P-specific transport	*phoW*; high-affinity P-specific transport; cytoplasmic membrane component	18001	3734, 4196, 4296, 79, 80
pstS	84.2	P-specific transport	*phoR2*, *nmpA*, *phoR2a*, *phoS*, *R2pho*; 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
psu	1.5	Pleiotropic suppressor	Temporary designation for pleiotropic suppressor gene; oxolinic acid resistance	37018	1160
pta	52.0	Phosphotransacetylase	Phosphotransacetylase (EC 2.3.1.8)	353	1548, 1573, 2094, 2512, 2813, 530
pth	27.1	Peptidyl tRNA hydrolase	*rap*; peptidyl-tRNA hydrolase; required for phage λ growth	352	1342, 1364, 1544, 1739, 1820, 3064, 976, 4269a
ptrA	63.7	Protease III	Protease III	351	1106, 1107, 1253, 220, 718, 775
ptrB	41.5	Protease III	Protease II	32339	2112
ptsG	24.9	Phosphotransferase system	*CR*, *car*, *cat*, *gpt*, *umg*; glucosephophotransferase enzyme II	349	1170, 2233, 2925, 3765, 4095, 459, 461, 557, 890
ptsH	54.6	Phosphotransferase system	*Hpr*, *ctr*, *hpr*; phosphohistidinoprotein-hexose phosphotransferase (EC 2.7.1.69)	348	9836, 2031, 2679, 3369, 3793, 4391, 508, 509, 510, 982, 983
ptsI	54.6	Phosphotransferase system	*ctr*; phosphotransferase system enzyme I	347	3369, 983, 983a, 983b, 1163, 1168, 2491, 3793, 4571, 508, 509, 510, 85, 982
ptsN	72.1	Phosphotransferase system	*pts* in the *rpoN* operon	38380	3517
ptsP	63.9	Phosphotransferase system	PEP-protein phosphotransferase (reuse of *manY* synonym)	53527	1171, 3648
purA	94.9	Purine	Adenylosuccinate synthetase (EC 6.3.4.4)	345	1681, 2788, 304, 4770
purB	25.6	Purine	Adenylosuccinate lyase (EC 4.3.2.2)	344	12, 1503, 2788, 1668, 1682
purC	55.9	Purine	ade_{g}; phosphoribosylaminoimidazole-succinocarboxamide synthetase (EC 6.3.2.6)	343	2788, 3364, 4415
purD	90.6	Purine	$\mathit{adth}_{\mathrm{a}}$; phosphoribosylglycinamide synthetase (EC 6.3.4.13)	342	1260, 2789, 28, 719
purE	11.9	Purine	*Pur2*, *ade3*, *adef*; phosphoribosylaminoimidazole carboxylase, catalytic subunit (EC 4.1.1.21)	341	1597, 2103, 4412
purF	52.3	Purine	ade_{ub}, *purC*; amidophosphoribosyl transferase (EC 2.4.2.14)	340	2727, 3211, 3719, 3826, 4117, 4483
purH	90.6	Purine	Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	338	1260, 2789, 28, 3410
purK	11.9	Purine	*purE2*; phosphoribosyl glucinamide formyltransferase	17995	2103, 4412

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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]
purL	58.0	Purine	*purI*; phosphoribosylformylglycinamide synthetase (EC 6.3.5.3)	336	1817, 3827, 3901
purM	56.5	Purine	*purG*; phosphoribosylaminoimidazole synthetase (EC 6.3.3.1)	335	1817, 4115, 4116
purN	56.5	Purine	ade$_C$; 5′-phosphoribosylglycinamide transformylase 1; see *purT*	17623	4116
purP	83.9	Purine	High-affinity purine transport	17992	578
purR	37.4	Purine	Purine repressor	17989	1681, 2222, 3718, 741
purT	41.6	Purine	Glycinamide ribonucleotide transformylase 2, non-folate-requiring; see *purN*	32348	2772, 3230
purU	27.7	Purine	*tgs*; formyltetrahydrofolate hydrolase	35231	3088, 3089, 444, 446, 447
pus	20.6	Reverse of *sup* (amber)	Reverses accentuation effects of amber suppressor on *relB* mutations	334	1044
putA	23.2	Proline utilization	*poaA*; proline dehydrogenase (EC 1.5.99.8)	333	1028, 2743, 2989, 3115, 3612, 4186, 4461, 4771, 4777
putP	23.2	Proline utilization	Proline/Na$^+$, Li$^+$ symport protein	332	2989, 3115, 3116, 3264, 3612, 4186, 4461, 4775, 4776, 4777, 4849
pykA	41.7	Pyruvate kinase	Pyruvate kinase A (II); (EC 2.7.1.40)	32363	1378, 3477, 4534
pykF	37.8	Pyruvate kinase	Pyruvate kinase I (EC 2.7.1.40); fructose-stimulated	17620	1378, 3255, 3477, 397
pyrB	96.3	Pyrimidine	Aspartate transcarbamylase, catalytic subunit (EC 2.1.3.2)	330	1797, 2275, 2510, 3140, 3383, 3715, 3729, 4499
pyrC	24.2	Pyrimidine	Dihydro-orotase (EC 3.5.2.3)	329	193, 2010, 4754
pyrD	21.6	Pyrimidine	Dihydro-orotate oxidase (EC 1.3.3.1)	328	2010, 2423
pyrE	82.2	Pyrimidine	Orotate phosphoribosyltransferase (EC 2.4.2.10)	327	2009, 3511–3514, 4367, 94
pyrF	28.9	Pyrimidine	Orotidine-5′-phosphate decarboxylase (EC 4.1.1.23)	326	1070, 2010, 407, 4498
pyrG	62.6	Pyrimidine	CTP synthetase (EC 6.3.4.2)	325	158, 3426, 4709
pyrH	4.1	Pyrimidine	*smbA*; UMP kinase	324	4104, 4843
pyrI	96.3	Pyrimidine	Aspartate transcarbamylase, regulatory subunit (EC 2.1.3.2)	323	1219, 1797, 2510, 3383, 3426, 3715, 3729, 4738
qin	35.1	Q independent	*kim*; cryptic lambdoid phage	17529	1177, 455
qmeC	75.3	Q membrane	Glycine resistance; penicillin sensitivity; membrane defect	321	4735
qmeD	64.4	Q membrane	Glycine resistance; penicillin sensitivity; membrane defect	320	4735
qmeE	37.9	Q membrane	Glycine resistance; penicillin sensitivity; membrane defect	319	4735
qor	91.8	Quinone oxidoreductase	Quinone oxidoreductase, NADPH dependent	36654	2549
qsr′	12.2	QSR replacement	DLP12; defective Q-independent lambdoid prophage, includes *intD* and *nmpD*	19200	115, 1751, 2085, 3059, 390
queA	9.1	Queuosine/queuine	*S*-Adenosylmethionine:tRNA ribosyltransferase-isomerase	29889	2651, 3654, 4094
rac	30.4	Recombination activation	Defective prophage Rac loci; see *recE*, *oriJ*, *trkG*, *sieB*, *lar*, *racC*, *racR*	318	1036, 1037, 1181, 2086, 2087, 2643, 355, 4750, 4751, 503, 759a
racC	30.5	Recombination activation	Element of defective prophage Rac	32076	748
racR	30.6	Recombination activation	Element of defective prophage Rac; repressor	37433	748, 759a
radA	99.7	Radiation	*sms*; sensitivity to gamma and UV radiation	15905	1059, 3160, 4136
radC	82.1	Radiation	Sensitivity to radiation	13913	1220
ranA	58.3		Affects RNA metabolism	317	121
rarD	86.2	Recombination and repair	Chloramphenicol resistance	34089	3259, 926
ras	9.9	Radiation sensitive	Sensitive to X rays and UV	316	4636, 4637
rbfA	71.4	Ribosome binding factor	Overexpression suppresses cold-sensitive 16S rRNA; ribosome binding factor	36919	2044, 590, 917
rbn	87.8	RNase BN	*o290*; RNase BN, tRNA processing enzyme	50482	3850, 618
rbsA	84.7	Ribose	*rbsP*, *rbsT*; D-ribose high-affinity transport system (may have chemotaxis function)	12082	1888, 242, 2630, 291
rbsB	84.8	Ribose	*prlB*, *rbsP*; D-ribose periplasmic binding protein	12092	1153, 1888, 2630
rbsC	84.8	Ribose	*rbsP*, *rbsT*; D-ribose high-affinity transport system	12089	1888, 2630, 291, 4915
rbsD	84.7	Ribose	*rbsP*; D-ribose high-affinity transport system	314	291
rbsK	84.8	Ribose	Ribokinase (EC 2.7.1.15)	315	1798, 1888, 2630, 4611
rbsR	84.8	Ribose	Regulatory gene	12086	2630

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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]
rcsA	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
rcsB	49.9	Regulation capsule synthesis	Positive regulatory gene for capsule (colanic acid) synthesis; when overexpressed, restores *ftsZ84* growth on low-salt medium	17977	1413, 1471, 2188, 4099, 4243–4245, 504
rcsC	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
rcsF	4.7	Regulation capsule synthesis	Overexpression confers mucoid phenotype, increases capsule synthesis; restores colony formation of *ftsZ84* mutants on low salt	29845	1412
rdgA	16.1	RecA-dependent growth	Dependence of growth upon *recA* gene product	17971	1317
rdgB	67.0	RecA-dependent growth	Dependence of growth and viability upon *recA*	17968	784
recA	60.8	Recombination	*srf*, *lexB*, *umuB*, *zab*; 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
recB	63.6	Recombination	*rorA*; recombination and repair; RecBCD enzyme (exonuclease V) subunit	311	1107, 1180, 1249, 1743, 3870, 4365, 690, 759, 4785a, 406a
recC	63.7	Recombination	Recombination and repair; RecBCD enzyme (exonuclease V) subunit	310	1107, 1252, 1262, 1743, 3870, 4365, 690, 759, 4785a
recD	63.6	Recombination	*hopE*; recombination and repair; RecBCD enzyme (exonuclease V) α-subunit	4975	1248, 3187, 348, 4365, 759, 87
recE	30.5	Recombination	Recombination and repair; in prophage rac locus; degrades one strand 5′–3′ in duplex DNA; exonuclease VIII	309	1181, 1287, 2086, 2087, 362, 4751, 748, 759, 760
recF	83.6	Recombination	*uvrF*; recombination and repair	308	10, 11, 132, 1517, 152, 2709, 3626, 3627, 379, 3846, 3847, 3848, 4611, 671, 759
recG	82.4	Recombination	*spoV*? branch migration of Holliday junctions, junction-specific DNA helicase (see *ruvABC*)	307	1281, 2100, 2593, 2596, 2597, 2598, 2599, 3086, 4721, 59
recJ	65.4	Recombination	Single-stranded DNA-specific exonuclease, 5′–3′	17965	2638, 2639, 2640, 2641, 2642, 4511, 759
recN	59.3	Recombination	*radB*; *lexA* regulon; recombination and repair	10872	2600, 2924, 3425, 3748, 3861, 3862
recO	58.2	Recombination	Conjugational recombination and repair; DNA-binding protein; RecA-like strand assimilation	17962	2297, 2657
recQ	86.3	Recombination	Conjugational recombination and repair, presynaptic stage of recombination; *lexA* regulon; RecQ helicase	17959	1923, 2883, 3123, 3124, 58, 926
recR	10.6	Recombination	Recombination and DNA repair	31049	2723
recT	30.4	Recombination	Locus in defective prophage rac; activated by *sbcA* mutation; DNA-annealing protein	32070	1612, 2298, 2378, 761
relA	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
relB	35.4	Relaxed	Stringent/relaxed response; regulation of RNA synthesis	305	1042, 266
relE	35.4	Relaxed	Function unknown	17956	1411, 266
relF	35.4	Relaxed	Function unknown; overproduction lethal	17953	1411, 266
relX	62.8	Relaxed	Control of ppGpp synthesis	304	3346
rep	85.3	Replicase	*dasC*, *mbrA*, *mmrA*; Rep helicase, a single-stranded DNA-dependent ATPase	303	1086, 1428, 257, 2613, 342, 343, 4388, 58, 610, 926
rer	89.9	Resistance to radiation	Resistance to UV and gamma radiation	302	4179
rfaB	81.9	Rough	*waaB*; UDP-galactose: (glucosyl)lipopolysaccharide-1,6-galactosyltransferase	17617	3361, 3522, 3726, 3921, 4128, 867
rfaC	81.8	Rough	*waaC*; 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]
rfaD	81.7	Rough	*htrM*; 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
rfaF	81.8	Rough	*waaF*; ADP-heptose;LPS heptosyltransferase 1	28434	2269, 3362, 3392, 3726, 3920, 3921, 4079, 4128, 702, 807
rfaG	82.0	Rough	*waaG*; LPS core biosynthesis; glucosyltransferase I	15583	172, 3361, 3362, 3522, 3726, 3920, 3921, 4128, 867
rfaH	86.7	Rough	*sfrB*; regulates LPS core biosynthesis, transcriptional activator	164	200, 201, 2959, 333, 3641, 3921, 867
rfaI	81.9	Rough	UDP-D-galactose: (glucosyl)lipopolysaccharide-1,3-D-galactosyltransferase	17614	3361, 3523, 3726, 3920, 3921, 4128, 867
rfaJ	81.9	Rough	UDP-D-glucose: (galactosyl)lipopolysaccharide glucosyltransferase	17611	3361, 3522, 3523, 3726, 3920, 3921, 4128, 867
rfaK	81.8	Rough	*waaK*; not similar to *Salmonella rfaK*; adds terminal GlcNac side branch to the lipopolysaccharide core prior to attachment of the O antigen	33791	1698a, 2269, 2271, 3726, 3920, 3921, 4128
rfaL	81.8	Rough	LPS core biosynthesis; O-antigen ligase	28438	2269, 2271, 3726, 3920, 3921, 4128, 1698a
rfaP	82.0	Rough	LPS core biosynthesis; phosphorylation of core	298	280, 3361, 3362, 3522, 3726, 3920, 3921, 4128
rfaQ	82.0	Rough	Heptose region of LPS core	33801	2268, 2271, 3361, 3362, 3435, 3522, 3523, 3726, 3920, 3921, 4128, 779
rfaS	81.9	Rough	LPS core, not affecting attachment of O antigen	28949	172, 2268, 2270, 2271, 3523, 3726, 3920, 3921
rfaY	81.9	Rough	LPS core biosynthesis	33828	2269, 3920, 3921, 4128
rfaZ	81.8	Rough	LPS core biosynthesis	33824	2269, 2271, 3920, 3921
rfbA	45.4	Rough	*som*; TDP-glucose pyrophosphorylase	297	2267, 2728, 4208, 4875
rfbB	45.4	Rough	*som*; TDP-glucose oxidoreductase-4,6 dehydratase	296	2267, 2728, 4208, 4875
rfbC	45.4	Rough	*rfbD*; dTDP-4-deoxyrhamnose-3,5-epimerase	38129	4875
rfbD	45.5	Rough	*rfbC*; TDP-rhamnose synthetase	295	2267, 4208, 4875
rfbX	45.4	Rough	Hydrophobic protein, O-antigen	37353	2267, 4875
rfc	45.4	Rough	O-antigen polymerase	53474	2658, 4875
rfe	85.5	Rough	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-P transferase; common and O-antigen synthesis, tunicamycin sensitivity	294	2866, 2867, 2868, 3268, 926
rffA	85.6	Rough	Lipid III biosynthesis in common antigen synthesis	33935	241, 2867
rffC	85.6	Rough	Synthesis of enterobacterial common antigen and chain elongation	33938	241, 2867
rffD	85.5	Rough	Synthesis of enterobacterial common antigen; UDP-ManNAcA dehydrogenase	293	2866, 2867, 2868, 3268
rffE	85.5	Rough	*nfrC*, *wecB*; synthesis of enterobacterial common antigen; UDP-GlcNAc-2-epimerase	33925	2770, 2867, 2868, 926
rffG	85.6	Rough	*rffE*? dehydratase activity	40941	2770, 926
rffH	85.6	Rough	Hypothetical protein in *rffE* operon	52957	394
rffM	85.7	Rough	UDP-ManNAcA transferase	33948	2867, 2868
rffT	85.7	Rough	Synthesis of enterobacterial common antigen; Fuc4NAc transferase	33930	2867, 2868
rhaA	88.2	Rhamnose	L-Rhamnose isomerase (EC 5.3.1.14)	292	2999, 3465, 4421
rhaB	88.2	Rhamnose	Rhamnulokinase (EC 2.7.1.5)	291	3465, 4421
rhaD	88.2	Rhamnose	Rhamnulosephosphate aldolase D (EC 4.1.2.19)	289	3465, 4421
rhaR	88.3	Rhamnose	*rhaC*; positive regulatory gene	290	3465, 4421, 4580
rhaS	88.3	Rhamnose	*rhaC*; positive regulatory gene	17950	3465, 4421, 4580
rhaT	88.3	Rhamnose	Rhamnose permease; L-rhamnose-H^+ symporter, membrane protein	34185	1362, 211, 4358, 4359, 4580
rhlB	85.4	RNA helicase like	Same as *mmrA*? protein with RNA helicase-like motif	36971	2099, 926
rhlE	17.9	RNA helicase like	DEAD-box protein family; ATP-dependent RNA helicase-like protein	33907	3260
rho	85.4	Rho termination factor	*nitA*, *nusD*, *psuA*, *rnsC*, *sun*, *tsu*; 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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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]
RhsA	81.0	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	17947	1232, 2557, 3790, 4596, 4950
RhsB	78.0	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	17944	2557, 3790, 4950
RhsC	15.7	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	17941	3790, 4950
RhsD	11.3	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	17938	3790, 3791, 4950
RhsE	32.9	Recombination hotspot	Repetitive sequence responsible for duplications within chromosome	33720	3791, 4950
ribA	28.8	Riboflavin	Riboflavin biosynthesis; GTP-cyclohydrolase II (EC 3.5.4.20)	287	216, 217, 2288, 3670, 4387
ribB	68.6	Riboflavin	*htrP*; *luxH*-like; riboflavin biosynthesis; 3,4-dihydroxy-2-butanone 4-phosphate synthase	286	216, 217, 3594, 3672, 4387
ribC	37.5	Riboflavin	Riboflavin synthase α chain; see *ribE*	11923	1110, 217, 4387
ribD	9.3	Riboflavin	*ribG*; riboflavin biosynthese; a deaminase	35685	3671, 4361
ribE	9.3	Riboflavin	*ribH*; riboflavin synthase β chain; see *ribC*	35688	4361
ribF	0.5	Riboflavin	Flavokinase and FAD synthetase	35833	185, E
ridA	73.1	Rifampin dependence	Rifampin resistance and dependence	285	898
ridB	85.5	Rifampin dependence	Transcription and translation; rifampin (rifamycin) sensitivity	17935	895
rimB	38.9	Ribosomal modification	50S ribosomal subunit maturation	284	546
rimC	26.2	Ribosomal modification	50S ribosomal subunit maturation	283	546
rimD	87.7	Ribosomal modification	50S ribosomal subunit maturation	282	546
rimE	74.1	Ribosomal modification	Ribosomal protein modification	281	2865
rimF?	0.8	Ribosomal modification	*res*; ribosomal modification; may be same as *rimG*	280	1379
rimG	0.7	Ribosomal modification	*ramB*; modification of 30S ribosomal subunit protein S4; probably same as *rimF* (*res*) in *E. coli* B	279	1379, 4961
rimH	13.6	Ribosomal modification	*stsB*; ribosomal modification	278	
rimI	99.3	Ribosomal modification	Modification of 30S ribosomal subunit protein S18; acetylation of N-terminal alanine	277	1939, 4895
rimJ	24.2	Ribosomal modification	*tcp*; modification of 30S ribosomal subunit protein S5; acetylation of N-terminal alanine	276	1988, 4728, 4729, 4895
rimK	19.2	Ribosomal modification	*nek*; modification of 30S ribosomal subunit protein S6 by addition of glutamic acid residues	31682	122, 1860, 2123
rimL	32.3	Ribosomal modification	Modification of 50S ribosomal subunit protein L7/L12; acetylation of N-terminal serine	275	1940, 4348
rimM	59.1	Ribosomal modification	*yfjA*; 21-kDa protein essential for 16S RNA processing	51908	589, 590
rit	89.2	Ribosomal thermolability	Affects thermolability of 50S ribosomal subunit	274	3298
rlpA	14.3	Rare lipoprotein	Minor lipoprotein	17932	4332
rlpB	14.5	Rare lipoprotein	Minor lipoprotein	17929	4332
rluA	1.3	rRNA, large, uridine modification	Dual specificity pseudouridine synthase for 23S rRNA and $tRNA^{phe}$	36966	1578, 2106, 4787
rluC	24.66[b]	Pseudouridine synthase	Responsible for pseudouridine at three positions in 23S RNA (not on map, Fig. 1)	57124	827a
rluD	48.9	Suppressor *ftsH*	*sfhB*; suppresses *ftsH*(ts) mutants; 23S rRNA pseudouridine synthase (pseudouridines at position 1911, 1915, and 1917)	53497	3079, 689a
rmf	21.9	Ribosome modulation factor	Associated with the 100S dimers of 70S ribosomes observed in stationary phase cells	31760	4622, 4624, 4832
rna	13.9	RNase A	*rnsA*; cleaves phosphodiester bond between two nucleotides; RNase I	273	2858
rnb	29.0	RNase B	RNase II; mRNA degradation	272	1069, 4958, 4959, 4960
rnc	58.2	RNase C	RNase III; cleaves double-stranded RNA	271	1910, 2753, 2810, 3134, 4679, 708, 4339
rnd	40.6	RNase D	Rnase D; processes tRNA precursors	270	1336, 4919, 4939, 4938
rne	24.6	RNase E	*ams*; 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
rnhA	5.1	RNase H	*cer*, *dasF*, *herA*, *rnh*, *sdrA*, *sin*; 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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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]
rnhB	4.4	RNase H	Degrades RNA of DNA-RNA hybrids; RNase HII (EC 3.1.26.4)	30604	1944
rnk	13.9	Regulator nucleoside-diP kinase	Regulator of nucleoside diphosphate kinase; suppresses *Pseudomonas algR2*	36984	3911, 3985
rnpA	83.7	RNase P	tRNA, 4.5S RNA-processing; RNase P, protein component	267	1632, 2074, 2293, 3328
rnpB	70.4	RNase P	RNase P, RNA component	266	1064, 123, 2293, 2311, 2663, 3019, 3634, 3635, 3811
rnr	94.3	RNase R	*vacB*; homology with *Shigella* virulence gene *vacB*; exoribonuclease R	34417	569, 719a, 4417a
rnt	37.2	RNase T	Degrades tRNA; RNase T (EC 3.1.13–)	32271	1843, 3331, 3656, 649
rob	99.8	Right *oriC* binding	*oriC*-binding protein, binds to right border of *oriC*	34661	131, 2093, 4086
rorB	85.1	Roentgen resistance	Sensitivity to ionizing radiation, mitomycin C	36611	991, 992
rpe	75.7	Ribulose-5-phosphate epimerase	D-Ribulose-5-phosphate epimerase, in *dam* operon	53572	2681
rph	82.2	RNase PH	RNase PH	33892	2009, 2011, 2192, 3309, 94
rpiA	65.9	Ribose-P isomerase	Ribose phosphate isomerase (constitutive) (EC 5.3.1.6)	264	1822
rpiB	92.9	Ribose-P isomerase	Allose-6-P isomerase; ribose P isomerase?	50228	2223, 4138
rpiR	92.9	Ribose-P isomerase	*alsR*; repressor for *als* operon and *rpiB*	50233	2223, 4138
rplA	90.0	Ribosomal protein, large	50S ribosomal subunit protein L1	263	1083, 1855, 2567, 2577, 2688, 3499, 3605, 537, 89
rplB	74.3	Ribosomal protein, large	50S ribosomal subunit protein L2	262	4969
rplC	74.4	Ribosomal protein, large	50S ribosomal subunit protein L3	261	4969
rplD	74.4	Ribosomal protein, large	*eryA*; 50S ribosomal subunit protein L4; erythromycin sensitivity	260	2538, 2559, 4293, 4762, 4927, 4969, 736
rplE	74.2	Ribosomal protein, large	50S ribosomal subunit protein L5	259	666
rplF	74.2	Ribosomal protein, large	50S ribosomal subunit protein L6; gentamicin sensitivity	258	554, 666
rplI	95.4	Ribosomal protein, large	50S ribosomal subunit protein L9	257	15, 1938, 3928
rplJ	90.0	Ribosomal protein, large	*strA*; 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
rplK	90.0	Ribosomal protein, large	*relC*; 50S ribosomal subunit protein L11; kasugamycin sensitivity	255	1083, 1855, 2567, 2577, 3065, 3165, 3499, 3605, 4210, 4377, 537, 89, 891, 918, 4398
rplL	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
rplM	72.8	Ribosomal protein, large	50S ribosomal subunit protein L13	253	1941, 894
rplN	74.3	Ribosomal protein, large	50S ribosomal subunit protein L14	252	666
rplO	74.2	Ribosomal protein, large	50S ribosomal subunit protein L15	251	1945, 666
rplP	74.3	Ribosomal protein, large	50S ribosomal subunit protein L16	250	4969
rplQ	74.1	Ribosomal protein, large	50S ribosomal subunit protein L17	249	275, 2865, 3496, 666
rplR	74.2	Ribosomal protein, large	50S ribosomal subunit protein L18	248	666
rplS	59.1	Ribosomal protein, large	50S ribosomal subunit protein L19	247	3407, 597
rplT	38.7	Ribosomal protein, large	*pdzA*; 50S ribosomal subunit protein L20	17608	1213
rplU	71.8	Ribosomal protein, large	50S ribosomal subunit protein L21	246	2013, 2246
rplV	74.3	Ribosomal protein, large	*eryB*; erythromycin sensitivity; 50S ribosomal subunit protein L22	245	4762, 4969, 736
rplW	74.3	Ribosomal protein, large	50S ribosomal subunit protein L23	244	4969
rplX	74.3	Ribosomal protein, large	50S ribosomal subunit protein L24	243	666, 896
rplY	49.2	Ribosomal protein, large	50S ribosomal subunit protein L25	242	
rpmA	71.8	Ribosomal protein, large	50S ribosomal subunit protein L27	241	2246
rpmB	82.1	Ribosomal protein, large	50S ribosomal subunit protein L28	240	1936, 2466, 2716, 4154
rpmC	74.3	Ribosomal protein, large	50S ribosomal subunit protein L29	239	4969
rpmD	74.2	Ribosomal protein, large	50S ribosomal subunit protein L30	238	666
rpmE	88.9	Ribosomal protein, large	50S ribosomal subunit protein L31	237	893
rpmF	24.7	Ribosomal protein, large	50S ribosomal subunit protein L32	17605	1988
rpmG	82.1	Ribosomal protein, large	50S ribosomal subunit protein L33	236	1936, 2466, 2716, 4154
rpmH	83.7	Ribosomal protein, large	*rimA*, *ssaF*; 50S ribosomal subunit protein L34	235	1631, 3285, 4611, 546
rpmI	38.8	Ribosomal protein, large	50S ribosomal subunit protein A (L35)	17602	4623
rpmJ	74.2	Ribosomal protein, large	50S ribosomal subunit protein X (L36)	17599	4623, 666

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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]
rpoA	74.1	RNA polymerase	*phs*, *sez*; phage P2 *vir1* resistance; RNA polymerase, α-subunit (EC 2.7.7.6)	234	1426, 2236, 275, 2865, 3318, 3496, 3497, 3754, 3755, 4292, 666
rpoB	90.1	RNA polymerase	*ftsR*, *groN*, *mbrD*, *nitB*, *rif*, *ron*, *stl*, *stv*, *tabD*, *sdgB*; 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
rpoC	90.2	RNA polymerase	*tabD*; 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
rpoD	69.2	RNA polymerase	*alt*; 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
rpoE	58.4	RNA polymerase	RNA polymerase σ^{E}-subunit, high-temperature transcription (heat shock and oxidative stress)	36181	1767, 3592
rpoH	77.5	RNA polymerase	*fam*, *hin*, *htpR*; heat-shock transcription RNA polymerase σ^{32}-subunit (EC 2.7.7.6)	618	1532, 1533, 2120, 2407, 3145, 4418, 4484, 4913, 612
rpoN	72.0	RNA polymerase	*glnF*, *ntrA*; RNA polymerase σ^{60}-subunit, transcription of N-source-controlled genes	17926	1770, 1864, 1904, 2904, 3517, 656, 657
rpoS	61.7	RNA polymerase	*abrD*, *dpeB*, *katF*, *nur*, *appR*; 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
rpoZ	82.3	RNA polymerase	*spoS*; RNA polymerase, ω subunit	28445	1400, 2597
rpsA	20.7	Ribosomal protein, small	*ssyF*; 30S ribosomal subunit protein S1	230	1099, 2247, 2248, 3390, 3926, 3927, 4027, 746
rpsB	4.1	Ribosomal protein, small	30S ribosomal subunit protein S2	229	2428, 296, 3133, 418, 88
rpsC	74.3	Ribosomal protein, small	30S ribosomal subunit protein S3	228	4969
rpsD	74.1	Ribosomal protein, small	*ramA*, *sud*$_2$; 30S ribosomal subunit protein S4	227	1662, 275, 3496, 3497, 666
rpsE	74.2	Ribosomal protein, small	*eps*, *spc*, *spcA*; 30S ribosomal subunit protein S5	226	1662, 2975, 666, 956
rpsF	95.3	Ribosomal protein, small	*sdgH*; 30S ribosomal subunit protein S6	225	1937, 3928
rpsG	74.8	Ribosomal protein, small	*K12*; 30S ribosomal subunit protein S7	224	3498
rpsH	74.2	Ribosomal protein, small	30S ribosomal subunit protein S8	223	666, 4784
rpsI	72.8	Ribosomal protein, small	30S ribosomal subunit protein S9	17596	1941, 897
rpsJ	74.4	Ribosomal protein, small	*nusE*; 30S ribosomal subunit protein S10	222	1012, 2559, 4927, 851
rpsK	74.1	Ribosomal protein, small	30S ribosomal subunit protein S11	221	275, 3496, 666
rpsL	74.8	Ribosomal protein, small	*asuB*; *strA*; 30S ribosomal subunit protein S12	220	489, 3498
rpsM	74.1	Ribosomal protein, small	30S ribosomal subunit protein S13	219	1212, 275, 3496, 666
rpsN	74.2	Ribosomal protein, small	30S ribosomal subunit protein S14	218	666
rpsO	71.3	Ribosomal protein, small	*secC*; 30S ribosomal subunit protein S15	217	1126, 1182, 1231, 2246, 2457, 3459, 3492, 3494, 3638, 3850, 4333, 4334
rpsP	59.1	Ribosomal protein, small	30S ribosomal subunit protein S16	216	1935, 3235, 3407, 599
rpsQ	74.3	Ribosomal protein, small	*neaA*; 30S ribosomal subunit protein S17	215	4969, 630
rpsR	95.3	Ribosomal protein, small	30S ribosomal subunit protein S18	214	1938, 3928, 891
rpsS	74.3	Ribosomal protein, small	30S ribosomal subunit protein S19	213	1935, 4969
rpsT	0.4	Ribosomal protein, small	*sup*$_{s20}$; 30S ribosomal subunit protein S20	212	2700, 2701, 4830
rpsU	69.2	Ribosomal protein, small	30S ribosomal subunit protein S21	211	2671, 2673, 3148, 579, 892
rrfA	87.0	Ribosomal RNA, 5S	5S rRNA of *rrnA* operon	210	1146, 4044, 439
rrfB	89.9	Ribosomal RNA, 5S	5S rRNA of *rrnB* operon	209	4044, 522, 523
rrfC	85.0	Ribosomal RNA, 5S	5S rRNA of *rrnC* operon	208	4044, 4904
rrfD	73.7	Ribosomal RNA, 5S	5S rRNA of *rrnD* operon	207	1096, 4044
rrfE	90.8	Ribosomal RNA, 5S	5S rRNA of *rrnE* operon	206	1146, 2543, 4044, 439
rrfF	73.7	Ribosomal RNA, 5S	*rrfD*β, *rrvD*; 5S rRNA of *rrnD* operon	33643	394
rrfG	58.7	Ribosomal RNA, 5S	5S rRNA of *rrnG* operon	205	1146, 4044
rrfH	4.8	Ribosomal RNA, 5S	5S rRNA of *rrnH* 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]
rrlA	87.0	Ribosomal RNA, 23S	23S rRNA of *rrnA* operon	203	1146, 1502, 3236, 4383, 439, 915, 926
rrlB	89.8	Ribosomal RNA, 23S	23S rRNA of *rrnB* operon	202	1502, 3063, 3236, 3785, 4383, 522, 523, 524, 915
rrlC	85.0	Ribosomal RNA, 23S	23S rRNA of *rrnC* operon	201	1502, 3236, 4383, 915
rrlD	73.8	Ribosomal RNA, 23S	23S rRNA of *rrnD* operon	200	1096, 1502, 3236, 4383, 915
rrlE	90.7	Ribosomal RNA, 23S	23S rRNA of *rrnE* operon	199	1146, 1502, 2543, 3236, 4383, 439, 915
rrlG	58.7	Ribosomal RNA, 23S	23S rRNA of *rrnG* operon	198	1146, 1502, 3236, 4383, 915
rrlH	4.8	Ribosomal RNA, 23S	23S rRNA of *rrnH* operon	197	1146, 1502, 3236, 4383, 4384, 915
rrmA	41.1	Ribosomal RNA modification	23S rRNA *m1G745* methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance	56816	1576
rrnA	96.9	Ribosomal RNA (operon)	See Fig. 1	23593	
rrnB	89.8	Ribosomal RNA (operon)	*cqsE*, *rrnB1*; see Fig. 1	195	1661, 248
rrnC	84.9	Ribosomal RNA (operon)	*cqsB*; see Fig. 1	19503	2056
rrnD	73.7	Ribosomal RNA (operon)	*cqsD*; see Fig. 1	193	1752
rrnE	90.7	Ribosomal RNA (operon)	*rrnD1*; see Fig. 1	192	1752, 2543
rrnG	58.7	Ribosomal RNA (operon)	See Fig. 1	10891	1661, 53
rrnH	4.8	Ribosomal RNA (operon)	See Fig. 1	190	
rrsA	86.9	Ribosomal RNA, 16S	16S RNA of *rrnA* operon	189	4458, 926
rrsB	89.8	Ribosomal RNA, 16S	16S RNA of *rrnB* operon	188	3063, 318, 3341, 3535, 440, 4458, 522, 523, 879
rrsC	84.9	Ribosomal RNA, 16S	16S RNA of *rrnC* operon	187	4458
rrsD	73.8	Ribosomal RNA, 16S	16S RNA of *rrnD* operon	186	4458
rrsE	90.7	Ribosomal RNA, 16S	16S RNA of *rrnE* operon	185	2543, 4458
rrsG	58.8	Ribosomal RNA, 16S	16S RNA of *rrnG* operon	184	1146, 4015, 4458
rrsH	4.8	Ribosomal RNA, 16S	16S RNA of *rrnH* operon	183	1146, 4058, 4458
rsd	94.4	Regulation of σ^D	Stationary phase protein, binds major σ-subunit	54664	2023
rseA	58.3	Regulation of σ^E	*mclA*; membrane protein, negative regulator of σ^E	37241	2965, 977
rseB	58.3	Regulation of σ^E	Binds *rseA*, negative regulation of σ^E	37244	2965, 977
rseC	58.3	Regulation of σ^E	Deletion does not affect σ^E activity	37247	2965, 977
rspA	35.5	Repressor of σ^S production	Prevents homoserine lactone-induced synthesis of σ^S, starvation induced	36959	1856
rspB	35.5	Repressor of σ^S production	Function unknown, transcribed with *rspA*, starvation induced	36962	1856
rssA	27.8	Regulation of σ^S	Two-component response regulator, affecting σ^S-dependent proteins	37468	1718
rssB	27.8	Regulation of σ^S	*mviA*, *spreE*, two-component response regulator, affecting σ^S-dependent proteins	37471	1718, 3034, 3532, 4952
rsuA	49.1	rRNA, small pseudouridine	16S RNA pseudouridine 516 synthase	36034	4786
rtcA	76.6	RNA terminal phosphate cyclase	Cyclase activity similar to human enzyme; RNA 3′-terminal phosphate cyclase	56879	1399a
rtcB	76.6	RNA terminal phosphate cyclase		56882	1399a
rtcR	76.6	RNA terminal phosphate cyclase		56885	1399a
rtn	48.9	Resistance to N4	Probable membrane protein; resistance to phages lambda and N4	54796	1605
rus	12.3	*ruv* suppressor	Resolvase; resolves Holliday structures	32471	2722, 2745, 4003
ruvA	41.9	Repair UV?	*lexA* regulon; Holliday junction recognition	17923	1281, 13, 163, 1966, 305, 306, 3373, 4049, 4478, 4479, 4712
ruvB	41.9	Repair UV?	*lexA* regulon; branch migration of Holliday structures	17920	1281, 13, 305, 306, 3373, 4712
ruvC	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
sad	34.3	Succinate-semialdehyde deHase	Succinate-semialdehyde dehydrogenase, NAD dependent (EC 1.2.1.24)	180	2759, 4088
sanA	48.1	Sensitivity vancomycin	Amplification abolishes vancomycin-sensitive permeability defects of mutants	50224	3673
sapA	29.2	Sensitivity to antimicrobial peptides	Peptide transport system periplasmic protein	51886	3371, 322a, 4792a
sapB	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[c]
sapC	29.1	Sensitivity to antimicrobial peptides	Peptide transport system permease	51880	I, H
sapD	29.1	Sensitivity to antimicrobial peptides	*trkE*; affects potassium transport; peptide transport system ATP-binding protein	35326	1161, 3371, 3372, 3914
sapF	29.1	Sensitivity to antimicrobial peptides	Peptide transport system ATP-binding protein	35323	3372
sbaA	96.5	Serine, branched-chain amino acids	Regulation of serine and branched-chain amino acid metabolism	179	919
sbcB	44.9	Suppression of *recBC*	*xonA*; suppresses *recB recC* mutations; exonuclease I	178	3156, 3417, 3418, 3529, 3845, 4291, 4834
sbcC	8.9	Suppression of *recBC*	Cosuppressor with *sbcB* of *recB recC* mutations	17917	2451, 2594, 2595, 3128, 4834, 676, 823
sbcD	8.9	Suppression of *recBC*	Cosuppressor with *sbcB* of *recB recC* mutations	30972	1423, 2451, 823
sbmA	8.5	Sensitivity B17 microcin	Methylmalonyl-CoA mutase (*mcm*)	17914	2435
sbmC	44.8	Sensitivity B17 microcin	*gyrI*; DNA gyrase inhibitor; in high copy protects cells from replication inhibitor MccB17; SOS induced; blocks MccB17 export	50396	222, 3114a
sbp	88.5	Sulfate binding protein	Periplasmic sulfate-binding protein	17911	1710
sdaA	40.8	Serine deaminase	L-Serine deaminase	32312	3987, 4258, 4260
sdaB	63.1	Serine deaminase	L-Serine deaminase, L-SD2	33324	3988, 4259
sdaC	63.1	Serine deaminase	*dcrA*; regulator of L-SD2; putative serine transporter	33329	2546, 3988, 4259
sdhA	16.3	Succinate dehydrogenase	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	17908	4741, 4773, 615, 866, 934, 3354
sdhB	16.3	Succinate dehydrogenase	Succinate dehydrogenase iron-sulfur protein	17905	4741, 4773, 615, 934, 3354
sdhC	16.3	Succinate dehydrogenase	*cybA*; succinate dehydrogenase membrane anchor subunit, cytochrome b_{556} (EC 1.3.99.1)	17902	3052, 3053, 615, 3354
sdhD	16.3	Succinate dehydrogenase	Succinate dehydrogenase hydrophobic subunit (EC 1.3.99.1)	17899	4741, 4773, 615, 3354
sdiA	43.0	Suppress division inhibitors	Suppresses inhibitory effect of the MinC/MinD division inhibitor, positive regulator *ftsQAZ*	30919	1361, 4659
sds	30.4	Suppresses disulfide bond	Motility defects		4792a
secA	2.3	Secretory	*azi*, *pea*, *prlD*; translocation ATPase for protein export	176	1079, 1241, 1279, 2329, 3286, 3287, 3358, 349, 3818, 3919, 598, 751, 921
secB	81.5	Secretory	Protein export; chaperone SecB	17896	1293, 2227, 2234, 2361, 2362, 2363, 2454, 260, 3519, 3919, 4675, 4676
secD	9.2	Secretory	Membrane component of protein export complex	17893	1366, 2329, 2651, 3469, 921
secE	90.0	Secretory	*prlG*; 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
secF	9.2	Secretory	Membrane protein with protein secretion function	29893	1198, 1365, 2329, 2651, 2817, 3467, 3469, 3794, 4264, 921
secG	71.6	Secretory	*prlH*; p12 cytoplasmic membrane protein involved with protein export	33484	1079, 1622, 3199, 3201, 450, 451, 4733
secY	74.2	Secretory	*prlA*; 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
selA	81.0	Selenium	*fdhA* (formate dehydrogenase activity); with SelD, converts serine residue to selenocysteine on tRNA	785	1276, 2480, 3887
selB	81.0	Selenium	*fdhA*; novel elongation factor promoting selenocysteine incorporation (specific for selenocysteyl tRNA)	17890	1274, 2480, 345, 3887
selC	82.6	Selenium	*fdhC*; selenocysteyl $tRNA_{UCA}$ (converted from serine tRNA)	17887	2313, 237, 2478, 2480, 3887
selD	39.8	Selenium	Selenophosphate synthase; reduced selenium donor for selenocysteic tRNA and protein	32292	1125, 1275, 2226, 2479, 3887, 4184

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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]
semA	40.5	Sensitivity to microcin	Sensitivity to microcin E492	17884	3552
seqA	15.4	Sequestration	*hobH*; DNA biosynthesis; negative modulator of replication initiation	31506	208, 2646, 4096, 4608, 471
serA	65.9	Serine	Phosphoglycerate dehydrogenase (EC 1.1.1.95)	173	3239, 4420, 4444, 4949, 73
serB	99.6	Serine	Phosphoserine phosphatase (EC 3.1.3.3)	172	3705
serC	20.6	Serine	*pdxC*, *pdxF*; phosphoserine aminotransferase (EC 2.6.1.52)	171	1019, 1020, 1099, 1370, 3161, 4034a
serR	2.3	Serine	Regulates level of seryl-tRNA synthetase		4392
serS	20.2	Serine	Serine hydroxamate resistance; seryl-tRNA synthetase (EC 6.1.1.11)	169	1659, 4444
serT	22.2	Serine	*divE*; serine tRNA$_1$	168	2313, 34, 4345
serU	44.0	Serine	*su*$_1$, *Su-1*, *ftsM*, *supD*, *supH* (amber suppressor); serine tRNA$_2$	167	2313, 2455, 3324, 4197, 4407, 1122a
serV	60.7	Serine	*supD* (ochre suppressor); serine tRNA$_3$	166	2313, 1122a
serW	19.9	Serine	*serW*α; *serWX* duplicate genes; serine tRNA$_5$	17881	2313, 3849, 1122a
serX	23.6	Serine	*serW*β; *serWX* duplicate genes; serine tRNA$_5$	17878	2313, 1122a
sfa	22.7	Suppressor of *fabA*	Suppresses *fabA6*	46624	3696
sfcA	33.5	*sbc* fusion C-terminal	Probably *maeA*, malic enzyme, NAD linked (EC 1.1.1.38)	32176	2719
sfiC	25.8	Septum formation inhibition	Element of e14, inhibitor of cell division	17875	1858, 1978, 2715, 933
sfsA	3.5	Sugar fermentation stimulation	*sfs1*; regulatory for maltose metabolism; overexpression increases amylomaltase	30524	2176
sfsB	71.8	Sugar fermentation stimulation	*nlp*, *sfs7*; Ner-like regulatory protein	35693	175, 2176, 744
shiA	44.1	Shikimate	Shikimate and dehydroshikimate permease	163	1185
sipC	82.6	Suppressor of increased permeability	Mutations reverse the susceptibility to vancomycin and other hydrophobic antibiotics caused by TraT plasmid gene	51306	3563
sipD	82.7	Suppressor of increased permeability	Same phenotype as that produced by *sipC*	36869	3563
sir	61.2	SOS-independent repair	SOS-independent repair of mitomycin C-induced DNA damage	36505	2366
sixA	52.9		Phosphohistidine phosphatase affecting His-Asp phosphorelay of ArcB, etc.	54917	3248
sloB	75.0	Slow growth	Tolerance for amidinopenicillin and nalidixic acid; slow growth rate	162	4716
slp	78.7	Stationary-phase lipoprotein	C starvation and stationary phase inducible; outer membrane lipoprotein	33726	3971, 63
slr	14.7	Selenolipoic acid resistant	Suppresses lipoate requirement of *lipA*; functions in lipoic acid synthesis	36705	3633
slt	99.8	Soluble lytic transglycosylase	Lytic transglycosylase, major autolysin	34819	1155, 332
slyD	74.9	Sensitivity to lysis	FK-506-BP-like lysis protein for ϕX174; metal ion-regulated peptidyl-prolyl *cis/trans*-isomerase, filamentation if overexpressed	35441	1809, 1814, 3730, 3731, 4804
slyX	74.9	Sensitivity to lysis	Required for ϕX174 lysis	54726	3731
smp	99.6	Serine B-contraposed membrane protein	Transcribed divergently from *serB*, overlapping promoter; membrane protein	34649	3162, 3163
smtA	21.0	SAM-dependent methyltransferase	Putative methyltransferase, SAM-dependent	50317	4844
sodA	88.3	SOD	Member of SoxRS regulon; superoxide dismutase, Mn	17593	1217, 301, 3178, 3540, 3541, 4338, 4445, 638, 819, 4355
sodB	37.4	SOD	Superoxide dismutase, Fe	15256	1217, 1529, 2204, 301, 3155, 3178, 3904, 638, 639
sodC	37.1	SOD	Superoxide dismutase, Cu, Zn	50310	1908, 302, 303
sohA	70.6	Suppressor of *htr*	*prlF*; suppressor of *htrA*; putative protease	35411	204, 2212, 4123
sohB	28.6	Suppressor of *htr*	Suppressor of *hyr*; homology with inner membrane protease IV, which digests cleaved signal peptides	31951	203
solA	24.1	Sarcosine oxidase-like	Homology with sarcosine oxidases, but stronger activity with methyltryptophan than with sarcosine	50669	2332
soxR	92.2	Superoxide	Regulatory protein of *soxRS* regulon; induces nine-protein *sox* regulon when superoxide levels increase	27798	1384, 1748, 3223, 3224, 4480, 4793, 78
soxS	92.1	Superoxide	Regulatory protein of *soxRS* regulon; induces nine-protein *sox* 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]
speA	66.4	Spermidine	Biosynthetic decarboxylase (EC 4.1.1.19)	161	2996, 3877, 472
speB	66.4	Spermidine	Agmatinase (EC 3.5.3.11)	160	3877, 472, 4318
speC	66.9	Spermidine	Ornithine decarboxylase (EC 4.1.1.17)	159	3877, 472
speD	2.9	Spermidine	*S*-Adenosylmethionine decarboxylase (EC 4.1.1.50)	158	4323, 4324
speE	2.9	Spermidine	Spermidine synthase	17590	4323, 4324
speF	15.5	Spermidine	Ornthine decarboxylase, inducible (EC 4.1.1.17)	31559	2149, 2153
speG	35.7	Spermidine	Spermidine acetyltransferase	53446	1334
spf	87.2	Spot 42	Spot 42 RNA	157	2067, 3473, 3661
spoT	82.3	Spot (magic spot)	Guanosine 5′-diphosphate, 3′-diphosphate pyrophosphatase, ppGpp synthetase II activity	156	2913, 3070, 3868, 3869, 4807a
sppA	39.8	Signal peptide peptidase	Protease IV; signal peptide peptidase	13763	1877, 4308
spr	48.9	Suppressor of *prc*	Suppresses thermosensitivity of *prc* mutants at low osmolality; in turn suppressed by multicopy expression of PBP 7	54675	1641
srlA	60.9	Sorbitol	*gutA*, *sbl*; D-glucitol-specific enzyme II of phosphotransferase system	155	3644, 437, 4749, 4822, 4823
srlB	60.9	Sorbitol	*gutB, sbl*; D-glucitol (sorbitol)-specific enzyme III of the phosphotransferase system	11886	4822, 4823
srlD	60.9	Sorbitol	*gutD*, *sbl*; sorbitol-6-phosphate dehydrogenase (EC 1.1.1.140)	153	4749, 4822, 4823
srlE	60.9	Sorbitol	*gutE*; protein encoded by reading frame adjacent to *srlA*	56893	3644a
slrR	60.9	Sorbitol	*gutR*; regulatory gene for *srl*	152	4749
srmB	58.4	Suppressor ribosomal mutant	*rbaB*, *rhlA*; ATP-dependent RNA helicase	32859	3191
srnA	9.4	Stable RNA	Degradation of stable RNA	151	3263
ssaE	52.5	Suppression secA	Suppresses *secA* mutations	17869	3285
ssaG	41.8	Suppression secA	Suppresses *secA* mutations	17866	3285
ssaH	94.1	Suppression *secA*	Suppresses *secA* mutations	17863	3285
ssb	92.1	Single-strand binding	*exrB*, *lexC*; single-strand DNA-binding protein; member of *lex* regulon	150	1435, 2237, 2393, 2916, 3568, 3835, 3837, 3917
sseA	57.1	Sensitivity to serine	Enhances serine sensitivity (inhibits homoserine deHase) on lactate; rhodanese-like protein	33023	1617
sseB	57.2	Sensitivity to serine	Enhances serine sensitivity (inhibits homoserine deHase) on lactate; weaker than *sseA*	33026	1617
sspA	72.7	Stringent starvation protein	*pog*; stress response protein	17860	1333, 1335, 3979, 3985, 4742
sspB	72.7	Stringent starvation protein	Stress response protein	33594	4742
ssrA	59.3	Small stable RNA	*sipB*; 10Sa RNA (nonribosomal); role in modulating DNA-binding proteins	35783	103, 1218, 2310, 2312, 3074, 3251, 3252, 3652, 3653, 692
ssrS	65.8	Small stable RNA	6S RNA	17857	1833, 2459
ssyA	57.1	Suppression of *secY*	Suppressor of *secY* mutation	17854	4026
ssyD	3.0	Suppression of *secY*	Suppressor of *secY* mutation	17848	4027
stfZ	2.3	*fts* in reverse	Antisense RNA blocks *ftsZ* mRNA translation, inhibits cell division	36124	1032
stkA	77.5	Suppressor of transposase killing	Suppresses cell aberrations and death caused by Tn*5* transposase overexpression	36083	4699
stkB	86.1	Suppressor of transposase killing	Suppresses cell aberrations and death caused by Tn*5* transposase overexpression	36093	4699
stkC	98.5	Suppressor of transposase killing	Suppresses cell aberrations and death caused by Tn*5* transposase overexpression	36087	4699
stkD	28.6	Suppressor of transposase killing	Suppresses cell aberrations and death caused by Tn*5* transposase overexpression	36090	4699
stpA	60.3	Suppressor of td mutant	*hnsB*; *hns*-like protein, suppresses T4 td mutant	34492	1300, 4024, 4133, 4933–4935
strC	7.0	Streptomycin	*strB*; low-level streptomycin resistance; modifies ribosome structure	149	3688
strM	78.3	Streptomycin	*asuF*?; control of ribosomal ambiguity	148	4272
stsA	84.7		Altered RNase activity	147	2493
sucA	16.3	Succinate	*lys*, *met*; α-ketoglutarate dehydrogenase (decarboxylase component)	146	3355, 4149, 4741, 4773, 553, 934, 935
sucB	16.4	Succinate	*lys*, *met*; dihydrolipoamide succinyltransferase component of α-ketoglutarate deHase (EC 2.3.1.61)	145	4149, 4150, 4151, 553
sucC	16.4	Succinate	Succinyl-CoA synthetase β-subunit	17845	4150, 4151, 552, 553
sucD	16.5	Succinate	Succinyl-CoA synthetase α-subunit	17842	552, 553
sufI	68.1	Suppressor of *ftsI*	*sui*; suppressor of *ftsI*	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]
sugE	94.3	Suppressor of *gro*	Suppresses *groL* mutation and mimics effects of *gro* overexpression	34460	1512
suhA	78.4	Suppressor heat-shock proteins	Induction of heat shock genes	17839	4419
suhB	57.4	Suppressor heat-shock proteins	Inositol monophosphate (EC 3.1.3.25)	32968	1910, 1911, 2804, 4870, 675
sulA	22.0	Suppressor of *lon*	*sfiA*; inhibits cell division and *ftsZ* ring formation	144	1391, 1857, 1978, 2027, 2984, 794
sup		Suppressor	Various suppressor tRNAs, see Table 2		
supQ	12.5	Suppressor	Uncharacterized suppressor	129	3780
surA	1.2	Survival	Affects stationary-phase survival	30326	2446, 2964, 3752, 4440
surE	61.8	Survival	*ygbC*; required for stationary-phase survival	33215	2523
syd	63.0	*secY-d1* suppression	Interacts with *secY*	36980	4036
tabC	86.3	T4 abortion	Mutants fail to support growth of T4	125	4329
tag	80.0	3-Methyl adenine glycosylase	3-Methyladenine DNA glycosylase I, constitutive	124	1184, 2144, 365, 3816, 3957, 4201, 773
talA	55.5	Transaldolase	Transaldolase A	54690	4164
talB	0.2	Transaldolase	Transaldolase B	36818	4165
tanA	41.6	Trehalose, anaerobic	Anaerobic growth on trehalose	37222	2799
tanB	68.1	Trehalose, anaerobic	Anaerobic growth on trehalose	37910	2799
tap	42.4	Taxis protein	Flagellar regulon; chemotactic membrane receptor for aspartate; methyl-accepting protein IV; peptide receptor	123	2342, 2951, 4101, 4102, 4651, 468
tar	42.4	Taxis, aspartate and repellents	*cheM*; chemotactic signal transducer protein II, methyl accepting; aspartate chemoreceptor	122	2206, 2342, 4101, 4102, 4650, 4651, 468
tas	64	Tyrosine auxotrophy suppressor	Suppresses tyrosine requirement of *tyrA14* O^6 strain	57111	4416a
tauA	8.3	Taurine	Uptake of taurine (probable S source)	51775	4549, 4550
tauB	8.3	Taurine	Taurine transport	51772	4549, 4550
tauC	8.3	Taurine	Taurine transport	51769	4549, 4550
tauD	8.3	Taurine	Taurine dioxygenase	51766	1131, 4549, 4550
tbpA	1.6	Thiamin binding protein	Periplasmic thiamin binding protein	34691	1785
tdcA	70.4	Threonine dehydratase, catabolic	Transcriptional activator of *tdc* operon	29702	1353, 1466, 1600, 3944, 3945, 689
tdcB	70.3	Threonine dehydratase, catabolic	*tdc*, *mukA*; threonine dehydratase (EC 4.2.1.16); LysR family of regulator proteins	17587	1466, 1467, 1468, 3944, 3945, 950
tdcC	70.3	Threonine dehydratase, catabolic	L-Threonine L-serine permease, membrane associated, anaerobically inducible	29709	1466, 3246, 3944, 3945
tdcD	70.3	Threonine dehydratase, catabolic	Propionate kinase, anaerobic	54712	1736, 3944
tdcE	70.2	Threonine dehydratase, catabolic	Pyruvate formate-lyase/ketobutyrate formate-lyase	54717	1736, 3944
tdcF	70.2	Threonine dehydratase, catabolic	Function unknown	54720	1736
tdcG	70.2	Threonine dehydratase, catabolic	Anaerobic pathway, L-serine deaminase, L-serine dehydratase	54723	1736, 3944
tdcR	70.4	Threonine dehydratase, catabolic	Positive regulatory protein for threonine dehydratase, TdcB	29692	3943, 3944
tdh	81.7	Threonine dehydrogenase	Threonine dehydrogenase	17584	141, 3619, 3620, 715
tdi	4.3	Transduction inhibition	Affects transduction, transformation, and rates of mutation	121	4181
tdk	27.9	Thymidine kinase	Deoxythymidine kinase	120	1763, 1887, 369, 405
tehA	32.3	Tellurite resistance	Multidrug resistance; K^+-tellurite ethidium and proflavin transport; membrane protein	32106	4372, 4500, 4501, 4645
tehB	32.3	Tellurite resistance	Multidrug resistance; K^+-tellurite ethidium and proflavin transport	32109	4372, 4500, 4501
TerA	28.8	Terminus	Terminus of DNA replication; replication fork inhibition	17836	1294, 1744, 1754, 1756, 1757, 3395, 979
TerB	36.2	Terminus	*psrB*; terminus of DNA replication; replication fork inhibition	17833	1097, 1294, 1744, 1754, 1756, 1757, 281, 3395, 352, 979
TerC	34.6	Terminus	*psrA*; terminus of DNA replication; replication fork inhibition	17830	1294, 1744, 297, 298, 454
TerD	27.6	Terminus	Terminus of DNA replication; replication fork inhibition	17827	1294, 1744
TerE	23.3	Terminus	Terminus of DNA replication; replication fork inhibition	29805	1746
TerF	50.0	Terminus	Terminus of DNA replication; replication fork inhibition	29289	3992
tesA	11.2	Thioesterase	*apeA*; 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]
tesB	10.2	Thioesterase	Thioesterase II	17581	3087, 3130
tgt	9.2	tRNA-guanine transglycosylase	tRNA-guanine transglycosylase	118	1358, 2651, 3205, 3654, 3655
thdA	10.5	Thiophene degradation	Degradation of furans and thiophenes; may be *tlnA*?	17824	3
thdC	94.2	Thiophene degradation	Degradation of furans and thiophenes	17821	3
thdD	99.8	Thiophene degradation	Degradation of furans and thiophenes	15908	3
thiA	90.3	Thiamin cluster	Hydroxyethylthiazole synthesis, cluster of genes	117	4564
thiB	90.3	Thiamin	Unidentified, not THI-P synthase, thiamine pyrophosphate pyrophosphorylase activity	116	4564
thiC	90.4	Thiamin (and thiazole)	Hydroxymethylpyrimidine synthesis; thiamin pyridine moiety biosynthesis	115	4564
thiD	47.2	Thiamin (and thiazole)	Phosphomethylpyrimidine kinase	114	1905
thiE	90.3	Thiamin (and thiazole)	*thiA*; thiamin-thiazole moiety synthesis	34301	4564
thiF	90.3	Thiamin (and thiazole)	*thiA*; thiamin-thiazole moiety synthesis	34298	4564
thiG	90.3	Thiamin (and thiazole)	*thiA*; thiamin-thiazole moiety synthesis	34295	4564
thiH	90.3	Thiamin (and thiazole)	*thiA*; thiamin-thiazole moiety synthesis	342952	4564
thiI	9.5	Thiamin (and thiazole)	Thiamin biosynthesis; also 4-thiouridine generation in tRNAs	56890	3032, 4681a
thiJ	47.1	Thiamin (and thiazole)	*thiA*, *thiN*; hydroxymethylpyrimidine kinase	37230	2977, 3122
thiK	25.1	Thiamin (and thiazole)	Thiamin kinase	113	1906, 2425
thiL	9.4	Thiamin (and thiazole)	*thiJ*; thiaminmonophosphate kinase	112	1906, 4681a
thiM	47.2	Thiamin (and thiazole)	Hydroxyethylthiazole kinase (EC 2.7.1.50)	34309	2976
thrA	0.0	Threonine	*thrD*, *Hs*; aspartokinase I-homoserine dehydrogenase I (EC 1.1.1.3 and EC 2.7.2.4)	111	1568, 2162, 2682, 4859, 845, 925
thrB	0.1	Threonine	Homoserine kinase (EC 2.7.1.39)	110	1568, 3801, 4948, 845, 846
thrC	0.1	Threonine	Threonine synthase (EC 4.2.99.2)	109	1568, 3375, 845, 846
thrS	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
thrT	90.0	Threonine	Threonine tRNA$_3$	107	1849, 2313, 2467, 3743, 90
thrU	89.9	Threonine	Threonine tRNA$_4$	106	1849, 2313, 2467, 3743, 90
thrV	73.7	Threonine	Threonine tRNA$_1$ in *rrnD*	105	1096, 1146, 2313, 3814, 818
thrW	5.6	Threonine	Threonine tRNA$_2$	10363	2313, 818, 914
thyA	63.9	Thymine	Aminopterin, trimethoprim resistance; thymidylate synthetase (EC 2.1.1.45)	104	1107, 1730, 1742, 286, 328, 3762, 3870, 658
tig	9.8	Trigger factor	Trigger factor; chaperone	35681	1583, 1737, 1738, 2119, 4236, 4525, 619
tktA	66.3	Transketolase	Transketolase (EC 2.2.1.1)	103	2059, 4161, 4162, 4947
tktB	55.6	Transketolase	Transketolase (EC 2.2.1.1)	29992	1889, 4947
tldD	73.0	Tolerance for *letD*	Tolerance for effects on DNA gyrase by sex factor F gene *letD*	50304	3061
tlnA	10.5	Thiolutin	*tlnI*; resistance or sensitivity to thiolutin; may be *thdA*?	102	4083
tmk	24.9	Thymidine kinase	Deoxythymidine kinase	17578	357, 3657, 967, 405
tnaA	83.8	Tryptophanase	*ind*, *tnaR*; tryptophanase (EC 4.1.99.1)	101	2927, 3170, 3171, 4222, 4611, 4677, 4911, 568, 996
tnaB	83.8	Tryptophanase	*trpP*; low-affinity Trp permease	69	1119, 2102, 3865, 4218, 568, 996
tnm	92.0	Tn migration	Transposition of Tn*9* and other transposons, development of phage Mu	100	1901, 1902, 4107, 4725
tolA	16.7	Tolerance	*cim*, *excC*, *lky*, *tol-2*; 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
tolB	16.7	Tolerance	*lkyA* (leakage of periplasmic proteins), *tol-3*; azaleucine resistant; tolerance to colicins E2, E, A, and K	98	1270, 1284, 2447, 2449, 2506, 3039, 4281, 4282, 484, 635, 957, 99
tolC	68.5	Tolerance	*colE1-i*, *mtcB*, *refI*, *weeA*, *toc* (topoisomerase compensation), *mukA*; 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
tolD	22.9	Tolerance	Bacteriocin tolerant; tolerance to colicins E2, E3, and ampicillin	96	1284, 484, 572, 957
tolE	22.9	Tolerance	Bacteriocin tolerant; tolerance to colicins E2, E3, and ampicillin	95	1284, 484, 635, 957
tolI	0.1	Tolerance	Bacteriocin tolerant; sensitivity to colicins Ia and Ib	94	484, 635, 957

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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]
tolJ	0.1	Tolerance	Bacteriocin tolerant; sensitivity to L, A, S4, E, and K	93	1284, 484, 635, 957
tolM	74.8	Tolerance	*cmt*; high-level tolerance to colicin M	92	1284, 1618, 1650, 2865, 3892, 484, 635, 957
tolQ	16.7	Tolerance	*fii*, *tolP*? 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
tolR	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
tonB	28.2	T-one	*T1rec*, *exbA*; sensitivity to T1, ϕ80, 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
topA	28.6	Topoisomerase	*supX*; topoisomerase I, omega protein I	89	1091, 2494, 2680, 2762, 3301, 3310, 4206, 4466, 4467, 4482, 4654
topB	39.7	Topoisomerase	*mutR*; topoisomerase III; *mutR* phenotype is decreased deletion formation between short repeats	29988	1048, 3931, 4653, 4730, 4937
torA	22.8	Trimethylamine oxide reductase	Molybdoprotein trimethylamine N-oxide reductase	17575	2874, 3377
torC	22.8	Trimethylamine oxide reductase	*c*-Type cytochrome	29977	2874
torD	22.9	Trimethylamine oxide reductase	Transcribed with *tor*; no similarity with other proteins in database	29980	2874
torR	22.8	Trimethylamine oxide reductase	Regulatory gene	36408	4071, 4072
torS	22.7	Trimethylamine oxide reductase	Sensor partner of TorRT, two-component system for trimethylamine N-oxide induction	50902	2061
torT	22.8	Trimethylamine oxide reductase	TorRT system	50188	2062
tpiA	88.6	Triose P isomerase	Triosephosphate isomerase	88	1710, 3423
tpr	27.7	*tyrT* region protamine	Protamine-like protein, apparently transcribed with *tyrT*	87	75
tpx	29.9	Thiol peroxidase	Thioredoxin-linked thiol peroxidase	46706	2225, 668
treA	26.8	Trehalose	*tre*; trehalase, periplasmic	17572	2865, 3651, 430
treB	96.2	Trehalose	IITre, translocation system, Tre-specific PTS enzyme II	34601	4253, 431
treC	96.2	Trehalose	Trehalose-6-phosphate hydrolase, osmoprotectant	34597	3677, 4253, 431
treF	79.0	Trehalose	Cytoplasmic trehalase	35861	1807
treR	96.2	Trehalose	Repressor	51427	1807, 1808, 2258
trg	32.1	Taxis to ribose and galactose	Methyl-accepting chemotaxis protein III, ribose acceptor, flagellar regulon	85	1646, 1678, 2865, 2991, 362, 363, 419
trkA	74.0	Transport K^+	Major constitutive K^+ transport system; potassium transport inner membrane protein subunit	84	1161, 1162, 1618, 2865, 3914, 448
trkD	84.7	Transport K^+	*kup*; major constitutive K^+ transport system	81	1161, 3910, 449, 4611
trkG	30.6	Transport K^+	Major constitutive K^+ transport system; membrane protein, perhaps inactive during anaerobic growth	29963	1074, 1162, 3915, 3916, 4453
trkH	86.9	Transport K^+	Potassium transport membrane protein subunit; binding of TrkA to membrane; mutants require high K^+	34066	1074, 1162, 3915, 448
trmA	89.7	tRNA methyltransferase	*rT*; tRNA (uracil-5)-methyltransferase (EC 2.1.1.35)	79	1577, 256, 2564, 3229, 3405
trmB	7.1	tRNA methyltransferase	tRNA (guanine-7)-methyltransferase (EC 2.1.1.33)	78	2763
trmC	52.6	tRNA methyltransferase	5-Methylaminoethyl-2-thiouridine in tRNA	77	1599, 366
trmD	59.1	tRNA methyltransferase	tRNA (guanine-7)-methyltransferase (EC 2.1.1.33)	76	1599, 3407, 594–596
trmE	83.7	tRNA methyltransferase	*thdF* (thiophene oxidation?); tRNA base modification, 5-methyl-aminoethyl, 2-thiouridine synthesis	17806	1147, 49, 568
trmF	84.8	tRNA methyltransferase	5-Methyl aminoethyl-2-thiouridine biosynthesis	17803	1147
trmH	82.4	tRNA methyltransferase	*spoU*; tRNA (Gm18) 2′-O-methyltransferase	33877	2319, 3406
trmU	25.7	tRNA methyltransferase	*asuE*; antisuppressor; tRNA base-modifying enzyme; 2-thiouridine synthesis	37613	1503, 3708, 4272

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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]
trnA	63.1	tRNA	Level of several tRNAs	75	724
trpA	28.3	Tryptophan	Tryptophan synthase subunit A (EC 4.2.1.20)	74	1157, 1470, 1551, 1760, 2819, 3173, 4314, 4788, 4789, 4871
trpB	28.4	Tryptophan	Tryptophan synthase subunit B (EC 4.2.1.20)	73	1157, 1470, 1760, 2819, 4871, 865
trpC	28.4	Tryptophan	Bifunctional enzyme *N*-(5-phosphoribosyl)anthranilate isomerase, indole-3-glycerolphosphate synthetase (EC 4.1.1.48)	72	1157, 1470, 1760, 1812, 2819, 4871, 747
trpD	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
trpE	28.4	Tryptophan	*anth*, *tryD*, *tryp-4*; anthranilate synthase component I (EC 4.1.3.27)	70	1157, 1470, 1703, 1760, 2819, 3026, 3174, 3175, 3321, 4871
trpR	99.8	Tryptophan	5-Methyltryptophan resistance; regulator of *trp* operon and *aroH*; autogenously regulated tryptophan repressor protein	68	1567, 1568, 210, 3705, 4078, 4872, 288
trpS	75.7	Tryptophan	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	67	1608, 1609, 410
trpT	85.0	Tryptophan	*su7* (UGA suppression), *supU* (UAG suppression), *su8*, *supV* (UAA suppression)[f]; tryptophan tRNA	66	2313, 3324, 4904, 926, 1122a
truA	52.4	tRNA uridine (modification to pseudouridine	*asuC*, *hisT*, *leuK*; pseudouridine synthase, anticodon stem and loop specific	623	142, 143, 144, 2784, 3211, 3226, 3363, 3955, 4523, 543
truB	71.3	tRNA uridine (modification to pseudouridine)	Pseudouridine synthase, ψ55 specific	35528	3226
trxA	85.4	Thioredoxin	*fipA*, *tsnC*; thioredoxin	65	1865, 2550, 2551, 2764, 2807, 3850, 3772, 3773, 3775, 3778, 3784, 4641, 58, 926
trxB	20.1	Thioredoxin	Thioredoxin reductase	17569	1009, 1613, 3774, 3776, 3777
trxC	58.6	Thioredoxin	Thioredoxin 2	54694	2953
tsaA	4.8	t6AtRNA-SAM-methyltransferase	N^6-threonylcarbamoyladenosine(t6A) modification of $tRNA^{Thr}$, adenosine A37 to threonylated adenosine; tRNA(m6t6A37) methyltransferase	53741	3564
tsf	4.1	Ts elongation factor	EF-Ts, elongation factor for transcription, stable	64	2428, 296, 418, 88
tsmA	40.1	Thymine suppression modifier	Affects suppression efficiency for nonsense and frameshift mutations of Thy^- strains	36603	1731
tsr	98.9	Taxis to serine and repellents	*cheD*; serine chemoreceptor; methyl accepting chemotaxis protein II, membrane receptor	63	1693, 2206, 3367, 4650, 467, 469, 617, 84
tsx	9.3	T-six	*T6rec*, *nupA*; T6, colicin K resistance; nucleoside channel	62	1635, 2651, 492, 494
ttdA	69.1	Tartrate dehydratase	L-Tartrate dehydratase subunit (EC 4.2.1.32)	33459	3628
ttdB	69.1	Tartrate dehydratase	L-Tartrate dehydratase subunit (EC 4.2.1.32)	33462	3628
ttk	82.2		Function unknown, TetR, AcrR family of regulators	52724	1144, 568
tufA	74.7	Tu elongation factor	*kirT*, *pulT*; duplicate gene for EF-Tu subunit; elongation factor, unstable	61	1561, 2042, 2334, 2379, 2433, 4342, 4543, 4548, 4732, 4887, 4928, 91
tufB	90.0	Tu elongation factor	*kirT*, *pulT*; 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
tus	36.3	Terminus utilization substance	*tau*; 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
tynA	31.2	Tyramine	*feaA*, *maoA*; tyramine oxidase (EC 1.4.3.4)	59	178, 3066, 4200, 4848
tyrA	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
tyrB	91.9	Tyrosine	Tyrosine aminotransferase (EC 2.6.1.5); TyrR regulon	57	1283, 2372, 4856
tyrP	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]
tyrR	29.8	Tyrosine	TyrR regulon repressor; regulates *aroF*, *aroG*, *tyrA*, and aromatic amino acid transport; autoregulation of *tyrR* not mediated by tyrosine	55	2436, 2819, 3441, 4640, 4740, 4855, 4857, 531, 623, 734, 785, 837, 838, 881, 882
tyrS	36.9	Tyrosine	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	54	1043, 236, 2398, 2938
tyrT	27.7	Tyrosine	*tyrT*α, *su*$_{\mathrm{III}}$, *Su-3*, *Su-4*, *supC* (ochre suppressor[f]), *supF* (amber suppressor), *supO*? tandemly duplicated tyrosine tRNA$_1$ (*tyrTV*)	53	2313, 3743, 3744, 445, 446, 447
tyrU	90.0	Tyrosine	*sup15B*, *supM* (ochre suppressor), *supZ* (amber suppressor[f]); tyrosine tRNA$_2$	52	1122a, 1849, 2313, 2467, 3743, 90
tyrV	27.7	Tyrosine	*tyrT*β; tandemly duplicated, tyrosine tRNA$_1$	51	3743, 1122a
ubiA	91.6	Ubiquinone	4-Hydroxybenzoate polyprenyltransferase	50	2549, 2576, 3195, 725
ubiB	86.7	Ubiquinone	*fadI*, *fre*, *fsrC*; 2-octaprenylphenol→2-octaprenyl-6-methoxyphenol; flavin reductase (EC 1.6.99.–)?	49	1273, 1385, 4174, 926
ubiC	91.6	Ubiquinone	Chorismate lyase	48	2549, 3176, 4124
ubiD	86.7	Ubiquinone	Reaction: 3-octaprenyl-4-hydroxybenzoate to 2-octaprenylphenol	47	858
ubiE	86.7	Ubiquinone	Reaction: 2-octaprenyl-6-methoxy-1,4-benzoquinone to 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	46	4902
ubiF	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
ubiG	50.4	Ubiquinone	Reaction: 1-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone to ubiquinone 8	44	1421, 1829, 3451
ubiH	65.8	Ubiquinone	*visB*; reaction: 2-octaprenyl-6-methoxyphenol to 2-octaprenyl-6-methoxy-1,4-benzoquinone	43	3100, 2974
ubiX	52.3	Ubiquinone	*dedF*; sequence homologous to *ubiX* of *S. typhimurium*, which codes for 3-octaprenyl 4-hydroxybenzoate carboxy-lyase	17797	3211
ucpA	54.8	Upstream *cysP*	Temporary name; protein with homology to short-chain dehydrogenases/reductases	51898	4080
udk	46.1	Uridine kinase	Uridine/cytidine kinase (EC 2.7.1.48)	42	2058, 3156, 3157
udp	86.5	Uridine phosphorylase	Uridine phosphorylase (EC 2.4.2.3)	41	1272, 3426, 3539, 58, 66, 926, 4646
ugpA	77.3	Uptake glycerol phosphate	*psiB*, *psiC*; glycerol P transport system, integral membrane protein	40	2147, 2931, 3320, 3539, 3946, 3948, 3949, 4261
ugpB	77.4	Uptake glycerol phosphate	*psiB*, *psiC*; periplasmic binding protein of *sn*-glycerol-3-phosphate transport system	39	2147, 2931, 3320, 3946, 3948, 3949, 4261
ugpC	77.3	Uptake glycerol phosphate	*sn*-Glycerol-3-P transport system; ABC family permease	17794	1701, 2147, 3320, 3948, 3949, 4261
ugpE	77.3	Uptake glycerol phosphate	*sn*-Glycerol-3-P transport system; membrane protein	17791	2147, 3320, 3948, 3949, 4261
ugpQ	77.3	Uptake glycerol phosphate	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.-); cytosolic	33697	548, 4261, 4428
uhpA	82.9	Utilization hexose phosphate	Response regulator (2-component system) required for *uhpT* transcription	15437	1316, 1933, 2079, 4006, 4717
uhpB	82.9	Utilization hexose phosphate	Membrane protein controlling UhpA activity, sensor kinase	15448	1316, 1933, 1934, 4717
uhpC	82.9	Utilization hexose phosphate	Membrane protein controlling UhpA activity, in concert with UhpB	15449	1316, 1933, 1934, 2079, 4006, 4717
uhpT	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
uidA	36.5	HexUronIDes	*gurA*, *gusA*; β-D-glucuronidase (EC 3.2.1.31)	36	2000, 386, 387, 3905
uidB	36.5	HexUronIDes	*gusB*, *uidP*; glucuronide permease	53467	33, 394
uidR	36.5	HexUronIDes	*gusR*; regulatory gene	35	384, 386, 387, 388
umuC	26.5	UV mutator	*uvm*; UV induction of mutations, error-prone repair; forms complex with UmuD and UmuD′	34	1068, 1145, 1297, 2245, 2776, 3404, 4041, 4778, 4779, 2284
umuD	26.5	UV mutator	*uvm*; 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
ung	58.5	Uracil nucleic acid glycosylase	Uracil-DNA-glycosylase	25	4567

Continued on following page

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]
upp	56.4	Uracil PRTase	*uraP*; uracil phosphoribosyltransferase (EC 2.4.2.9)	24	1621, 1799, 97
ups	27.1	Up-suppression?	Efficiency of nonsense suppressors; see *prfA*	23	3782, 854
uraA	56.4	Uracil	Uracil concentration dependence of *pyr* mutants; Ura ABC transporter	33043	96
uro	85.9	Uroporphyrinogen	*hemC-Y* operon	37849	3871, 60
usg1	52.5	Upstream gene, temporary	Temporary name for gene in *pdxB* operon, unknown function	32746	144
ushA	10.9	UDP sugar hydrolase	UDP-glucose hydrolase (5′-nucleotidase)	22	574, 854
uspA	78.4	Universal stress protein	Global regulatory gene for stress response	28127	1046, 1302, 3232, 3233
uup	21.7		Precise excision of insertion elements	17785	1799, 3631
uvh	90.2	UV hyperresistant to UVC	Resistance to UVC, peroxide and antibiotics; may affect SOS repair	51073	21
uvrA	92.0	Ultraviolet resistant	*dar*; *lex* regulon; repair of UV damage to DNA; excision nuclease subunit A	21	1867, 2201, 3831, 3834, 3837, 3838, 3479
uvrB	17.5	UV resistant	*dar-1*, *dar-6*; DNA repair; excision nuclease subunit B, ATPase I and helicase II	20	1268, 128, 191, 3345, 1831, 3836, 3838, 3839, 4319, 4547
uvrC	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
uvrD	86.1	UV resistant	*dar-2*, *dda*, *mutU*, *pdeB*, *rad*, *recL*, *srjC*, *uvr502*, *uvrE*; DNA-dependent ATPaseI-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
uvs	91.1	UV sensitivity	UV-sensitive mutants, locus linked to *uvr*	51076	21
uxaA	69.8	Utilization hexuronate galacturonate	Altronate hydrolase (EC 4.2.1.7)	17	1851, 3489, 3682, 892
uxaB	34.6	Utilization hexuronate galacturonate	Altronate oxidoreductase (EC 1.1.1.58); *exu* regulon	16	1854, 2796, 381, 383, 394
uxaC	69.9	Utilization hexuronate galacturonate	Uronate isomerase (EC 5.3.1.12)	15	1851, 2795, 2796, 3489, 3682, 382, 892
uxuA	98.1	Utilization hexuronide glucuronate	Mannonate hydrolase (EC 4.2.1.8)	14	1305, 3681, 3687, 385
uxuB	98.1	Utilization hexuronide glucuronate	Mannonate oxidoreductase (EC 1.1.1.57)	13	1304, 3681, 3687, 385
uxuR	98.1	Utilization hexuronide glucuronate	Regulatory gene for *uxuBA* operon	12	3680, 3681, 3687
valS	96.5	Valine	*val-act*; valyl-tRNA synthetase (EC 6.1.1.9)	11	1660, 1691, 1692, 197, 4091
valT	16.8	Valine	*valT*α; duplicate gene with triplicated *valUXY*; valine $tRNA_1$	10	2313, 3324, 4898
valU	54.3	Valine	*valU*α, *valU*γ; tandemly triplicate *valUXY*; valine $tRNA_1$	17782	2313, 3238, 538, 539
valV	37.6	Valine	Valine $tRNA_{2B}$	17563	2313
valW	37.6	Valine	Valine $tRNA_{2A}$	17560	2313
valX	54.3	Valine	*valU*γ; tandemly triplicate *valUXY*; valine $tRNA_1$	28696	3238, 539
valY	54.3	Valine	*valU*γ; tandemly triplicate *valUXY*; valine $tRNA_1$	28699	3238, 539
valZ	16.8	Valine	*valT*β; valine $tRNA_1$	51028	394
vsr	43.7	Very short (patch) repair	Repairs mismatches; minimizes effects of C methylation	28927	1282, 2540, 2541, 2697, 336, 4130, 1720
wrbA	23.0	W(Trp) repressor binding	Affects association between Trp repressor and operators in stationary phase	31836	4865
xapA	54.4	Xanthosine P	*pndA*; xanthosine phosphorylase	41105	539
xapB	54.3	Xanthosine P	Xanthosine transport protein, NupG-like	41101	3962
xapR	54.3	Xanthosine P	*pndR*; regulatory gene for *xapA*	8	2282, 3962, 539, 586
xasA	33.8	Extreme acid survival	Glutamate-dependent enzyme, may function in protection against cytoplasmic acidification	36518	1732
xerC	86.1	*cer*-specific recombination	Recombinase, site specific	30184	2841, 376, 377, 378, 812
xerD	41.7	*cer*-specific recombination	*xprB*; recombinase, site specific	30201	2639, 2641, 376, 377
xni	63.1	Exonuclease nine	*exo*; exonuclease IX, a 3′–5′ exonuclease acting preferentially on single-stranded DNA, probable excision repair function	56869	3983a
xseA	56.7	Exonuclease VII	Exonuclease VII, large subunit	6	4535, 687
xseB	9.5	Exonuclease VII	Exonuclease VII, small subunit	17557	4535, 4536
xthA	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[c]
xylA	80.3	Xylose	D-Xylose isomerase (EC 5.3.1.5)	5	2377, 2437, 2741, 3735, 3896, 4128, 502
xylB	80.3	Xylose	Xylulokinase (EC 2.7.1.17)	4	2741, 3735, 4128, 502
xylE	91.4	Xylose	Xylose-proton symport	17776	1295, 2376, 4277, 961, 962
xylF	80.4	Xylose	*xylT*; xylose-binding protein, transport system	17773	2377, 3735, 4128, 4277, 961
xylG	80.4	Xylose	Xylose transport gene	33780	4128
xylH	80.4	Xylose	Xylose permease protein	33783	4128
xylR	80.5	Xylose	Regulatory gene	3	2741, 3735, 4128
yhhP	77.7	Temporary name	*sirA*; provisional name for small protein required for cell growth	55460	4847
yihG	87.1	Temporary name	Poly(A) polymerase II; see also *pcnB*	50490	631
yjaB	90.8	Temporary name	*f147*; temporary names for protein transcribed divergently from a promoter that overlaps the *metA* promoter, divergent from *metA*	51779	1414
yohF	47.9	Temporary name	RpoS regulon, acid sensitive, induced by ALS inhibition, similarity to insect-type ADH	55069	4552
zipA	54.5	*ftsZ*-interacting protein	Essential gene, affects cell division and growth; septal ring structural protein	51069	1602
zntA	77.7	Zn translocation	Zn^{2+} translocating P-type ATPase; hypersensitive to Zn and Cd salts	53884	3650
znuA	41.8	Zn uptake	High-affinity ABC transport system for zinc	52879	3381
znuB	41.8	Zn uptake	High-affinity ABC transport system for zinc	52882	3381
znuC	41.8	Zn uptake	High-affinity ABC transport system for zinc	52886	3381
zur	91.8	Zn uptake regulation	Regulatory gene for high-affinity transport of zinc	52889	3381
zwf	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
abrD	*rpoS*	*air*	*aer*, *aegA*?
acpS	*acpX*	*ala-act*	*alaS*
acrB	*gyrB*	*alaW*β	*alaX*
acrE	*acrB*	*alaW*α	*alaW*
acrS	*envR*	*ald*	*fbaA*, *aldA*
act	*alaS*, *glyS*, *pflA*	*alnA*	*dadB*
ade$_{c}$	*purN*	*alnR*	*dadQ*
ade3	*purE*	*alt*	*rpoD*
ade$_{f}$	*purE*	*alu*	*dpp*
ade$_{g}$	*purC*	*ampA*	*ampC*
ade$_{ub}$	*purF*	*ams*	*rne*
adhC	*adhE*	*amt*, *amtA*	*cysQ*
adi	*adiA*	*ana*	*adhE*
ads	*folD*	*anr*	*osmE*
adth$_{a}$	*purD*	*ant*	*nhaA*, *mutS*
aeg-46.5	*ccm-nap* operon	*anth*	*trpE*
aidA	*alkA*	*apbC*	*mrp*
aidC	*nrfA*, *nrfG*	*apeA*	*tesA*
aidD	*alkB*	*apk*	*lysC*

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TABLE 2—*Continued*

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

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TABLE 2—*Continued*

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

Continued on following page

TABLE 2—*Continued*

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

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TABLE 2—*Continued*

Synonym	Gene symbol from Table 1
lig	*ligA*
lipP	nike?
lir	*acrA*
livR	*lrp*
lky	*tolA*, *B*
lkyA	*tolB*
lnt	*cutE*
lolB	*hemM*
LopC	*clpX*
LopP	*clpP*
lov	*argS*
lovB	*alaS*
loxB	*attP1,P7*
lrs	*lrp*
lss	*lrp*
lstR	*lrp*
luxH-like	*ribB*
*lysT*α, β, γ	*lysT*, *W*, *Y*
mac	*maa*
malB	*malK*
maoA	*tynA*
maoB	*feaR*
mas	*aceB*
mazE	*chpR*
mazF	*chpA*
Mb	*acrA*
mbf	*lrp*
mbl	*acrA*
mbrA	*rep*
mcb	*pmbA*
mclA	*rseA*
mdaA	*nfsA*
mdfA	*cmr*
mdrA	*cydC*
mdrH	*cydC*
mec	*dcm*
mel-4	*melB*
mel-7	*melA*
meoA	*ompC*
met-1	*metB*
metM	*metL*
*metT*β	*metU*
*metZ*β	*metV*
mglD	*galS*
mglP	*mglA*, *C*
mhpS	*mhpD*
micA	*mutY*
mlc	*dgsA*
mlpA	*lpp*
mmrA	*rep*, *rhlB*?
mni	*manC*
modR	*modE*
molA	*malM*
momR	*oxyR*
mon	*mreB*
mopA	*groS*
mopB	*groL*
mor	*oxyR*
motD	*fliN*
mpt	*manX*, *Z*
mra	*murF*
mrbA	*murA*
mrc	*lpcB*
mrsA	*glmM*
mrsC	*hflB*
msgA	*ftsN*
msmA	*dksA*
msmB	*cspC*
msmC	*cspE*
msp	*arcA*
mssA	*cmk*
mssB	*deaD*
msuA	*dadX*?
msyA	*hns*
mtcA	*acrA*
mtcB	*tolC*
muc	*lon*
mukA	*tolC*
mukE	*kicA*
mukF	*kicB*
murZ	*murA*
mutA	*glyV*
mutC	*glyW*
mutD	*dnaQ*
mutH	*dnaX*
mutR	*topB*
mutU	*uvrD*
mvrA	*fpr*
mvrC	*emrE*
nagR	*nagC*
nalA	*gyrA*
nalC	*gyrB*
nalD	*gyrB*
nam	*pncA*
narA	*moaA*
narB	*mobA*
narC	*narG*
narD	*modC*, *E*, *F*
narR	*narL*, *X*
nbp	*fis*
ncf	*hemB*
neaA	*rpsQ*
nek	*rimK*
nfrC	*rffE*
nfsB	*nfnB*
nfsI	*nfnB*
nfxA	*gyrA*
nfxC	*marA*
nfxD	*parE*
nic	*nadB*
nirA	*fnr*
nirR	*fnr*
nitA	*rho*
nitB	*rpoB*
nlp	*sfsB*
nlpE	*cutF*
nmpA	*pst*, *pstS*
nmpB	*phoR*
norA	*gyrA*
norB	*marA*?
nov	*cls*
ntr	*nfnB*
ntrA	*rpoN*
ntrB	*glnL*
ntrC	*glnG*
ntrL	*nadE*
nucR	*deoR*
nupA	*tsx*
nur	*rpoS*
nusD	*rho*
nusE	*rpsJ*
oldB	*fadB*
ole	*fadR*
ompB	*envZ*, *ompR*
ompE	*phoE*
ompH	*hlpA*

Continued on following page

TABLE 2—*Continued*

Synonym	Gene symbol from Table 1
omsA	*lpxD*
opdA	*prlC*
oppI	*lrp*
optA	*dgt*
osmZ	*hns*
osrA	*proU*
ossA	*fnr*
ossB	*gltB*, *D*, *F*
ostA	*imp*
padA	*feaB*
panK	*coaA*
papA	*atpA*
papC	*atpG*
papD	*atpB*, *D*
papE	*atpH*
papF	*atpF*
papG	*atpC*
papH	*atpE*
par	*ompC*
parB	*dnaG*
parD	*gyrA*
parvA	*ppiC*
paxA	*dcd*
pbpA	*mrdA*
pbpB	*ftsI*
pbpF	*mrcB*
pcbA	*gyrB*
pcsA	*dinD*
pdeB	*uvrD*
pdeC	*ligA*
pdxC	*serC*
pdxF	*serC*
pdzA	*rplT*
pea	*secA*
pel	*manY*
perA	*envZ*
pexB	*dps*
pfv	*dacA*
pgsB	*lpxB*
phd	*hcaA*, *B*
phe-act	*pheS*
pheR	*pheU*
pheW	*pheU*
phmA	*nmpC*
phoM	*creC*
phoM-orf2	*creB*
phoR1	*phoR*
phoR2a	*pstS*
phoR2b	*pstA*
phoRc	*phoB*
phoS	*pstS*
phoT	*phoB*, *U*, *pstA*, *B*
phoW	*pstC*
phrA	*modF*
phs	*rpoA*
phsE?	*dacD*
pil	*fim*, *fimB*, *C*, *D*
pilA	*fimA*
pilB	*fimC*
pilC	*fimD*
pilD	*fimF*, *G*
pilE	*fimH*
pilG	*hns*
pilH	*fimE*
pin	*argU*
pinO	*pioO*
plsA	*adk*
PMG	*mgl*
pmi	*manA*
pmsR	*msrA*
pndR	*xapR*
poaA	*putA*
pog	*sspA*
poh	*oriC*
polC	*dnaE*
pon	*lpcB*
ponA	*mrcA*
ponB	*mrcB*
popA	*hemH*
popB	*hemF*
popC	*hemL*
popE	*hemC*
ppfA	*dsbA*
ppsA	*pps*
prd	*fucP*
prlA	*secY*
prlB	*rbsB*
prlD	*secA*
prlF	*sohA*
prlG	*secE*
prlH	*secG*
Pro2	*proC*
pro$_1$	*proA*
pro$_2$	*proB*
pro$_3$	*proC*
prv	*mutH*
psiB	*ugpA*, *B*
psiC	*ugpA*, *B*
psiD	*phn*, *phnD*
psiH	*phoH*
psrA, *B*	*TerC*, *B*
psuA	*rho*
pts	*man*
ptsF	*fruA*
ptsL	*manX*
ptsM	*manX*, *Y*, *Z*
ptsN	*nagE*
ptsO	*npr*
ptsP	*manY*
ptsX	*manX*, *Z*
pulT	*tufA*, *B*
pup	*deoD*
Pur2	*purE*
purC	*purF*
purE2	*purK*
purG	*purM*
purI	*purL*
pyrA	*carA*, *B*
qmeA	*fabI*
R1pho	*phoR*
R2pho	*pstA*, *S*
rad	*uvrD*
radB	*recN*
ramA	*rpsD*
ramB	*rimG*
rap	*pth*
rapA	*hepA*
rbaB	*srmB*
rblA	*lrp*
rbsP	*rbsA*, *B*, *C*, *D*
rbsT	*rbsA*, *C*
recA	*lexA*
recL	*uvrD*
refI	*tolC*
refII	*creD*
relC	*rplK*

Continued on following page

TABLE 2—*Continued*

Synonym	Gene symbol from Table 1
res	*rimF*
resA	*polA*
rfbC	*rfbD*
rfbD	*rfbC*
rffE	*rffG*?
rglA	*mcrA*
rglB	*mcrB*
rhaC	*rhaR*, *S*
rhlA	*srmB*
ribE	*ribC*
ribG	*ribD*
ribH	*ribE*
rif	*rpoB*
rimA	*rpmH*
rm	*hsdM*, *R*
rnh	*rnhA*
rnsA	*rna*
rnsC	*rho*
rodA	*mrdB*
rodY	*mreB*
ron	*rpoB*
rorA	*recB*
rot	*ppiA*
rpoF	*fliA*
*rrfD*β	*rrfF*
rrnB1	*rrnB*
rrnD1	*rrnE*
rrvD	*rrfF*
rsgA	*ftn*
rT	*trmA*
rts	*coaA*
sac	*ascB*, *F*
sbl	*srlA*, *B*, *D*
sdgA	*dnaG*
sdgB	*rpoB*
sdgE	*era*
sdrA	*rnhA*
sec	*hemF*
secC	*rpsO*
sefA	*fabZ*
seg	*arcA*, *dnaK*
sep	*ftsI*
sez	*rpoA*
sfcA	*mae*?
sfhB	*rluD*
sfiA	*sulA*
sfiB	*ftsZ*
sfrA	*arcA*
sfrB	*rfaH*
sfs1	*sfsA*
sfs7	*sfsB*
shl	*fruR*
sin	*rnhA*
sipB	*acrA*, *ssrA*
sirA	*yhhP*
skp	*hlpA*, *lpxD*
slpA	*intA*
slr	*lplA*
slt	*mltB*
smbA	*pyrH*
sms	*radA*
sof	*dut*
som	*rfbA*, *B*
soxQ	*marA*, *R*
spcA	*rpsE*
spoS	*rpoZ*
spoU	*trmH*
spoV	*recG*?
spr	*lexA*
srf	*recA*
srgA	*priA*
srjA	*infC*
srjB	*helD*
srjC	*uvrD*
ssaD	*nusB*
ssaF	*rpmH*
ssc	*lpxD*
ssd	*cpxA*
ssyB	*nusB*
ssyF	*rpsA*
ssyG	*infB*
stc	*micF*
stl	*rpoB*
strA	*rpsL*
strB	*strC*
stsB	*rimH*
stv	*rpoB*
Su-1	*serU*
Su-2	*glnV*, *X*
Su-3	*tyrT*
Su-4	*tyrT*
Su-6	*leuX*
Suβ	*lysT*
Su_{II}	*glnV*, *X*
su_{I}	*serU*
su_{B}	*glnU*
su_{III}	*tyrT*
su7	*trpT*
su8	*trpT*
suA36	*glyU*
sud_{2}	*rpsD*
sueB	*prfA*
sufD	*glyU*
sui	*sufI*
sulB	*ftsZ*
sumA	*glyT*, *U*
sumB	*glyU*
sun	*rho*
sup_{S20}	*rpsT*
sup15B	*tyrU*
supB	*glnU*, *W*
supC	*tyrT*
supD	*serU*, *V*
supE	*glnV*, *X*
supF	*tyrT*
supG	*lysT*
supH	*serU*
supK	*prfB*
supL	*lysT*
supM	*tyrU*
supN	*lysV*
supO	*tyrT*?
supP	*leuX*
supT	*glyU*
supU	*trpT*
supV	*trpT*
supX	*topA*
supZ	*tyrU*
sur	*bcr*
surB	*cydC*
suxA	*bcr*
T1	*fhuA*
T1rec	*tonB*
T5rec	*fhuA*
T6rec	*tsx*
tabB	*groE*

Continued on following page

TABLE 2—*Continued*

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

[a] Temporary names (*y* names, *orf*s) are not included.

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