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Linkage Map of *Escherichia coli* K-12, Edition 7

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INTRODUCTION

The first linkage map in this series was published in 1964 (567), at which time 99 gene loci had been identified and positioned on the map. Since that time, gene loci have been added at an almost steady rate through six revisions of the map (20, 21, 566, 568, 569). In the 1983 linkage map herein, 1,027 loci are drawn on Fig. 1 and listed in Table 1. One hundred forty-six genes have been added to the map since the 1980 edition. A number of "loci" have been removed from the map, usually because they have been found to represent sequences controlling transcription and translation or have been shown to be identical to genes placed on the map earlier.

This review is based upon all data cited in earlier editions of the map, on the experimental literature published between June 1979 and July 1982, on manuscripts of later-appearing papers received before publication, and on personal communications of mapping data. Review articles have been included only if they present original data. References to data on restriction mapping have been included in this edition of the linkage map.

The literature on the mapping of genes in *Escherichia coli* is now so voluminous that it was not possible to include, in the Literature Cited in this review, the publications cited in earlier editions of the map. In Table 1, under References, the letter A refers the reader to the references in the 1976 edition of the map (21) and the letter B refers to the 1980 edition (20).

The reader should be cautioned, as before, that these reviews are intended as guides to the literature and not as substitutes for the original research papers. It should be emphasized that the positions shown for many loci in Fig. 1 are the result of estimates based on widely varying, or even contradictory, data.

MAP UNITS

The units of the map as drawn in Fig. 1 are minutes as determined by time-of-entry in interrupted-conjugation experiments (21). The entire linkage group is now linked by cotransduction data as well as by time-of-entry data. However, the uncertainties of the transductional data for several regions of the map are so great that the overall length of these regions can be judged only by time-of-entry data.

A significant portion of the map has been covered by physical mapping. Many small regions, mostly of less than 1 min in length, have been mapped in kilobases (kb) by restriction analysis. Note, however, that it is not possible to represent accurately on Fig. 1 distances of less than ca. 4.5 kb. Two long segments of the linkage group have been mapped physically since 1980. The length of the region between *proAB* and *purE* has been reinvestigated, this time by restriction analysis (223). A 470-kb region flanking the terminus of DNA replication, extending from *attϕ80* to *manA*, has been mapped physically (58, 59). This elegant work has settled definitively the question as to whether or not this long relatively silent region on the map represents an artifact of time-of-entry data. This region has also been spanned by cotransductional data, using transposon insertions (47, 185). The results of the physical mapping are in good agreement with the time-of-entry map, in that they agree with the rather arbitrarily chosen figure of ca. 45 kb/min which I have used to convert physically determined distances to map lengths in this review.

Cotransductional data have been converted to map distances by the formula of Wu (624a) and assuming that the effective length of the phage P1 transducing fragment is 2 min.

GENETIC NOMENCLATURE

The system of nomenclature used in this edition of the map is that of Demerec et al. (147), as in previous editions. In the 1980 map a modification of this system was proposed for designating mutations in sequences controlling transcription (operators, promoters, leaders, attenuators, and the like). In this edition of the map, these sequences have been neither drawn on Fig. 1 nor listed in Table 1. Thus, a good many "loci" have

been removed from the map. References to these elements will be found listed under the genes to which they are related.

Proposals to change gene symbols so that they might represent acronyms based on biochemical steps or on the names of enzymes have been resisted for the most part, on the grounds that this leads to confusion or loss of continuity when the older literature is consulted. The genetic nomenclature is intended to be conservative, and its value is lessened when changes of gene symbols are made. Gene symbols used formerly or proposed as alternatives for those used in Table 1 are listed in Table 2 beside the symbols used in Table 1 for the corresponding loci.

Nevertheless, the names of a few loci have been changed, for a variety of reasons. The well-known locus *tonA* has been discovered to be one of two or three clustered genes involved in hydroxamate-dependent iron uptake (290). So that these closely related genes might all have the same appropriate symbol, *tonA* has been changed to *fhuA*.

The most serious problem to have arisen involves the genes called *purG* and *purI*. It has recently been determined that the functions ascribed to these genes in previous *E. coli* linkage maps are incorrect. The gene which maps between *upp* and *guaAB* has been called *purG* and has been said to code for phosphoribosylformylglycineamide synthetase. It has now been established (253; J. Gots, personal communication) that this locus codes for phosphoribosylaminoimidazole synthetase (EC 6.3.3.1) and is thus homologous to the *purI* gene of *Salmonella typhimurium*, which is located between *purC* and *guaB* on the *S. typhimurium* linkage map (512a). The gene which maps between *glyA* and *nadB* has been called *purI* and has been said to code for phosphoribosylaminoimidazole synthetase. It has now been established that this locus codes for phosphoribosylformylglycineamide synthetase (EC 6.3.5.3) and is thus homologous to the *purG* gene of *S. typhimurium*, which is located between *glyA* and *nadB* on the *S. typhimurium* linkage map (512a). This problem could be solved by switching the designations of these two loci, so that *purG* becomes *purI* and *purI* becomes *purG*, as well as redefining the gene functions. However, it seems likely that such a solution would lead to endless confusion. Upon reading the symbol *purG* or *purI* in a paper or in a strain description, the reader would have no way of knowing whether or not the author was aware of the switch in locus designations unless this was specifically stated whenever these designations were used. For this reason, the locus designations have been changed to *purM* (formerly *purG*) and *purL* (formerly *purI*) in this revision of the map.

COMMENTS ON THE LINKAGE MAP

The two cotransduction gaps remaining on the 1980 edition of the map (20) have now been closed. The large gap between *recE* and *relB* has been spanned both by cotransduction (47, 185) and by physical mapping (58, 59), as discussed above. The gap between *pit* and *kdgK* has been closed by cotransductional mapping (136; M. Jones-Mortimer, personal communication).

There are still regions of the map for which the existing data are very unsatisfactory, however. The region between *udk* and *gyrA* is perhaps the most puzzling, and the order of loci shown in Fig. 1 is very uncertain. This region was discussed in the 1980 map (20). The recent data are even more confusingly contradictory than were those available in 1980. Altogether, the data for this region suggest that perhaps one (or more) of the strains which have been used in several laboratories in the mapping of this region carries an inversion of the chromosome between *udk* and *gyrA*. Such an inversion could account for the contradictory results reported in these and previous papers on the mapping of genes in this region. (In this connection, it is interesting that a hitherto undetected inversion of nearly 20% of the chromosome has been demonstrated recently in a widely used old ancestral stock, strain W3110 [244].) Because of the uncertainty of the cotransductional mapping across this region and the repeated suggestions in the literature that the distance between *his* and *gyrA* is longer than has been indicated on recent maps, the distance between *his* and *gyrA* has been increased by about 0.5 min in Fig. 1, although the time-of-entry data argue for a shorter distance (21).

The distance between *pyrB* and *uxuBA* also is somewhat uncertain. Of necessity, many of the cotransductional data in this region have been obtained by using widely separated markers. As discussed in the 1976 map (21), the use of very low cotransduction frequencies leads to shorter calculated map distances than does the use of cumulative distance calculated from cotransductional data for shorter intervals of the same region. However, the distance between *pyrB* and *pil* has been shortened by 0.5 min in Fig. 1 because of suggestions in the literature that this region is shorter than has been indicated in previous drawings of the map. The data are rather tenuous, however, and the length of this region should be regarded as being uncertain.

On going through all of the data from previous map reviews (20, 21), I found that the distance between *pyrD* and *pyrC* has not been determined accurately by transduction and that the data for the distance between *pyrC* and *purB* are rather contradictory. The latter data fall into two discontinuous groups, one of which gives an aver-

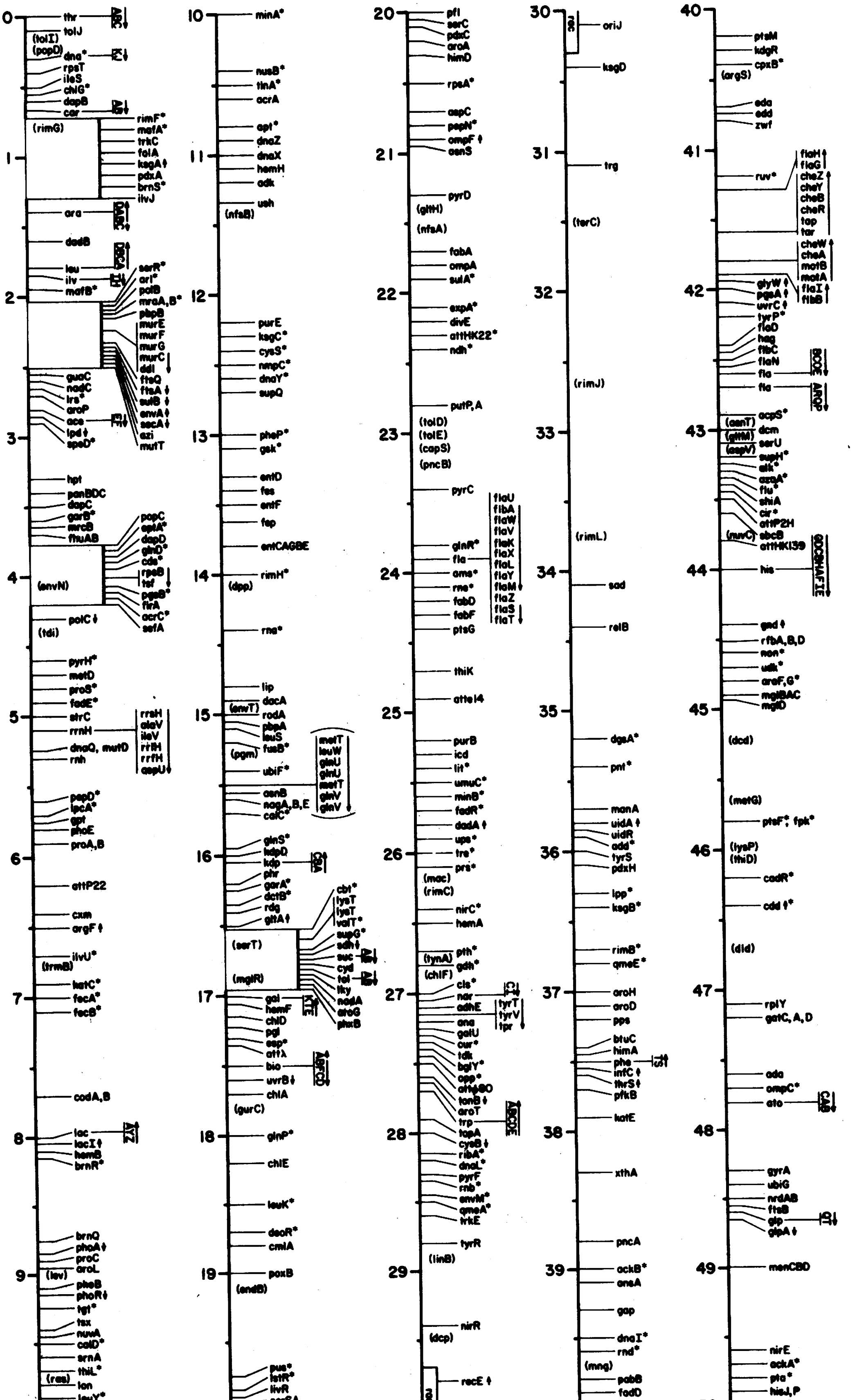
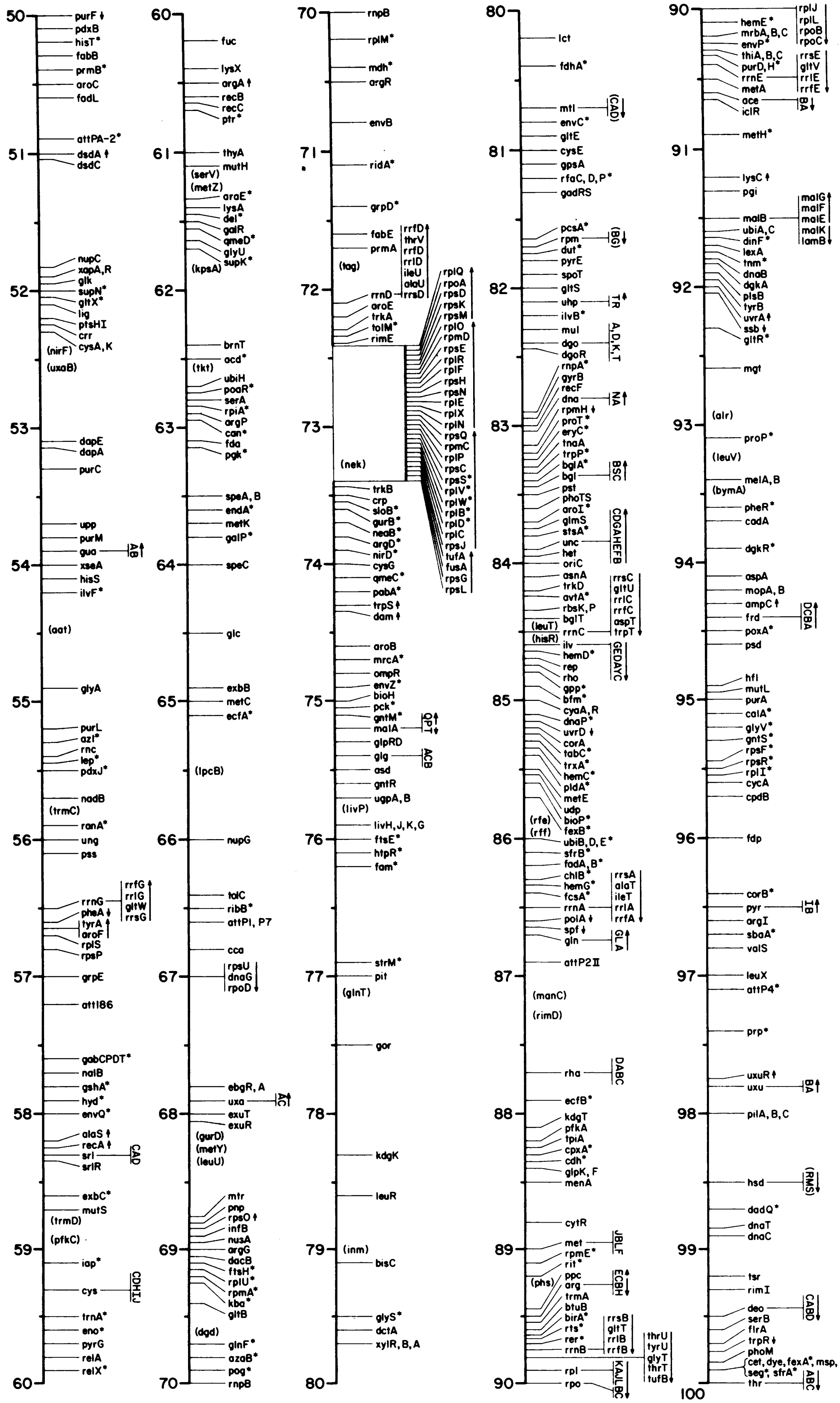


FIG. 1. Linear scale drawings representing the circular map of *E. coli* K-12. The time scale of 100 min, beginning arbitrarily with zero at the *thr* locus, is based on the results of interrupted-conjugation experiments. The genetic symbols used in this figure are defined in Table 1. Parentheses around a gene symbol indicate that the position of that marker is not well known and may have been determined only within 5 to 10 min. An asterisk



indicates that a marker has been mapped more precisely but that its position with respect to nearby markers is not known. Arrows above genes and operons indicate the direction of transcription of these loci. Parentheses around an operon indicate that, although the direction of transcription of the genes in the operon is known, the orientation of the operon on the chromosome is not known.

TABLE 1. Genetic markers of *E. coli* K-12

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
aat		(54)	Aminoacyl-tRNA-protein-transferase (EC 2.3.2.6)	B
acd		63	Acetaldehyde-CoA dehydrogenase	102
aceA	Acetate	91	*icl*; utilization of acetate; isocitrate lyase (EC 4.1.3.1)	A, 366
aceB	Acetate	91	*mas*; utilization of acetate; malate synthase A (EC 4.1.3.2)	A, 366
aceE	Acetate	3	*aceE1*; acetate requirement; pyruvate dehydrogenase (decarboxylase component)	A, B, 215, 217
aceF	Acetate	3	*aceE2*; acetate requirement; pyruvate dehydrogenase (dihydrolipoyl-transacetylase component)	A, B, 215, 217
ackA		50	Acetate kinase (EC 2.7.2.1) activity	B, 213, 340
ackB		39	Acetate kinase (EC 2.7.2.1) activity	457
acpS		43	CoA:apo-[acyl-carrier-protein]pantetheinephosphotransferase (EC 2.7.8.7); holo-[acyl-carrier-protein]synthase	464
acrA	Acridine	11	*lir, Mb, mbl, mtc*; sensitivity to acriflavine, phenethyl alcohol, sodium dodecyl sulfate	A, 110, 240
acrC	Acridine	4	Sensitivity to acriflavine	410
ada		48	Inducible DNA repair system protecting against methylating and alkylating agents	175, 282, 527
add		36	Adenosine deaminase (EC 3.5.4.4.)	B
adhE		27	Alcohol dehydrogenase (EC 1.1.1.1)	B, 351
adk		11	*dnaW, plsA*; adenylate kinase (EC 2.7.4.3) activity; pleiotropic effects on glycerol-3-phosphate acyltransferase activity	A, B, 173, 239
alaS	Alanine	58	*ala-act*; alanyl-tRNA synthetase (EC 6.1.1.1.7)	A, B, 473–475
alaT	Alanine	87	*talA*; alanine tRNA 1B; in *rrnA* operon	B
alaU	Alanine	72	*talD*; alanine tRNA 1B; in *rrnD* operon	B
alaV	Alanine	5	Alanine tRNA 1B in *rrnH* operon	170
alk	Alkylation	43	3-Methyl-adenine DNA glycosylase II, inducible	B, 175
alr		(93)	Alanine racemase (EC 5.1.1.1)	A
ampC	Ampicillin	94	β-Lactamase; penicillin resistance	A, B, 162, 163, 211, 212, 280, 281
ams		24	Alteration of mRNA stability	441
ana		27	Alcohol dehydrogenase (EC 1.1.1.1) and acetaldehyde dehydrogenase (EC 1.2.1.10) activities	B, 457
ansA		39	Cytoplasmic L-asparaginase activity	143
apt		11	Adenine phosphoribosyltransferase (EC 2.4.2.7)	B
araA	Arabinose	1	L-Arabinose isomerase (EC 5.3.1.4)	A, B
araB	Arabinose	1	Ribulokinase (EC 2.7.1.16)	A, B, 335, 389, 433
araC	Arabinose	1	Regulatory gene; activator and repressor protein	A, B, 87, 313, 335, 433, 557
araD	Arabinose	1	L-Ribulosephosphate 4-epimerase (EC 5.1.3.4)	A, B
araE	Arabinose	61	Low-affinity L-arabinose transport system	A, 312, 313, 364
araF	Arabinose	45	L-Arabinose-binding protein	B, 99, 312, 313, 319
araG	Arabinose	45	High-affinity L-arabinose transport system	312, 313, 319

Continued on next page

TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
argA	Arginine	61	*argB*, *ArgI*, Arg_2; amino-acid acetyltransferase (EC 2.3.1.1)	A, B, J
argB	Arginine	90	*ArgC*; acetylglutamate kinase (EC 2.7.2.8)	A, B, 121, 394
argC	Arginine	90	*argH*, *Arg2*; *N*-acetyl-γ-glutamyl-phosphate reductase (EC 1.2.1.38)	A, B, 121, 394
argD	Arginine	74	*argG*, Arg_I; acetylornithine aminotransferase (EC 2.6.1.11)	A
argE	Arginine	90	*argA*, *Arg4*; acetylornithine deacetylase (EC 5.1.1.16)	A, B, 121, 394
argF	Arginine	7	*argD*, *Arg5*; ornithine carbamoyltransferase (EC 2.1.3.3) (duplicate gene)	A, B, 121, 223, 256, 392, 393, 631
argG	Arginine	69	*argE*, *Arg6*; argininosuccinate synthetase (EC 6.3.4.5)	A
argH	Arginine	90	*argF*, *Arg7*; argininosuccinate lyase (EC 4.3.2.1)	A, B, 121, 394
argI	Arginine	97	Ornithine carbamoyltransferase (EC 2.1.3.3) (duplicate gene)	A, B
argP	Arginine	63	Transport of arginine, ornithine, and lysine	A
argR	Arginine	71	*Rarg*; regulatory gene	A, 161
argS	Arginine	(40)	Arginyl-tRNA synthetase (EC 6.1.1.19)	A
arl		2	Level of recombination	232, 318
aroA	Aromatic	20	3-Enolpyruvylshikimate-5-phosphate synthetase	A
aroB	Aromatic	75	Dehydroquinate synthetase	A
aroC	Aromatic	51	Chorismate synthetase	A
aroD	Aromatic	37	5-Dehydroquinate dehydratase (EC 4.2.1.10)	A, 308
aroE	Aromatic	72	Dehydroshikimate reductase	A
aroF	Aromatic	57	DAHP synthetase, tyrosine-repressible	A
aroG	Aromatic	17	DAHP synthetase, phenylalanine-repressible	A, 134
aroH	Aromatic	37	DAHP synthetase, tryptophan-repressible	A, 134, 644
aroI	Aromatic	84	Function unknown	A
aroL	Aromatic	9	Shikimate kinase II (EC 2.7.1.71)	B, D
aroP	Aromatic	3	General aromatic amino acid transport	A, 215, 217
aroT	Aromatic	28	*aroR*, *trpR*; transport of aromatic amino acids, alanine, and glycine	A, B
asd		76	*dap* + *hom*; aspartate semialdehyde dehydrogenase (EC 1.2.1.11)	A, 235, 236, 438
asnA	Asparagine	84	Asparagine synthetase A (EC 6.3.1.1)	A, B, 245, 262, 412, 595, 596
asnB	Asparagine	16	Asparagine synthetase B (EC 6.3.1.1)	B, 262
asnS	Asparagine	21	*lcs*; asparaginyl-tRNA synthetase (EC 6.1.1.22)	B, 580
asnT	Asparagine	(43)	Asparagine tRNA	B, 448
aspA	Aspartate	94	Aspartate ammonia-lyase (aspartase) (EC 4.3.1.1)	A, B
aspC	Aspartate	21	Aspartate aminotransferase (EC 2.6.1.1)	B
aspT	Aspartate	85	*tasC*; aspartate tRNA 1, duplicate gene; in *rrnC* operon	B, 633
aspU	Aspartate	5	Aspartate tRNA 1, duplicate gene; in *rrnH* operon	170
aspV	Aspartate	43	Aspartate tRNA	448
atoA	Acetoacetate	48	Acetate CoA-transferase (EC 2.8.3.-)	A
atoB	Acetoacetate	48	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	A
atoC	Acetoacetate	48	Regulatory gene	A

Continued on next page

TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
attel4	Attachment	25	Attachment site for element el4	209
attHK22	Attachment	22	*atthtt*; attachment site for phage HK022	148
attHK139	Attachment	44	Attachment site for phage HK139	149
attλ	Attachment	17	Integration site for prophages λ, 82, and 434	A, B, 255
attP1,P7	Attachment	67	*loxB*; integration site for phages P1 and P7	93, 553
attP2H	Attachment	44	Phase P2 integration site H	A
attP2II	Attachment	87	Phage P2 integration site II	A
attP4	Attachment	97	Integration site for phage P4	81
attP22	Attachment	6	*ata*; integration site for phage P22	A
attPA-2	Attachment	51	Integration site for phage PA-2	B
attφ80	Attachment	28	Integration site for prophage φ80	A, B
att186	Attachment	57	Integration site for prophage 186	A
avtA		84	Alanine-α-ketoisovalerate transaminase, transminase C	176, 608
azaA	Azaserine	43	Resistance or sensitivity to azaserine	615
azaB	Azaserine	70	Resistance or sensitivity to azaserine	615
azi	Azide	2	*pea*; resistance or sensitivity to sodium azide or phenethyl alcohol; filament formation at 42°C	A
azl	Azaleucine	55	Regulation of *ilv* and *leu* genes; azaleucine resistance	A
bfm		85	Phase BF23 multiplication	A
bglA	β-Glucoside	83	*bglD*; phospho-β-glucosidase A	A, B
bglB	β-Glucoside	83	*bglA*; phospho-β-glucosidase B	A, B, O, 479, 595
bglC	β-Glucoside	83	*bglB*; β-glucoside transport	A, B, O, 479, 595
bglS	β-Glucoside	83	*bglC*; regulatory gene	A, O
bglT	β-Glucoside	84	*bglE*; regulatory gene for phospho-β-glucosidase A synthesis	A
bglY	β-Glucoside	27	Regulatory gene; possibly repressor protein of *bgl* operon	141
bioA	Biotin	18	Group 2; 7KAP → DAPA	A, B, 25, 28, 320
bioB	Biotin	18	Conversion of dethiobiotin to biotin	A, B, 25, 28, 320
bioC	Biotin	18	Block before pimeloyl CoA	A, B
bioD	Biotin	18	Dethiobiotin synthetase	A, B
bioF	Biotin	18	Pimeloyl CoA → 7KAP	A, B
bioH	Biotin	75	*bioB*; block before pimeloyl CoA	A, 25
bioP	Biotin	86	*birB*; biotin transport	A, B, 84, 186
birA	Biotin retention	89	*bioR*, *dhbB*; biotin-[acetyl-CoA carboxylase]holoenzyme synthetase	A, B, 25–27, 84
bisC	Biotin sulfoxide	79	Biotin sulfoxide reductase, structural gene	B, 142
brnQ	Branched chain	9	Transport system 1 for isoleucine, leucine, and valine	A, B
brnR	Branched chain	8	Component of transport systems 1 and 2 for isoleucine, leucine, and valine	A
brnS	Branched chain	1	Transport system for isoleucine, leucine, and valine	A
brnT	Branched chain	62	Low-affinity transport system for isoleucine	B
btuB	B_{12} uptake	90	*bfe*, *btuA*, *cer*; receptor for vitamin B_{12}, E colicins, and bacteriopahge BF23	A, B, 394
btuC	B_{12} uptake	37	Vitamin B_{12} transport	B
bymA		(93)	Bypass of maltose permease at *malB*	A
cadA	Cadaverine	94	Lysine decarboxylase (EC 4.1.1.18)	561
cadR	Cadaverine	46	Regulatory gene for lysine decarboxylase	561

Continued on next page

TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
calA	Calcium	95	Calcium transport	67
calC	Calcium	16	Calcium transport	67
calD	Calcium	10	Calcium transport	67
can	Canavanine	63	Canavanine resistance	A
capS	Capsule	(23)	Regulation of *galU* and of capsular polysaccharide synthesis	A
carA		1	*arg* + *ura*, *cap*, *pyrA*; carbamoylphosphate synthase (EC 2.7.2.9), glutamine (light) subunit	A, 122, 197
carB		1	*arg* + *ura*, *cap*, *pyrA*; carbamoylphosphate synthase (EC 2.7.2.9), ammonia (heavy) subunit	A, 122, 197
cbt		17	Dicarboxylate-binding protein production	A, 44
cca		67	tRNA nucleotidyl transferase	A
cdd		46	Deoxycytidine deaminase (EC 3.5.4.5)	A, B, 55, 286, 287, 561
cdh		88	CDP-diglyceride hydrolase	74
cds		4	CDP-diglyceride synthase	190
cet	Colicin E2	100	*ref*, *refII*; tolerance to colicin E2	A, 221
cheA	Chemotaxis	42	Chemotactic response	A, B, 544
cheB	Chemotaxis	42	Chemotactic response; protein methylesterase activity	A, B, 61
cheR	Chemotaxis	42	*cheX*; chemotactic response; protein methylesterase activity	B, 61, 387
cheW	Chemotaxis	42	Chemotactic response	B
cheY	Chemotaxis	42	Chemotactic response	B, 61
cheZ	Chemotaxis	42	Chemotactic response	B, 61
chlA	Chlorate	18	*bisA*, *narA*; nitrate reductase, formate dehydrogenase, and biotin sulfoxide reductase activities; molybdenum-containing factor	A, B, 142
chlB	Chlorate	86	*narB*; nitrate reductase, formate dehydrogenase, and biotin sulfoxide reductase activities; molybdenum-containing factor	A, B, 142
chlD	Chlorate	17	*narD*; nitrate reductase, formate dehydrogenase, and biotin sulfoxide reductase activities; molybdenum-containing factor; possibly Mo uptake	A, B, 142
chlE	Chlorate	18	*bisB*, *narE*; nitrate reductase, formate dehydrogenase, and biotin sulfoxide reductase activities; molybdenum-containing factor; regulatory function	A, B, 142, 456, 556
chlF	Chlorate	(27)	Formate dehydrogenase (EC 1.2.2.1) structural gene	A
chlG	Chlorate	0	*bisD*; nitrate reductase and biotin sulfoxide reductase activities	A, 142, 283, 284, 556
cir	Colicine I resistance	43	*feuA*; production of colicin I receptor	A, B, 622
cls		27	Cardiolipin synthase activity	B
cmlA	Chloramphenicol	19	Resistance or sensitivity to chloramphenicol	A
codA		8	Cytosine deaminase (EC 3.5.4.1)	A
codB		8	Cytosine transport	A
corA	Cobalt resistance	85	Mg^{2+} transport, system I	B, 367, 431, 432
corB	Cobalt resistance	96	Mg^{2+} transport, system I	B
cpdB		96	2′:3′-Cyclic-nucleotide 2′-phosphodiesterase (EC 3.1.4.16)	32
cpxA		88	F-pilus formation; surface exclusion; conjugal donor activity	370, 371, 534
cpxB		40	F-pilus formation; surface exclusion; conjugal donor activity	370, 371

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
crp		74	*cap*; cyclic AMP receptor protein	A, 2, 113, 218
crr		52	Phosphocarrier protein for glucose of the PTS system; III^{Glc}, structural gene	B, 75, 375
cur		27	Capsular polysaccharide production; resistance or sensitivity to antibiotics; uracil pool	153
cxm		6	*cxr*; methylglyoxal synthesis	A, B
cyaA		85	Adenylate cyclase (EC 4.6.1.1)	A, B, 494
cyaR		85	Possible regulatory locus for *cya*	218
cycA	Cycloserine	96	*dagA*; resistance to D-cycloserine and D-serine; transport of D-alanine, D-serine, and glycine	A, B
cyd		17	Cytochromes *d*, a_1, and b_{558}	206
cysA	Cysteine	52	Sulfate permease; chromate resistance	A, B
cysB	Cysteine	28	Regulatory gene for cysteine biosynthesis	A, B, 279
cysC	Cysteine	59	Adenylylsulfate kinase (EC 2.7.1.25)	A
cysD	Cysteine	59	Sulfate adenylyltransferase (EC 2.7.7.4)	A
cysE	Cysteine	81	Serine acetyltransferase (EC 2.3.1.30)	A, B
cysG	Cysteine	74	*nirB*?; sulfite reduction and possibly nitrite reduction	A, 105
cysH	Cysteine	59	Adenylylsulfate reductase (EC 1.8.99.2)	A
cysI	Cysteine	59	*cysQ*; sulfite reductase activity	A
cysJ	Cysteine	59	*cysP*; sulfite reductase activity	A
cysK	Cysteine	52	Cysteine synthase (EC 4.2.99.8)	B, 611
cysS	Cysteine	12	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	50
cytR		89	Regulatory gene for *deo* operon, *udp* and *cdd*	A, B
dacA		15	D-Alanine carboxypeptidase, fraction A; penicillin-binding protein 5	A, B, 427, 547
dacB		69	D-Alanine carboxypeptidase, fraction B; penicillin-binding protein 4	B, 562
dadA		26	*dadR*; D-amino acid dehydrogenase subunit	A, B, 612, 613
dadB		2	*alnA*: D-amino acid dehydrogenase subunit	A, B, 186
dadQ		99	*alnR*; regulatory gene for *dad* regulon	A, 186
dam		74	DNA adenine methylase	A, B, 225, 374
dapA	Diaminopimelate	53	Dihydropicolinate synthase (EC 4.2.1.52)	A
dapB	Diaminopimelate	1	Dihydropicolinate reductase	A, 361
dapC	Diaminopimelate	4	Tetrahydropicolinate succinylase	A, 191
dapD	Diaminopimelate	4	Succinyl-diaminopimelate aminotransferase	A, 38, 191
dapE	Diaminopimelate	53	*dapB*; *N*-succinyl-diaminopimelate deacylase	A
dcd		(45)	*paxA*; 2α-deoxycytidine 5α-triphosphate deaminase (EC 3.5.4.-) activity	B
dcm		43	*mec*; DNA cytosine methylase	A, B
dcp		(30)	Dipeptidyl carboxypeptidase	B
dctA		80	Uptake of C_4 dicarboxylic acids	A
dctB		16	Uptake of C_4 dicarboxylic acids	A
ddl		2	D-Alanine:D-alanine ligase	A, B, 357, 358
del	Deletion	61	Frequency of IS*1*-mediated deletion	B
deoA	Deoxyribose	100	*tpp*, *TP*; thymidine phosphorylase (EC 2.4.2.4)	A, B, 182, 588, 590
deoB	Deoxyribose	100	*drm*, *thyR*; phosphopentomutase (EC 2.7.5.6)	A, B, 182, 588, 590
deoC	Deoxyribose	100	*dra*, *thyR*; deoxyribose-phosphate aldolase (EC 4.1.2.4)	A, B, 3, 182, 588, 589, 590
deoD	Deoxyribose	100	*pup*; purine-nucleoside phosphorylase (EC 2,4,2,1)	A, B, 182, 487, 588, 590
deoR	Deoxyribose	19	*nucR*; regulatory gene for *deo* operon	A, B
dgd		(70)	D-Galactose dehydrogenase production	B

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
dgkA	Diglyceride	92	Diglyceride kinase	B, 343
dgkR	Diglyceride	94	Level of diglyceride kinase	476
dgoA	D-Galactonate	82	2-Oxo-3-deoxygalactonate 6-phosphate aldolase (EC 4.1.2.21)	B
dgoD	D-Galactonate	82	Galactonate dehydratase (EC 4.2.1.6)	B
dgoK	D-Galactonate	82	2-Oxo-3-deoxygalactonate kinase (EC 2.7.1.58)	B
dgoR	D-Galactonate	82	Regulatory gene	B
dgoT	D-Galactonate	82	Galactonate transport	B
dgsA		35	Function of enzyme IIA/IIB of PTS system	488
dinF		92	Locus induced by UV and mitomycin C; subject to *recA* and *lexA* regulation	304, 381
divE	Division	22	Membrane protein biosynthesis	B
dld		(47)	D-Lactate dehydrogenase (EC 1.1.1.28)	287
dnaA	DNA	83	DNA biosynthesis; initiation	A, B, 228, 229, 307, 382, 402, 501, 502, 595, 635
dnaB	DNA	92	*groP*, *grpA*; DNA biosynthesis; chain elongation	A, B, 343, 526
dnaC	DNA	99	*dnaD*; DNA biosynthesis; initiation and chain elongation	A, B
dnaE	DNA	4	see *polC*	
dnaG	DNA	67	DNA biosynthesis; primase	A, B, 210, 355, 356, 413
dnaI	DNA	40	DNA biosynthesis	A
dnaJ	DNA	0	*groPAB*, *groPC*; DNA biosynthesis	B
dnaK	DNA	0	*groPAB*, *groPC*, *groPF*, *grpF*; DNA biosynthesis	B
dnaL	DNA	28	*dnaK*; DNA biosynthesis	B
dnaN	DNA	83	DNA biosynthesis; DNA polymerase III holoenzyme, β-subunit	76, 228, 307, 478, 500–502, 635
dnaP	DNA	85	DNA biosynthesis; initiation	A
dnaQ	DNA	5	Mutator activity and DNA biosynthesis	B, 250
dnaT	DNA	99	DNA biosynthesis; termination	B
dnaX	DNA	11	DNA biosynthesis; subunit of DNA polymerase III holoenzyme; DNA elongation factor III	B, 257
dnaY	DNA	13	DNA biosynthesis	B, 240
dnaZ	DNA	11	DNA biosynthesis; γ subunit of DNA polymerase III holoenzyme; DNA elongation factor II	A, B, 240, 257, 258
dpp	Dipeptide	(14)	Transport of dipeptides	A, B
dsdA	D-Serine	51	D-Serine deaminase	A, B, 86
dsdC	D-Serine	51	Regulatory gene for *dsdA*	A, 86
dut	dUTPase	82	*dnaS*, *sof*; deoxyuridinetriphosphatase (EC 3.6.1.23)	A, B, 565
dye		100	Resistance or sensitivity to methylene blue	B, 487
ebgA		68	Second β-galactosidase activity appears as result of mutation	A, B
ebgR		68	Regulatory gene	B
ecfA	Energy-coupling factor	65	Pleiotropic effects on active transport coupling to metabolic energy; may be *metC*	B
ecfB	Energy-coupling factor	88	*ssd*; generalized resistance to aminoglycoside antibiotics; coupling of metabolic energy to active transport	B, 397, 419
eda		41	*kdgA*, *kga*; 2-keto-3-deoxygluconate 6-phosphate aldolase (EC 4.1.2.14)	A

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
edd		41	Phosphogluconate dehydratase (EC 4.2.1.12)	A
endA		64	DNA-specific endonuclease I	B
eno		60	Enolase (EC 4.2.1.11)	A, B, 19
entA	Enterochelin	14	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase	A, B, 324, 325
entB	Enterochelin	14	2,3-dihydro-2,3-dihydroxybenzoate synthetase	A, B, 324, 325
entC	Enterochelin	14	Isochorismate synthetase	A, B, 324, 325
entD	Enterochelin	13	Enterochelin synthetase, component D	A, B, 324, 325
entE	Enterochelin	14	Enterochelin synthetase, component E	A, B, 324, 325
entF	Enterochelin	14	Enterochelin synthetase, component F	A, B, 324, 325
entG	Enterochelin	14	Enterochelin synthetase, component G	A, B, 324, 325
envA	Envelope	2	Anomalous cell division; chain formation	A, B, 357, 358
envB	Envelope	71	*mon*, *rodY*; anomalous formation of spheroidal cells	A, B
envC	Envelope	81	Anomalous cell division; chain formation	A
envM	Envelope	28	Osmotically remedial envelope defect	A
envN	Envelope	(4)	Osmotically remedial envelope defect	A
envP	Envelope	90	Osmotically remedial envelope defect	A
envQ	Envelope	58	Osmotically remedial envelope defect	A
envT	Envelope	(15)	Osmotically remedial envelope defect	A
envZ	Envelope	75	*ompB*, *perA*, *tpo*; production of outer membrane proteins; regulatory gene	226, 227, 354, 391, 599, 604
eryC	Erythromycin	83	Erythromycin resistance; ribosome assembly	B
esp		17	Site for efficient packaging of phage T1	B
exbB		59	Uptake of enterochelin; resistance or sensitivity to colicins	A, B
exbC		59	Uptake of enterochelin; resistance or sensitivity to colicins	B
expA		22	Expression of a group of exported proteins	132
exuR		68	Regulatory gene for *uxaAC*, *uxuB*, and *exuT*	B, 261, 466, 483, 484
exuT		68	Transport of hexuronates	B, 466, 483
fabA	Fatty acid biosynthesis	22	β-Hydroxydecanoylthioester dehydrase (EC 4.2.1.60)	A
fabB	Fatty acid biosynthesis	50	*fabC*; β-ketoacyl-acyl carrier protein synthase I (EC 2.3.1.41)	A, B, 192, 193
fabD	Fatty acid biosynthesis	24	Malonyl-CoA-acyl carrier protein transacylase (EC 2.3.1.39)	A, 193
fabE	Fatty acid biosynthesis	72	Acetyl-CoA carboxylase (EC 6.4.1.2)	B
fabF	Fatty acid biosynthesis	24	*cvc*; β-ketoacyl-acyl carrier protein synthase II (EC 2.3.1.41)	B, 192, 193
fadA	Fatty acid degradation	86	*oldA*; thiolase I (EC 2.3.1.16)	A, 100
fadB	Fatty acid degradation	86	*oldB*; 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	A
fadD	Fatty acid degradation	40	*oldD*; acyl-CoA synthetase (EC 6.2.1.3)	A, B
fadE	Fatty acid degradation	5	Electron transport flavoprotein (ETF) of β-oxidation	A, 100
fadL	Fatty acid degradation	51	Transport of long-chain fatty acids	B
fadR	Fatty acid degradation	26	*oleR*; negative regulatory gene for *fad* regulon and *aceBA* operon	B, 100, 366, 535, 536
fam		76	Anomalous filament formation	581
fcsA		86	Cell division; septation	B
fda		63	*ald*; fructose-biphosphate aldolase	A
fdhA		80	Formate dehydrogenase activity	B
fdp		96	Fructosediphosphatase (EC 3.1.3.11)	A
fecA	Iron	7	Citrate-dependent iron transport, outer membrane receptor	B, 263, 598
fecB	Iron	7	Citrate-dependent iron transport	B, 263

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
fep	Iron	14	*cbr*, *cbt*, *feuB*; receptor for ferrienterochelin and colicins F and D; enterochelin-dependent iron transport	A, B, 324, 325
fes	Iron	13	Enterochelin esterase	A, B, 324, 325
fexA		100	*sfrA*; F-pilus synthesis, conjugal donor activity, and surface exclusion	B, 339
fexB		86	FexA phenotype affected	339
fhuA	Ferric hydroxamate uptake	4	*tonA*, *T1*,*T5rec*; outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and ϕ80	A, B, 290
fhuB	Ferric hydroxamate uptake	4	Hydroxamate-dependent iron uptake	290
firA		4	RNA polymerase function	B
flaA	Flagella	43	*cheC*; flagellar synthesis and chemotaxis	A, B, 314, 316, 317
flaB	Flagella	43	Flagellar synthesis	A, B, 314, 316
flaC	Flagella	43	Flagellar synthesis	A, B, 316
flaD	Flagella	42	Flagellar synthesis	A, B, 314
flaE	Flagella	43	Flagellar synthesis; length of basal hook	A, B
flaG	Flagella	41	Flagellar synthesis	A, 314
flaH	Flagella	41	Flagellar synthesis	A
flaI	Flagella	42	Regulation of flagellar synthesis	A
flaK	Flagella	24	Flagellar hook subunit protein	B
flaL	Flagella	24	Flagellar synthesis; basal body	B
flaM	Flagella	24	Flagellar synthesis; basal body	B
flaN	Flagella	43	Flagellar synthesis	A, B, 314
flaO	Flagella	43	Flagellar synthesis	A, B
flaP	Flagella	43	Flagellar synthesis	A, B
flaQ	Flagella	43	Flagellar synthesis	A, B
flaR	Flagella	43	Flagellar synthesis	A, B, 317
flaS	Flagella	24	Flagellar synthesis; basal body	B, 314
flaT	Flagella	24	Flagellar synthesis; basal body	B
flaU	Flagella	24	Flagellar synthesis	B, 314, 316
flaV	Flagella	24	Flagellar synthesis; basal body	B
flaW	Flagella	24	Flagellar synthesis	B, 316
flaX	Flagella	24	Flagellar synthesis	B, 316
flaY	Flagella	24	Flagellar synthesis; basal body	B, 316
flaZ	Flagella	24	Flagellar synthesis; basal body	B, 314, 316
flbA	Flagella	24	Flagellar synthesis	B, 314
flbB	Flagella	42	Flagellar synthesis	B, 314
flbC	Flagella	43	Flagellar synthesis	B, 314
flrA	Fluoroleucine	100	Regulation of *ilv* and *leu* genes; fluoroleucine resistance	A
flu	Fluffing	43	Metastable gene affecting surface properties, piliation, and colonial morphology	B
fnr		29	See *nirR*	
folA	Folate	1	*tmrA*; dihydrofolate reductase (EC 1.5.1.3); trimethoprim resistance	A, B, 10, 277, 490, 540–542
fpk		46	Fructose-1-phosphate kinase (EC 2.7.1.3)	A, B, 55
frdA		94	Fumarate reductase (EC 1.3.99.1), flavoprotein subunit	A, B, 106–109, 163, 211, 350
frdB		94	Fumarate reductase (EC 1.3.99.1), iron-sulfur protein subunit	107, 109, 211, 350
frdC		94	Fumarate reductase (EC 1.3.99.1), membrane anchor polypeptide	211, 336
frdD		94	Fumarate reductase (EC 1.3.99.1), membrane anchor polypeptide	211, 336

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
ftsA		2	*divA*; anomalous filamentous growth	A, B, 357, 358
ftsB		49	Anomalous filamentous growth; cell division	428, 625
ftsE		76	Anomalous filamentous growth	B
ftsH		69	Anomalous filamentous growth	B
ftsQ		2	Anomalous filamentous growth	36
fuc	Fucose	60	*prd*; L-fucose utilization	A, B
fusA	Fusidic acid	73	*far*; protein chain elongation factor EF-G	A, B, 471
fusB	Fusidic acid	15	Pleiotropic effects on RNA synthesis, ribosomes, and ribosomal protein S6	B
gabC	γ-Aminobutyrate	58	Regulatory gene for *gabP,D,T*	A, B, 378
gabD	γ-Aminobutyrate	58	Succinate-semialdehyde dehydrogenase (EC 1.2.1.16), NADP-dependent, activity	B, 378
gabP	γ-Aminobutyrate	58	Transport of γ-aminobutyrate	B, 378
gabT	γ-Aminobutyrate	58	Aminobutyrate aminotransferase (EC 2.6.1.19) activity	A, B, 378
gadR		81	Regulatory gene for *gadS*	A
gadS		81	Glutamate decarboxylase (EC 4.1.1.15)	A
galE	Galactose	17	*galD*; UDPgalactose 4-epimerase; hexose-1-phosphate uridylyltransferase (EC 2.7.7.12)	A, B, 1, 79
galK	Galactose	17	*galA*; galactokinase (EC 2.7.1.6)	A
galP	Galactose	64	*Pgal*; galactose permease activity	B
galR	Galactose	62	*Rgal*; regulatory gene; repressor of *galETK* operon	A, 364, 597
galT	Galactose	17	*galB*; galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)	A
galU	Galactose	27	Glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	A, B
gap		39	*gad*; glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)	A, B
garA	Glucarate	16	Glucarate utilization	485
garB	Glucarate	4	Glucarate utilization	485
gatA	Galactitol	47	Galactitol-specific enzyme II of phosphotransferase system	B, 55, 146, 287
gatC	Galactitol	47	Regulatory gene	B, 55, 287
gatD	Galactitol	47	Galactitol-1-phosphate dehydrogenase	B, 55, 287
gdh		27	Glutamate dehydrogenase	B, 116, 512
glc	Glycolate	65	Utilization of glycolate; malate synthase G (EC 4.1.3.2)	A
glgA	Glycogen	75	Glycogen synthase (EC 2.4.1.21)	A, B, 438
glgB	Glycogen	75	1,4-α-glucan branching enzyme (EC 2.4.1.18)	A, B, 438
glgC	Glycogen	75	Glucose-1-phosphate adenylyltransferase (EC 1.7.7.27)	A, B, 438
glk		52	Glucokinase (EC 2.7.1.2)	A
glmS	Glucosamine	84	Glucosaminephosphate isomerase (EC 5.3.1.19)	A, B, 595
glnA	Glutamine	87	Glutamine synthetase (EC 6.3.1.2)	A, B, 22, 116, 222, 362, 363, 373, 403, 449, 492
glnD	Glutamine	4	Uridylyltransferase	B, 191
glnF	Glutamine	70	*ntrA*; positive regulatory gene for *glnA*	B, 372
glnG	Glutamine	87	*glnT*, *ntrC*; negative regulatory gene for *glnA*	22, 362, 363, 372, 373, 449, 450
glnL	Glutamine	87	*glnR*, *ntrB*; negative regulatory gene for *glnA*	22, 90, 363, 372, 373, 449

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TABLE 1—Continued

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
glnP	Glutamine	18	L-Glutamate periplasmic-binding protein	369
glnR	Glutamine	24	Affects level of glutaminyl-tRNA synthetase	94
glnS	Glutamine	16	Glutaminyl-tRNA synthetase (EC 6.1.1.18)	A
glnT	Glutamine	(77)	Affects levels of glutamine tRNA1 and glutamine synthetase	B
glnU	Glutamine	16	*supB*; glutamine tRNA1 (tandemly duplicated gene)	B, 269, 408, 409
glnV	Glutamine	16	*supE*, *Su2*, *suII*; glutamine tRNA2 (tandemly duplicated gene)	B, 268, 269, 408, 409
glpA	Glycerol phosphate	49	Glycerol-3-phosphate dehydrogenase (anaerobic) (EC 1.1.99.5)	A, B, 326, 523
glpD	Glycerol phosphate	75	*glyD*; glycerol-3-phosphate dehydrogenase (aerobic) (EC 1.1.99.5)	A
glpF	Glycerol phosphate	88	Facilitated diffusion of glycerol	A
glpK	Glycerol phosphate	88	Glycerol kinase (EC 2.7.1.30)	A
glpQ	Glycerol phosphate	49	Glycerol-3-phosphate diesterase	326
glpT	Glycerol phosphate	49	*sn*-Glycerol-3-phosphate permease	A, B, 326, 523, 625
glpR	Glycerol phosphate	75	Regulatory gene	A
gltA	Glutamate	17	*glut*; citrate synthasee (EC 4.1.3.7)	A, 214, 546
gltB	Glutamate	69	*aspB*; glutamate synthase (EC 2.6.1.53)	A, B, 116, 353
gltE	Glutamate	81	Glutamyl-tRNA synthetase; possible regulatory subunit	A
gltH	Glutamate	(21)	Requirement	A
gltM	Glutamate	(43)	Glutamyl-tRNA synthetase (EC 6.1.1.17)	A
gltR	Glutamate	92	Regulatory gene for glutamate permease	A
gltS	Glutamate	82	Glutamate permease	A, E, G
gltT	Glutamate	90	*tgtB*; glutamate tRNA2; in *rrnB* operon	B, 69, 70
gltU	Glutamate	85	*tgtC*; glutamate tRNA2; in *rrnC* operon	B
gltV	Glutamate	90	*tgtE*; glutamate tRNA2; in *rrnE* operon	B
gltW	Glutamate	57	Glutamate tRNA2; in *rrnG* operon	170
gltX	Glutamate	52	Catalytic subunit for glutamyl-tRNA synthetase	A
glyA	Glycine	55	Serine hydroxymethyltransferase (EC 2.1.2.1)	A, 552
glyS	Glycine	80	*gly-act*; glycyl-tRNA synthetase (EC 6.1.1.14)	A
glyT	Glycine	90	*supA36*, *sumA*; glycine tRNA2	A, B, 6, 259, 333
glyU	Glycine	62	*suA36*, *sufD*, *sumB*, *supT*; glycine tRNA1	A
glyV	Glycine	95	*suA58*, *suA78;* glycine tRNA3 (duplicate gene)	A, B
glyW	Glycine	42	*suA58*, *suA78*; glycine tRNA3 (duplicate gene)	A, 585
gnd		44	Gluconate-6-phosphate dehydrogenase (EC 1.1.1.43)	A, 415, 617
gntM	Gluconate	75	*usgA*; transport and phosphorylation of gluconate	A, B
gntR	Gluconate	76	Regulatory gene for *edd*; transport and phosphorylation of gluconate	A, B
gntS	Gluconate	95	Second system for transport, and possibly phosphorylation of gluconate	B
gor		78	Glutathione oxidoreductase (EC 1.6.4.2)	136
gpp		85	Guanosine pentaphosphatase activity	B
gpsA		81	*sn*-Glycerol-3-phosphate dehydrogenase [NAD(P)$^+$] (EC 1.1.1.94)	A, B
gpt		6	*gpp*, *gxu*; guanine-hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	A, B
grpD		71	Initiation of lambda DNA replication; host DNA synthesis	B

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
grpE		57	Phage lambda replication; host DNA synthesis	B
gshA		58	γ-Glutamyl-cysteine synthetase (EC 6.3.2.2) activity	B
gsk		13	Guanosine kinase	B
guaA	Guanine	54	gua_b; GMP synthetase (EC 6.3.4.1)	A, B
guaB	Guanine	54	gua_a; IMP dehydrogenase (EC 1.2.1.14)	A, B
guaC	Guanine	3	GMP reductase (EC 1.6.6.8)	A, F
gurB		74	Utilization of methyl-β-D-glucuronide; possibly *crp*	A
gurC		(18)	Utilization of methyl-β-D-glucuronide	A
gurD		(68)	Utilization of methyl-β-D-glucuronide	A
gyrA	Gyrase	48	*nalA*; DNA gyrase, subunit A; resistance or sensitivity to nalidixic acid	A, B, 321
gyrB	Gyrase	83	*acrB*, *cou*, *himB*, *nalC*; DNA gyrase, subunit B; resistance or sensitivity to coumermycin	B, 384, 595
hag	H antigen	42	*flaF*, *H*; flagellin, structural gene; flagellar (H) antigen	A, B, 314, 315
hemA	Hemin	27	δ-Aminolevulinate synthase (EC 2.3.1.37)	A
hemB	Hemin	8	*nef*; δ-aminolevulinate dehydratase (EC 4.2.1.24) activity	A, B
hemC	Hemin	85	*popE*; uroporphyrinogen I synthase (EC 4.3.1.8) activity	B
hemD	Hemin	85	Uroporphyrinogen III cosynthase	B
hemE	Hemin	90	*hemC*; uroporphyrinogen decarboxylase (EC 4.1.1.37)	A
hemF	Hemin	17	*popB*, *sec*; coproporphyrinogen III oxidase (EC 1.3.3.3)	A
hemG	Hemin	86	Protoporphyrinogen oxidase activity	516
hemH	Hemin	11	*hemG*, *popA*; ferrochelatase (EC 4.99.1.1)	A
het		84	*cop*; binding of DNA sequences in *oriC* region to outer membrane; possibly structural gene for DNA-binding protein	A, 434, 596, 618
hfl		95	High frequency of lysogenization by phage lambda	A
himA		37	*hid*; integration host factor (IHF), α-subunit	112, 383, 384, 386
himD		20	*hip*; integration host factor (IHF), β-subunit	I, 384, 385
hisA	Histidine	44	*N*-(5′-Phospho-L-ribosylformimino)-5-amino-1-(5′-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	A
hisB	Histidine	44	Imidazoleglycerolphosphate dehydratase (EC 4.2.1.19) and histidinol phosphatase (EC 3.1.3.15)	A
hisC	Histidine	44	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	A
hisD	Histidine	44	L-Histidinol:NAD^+ oxidoreductase (EC 1.1.1.23)	A, 72
hisE	Histidine	44	Phosphoribosyl-ATP pyrophosphohydrolase	A
hisF	Histidine	44	Cyclase	A
hisG	Histidine	44	ATP phosphoribosyltransferase (EC 2.4.2.17)	A, B, 72, 189, 593
hisH	Histidine	44	Amido transferase	A
hisI	Histidine	44	Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19)	A
hisJ	Histidine	50	Histidine-binding protein of high-affinity histidine transport system	15, 340
hisP	Histidine	50	Histidine permease	15

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
hisR	Histidine	(85)	*hisT*; histidine tRNA	B
hisS	Histidine	54	Histidyl-tRNA synthetase (EC 6.1.1.21)	B, 166, 167
hisT	Histidine	50	Pseudouridylate synthetase	B, 454
hpt		3	Hypoxanthine phosphoribosyltransferase	A
hsdM	Host specificity	99	*hs*, *hsm*, *hsp*, *rm*; host modification; DNA methylase M	A, 498, 634
hsdR	Host specificity	99	*hs*, *hsp*, *hsr*, *rm*; host restriction; endonuclease R	A, 498, 634
hsdS	Host specificity	99	*hss*; specificity determinant for *hsdM* and *hsdR*	A, 498, 634
htpR		76	*hin*; regulatory gene for proteins induced at high temperatures	417, 626
hyd		58	Hydrogenase activity	B
iap		59	Altered isozyme pattern of alkaline phosphatase	B
icd		25	Isocitrate dehydrogenase, $NADP^+$-specific (EC 1.1.1.42)	B, 14
iclR		91	Regulatory gene for *aceBA* operon	A, 366
ileS	Isoleucine	1	Isoleucyl-tRNA synthetase (EC 1.1.1.5)	A, B
ileT	Isoleucine	87	*tilA*; isoleucine tRNA1; in *rrnA* operon	B
ileU	Isoleucine	72	*tilD*; isoleucine tRNA1; in *rrnD* operon	B
ileV	Isoleucine	5	Isoleucine tRNA1; in *rrnH* operon	170
ilvA	Isoleucine-valine	85	*ile*; threonine deaminase (EC 4.2.1.16)	A, B, 205
ilvB	Isoleucine-valine	82	Acetolactate synthase I (EC 4.1.3.18), valine-sensitive	A, B, 323, 420, 421
ilvC	Isoleucine-valine	85	*ilvA*; ketol-acid reductoisomerase (EC 1.1.1.86)	A, B, 45
ilvD	Isoleucine-valine	85	*ilvB*; dihydroxyacid dehydrase (EC 4.2.1.9)	A, B, 40, 205
ilvE	Isoleucine-valine	85	*ilvC*, *ilvJ*; branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	A, B, 39, 205, 331, 559, 587
ilvF	Isoleucine-valine	54	Production of valine-resistant acetolactate synthase activity	A
ilvG	Isoleucine-valine	85	Acetolactate synthase II (EC 4.1.3.18), valine-insensitive	A, B, 39, 196, 205, 328–331, 414, 558, 559, 587
ilvH	Isoleucine-valine	2	Acetolactate synthase II (EC 4.1.3.18), valine-sensitive	A, B, 323, 551
ilvI	Isoleucine-valine	2	Acetolactate synthase II (EC 4.1.3.18), valine-sensitive	A, B, 323, 551
ilvJ	Isoleucine-valine	2	Acetolactate synthase IV (EC 4.1.3.18), valine-resistant	278, 486
ilvU	Isoleucine-valine	7	Regulation of *ileS* and modification of isoleucine tRNA2 and valine tRNA2	177
ilvY	Isoleucine-valine	85	Positive regulatory locus for *ilvC*	B, 45
infB		69	Protein chain initiation factor 2	461
infC		38	Protein chain initiation factor 3	B, 463, 497, 549
inm		(79)	Susceptibility to mutagenesis by nitrosoguanidine	496
katC	Catalase	7	Catalase activity	B
katE	Catalase	38	Catalase activity	K
kba		69	Ketose-bis-phosphate aldolase, temperature-sensitive enzyme, active on D-tagatose-1,6-diphosphate	B
kdgK	Ketodeoxygluconate	78	Ketodeoxygluconokinase (EC 2.7.1.45)	A
kdgR	Ketodeoxygluconate	40	Regulatory gene for *kdgK*, *kdgT*, and *eda*	A
kdgT	Ketodeoxygluconate	88	Ketodeoxygluconate transport system, structural gene	A, B

Continued on next page

TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
kdpA	Potassium dependence	16	*kac*; high-affinity potassium transport system; probably K^+-stimulated ATPase	A, B
kdpB	Postassium dependence	16	*kac*; high-affinity potassium transport system	A, B
kdpC	Potassium dependence	16	*kac*; high-affinity potassium transport system	A, B
kdpD	Potassium dependence	16	*kac*; high-affinity potassium transport system; regulatory gene	A, B
kpsA	K-polysaccharide	(62)	Acidic polysaccharide capsular (K) antigen	A
ksgA	Kasugamycin	1	*S*-Adenosylmethionine-6-*N'*,*N'*-adenosyl (rRNA) dimethyltransferase	A, 10–12
ksgB	Kasugamycin	36	Second-step (high-level) resistance to kasugamycin	A, B, 154, 184
ksgC	Kasugamycin	12	Kasugamycin resistance; affects ribosomal protein S2	B
ksgD	Kasugamycin	30	Kasugamycin resistance	184
lacA	Lactose	8	*a*, *lacAc*; galactoside acetyltransferase (EC 2.3.1.18)	A, B
lacI	Lactose	8	*i*; regulatory gene; repressor protein of *lac* operon	A, B, 82
lacY	Lactose	8	*y*; galactoside permease (M protein)	A, B, 73, 165
lacZ	Lactose	8	*z*; β-D-galactosidase (EC 3.2.1.23)	A, B, 223
lamB	Lambda	92	*malB*; phage lambda receptor protein; maltose high-affinity uptake system	A, B, 103, 111, 171, 238, 246, 524
lct	Lactate	80	Lactate dehydrogenase (EC 1.1.1.27)	A
lep		55	Leader peptidase	533
leuA	Leucine	2	α-Isopropylmalate synthase (EC 4.1.3.12)	A, 135, 607
leuB	Leucine	2	β-Isopropylmalate dehydrogenase	A, 135
leuC	Leucine	2	α-Isopropylmalate isomerase subunit	A, 135
leuD	Leucine	2	α-Isopropylmalate isomerase subunit	A, 135
leuK	Leucine	19	Regulation of biosynthetic enzymes for leucine, isoleucine-valine, histidine, and tryptophan	B
leuR	Leucine	79	Level of leucyl-tRNA synthetase	B
leuS	Leucine	15	Leucyl-tRNA synthetase (EC 6.1.1.4)	A, B, 547
leuT	Leucine	(84)	Leucine tRNA1 (duplicate gene)	B
leuU	Leucine	(68)	Leucine tRNA2	B
leuV	Leucine	(93)	Leucine tRNA1 (duplicate gene)	B
leuW	Leucine	16	A leucine tRNA	B, 408, 409
leuX	Leucine	97	*Su-6*, *supP*; a leucine tRNA	B, 17
leuY	Leucine	10	Level of leucyl-tRNA synthetase	B
lev	Levallorphan	(9)	Resistance to levallorphan	B
lexA		92	*exrA*, *spr*, *tsl*, *umuA*; resistance or sensitivity to X-rays and UV	A, B, 62, 65, 66, 249, 347, 348, 368, 381
lig	Ligase	52	*dnaL*, *pdeC*; DNA ligase	A, B
linB	Lincomycin	(29)	High-level resistance to lincomycin	A
lip	Lipoate	15	Requirement	A, 547
lit		25	Phage T4 late gene expression	B
livG	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system	445, 627
livH	Leucine, isoleucine, and valine	76	High-affinity branched-chain amino acid transport system	B, 445, 627
livJ	Leucine, isoleucine, and valine	76	Binding protein, high-affinity branched-chain amino acid transport system	B, 445, 627
livK	Leucine, isoleucine, and valine	76	Leucine-specific periplasmic binding protein; high-affinity branched-chain amino acid transport system	B, 445, 446, 627

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
livR	Leucine, isoleucine, and valine	20	*lss*; regulatory gene; high-affinity branched-chain amino acid transport system	B
ikyA	Leaky	17	Retention of periplasmic enzymes; colicin sensitivity; may be *tolA* or *tolB*	9
lon	Long form	10	*capR*, *deg*, *dir*, *muc*; DNA-binding, ATP-dependent protease La	A, B, 89, 98, 522, 638, 639
lpcA	Lipopolysaccharide core	6	*tfrA*; lipopolysaccharide core synthesis; resistance to phages T4, T7, and P1; deficiency in conjugation	A, B
lpcB	Lipopolysaccharide core	(65)	*pon*; lipopolysaccharide core synthesis	A
lpd		3	*dhl*; lipoamide dehydrogenase (NADH) (EC 1.6.4.3)	A, B, 215, 217
lpp	Lipoprotein	36	*mlpA*; murein lipoprotein structural gene	B, 411
lrs		3	Level of leucine tRNA	586
lstR		20	Leucine-specific transport	B
lysA	Lysine	61	Diaminopimelate decarboxylase (EC 4.1.1.20)	A, 91
lysC	Lysine	91	*apk*; aspartokinase III	A, B, 60
lysP	Lysine	(46)	Regulatory gene affecting *cadA* and lysine transport	465
lysT	Lysine	17	*suβ*, *supL*; lysine tRNA (tandemly duplicated gene)	B
lysX	Lysine	60	Lysine excretion	A
mac	Macrolide	(26)	Erythromycin growth dependence	A
mafA		1	Maintenance of F-like plasmids	A, B
mafB		2	Maintenance of F-like plasmids	B
malE	Maltose	92	*malB*; periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis	A, B, 34, 35
malF	Maltose	92	*malB*; maltose transport; cytoplasmic membrane protein	A, B
malG	Maltose	92	*malB*; active transport of maltose and maltodextrins	B
malK	Maltose	92	*malB*; maltose permeation	A, B, 35, 111
malP	Maltose	75	*malA*; maltodextrin phosphorylase (EC 2.4.1.1)	A, B, 137, 477
malQ	Maltose	75	*malA*; amylomaltase (EC 2.4.1.25)	A
malT	Maltose	75	*malA*; positive regulatory gene for *mal* regulon	A, B, 137, 138, 139, 477
manA	Mannose	36	Mannosephosphate isomerase (EC 5.3.1.8)	A, 49
manC	Mannose	(87)	*mni*; D-mannose isomerase regulation; utilization of D-lyxose	B
mdh		70	Malate dehydrogenase (EC 1.1.1.37)	A
melA	Melibiose	93	*mel-7*; α-galactosidase (EC 3.2.1.22)	A
melB	Melibiose	93	*mel-4*; thiomethylgalactoside permease II	A
menA	Menaquinone	89	Conversion of 1,4-dihydroxy-2-naphthoate to demethylmenaquinone	A, B
menB	Menaquinone	49	Conversion of 2-succinylbenzoate to 1,4-dihydroxy-2-naphthoate	B, 213, 216
menC	Menaquinone	49	Conversion of chorismate to 2-succinylbenzoate	B, 213, 216
menD	Menaquinone	49	Menaquinone biosynthesis	213, 216
metA	Methionine	91	*met*$_3$; homoserine transsuccinylase (EC 2.3.1.46)	A, 380
metB	Methionine	90	*met-1*, *met*$_1$; cystathionine γ-synthase (EC 4.2.99.9)	A, 322, 636
metC	Methionine	65	Cystathionine γ-lyase (EC 4.4.1.1.)	A
metD	Methionine	5	High-affinity uptake of D- and L-methionine	A, B

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
metE	Methionine	86	*metB₁₂*; tetrahydropteroyltriglutamate methyltransferase (EC 2.1.1.14)	A
metF	Methionine	89	*met-2*, *met₂*; 5,10-methylenetetrahydrofolate reductase (EC 1.1.1.68)	A, 322, 636
metG	Methionine	(46)	Methionyl-tRNA synthetase	A, B
metH	Methionine	91	B_{12}-Dependent homocysteine-N^5-methyltetrahydrofolate transmethylase	A, B
metJ	Methionine	89	Regulatory gene	A, B, 322, 636
metK	Methionine	64	Methionine adenosyltransferase (EC 2.5.1.6)	A, B
metL	Methionine	89	*metM*; aspartokinase II-homoserine dehydrogenase II	A, 133, 322, 636
metT	Methionine	16	Methionine $tRNA_m$ (duplicated gene)	B, 269, 408, 409
metY	Methionine	(68)	Methionine $tRNA_f2$	B
metZ	Methionine	(61)	Methionine $tRNA_f1$	B
mglA	Methyl-galactoside	45	*mglP*; methyl-galactoside transport and galactose taxis	A, B, 55, 493
mglB	Methyl-galactoside	45	*mglP*; galactose-binding protein; receptor for galactose taxis	A, B, 493
mglC	Methyl-galactoside	45	*mglP*; methyl-galactoside transport and galactose taxis	A, B, 493
mglD	Methyl-galactoside	45	Regulatory locus for methyl-galactoside transport	B, 493
mglR	Methyl-galactoside	(17)	R-MG; regulatory gene	A
mgt	Magnesium transport	93	Mg^{2+} transport, system II	B
minA	Minicell	10	Formation of minute cells containing no DNA	A
minB	Minicell	26	Formation of minute cells containing no DNA	A, 519
mng	Manganese	(40)	Resistance or sensitivity to manganese	A
mopA	Morphogenesis of phages	94	*groE*, *hdh*, *tabB*; head assembly of phages T4 and lambda	A, B, 416, 574
mopB	Morphogenesis of phages	94	*groE*, *hdh*, *tabB*; head assembly of phages T4 and lambda	A, B, 416, 574
motA	Motility	42	*flaJ*; flagellar paralysis	A, B
motB	Motility	42	*flaJ*; flagellar paralysis	A, B
mraA	Murein	2	D-Alanine carboxypeptidase	A
mraB	Murein	2	D-Alanine requirement; cell wall peptidoglycan biosynthesis	A
mrbA	Murein	90	UDP-*N*-acetylglucosaminyl-3-enolpyruvate reductase activity	A
mrbB	Murein	90	D-Alanine requirement; cell wall peptidylglycan biosynthesis	A
mrbC	Murein	90	Cell wall peptidylglycan biosynthesis	A
mrcA	Murein	75	*ponA*; peptidoglycan synthetase; cell wall synthesis; penicillin-binding protein 1A	B, 273, 562
mrcB	Murein	4	*ponB*; peptidoglycan synthetase; cell wall synthesis; penicillin-binding protein 1Bs	B, 406, 407, 560, 562, 564
msp	Male-specific phage	100	Sensitivity or resistance of male strains to male-specific phages R17 and μ2	B
mtlA	Mannitol	81	Mannitol-specific enzyme II of phosphotransferase system	A, B, 332
mtlC	Mannitol	81	Regulatory locus	A, B
mtlD	Mannitol	81	Mannitol-1-phosphate dehydrogenase (EC 1.1.1.17)	A, B, 322
mtr	Methyltryptophan	69	Resistance to 5-methyltryptophan	A, B
mul		82	Mutability of UV-irradiated phage λ	A
murC	Murein	2	L-Alanine-adding enzyme	A, B, 357, 358
murE	Murein	2	*meso*-Diaminopimelate-adding enzyme	A, B
murF	Murein	2	*mra*; D-alanyl:D-alanine-adding enzyme	A, B
murG	Murein	2	Murein or envelope biosynthesis	503

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
mutD	Mutator	5	Generalized high mutability; may be *dnaQ*	A, 118
mutH	Mutator	61	*mutR*, *prv*; increased rates of frameshift and base substitution mutations	A, B
mutL	Mutator	95	*mut-25*; high rate of AT ⇌ GC transitions	A
mutS	Mutator	59	High rate of AT ⇌ GC transitions	A, B
mutT	Mutator	3	High rate of AT ⇌ GC transversions	A, B
nadA	Nicotinamide adenine dinucleotide	17	*nicA*; quinolinate synthetase, A protein	A
nadB	Nicotinamide adenine dinucleotide	56	*nicB*; quinolinate synthetase, B protein	A
nadC	Nicotinamide adenine dinucleotide	3	Quinolinate phosphoribosyl transferase	A, 215, 217
nagA	*N*-Acetylglucosamine	16	*N*-Acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	A
nagB	*N*-Acetylglucosamine	16	*glmD*; glucosamine-6-phosphate deaminase	A
nagE	*N*-Acetylglucosamine	16	*ptsN*; *N*-acetylglucosamine-specific enzyme II of phosphotransferase system	285
nalA	Nalidixic acid	48	See *gyrA*	
nalB	Nalidixic acid	58	Resistance or sensitivity to nalidixic acid	A
narC	Nitrate reductase	27	*chlC*; nitrate reductase (EC 1.7.99.4) α-subunit	A, B, 29, 54, 95, 181, 204, 555, 556
narI	Nitrate reductase	27	*chlI*; cytochrome b_{NR}, structural gene	54, 95, 442, 556
ndh		22	Respiratory NADH dehydrogenase	B, 632
neaB	Neamine	74	Resistance to neamine	A, B
nek		73	*amk*; resistance to neomycin, kanamycin, and other aminoglycoside antibiotics	A, B
nfsA	Nitrofurazone sensitivity	(22)	Nitrofuran reductase I activity	B
nfsB	Nitrofurazone sensitivity	(11)	Nitrofuran reductase I activity	B
nirC	Nitrite reductase	26	NADH-nitrite reductase (EC 1.6.6.4) activity	B
nirD	Nitrite reductase	74	NADH-nitrite reductase (EC 1.6.6.4) activity	B
nirE	Nitrite reductase	50	NADH-nitrite reductase (EC 1.6.6.4) activity	B
nirF	Nitrite reductase	(53)	NADH-nitrite reductase (EC 1.6.6.4) activity	B
nirR	Nitrite reductase	29	*fnr*, *nirA*; regulatory gene for nitrite and nitrate reductases, hydrogenase, and fumurate reductase	A, B, 95, 530
nmpC	New membrane protein	13	Production of an outer membrane protein	B
non	Nonmucoid	45	Capsule formation	A
nrdA		49	*dnaF*; ribonucleoside diphosphate reductase (EC 1.17.4.1) subunit B1	A, B, 460, 625
nrdB		49	Ribonucleoside diphosphate reductase (EC 1.17.4.1) subunit B2	A, B, 460, 625
nupC		52	Transport of nucleosides, except guanosine	B, 80
nupG		66	Transport of nucleosides	B
nusA		69	Transcription termination; L factor	B, 207, 208, 461 606
nusB		10	Transcription termination; L factor	B, 606
nuvA		9	Uridine thiolation factor A activity	B
nuvC		(44)	Uridine thiolation factor C activity	B
ompA	Outer membrane protein	22	*con*, *tolG*, *tut*; outer membrane protein 3a (II*;G;d), structural gene	A, B, 33, 37, 399–401
ompC	Outer membrane protein	48	*meoA*, *par*; outer membrane protein 1b (Ib;c), structural gene	B, 517

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
ompF	Outer membrane protein	21	*cmlB*, *coa*, *cry*, *tolF*; outer membrane protein 1a (Ia;b;F), structural gene	B, 404, 405, 517, 579, 580
ompR	Outer membrane protein	75	*ompB*; positive regulatory gene for *ompC* and *ompF*	B, 226, 227, 391, 525, 570
opp		27	Oligopeptide transport	A, B, 338
optA		4	Phage T7 DNA metabolism	499
oriC	Origin of replication	84	*poh*?; origin of replication of chromosome	B, 18, 230, 245, 352, 377, 437, 545, 595, 596, 645
oriJ	Origin of replication	30	Origin function of *rac* prophage	150, 152, 291
pabA	ρ-Aminobenzoate	74	Requirement	A
pabB	ρ-Aminobenzoate	40	Requirement	A, B
panB	Pantothenate	3	Ketopantoate hydroxymethyltransferase (EC 4.1.2.12)	A, B, 124
panC	Pantothenate	3	Pantothenate synthetase (EC 6.3.2.1)	A, B, 124
panD	Pantothenate	3	Aspartate 1-decarboxylase (EC 4.1.1.11)	A, B, 124
pbpA	Penicillin-binding protein	15	*mrdA*; penicillin-binding protein 2	B, 547, 563
pbpB	Penicillin-binding protein	2	*ftsI*, *sep*; peptidoglycan synthetase; septum formation; penicillin-binding protein 3	B, 272, 562
pck		75	Phosphoenolpyruvate carboxykinase (EC 4.1.1.49)	200, 201
pcsA		82	Cell division; chromosome segregation	B
pdxA	Pyridoxine	1	Requirement	A, B, 10, 11
pdxB	Pyridoxine	50	Requirement	A, B
pdxC	Pyridoxine	20	Requirement	A
pdxH	Pyridoxine	36	Pyridoxinephosphate oxidase	A, B
pdxJ	Pyridoxine	56	Requirement	A, B
pepD	Peptides	6	*pepH*; peptidase D, a dipeptidase	A, B
pepN	Peptides	21	Aminopeptidase N	B, 179
pfkA		88	6-Phosphofructokinase I (EC 2.7.1.11)	A, B
pfkB		38	Level of 6-phosphofructokinase II; suppressor of *pfkA*	A, B, 112, 130
pfkC		(59)	Modifier of 6-phosphofructokinase activity	A
pfl		20	Pyruvate formate lyase	B
pgi		91	Glucosephosphate isomerase (EC 5.3.1.9)	A
pgk		63	Phosphoglycerate kinase (EC 2.7.2.3)	A, B
pgl		17	*blu*; 6-phosphogluconolactonase (EC 3.1.1.31)	A
pgm		(15)	Phosphoglucomutase (EC 2.7.5.1)	A
pgsA		42	Phosphatidylglycerophosphate synthetase (EC 2.7.8.5)	A, B, 436, 585
pgsB		4	Lipopolysaccharide synthesis	426
pheA	Phenylalanine	57	Chorismate mutase-P–prephenate dehydrogenase	A, B, 202, 203
pheP	Phenylalanine	13	Phenylalanine-specific transport system	609, H
pheR	Phenylalanine	94	Regulatory gene for *pheA*	203
pheS	Phenylalanine	38	*phe-act*; phenylalanyl-tRNA synthetase (EC 6.1.1.20) α-subunit	A, B, 462, 463, 549
pheT	Phenylalanine	38	*pheS*; phenylalanyl-tRNA synthetase (EC 6.1.1.20) β-subunit	A, B, 462, 463, 549
phoA	Phosphate	9	Alkaline phosphatase (EC 3.1.3.1)	A, B, 41, 52, 223, 270, 271, 306, 514, 515, 605
phoB	Phosphate	9	*phoRc*, *phoT*; positive regulatory gene for *pho* regulon	A, B, 52, 223, 575, 605
phoE	Phosphate	6	*ompE*; outer membrane protein e (E,Ic,NmpAB), structural gene	577, 578, 580

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
phoM	Phosphate	100	Positive regulatory gene for *pho* regulon	602, 603
phoR	Phosphate	9	*nmpB*, *phoR1*, *R1pho*; positive and negative regulatory gene for *pho* regulon	A, B, 575, 576
phoS	Phosphate	84	*nmpA*, *phoR2a*, *R2pho*; periplasmic phosphate-binding protein	A, B, 120, 341, 576, 595, 643
phoT	Phosphate	84	*nmpA*, *phoS*; inorganic phosphate transport; may be *phoS*	A, B, 120, 341, 576, 643
phr	Photoreactivation	16	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	A, B
phs		(89)	Sodium/proton antiporter activity	642
phxB	Phi-X	17	Adsorption of φX174	B
pilA	Pili	98	*fim*; formation of type 1 somatic pili	A, B, 169
pilB	Pili	98	*fim*; formation of type 1 somatic pili	A, B, 169
pilC	Pili	98	*fim*; formation of type I somatic pili	A, B, 169
pit	P_i transport	77	Inorganic phosphate transport system	A
pldA		85	Detergent-resistant phospholipase A activity	A
plsA	Phospholipid synthesis	11	See *adk*	
plsB	Phospholipid synthesis	92	Glycerolphosphate acyltransferase activity	A, B, 343
pncA	Pyridine nucleotide cycle	39	*nam*; nicotinamide deamidase (EC 3.5.1.19)	A, B
pncB	Pyridine nucleotide cycle	(23)	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	337
pnp		69	Polynucleotide phosphorylase (EC 2.7.7.8)	A, 467, 468
pnt		35	Pyridine nucleotide transhydrogenase (EC 1.6.1.1)	B
poaR		63	Regulation of proline oxidase production	A
pog		70	Growth of phage P1	M
polA	Polymerase	87	*resA*; DNA polymerase I (EC 2.7.7.7)	A, B, 289, 302, 303, 403
polB	Polymerase	2	DNA polymerase II (EC 2.7.7.7)	A
polC	Polymerase	4	*dnaE*; DNA biosynthesis; DNA polymerase III, α-subunit	A, B, 38
popC	Porphyrin	4	Synthesis of δ-aminolevulinate	A
popD	Porphyrin	(1)	Level of 5-aminolevulinate dehydratase (EC 4.2.1.24) activity	A, B
poxA		95	Regulatory gene for *poxB*	88
poxB		19	Pyruvate:cytochrome *b* oxidoreductase (EC 1.2.2.2)	C
ppc	Phosphoenolpyruvate	89	*glu*, *asp*; phosphoenolpyruvate carboxylase (EC 4.1.1.31)	A, B, 394
pps	Phosphoenolpyruvate	37	Phosphoenolpyruvate synthase	A
prmA		72	*prm-1*; methylation of 50S ribosomal subunit protein L11	B
prmB		50	*prm-2*; methylation of 50S ribosomal subunit protein L3	B
proA	Proline	6	*pro₁*; γ-glutamyl phosphate reductase (EC 1.2.1.41)	A, 223, 233
proB	Proline	6	*pro₂*; γ-glutamyl kinase (EC 2.7.2.11)	A, 223, 233
proC	Proline	9	*pro₃*, *Pro2*; pyrroline-5-carboxylate reductase (EC 1.5.1.2)	A, 52, 223
proP	Proline	93	Proline permease, minor	376
proS	Proline	5	Prolyl-tRNA synthetase (EC 1.1.1.15)	51
proT	Proline	83	Proline transport	B, 398
prp	Propionate	97	Propionate metabolism	548
prs		26	Phosphoribosylpyrophosphate synthetase (EC 2.7.6.1)	254
psd		95	Phosphatidylserine decarboxylase	A, B
pss		56	Phosphatidylserine synthetase (EC 2.7.8.8)	B, 101, 435

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
pst		84	*nmpA*; inorganic phosphate transport system	A, B, 120, 576, 595, 643
pta		50	Phosphotransacetylase (EC 2.3.1.8) activity	B, 213, 340
pth		27	Peptidyl-tRNA hydrolase	A
ptr		61	Protease III	92
ptsF	Phosphotransferase system	46	Fructosephosphotransferase enzyme II	A, B, 55, 287
ptsG	Phosphotransferase system	24	*car*, *CR*, *gpt*, *gptA*, *tgl*, *umg*; glucosephosphotransferase enzyme II	A, B
ptsH	Phosphotransferase system	52	*ctr*, *Hpr*; phosphohistidinoprotein-hexose phosphotransferase (EC 2.7.1.69)	A, B
ptsI	Phosphotransferase system	52	*ctr*; phosphotransferase system enzyme I	A, B
ptsM	Phosphotransferase system	40	*gptB*, *mpt*, *pel*, *ptsX*; mannosephosphotransferase enzyme II	A, B
purA	Purine	95	ade_k, Ad_4; adenylosuccinate synthetase (EC 6.3.4.4)	A
purB	Purine	25	ade_h; adenylosuccinate lyase (EC 4.3.2.2)	A
purC	Purine	53	ade_g; phosphoribosylaminoimidazole-succinocarboxamide synthetase (EC 6.3.2.6)	A
purD	Purine	90	$adth_a$; phosphoribosylglycineamide synthetase (EC 6.3.4.13)	A
purE	Purine	12	ade_3, ade_f, Pur_2; phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21)	A, 223
purF	Purine	50	$ade_{u,b}$, *purC*; amidophosphoribosyl transferase (EC 2.4.2.14)	A, 543, 584
purG	Purine		See *purM*	
purH	Purine	90	ade_i; phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	A
purI	Purine		See *purL*	
purL	Purine	55	*purI*; phosphoribosylformylglycineamide synthetase (EC 6.3.5.3); homologous to *purG* of *Salmonella*	A, 253, F
purM	Purine	54	*purG*; phosphoribosylaminoimidazole synthetase (EC 6.3.3.1); homologous to *purI* of *Salmonella*	A, B, 253, F
pus		20	Effect of suppressors on $RelB^-$ phenotype	156
putA	Proline utilization	23	*poaA*; proline oxidase	A, 619, 621
putP	Proline utilization	23	Proline uptake	619–621
pyrA	Pyrimidine	1	See *car*	
pyrB	Pyrimidine	97	Aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit	A, B, 458
pyrC	Pyrimidine	23	Dihydro-orotase (EC 3.5.2.3)	A
pyrD	Pyrimidine	21	Dihydro-orotate oxidase (EC 1.3.3.1)	A
pyrE	Primidine	82	Orotate phosphoribosyltransferase (EC 2.4.2.10)	A, 565
pyrF	Pyrimidine	28	Orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	A
pyrG	Pyrimidine	60	CTP synthetase (EC 6.3.4.2)	B, 19, 459
pyrH	Pyrimidine	5	UMP kinase	A, 459
pyrI	Pyrimidine	97	Aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit	178, 458, 459, 614
qmeA		29	*gts*; unspecified membrane defect	A
qmeC		74	Unspecified membrane defect; tolerance to glycine; penicillin sensitivity	A
qmeD		62	Unspecified membrane defect; tolerance to glycine; penicillin sensitivity	A

Continued on next page

TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
qmeE		37	Unspecified membrane defect	A
rac			Defective prophage rac; see *recE* and *oriJ*	A, 46, 150, 151, 174, 291, 292
ranA		56	RNA metabolism	A
ras	Radiation sensitivity	(10)	Sensitivity to UV and X rays	A
rbsK	Ribose	84	Ribokinase (EC 2.7.1.15)	A, B, 595
rbsP	Ribose	84	D-Ribose permease	A, B, 595
rdg		16	Dependence of growth upon *recA* gene product	187
recA	Recombination	58	*lexB*, *recH*, *rnmB*, *tif*, *umuB*, *zab*; general recombination, repair of radiation damage, and induction of phage lambda	A, B, 66, 248, 346, 348, 508, 573, 594, 616
recB	Recombination	61	*rorA*; recombination and repair of radiation damage; exonuclease V subunit	A, B, 242
recC	Recombination	61	Recombination and repair of radiation damage; exonuclease V subunit	A, B, 242
recE	Recombination	30	*rac*; locus of rac prophage; exonuclease VIII	A, B, 47, 174, 291, 292
recF	Recombination	83	*uvrF*; recombination and repair of radiation damage	A, B, 478, 595
recG	Recombination	(82)	Recombination	A
relA	Relaxed	60	*RC*; regulation of RNA synthesis; stringent factor; ATP:GTP 3'-pyrophosphotransferase	A, B
relB	Relaxed	34	Regulation of RNA synthesis	B, 154
relX	Relaxed	60	Control of synthesis of guanosine-5'-diphosphate-3'-diphosphate	B
rep		85	DNA-melting activity involved in replication of certain phages	A, B, 572
rer		90	Resistance to UV and gamma radiation	B
rfa	Rough	81	*con*, *lpsA*, *phx*; cluster of genes coding for enzymes involved in lipopolysaccharide core biosynthesis	A, B
rfaC	Rough	81	Lipopolysaccharide core biosynthesis; core heptose	37
rfaD	Rough	81	D-Glycero-D-mannoheptose epimerase	110
rfaP	Rough	81	Lipopolysaccharide core biosynthesis; phosphorylation of core heptose	37
rfbA	Rough	45	TDP-glucose pyrophosphorylase	A
rfbB	Rough	45	TDP-glucose oxidoreductase	A
rfbD	Rough	45	TDP-rhamnose synthetase	A
rfe	Rough	(86)	Synthesis of enterobacterial common antigen and O antigen	B
rff	Rough	(86)	Synthesis of enterobacterial common antigen	B
rhaA	Rhamnose	88	L-Rhamnose isomerase (EC 5.3.1.14)	A
rhaB	Rhamnose	88	Rhamnulokinase (EC 2.7.1.5)	A
rhaC	Rhamnose	88	Regulatory gene	A
rhaD	Rhamnose	88	Thamnulosephosphate aldolase (EC 4.1.2.19)	A
rho		85	*nitA*, *psu*, *rnsC*, *SuA*, *sun*, *tsu*; transcription termination factor rho; polarity suppressor	A, B, 572, 587
ribA	Riboflavin	28	Riboflavin biosynthesis	24
ribB	Riboflavin	66	Riboflavin biosynthesis	24
ridA		70	Transcription and translation; dependence upon rifampicin and kasugamycin	129
rimB	Ribosomal modification	37	Maturation of 50S ribosomal subunit	A
rimC	Ribosomal modification	(26)	Maturation of 50S ribosomal subunit	A
rimD	Ribosomal modification	(87)	Maturation of 50S ribosomal subunit	A

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
rimE	Ribosomal modification	72	Modification of ribosomal proteins	B
rimF	Ribosomal modification	1	*res*; ribosomal modification	A
rimG	Ribosomal modification	(1)	*ramB*; modification of 30S ribosomal subunit protein S4	A
rimH	Ribosomal modification	14	*stsB*; ribosomal modification	A, B
rimI	Ribosomal modification	99	Modification of 30S ribosomal subunit protein S18; acetylation of N-terminal alanine	B, 274
rimJ	Ribosomal modification	(33)	Modification of 30S ribosomal subunit protein S5; acetylation of N-terminal alanine	B
rimL	Ribosomal modification	(34)	Modification of 30S ribosomal subunit protein L7; acetylation of N-terminal serine	275
rit		89	Affects thermolability of 50S ribosomal subunit	B
rna	Ribonuclease	14	*rns*, *rnsA*; ribonuclease I	A
rnb	Ribonuclease	28	Ribonuclease II	B, 157
rnc	Ribonuclease	55	Ribonuclease III	A, B
rnd	Ribonuclease	40	Ribonuclease D	637
rne	Ribonuclease	24	Ribonuclease E activity	B, 388
rnh	Ribonuclease	5	Ribonuclease H	16, 85, 250
rnpA	Ribonuclease	83	Ribonuclease P, protein component	B, 311
rnpB	Ribonuclease	70	Ribonuclease P, RNA component	B, 13, 311
rodA	Rod shape	15	*mrdB*; rounded morphology, radiation resistance, and drug sensitivities	A, B, 427, 547, 563
rpiA		63	Ribose phosphate isomerase (EC 5.3.1.6) (constitutive)	A
rplA	Ribosomal protein, large	90	50S ribosomal subunit protein L1	A, B, 7, 71, 345, 349, 359
rplB	Ribosomal protein, large	73	50S ribosomal subunit protein L2	A, B
rplC	Ribosomal protein, large	73	50S ribosomal subunit protein L3	A, B
rplD	Ribosomal protein, large	73	*eryA*; 50S ribosomal subunit protein L4	A, B, 344, 641
rplE	Ribosomal protein, large	73	50S ribosomal subunit protein L5	A, B
rplF	Ribosomal protein, large	73	50S ribosomal subunit protein L6	A, B
rplI	Ribosomal protein, large	96	50S ribosomal subunit protein L9	B
rplJ	Ribosomal protein, large	90	50S ribosomal subunit protein L10	A, B, 7, 30, 31, 71, 180, 247, 345, 349, 359, 418, 571
rplK	Ribosomal protein, large	90	*relC*; 50S ribosomal subunit protein L11	A, B, 7, 71, 345, 349, 418, 571
rplL	Ribosomal protein, large	90	50S ribosomal subunit protein L7/L12	A, B, 7, 30, 31, 71, 247, 345, 349, 359, 418
rplM	Ribosomal protein, large	70	50S ribosomal subunit protein L13	128
rplN	Ribosomal protein, large	73	50S ribosomal subunit protein L14	A, B
rplO	Ribosomal protein, large	73	50S ribosomal subunit protein L15	A, B
rplP	Ribosomal protein, large	73	50S ribosomal subunit protein L16	A, B
rplQ	Ribosomal protein, large	73	50S ribosomal subunit protein L17	A, B, 469

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
rplR	Ribosomal protein, large	73	50S ribosomal subunit protein L18	A, B
rplS	Ribosomal protein, large	57	50S ribosomal subunit protein L19	B
rplU	Ribosomal protein, large	69	50S ribosomal subunit protein L21	B
rplV	Ribosomal protein, large	73	50S ribosomal subunit protein L22	A, B
rplW	Ribosomal protein, large	73	50S ribosomal subunit protein L23	B
rplX	Ribosomal protein, large	73	50S ribosomal subunit protein L24	A, B
rplY	Ribosomal protein, large	47	50S ribosomal subunit protein L25	B
rpmA	Ribosomal protein, large	69	50S ribosomal subunit protein L27	B
rpmB	Ribosomal protein, large	82	50S ribosomal subunit protein L28	B, 276, 334
rpmC	Ribosomal protein, large	73	50S ribosomal subunit protein L29	A, B
rpmD	Ribosomal protein, large	73	50S ribosomal subunit protein L30	A, B
rpmE	Ribosomal protein, large	89	50S ribosomal subunit protein L31	127
rpmG	Ribosomal protein, large	82	50S ribosomal subunit protein L33	B, 276, 334
rpmH	Ribosomal protein, large	83	*rimA*; 50S ribosomal subunit protein L34	229, 595
rpoA	RNA polymerase	73	RNA polymerase (EC 2.7.7.6), α-subunit	A, B, 469, 470
rpoB	RNA polymerase	90	*groN*, *nitB*, *rif*, *ron*, *stl*, *stv*, *tabD*; RNA polymerase (EC 2.7.7.6), β-subunit	A, B, 7, 30, 31, 71, 145, 247, 293, 345, 349, 359, 418, 443
rpoC	RNA polymerase	90	*tabD*; RNA polymerase (EC 2.7.7.6), β′-subunit	A, B, 7, 30, 31, 71, 247, 293, 345, 349, 359, 418, 443, 444, 550
rpoD	RNA polymerase	67	*alt*; RNA polymerase (EC 2.7.7.6), σ-subunit	B, 77, 78, 210, 342, 356, 413
rpsA	Ribosomal protein, small	21	30S ribosomal subunit protein S1	B, 96, 309, 310, 520, 521
rpsB	Ribosomal protein, small	4	30S ribosomal subunit protein S2	A, B, 5, 38, 53, 327
rpsC	Ribosomal protein, small	73	30S ribosomal subunit protein S3	A, B
rpsD	Ribosomal protein, small	73	*ramA*, *sud2*; 30S ribosomal subunit protein S4	A, B, 469, 470
rpsE	Ribosomal protein, small	73	*eps*, *spcA*, *spc*; 30S ribosomal subunit protein S5	A, B
rpsF	Ribosomal protein, small	95	30S ribosomal subunit protein S6	A, B
rpsG	Ribosomal protein, small	73	*K12*; 30S ribosomal subunit protein S7	A, B, 471
rpsH	Ribosomal protein, small	73	30S ribosomal subunit protein S8	A, B
rpsJ	Ribosomal protein, small	73	30S ribosomal subunit protein S10	A, B, 144, 344, 641
rpsK	Ribosomal protein, small	73	30S ribosomal subunit protein S11	A, B, 469
rpsL	Ribosomal protein, small	73	*strA*; 30S ribosomal subunit protein S12	A, B, 471

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
rpsM	Ribosomal protein, small	73	30S ribosomal subunit protein S13	A, B, 469
rpsN	Ribosomal protein, small	73	30S ribosomal subunit protein S14	A, B
rpsO	Ribosomal protein, small	69	30S ribosomal subunit protein S15	B, 461, 467
rpsP	Ribosomal protein, small	57	30S ribosomal subunit protein S16	B
rpsQ	Ribosomal protein, small	73	*neaA*; 30S ribosomal subunit protein S17	A, B
rpsR	Ribosomal protein, small	96	30S ribosomal subunit protein S18	A, B
rpsS	Ribosomal protein, small	73	30S ribosomal subunit protein S19	A, B
rpsT	Ribosomal protein, small	0	*supS20*; 30S ribosomal subunit protein S20	A, B
rpsU	Ribosomal protein, small	67	30S ribosomal subunit protein S21	B, 126, 356
rrfA	rRNA, 5S	87	5S rRNA gene of *rrnA* operon	B, 57, 170
rrfB	rRNA, 5S	90	5S rRNA gene of *rrnB* operon	B, 69, 70
rrfC	rRNA, 5S	85	5S rRNA gene of *rrnC* operon	B, 633
rrfD	rRNA, 5S	72	5S rRNA gene of *rrnD* operon	160
rrfE	rRNA, 5S	90	5S rRNA gene of *rrnE* operon	B, 57, 170
rrfG	rRNA, 5S	57	5S rRNA gene of *rrnG* operon	170
rrfH	rRNA, 5S	5	5S rRNA gene of *rrnH* operon	170
rrlA	rRNA, 23S	87	23S rRNA gene of *rrnA* operon	A, B, 57, 170
rrlB	rRNA, 23S	90	23S rRNA gene of *rrnB* operon	B, 68, 69, 70
rrlC	rRNA, 23S	85	23S rRNA gene of *rrnC* operon	B
rrlD	rRNA, 23S	72	23S rRNA gene of *rrnD* operon	B, 160
rrlE	rRNA, 23S	90	23S rRNA gene of *rrnE* operon	B, 57, 170
rrlG	rRNA, 23S	57	23S rRNA gene of *rrnG* operon	B, 170
rrlH	rRNA, 23S	5	23S rRNA gene of *rrnH* operon	170
rrnA	rRNA	87	*cqsA*; rRNA operon	A, B, 57, 170
rrnB	rRNA	90	*cqsE*, $rrnB_I$; rRNA operon	A, B, 57, 69, 70, 125, 170, 451, 571
rrnC	rRNA	85	*cqsB*, *rrnB*, $rrnB_2$; rRNA operon	A, B, 57, 170, 595
rrnD	rRNA	72	*cqsD*; rRNA operon	B, 57, 160, 170
rrnE	rRNA	90	*rrnD*; rRNA operon	B, 57, 170
rrnG	rRNA	57	rRNA operon	B, 57, 170, 244, 531
rrnH	rRNA	5	rRNA operon	170, 244
rrsA	rRNA, 16S	87	16S rRNA gene of *rrnA* operon'	B
rrsB	rRNA, 16S	90	16S rRNA gene of *rrnB* operon	B, 69, 70, 125, 451
rrsC	rRNA, 16S	85	16S rRNA gene of *rrnC* operon	B
rrsD	rRNA, 16S	72	16S rRNA gene of *rrnD* operon	B
rrsE	rRNA, 16S	90	16S rRNA gene of *rrnE* operon	B
rrsG	rRNA, 16S	57	16S rRNA gene of *rrnG* operon	B, 170, 531
rrsH	rRNA, 16S	5	16S rRNA gene of *rrnH* operon	170
rts		90	*ts-9*; uncharacterized growth defect	A, B, 6, 7
ruv		41	Filament formation and sensitivity to UV radiation	A
sad		34	Succinate-semialdehyde dehydrogenase (EC 1.2.1.16), NAD-dependent	538
sbaA		97	Regulation of serine and branched-chain amino acid metabolism	131
sbcB		44	*xonA*; exonuclease I; suppressor of *recB*, *recC*	A
sdh		17	Succinate dehydrogenase (EC 1.3.99.1)	A, 546
secA		2	Secretion of envelope proteins	439, 440
sefA		4	Septum formation	B
seg	Segregation	100	Replication of F-factors	A, B

Continued on next page

TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
serA	Serine	63	Phosphoglycerate dehydrogenase (EC 1.1.1.95)	A
serB	Serine	100	Phosphoserine phosphatase (EC 3.1.3.3)	A, 487
serC	Serine	20	*pdxF*; phosphoserine aminotransferase (EC 2.6.1.52)	A, B
serR	Serine	2	Level of seryl-tRNA synthetase	B
serS	Serine	20	Seryl-tRNA synthetase (EC 6.1.1.11)	A
serT	Serine	(17)	Serine tRNA1	B
serU	Serine	43	*supD*, *Su-1*, su_I; serine tRNA2	448, N
serV	Serine	(61)	Serine tRNA3	B
sfrA		100	Expression of F-factor conjugation cistrons; antiterminator	42, 43
sfrB		86	Expression of F-factor conjugation cistrons; antiterminator	42, 43
shiA	Shikimate	43	Shikimate and dehydroshikimate permease	A
sloB	Slow growth	74	Low growth rate; tolerance to amidinopenicillin and nalidixic acid	B
speA	Spermidine	64	Arginine decarboxylase (EC 4.1.1.19)	A
speB	Spermidine	64	Agmatinase (EC 3.5.3.11)	A
speC	Spermidine	64	Ornithine decarboxylase (EC 4.1.1.17)	A, B
speD	Spermidine	3	*S*-Adenosylmethionine decarboxylase (EC 4.1.1.50)	B
spf		87	"Spot 42" RNA	288, 480
spoT		82	Guanosine 5′-diphosphate, 3′-diphosphate pyrophosphatase	A, B
srlA	Sorbitol	58	*gutA*, *sbl*; D-glucitol-specific enzyme II of phosphotransferase system	A, B, 56, 616
srlC	Sorbitol	58	*gutC*, *sbl*; regulatory gene	A, B, 616
srlD	Sorbitol	58	*gutD*, *sbl*; sorbitol-6-phosphate dehydrogenase (EC 1.1.1.140)	A, B, 616
srlR	Sorbitol	58	Regulatory gene	B, 616
srnA		10	Degradation of stable RNA	A
ssb	Single-strand binding	92	*exrB*, *lexC*; single-strand DNA-binding protein	B, 198, 379, 509, 510
strC	Streptomycin	5	*strB*; low-level streptomycin resistance	A
strM	Streptomycin	77	Control of ribosomal ambiguity	A
stsA		84	Altered ribonuclease activity	A
sucA	Succinate	17	*lys* + *met*; succinate requirement; α-ketoglutarate dehydrogenase (decarboxylase component)	A, 546
sucB	Succinate	17	*lys* + *met*; succinate requirement; α-ketoglutarate dehydrogenase (dihydrolipoyltranssuccinase component)	A, 546
sulA		22	*sfiA*, *suf*; suppressor of *lon*	A, B
sulB		2	*ftsZ*, *sfiB*; suppressor of *lon*	B, 356a, 357, 358
supB	Suppressor	16	su_B; suppressor of ochre (UAA) and amber (UAG) mutations; see *glnU*	
supC	Suppressor	27	su_C, *Su-4*; suppressor of ochre (UAA) and amber (UAG) mutations; see *tyrT*	
supD	Suppressor	43	su_I, *Su-1*; suppressor of amber (UAG) mutations; see *serU*	
supE	Suppressor	16	su_{II}, *Su-2*; suppressor of amber (UAG) mutations; see *glnV*	
supF	Suppressor	27	su_{III}, *Su-3*; suppressor of amber (UAG) mutations; see *tyrT*	
supG	Suppressor	17	*Su-5*; suppressor of ochre (UAA) and amber (UAG) mutations	A, B
supH	Suppressor	43	Suppressor	A
supK	Suppressor	62	Suppressor of opal (UGA) mutations; a tRNA methylase	B
supL	Suppressor	17	Su_B; suppressor of ochre (UAA) and amber (UAG) mutations; see *lysT*	

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
supM	Suppressor	90	Suppressor of ochre (UAA) and amber (UAG) mutations; see *tyrU*	
supN	Suppressor	52	Suppressor of ochre (UAA) and amber (UAG) mutations	A
supO	Suppressor	27	Suppressor of ochre (UAA) and amber (UAG) mutations; may be *supC*	A
supP	Suppressor	97	*Su-6*; suppressor of amber (UAG) mutations; see *leuX*	
supQ	Suppressor	13	Suppressor	A
supT	Suppressor	62	Suppressor; see *glyU*	
supU	Suppressor	85	*su7*; suppressor of amber (UAG) mutations; see *trpT*	
supV	Suppressor	85	*su8*; suppressor of ochre (UAA) and amber (UAG) mutations; see *trpT*	
tabC		85	Development of phage T4	B
tag		(72)	3-Methyl-adenine DNA glycosylase I, constitutive	B, 175, 300, 527
tap		42	Methyl-accepting chemotaxis protein IV	61, 387, 601
tar		42	*cheM*; methyl-accepting chemotaxis protein II	B, 61, 600, 601
tdi		(4)	Transduction, transformation, and rates of mutation	B
tdk		27	Thymidine kinase (EC 2.7.1.75)	A, B, L
terC	Terminus	(32)	*tre*; terminus of replication	B, 59
tgt		9	tRNA-guanine transglycosylase	429
thiA	Thiamine	90	Thiamine thiazole requirement	A
thiB	Thiamine	90	Thiaminphosphate pyrophosphorylase (EC 2.5.1.3)	A
thiC	Thiamine	90	Thiamine pyrimidine requirement	A
thiD	Thiamine	46	Phosphomethylpyrimidine kinase activity	266
thiK	Thiamine	25	Thiamine kinase	267
thiL	Thiamine	10	Thiamine monophosphate kinase	267
thrA	Threonine	0	*HS*, *thrD*; aspartokinase I–homoserine dehydrogenase I (EC 2.7.2.4–EC 1.1.1.3)	A, B, 114, 221, 301
thrB	Threonine	0	Homoserine kinase (EC 2.7.1.39)	A, 114, 115, 221
thrC	Threonine	0	Threonine synthase (EC 4.2.99.2)	A, 114, 115, 221
thrS	Threonine	38	Threonyl-tRNA synthetase (EC 6.1.1.3)	B, 188, 463, 549
thrT	Threonine	90	Threonine tRNA3	A, B, 6, 259, 333
thrU	Theonine	90	Threonine tRNA4	B, 6, 259, 333
thrV	Threonine	72	Threonine tRNA gene at distal end of *rrnD* operon	160, 170
thyA	Thymine	61	Thymidylate synthase (EC 2.1.1.45)	A, 241, 495
tkt		(63)	Transketolase (EC 2.2.1.1)	A
tlnA		11	*tlnI*; resistance or sensitivity to thiolutin	537
tnaA		83	*ind*, *tnaR*; tryptophanase (EC 4.1.99.1)	A, B, 140, 382, 595
tnm			Transposition of Tn*9* and other transposons; development of phage Mu	264, 265, 539, 610
tolA	Tolerance	17	*cim*, *tol-2*; tolerance to colicins E2, E3, A, and K	A
tolB	Tolerance	17	*tol-3*; tolerance to colicins E1, E2, E3, A, and K	A
tolC	Tolerance	66	*colE1-i*, *mtcB*, *refI*, *tol-8*; specific tolerance to colicin E1; expression of outer membrane proteins	A, 395, 396
tolD	Tolerance	(23)	Tolerance to colicins E2 and E3; ampicillin resistance	A
tolE	Tolerance	(23)	Tolerance to colicins E2 and E3; ampicillin resistance	A
tolI	Tolerance	(0)	Tolerance to colicins Ia and Ib	A

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TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
tolJ	Tolerance	0	Resistance to colicins L, A, and S4; partial resistance to colicins E and K	B
tolM	Tolerance	72	*cmt*; high-level tolerance to colicin M	63, 518
tonA	T-one	4	See *fhuA*	
tonB	T-one	28	*exbA*, *T1rec*; uptake of chelated iron and cyanocobalamin; sensitivity to phages T1 and 80 and colicins	A, B, 472
topA	Topoisomerase	28	*supX*; DNA topoisomerase I, ω protein	338, 554, 582, 583
tpiA		88	Triosephosphate isomerase (EC 5.3.1.1)	A, B
tpr		27	A protamine-like protein	4
tre	Trehalose	26	Utilization of trehalose	B
trg		31	Methyl-accepting chemotaxis protein III	B, 47, 48, 234
trkA		72	Transport of postassium	A
trkB		73	Transport of potassium	A
trkC		1	Transport of potassium	A
trkD		84	Transport of potassium	A, B, 595
trkE		29	Transport of potassium	A
trmA	tRNA methyltransferase	90	tRNA (uracil-5)-methyltransferase (EC 2.1.1.35)	A, B, 430
trmB	tRNA methyltransferase	(7)	tRNA (guanine-7)-methyltransferase (EC 2.1.1.33)	A
trmC	tRNA methyltransferase	(56)	5-Methylaminomethyl-2-thio-uridine in tRNA	A, B
trmD	tRNA methyltransferase	(59)	tRNA (guanine-1)-methyltransferase (EC 2.1.1.31)	B
trnA		60	*glnU*; level of several tRNAs	94
trpA	Tryptophan	28	*tryp-2*; tryptophan synthase (EC 4.2.1.20), A protein	A, B, 172, 424, 623, 624, 628
trpB	Tryptophan	28	*tryp-1*; tryptophan synthase (EC 4.2.1.20), B protein	A, 123, 172, 628
trpC	Tryptophan	28	*tryp-3*; *N*-(5-phosphoribosyl)anthranilate isomerase–indole-3-glycerolphosphate synthetase	A, B, 97, 172, 252, 628
trpD	Tryptophan	28	*tryE*; glutamine amidotransferase–phosphoribosyl anthranilate transferase	A, 172, 251, 252, 422, 628
trpE	Tryptophan	28	*anth*, *tryp-4*, *tryD*; anthranilate synthase (EC 4.1.3.27)	A, B, 172, 422, 423, 447, 628
trpP	Tryptophan	83	Low-affinity tryptophan-specific permease	140, 164
trpR	Tryptophan	100	*Rtry*; regulation of *trp* operon and *aroH*; *trp* aporepressor	A, B, 220, 221, 487
trpS	Tryptophan	74	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	A, B, 224, 225
trpT	Tryptophan	85	*su7*, *su8*, *su9*, *supU*, *supV*; tryptophan tRNA gene at distal end of *rrnC* operon	A, B, 448, 633
trxA	Thioredoxin	85	*tsnC*; thioredoxin deficiency	B
tsf		4	Protein chain elongation factor, EF-Ts	B, 5, 38, 53, 327
tsr		99	*cheD*; methyl-accepting chemotaxis protein I	B, 61, 237, 455, 600
tsx	T-six	9	*nupA*, *T6rec*; nucleoside uptake; receptor for phage T6 and colicin K	A, B
tufA		74	Protein chain elongation factor, EF-Tu (duplicate gene)	A, B, 8, 592, 630, 640
tufB		90	Protein chain elongation factor, EF-Tu (duplicate gene)	A, B, 6, 7, 259, 333, 345, 390, 571, 592
tynA		(27)	Tyramine oxidase (EC 1.4.3.4)	B
tyrA	Tyrosine	57	Chorismate mutase T (EC 5.4.99.5)–prephenate dehydrogenase (EC 1.3.1.12)	A

Continued on next page

TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
tyrB	Tyrosine	92	Tyrosine aminotransferase (EC 2.6.1.5), tyrosine-repressible	B
tyrP	Tyrosine	42	Tyrosine-specific transport system	H, 609
tyrR	Tyrosine	29	Regulation of *aroF*, *aroG*, and *tyrA* and aromatic amino acid transport systems	A, B, 83, 104
tyrS	Tyrosine	36	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	A, B, 155
tyrT	Tyrosine	27	*su_{III}*, *Su-3*, *su_c*, *Su-4*, *supF*, *supE*; tyrosine tRNA1 (tandemly duplicated gene)	A, B, 491
tyrU	Tyrosine	89	*supM*, *sup15B*; tyrosine tRNA2	A, B, 6, 259, 333
tyrV	Tyrosine	27	*su_{III}*, *Su-3*, *supF*; tyrosine tRNA1 (tandemly duplicated gene)	A, B
ubiA	Ubiquinone	92	4-Hydroxybenzoate → 3-octaprenyl 4-hydroxybenzoate	A, 347
ubiB	Ubiquinone	86	2-Octaprenylphenol → 2-octaprenyl-6-methoxy-phenol	A
ubiC	Ubiquinone	92	Chorismate lyase	A
ubiD	Ubiquinone	86	3-Octaprenyl-4-hydroxybenzoate → 2-octaprenylphenol	A
ubiE	Ubiquinone	86	2-Octaprenyl-6-methoxy-1,4-benzoquinone → 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone	A
ubiF	Ubiquinone	15	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone → 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone	A
ubiG	Ubiquinone	48	2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone → ubiquinone 8	A, B, 460
ubiH	Ubiquinone	63	2-Octaprenyl-6-methoxyphenol → 2-octaprenyl-6-methoxy-1,4-benzoquinone	A
udk		45	Uridine kinase (EC 2.7.1.48)	A, 287
udp		86	Uridine phosphorylase (EC 2.4.2.3)	A, J
ugpA		76	*sn*-Glycerol-3-phosphate transport system	525
ugpB		76	Binding protein of *sn*-glycerol-3-phosphate transport system	525
uhpR		82	Regulation of hexose phosphate transport; possibly outer membrane receptor for glucose 6-phosphate	A, B, 199
uhpT		82	Hexose phosphate transport	A, B, 529
uidA		36	*gurA*; β-D-glucuronidase (EC 3.2.1.31)	A, B, 49
uidR		36	Regulatory gene	A, B, 49
umuC		26	Induction of mutations by UV; sensitivity to UV	B
uncA	Uncoupling	84	*atpA*, *papA*; membrane-bound ATP synthase (EC 3.6.1.3), F_1 sector, α-subunit	A, B, 159, 194, 219, 231, 295, 298, 299, 425, 595
uncB	Uncoupling	84	*atpB*, *papD*; membrane-bound ATP synthase (EC 3.6.1.3), F_0 sector, subunit a	A, B, 158, 159, 219, 231, 296, 297, 299, 425, 513, 595
uncC	Uncoupling	84	*atpC*, *papG*; membrane-bound ATP synthase (EC 3.6.1.3), F_1 sector, ε-subunit	B, 119, 159, 219, 231, 294, 513, 595
uncD	Uncoupling	84	*atpD*, *papB*; membrane-bound ATP synthase (EC 3.6.1.3), F_1 sector, β-subunit	B, 119, 159, 219, 231, 294, 295, 299, 513, 595

Continued on next page

TABLE 1—*Continued*

Gene Symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected[b]	Reference(s)[c]
uncE	Uncoupling	84	*atpE*, *papH*; membrane-bound ATP synthase (EC 3.6.1.3), F_0 sector, subunit c; DCCD-binding protein	B, 158, 159, 195, 219, 231, 298, 425, 595
uncF	Uncoupling	84	*atpF*; membrane-bound ATP synthase (EC 3.6.1.3), F_0 sector, subunit b	158, 195, 219, 231, 297, 425, 595
uncG	Uncoupling	84	*atpG*, *papC*; membrane-bound ATP synthase (EC 3.6.1.3), F_1 sector, γ-subunit	B, 159, 219, 231, 295, 513, 595
uncH	Uncoupling	84	*atpH*, *papE*; membrane-bound ATP synthase (EC 3.6.1.3), F_1 sector, δ-subunit	219, 231, 360, 425, 595
ung		56	Uracil-DNA-glycosylase	B
upp		54	*uraP*; uracil phosphoribosyltransferase (EC 2.4.2.9)	A, B
ups		27	Efficiency of nonsense suppressors	B
ush		11	UDP-glucose hydrolase (F′-nucleotidase)	A, B, 117
uvrA	UV	92	*dar*; repair of UV damage to DNA; excision nuclease	A, B, 62, 305, 506, 507, 509
uvrB	UV	18	*dar-1,6*; repair of UV damage to DNA; excision nuclease	A, B, 183, 453, 504 506, 511, 591
uvrC	UV	42	*dar4,5*; repair of UV damage to DNA; excision nuclease	A, 505, 506, 528, 585, 629
uvrD	UV	85	*dar-2*, *mutU*, *pdeB*, *recL*, *uvrE*, *uvr502*; repair of UV damage to DNA; DNA-dependent ATPase; helicase II	A, B, 367, 431, 432, 532
uxaA		68	Altronate hydrolase (EC 4.2.1.7)	A, B, 126, 260, 466, 483
uxaB		(53)	Altronate oxidoreductase (EC 1.1.1.58)	A, B
uxaC		68	Uronate isomerase (EC 5.3.1.12)	A, B, 126, 260, 466, 483
uxuA		98	Mannonate hydrolase (EC 4.2.1.8)	A, B, 482, 484
uxuB		98	Mannonate oxidoreductase (EC 1.1.1.57)	A, B, 482, 484
uxuR		98	Regulatory gene for *uxuBA* operon	B, 481, 482, 484
valS	Valine	97	*val-act*; valyl-tRNA synthetase (EC 6.1.1.9)	A, B, 23
valT	Valine	17	Valine tRNA1	B, 448
xapA		52	Xanthosine phosphorylase	80
xapR		52	Regulatory gene	80
xthA		38	Exonuclease III	A, B, 489
xseA		54	Exonuclease VII	B
xylA	Xylose	80	D-Xylose isomerase (EC 5.3.1.5)	A, 365
xylB	Xylose	80	Xylulokinase (EC 2.7.1.17)	A, 365
xylR	Xylose	80	Regulatory gene	A, 365
zwf	Zwischenferment	41	Glucose 6-phosphate dehydrogenase (EC 1.1.1.49)	A

[a] Numbers refer to time scale shown in Fig. 1. Parentheses indicate approximate map locations.

[b] Abbreviations: DAHP, 3-Deoxy-D-arabinoheptulosonate-7-phosphate; 7KAP, 7-oxo-8-aminopelargonate; DAPA, 7,8-diaminopelargonate; CoA, coenzyme A; tRNA, transfer ribonucleic acid; rRNA, ribosomal ribonucleic acid; DNA, deoxyribonucleic acid; ATP, GTP, and CTP, adenosine, guanosine, and cytosine 5′-triphosphate, respectively; CDP, UDP, and TDP, cytidine, uridine, and thymidine 5′-diphosphate, respectively; IMP, UMP, and GMP, inosine, uridine, and guanosine 5′-monophosphate, respectively; cyclic AMP, adenosine 3′,5′-phosphate; ATPase, adenosine triphosphatase; dUTPase, deoxyuridine triphosphatase; NAD, nicotinamide adenine dinucleotide; NADH, reduced NAD; NADP, NAD phosphate; UV, ultraviolet light; PTS, phosphotransferase; P_i, inorganic phosphate; DCCD, dicyclohexylcarbodiimide.

[c] Numbers refer to Literature Cited. (A) refers to literature cited in Table 2 of reference 21. (B) refers to literature cited in Table 1 of reference 20. The other letters refer to personal communications from the following individuals: (C) Y.-Y. Chang and J. E. Cronan, Jr.; (D) R. DeFeyter and A. J. Pittard; (E) R. Essenberg; (F) J. S. Gots; (G) R. J. Kadner; (H) P. A. Kasian and A. J. Pittard; (I) A. Kikuchi and R. Weisberg; (J) S. Kushner; (K) P. Loewen; (L) A. Markovitz; (M) H. M. Race; (N) D. Steege; (O) A. Wright.

TABLE 2. Alternate gene symbols

Alternate symbol	Symbol in Table 1
acrB	*gyrB*
ade	*pur*
ald	*fda*
$adth_a$	*purD*
$adth_b$	*purG*
ala-act	*alaS*
alnA	*dadB*
alnR	*dadQ*
alt	*rpoD*
amk	*nek*
anth	*trpE*
apk	*lysC*
arg + ura	*car*
aroR	*aroT*
asp	*ppc*
aspB	*gltB*
ata	*attP22*
atp	*unc*
bfe	*btuB*
bioR	*birA*
birB	*bioP*
bisA	*chlA*
bisB	*chlE*
bisD	*chlG*
blu	*pgl, pgm, malP*
brnP	*ilvH*
cap	*car, crp*
capR	*lon*
car	*ptsG*
cat	*ptsG*
cbr	*fep*
cbt	*fep*
cer	*btuB*
cheC	*flaA*
cheD	*tsr*
cheM	*tar*
cheX	*cheR*
chlC	*narC*
chlI	*narI*
cim	*tolA*
cmlB	*ompF*
cmt	*tolM*
coa	*ompF*
colE1-i	*tolC*
cop	*het*
con	*ompA, rfa*
Cou	*gyrB*
cqsA	*rrnA*
cqsB	*rrnC*
cqsD	*rrnD*
CR	*ptsG*
cru	*nupC*
cry	*ompR, ompF*
ctr	*ptsH, ptsI*
cxr	*cxm*
dagA	*cycA*
dap + hom	*asd*
dar	*uvr*
deg	*lon*
dhbB	*bioR*
dhl	*lpd*
dir	*lon*
divA	*ftsA*
dnaF	*nrdA*
dnaL	*lig*
dnaS	*dut*
dnaW	*adk*
dra	*deoC*
drm	*deoB*
eps	*rpsE*
eryA	*rplD*
eryB	*rplV*
exbA	*tonB*
exrA	*lexA*
exrB	*ssb*
far	*fusA*
feuA	*cir*
feuB	*fep*
fim	*pil*
flaJ	*motA, motB*
flaF	*hag*
fnr	*nirR*
frdB	*nirR*
ftsI	*pbpB*
ftsZ	*sulB*
gad	*gap*
glmD	*nagB*
glu	*ppc*
glut	*gltA*
gly-act	*glyS*
glyD	*gpt*
gpp	*gpt*
gpt	*ptsG*
gptB	*ptsM*
groE	*mop*
groN	*rpoB*
groP	*dnaB, dnaJ, dnaK*
grpA	*dnaB*
grpC	*dnaJ, dnaK*
grpF	*dnaK*
gts	*qmeA*
gurA	*uidA*
gut	*srl*
gxu	*gpt*
H	*hag*
hdh	*mop*
hid	*himA*
himB	*gyrB*
hin	*htpR*
hip	*himD*
Hpr	*ptsH*
hrbA	*brnQ*
hrbB,C,D	*livG,H,J,K*
hs	*hsd*
Hs	*thrA*
hsm	*hsdM*
hsp	*hsd*
hsr	*hsdR*
hss	*hsdS*
icl	*aceA*
ile	*ilvA*
ind	*tnaA*
ins	*glyV, glyW*
K12	*rpsG*
kac	*kdp*
kdgA	*eda*
kga	*eda*
kmt	*ompB*

Continued on next page

TABLE 2—*Continued*

Alternate symbol	Symbol in Table 1	Alternate symbol	Symbol in Table 1
lcs	*asnS*	*pon*	*lpcB, mrc*
lexB	*recA*	*popA*	*hemH*
lexC	*ssb*	*popB*	*hemF*
lir	*acrA*	*popE*	*hemC*
lop	*ligA*	*prd*	*fuc*
loxB	*attP1,P7*	*prv*	*mutH*
lps	*rfa*	*psuA*	*rho*
lss	*livR*	*ptsN*	*nagE*
lys + met	*sucA, sucB*	*pup*	*deoD*
mas	*aceB*	*pyrA*	*car*
Mb	*acrA*	*rad*	*uvrD*
mbl	*acrA*	*ramA*	*rpsD*
mec	*dcm*	*ramB*	*rimG*
meoA	*ompC*	*RC*	*rel*
mlpA	*lpp*	*recL*	*uvrD*
mon	*envB*	*refI*	*tolC*
mni	*manC*	*refII*	*cet*
mpt	*ptsM*	*relC*	*rplK*
mra	*murF*	*res*	*rimF*
mrdA	*pbpA*	*resA*	*polA*
mrdB	*rodA*	*rif*	*rpoB*
mtcA	*acrA*	*rimA*	*rpmH*
mtcB	*tolC*	*RMG*	*mglR*
muc	*lon*	*rm*	*hsd*
mutU	*uvrD*	*rnsA*	*rna*
nalA	*gyrA*	*rnsC*	*rho*
nalC,D	*gyrB*	*rodY*	*envB*
nam	*pncA*	*ron*	*rpoB*
nar	*chl*	*rorA*	*recB*
ncf	*hemB*	*rpx*	*rps*
neaA	*rpsQ*	*rpy*	*rpl*
nic	*nad*	*rpz*	*rpm*
nirA	*nirR*	*sbl*	*srl*
nirB	*cysG*	*sec*	*hemF*
nitA	*rho*	*sep*	*pbpB*
nitB	*rpoB*	*sfiA*	*sulA*
nmpA	*pst, phoS,T*	*sfiB*	*sulB*
nmpB	*phoR*	*sof*	*dut*
ntrA	*glnF*	*som*	*rfb*
ntrB	*glnL*	*spcA*	*rpsE*
ntrC	*glnG*	*spr*	*lexA*
nucR	*deoR*	*ssd*	*ecfB*
nupA	*tsx*	*stl*	*rpoB*
nusE	*rpsJ*	*strA*	*rpsL*
old	*fad*	*stsB*	*rimH*
ole	*fadR*	*stv*	*rpoB*
ompB	*envZ, ompR*	*Su, su*	*sup*
ompE	*phoE*	sud_2	*rpsD*
par	*ompC*	*sufD*	*glyU*
paxA	*dcd*	*sumA*	*glyT*
pbpF	*mrcB*	*sumB*	*glyU*
pdeB	*uvrD*	*sun*	*rho*
pdeC	*lig*	sup_{s20}	*rpsT*
pdxF	*serC*	*T1rec*	*tonB*
pea	*azi*	*T1, T5rec*	*fhuA*
pel	*ptsM*	*T6rec*	*tsx*
perA	*envZ*	*tabB*	*mop*
pfv	*dacA*	*tabD*	*rpoB, rpoC*
phe-act	*pheS*	*talA*	*alaT*
phx	*rfa*	*talD*	*alaU*
PMG	*mgl*	*tasC*	*aspT*
poaA	*putA*	*tfrA*	*lpcA*
poh	*oriC*	*tgl*	*ptsG*
polC	*dnaE*	*tgtB*	*gltT*

Continued on next page

TABLE 2—*Continued*

Alternate symbol	Symbol in Table 1
tgtC	*gltU*
tgtE	*gltV*
thyR	*deoB, deoC*
tif	*recA*
tmr	*fol*
tolF	*ompF*
tolG	*ompA*
tonA	*fhuA*
TP	*deoA*
tpp	*deoA*
tpo	*envZ*
tre	*terC*
trpP	*aroT*
try	*trp*
tryp	*trp*
ts-9	*rts*
tsl	*lexA*
tsnC	*trxA*
tsu	*rho*
tss	*asnS*
tut	*ompA*
umg	*ptsG*
umuA	*lexA*
umuB	*recA*
uraP	*upp*
usgA	*gntM*
uvrF	*recF*
val-act	*valS*
xonA	*sbcB*
zab	*recA*

age of 1.4 min and the other of which gives an average of 2 min for this distance. It is tempting to speculate that the presence or absence of the element "e14," said to be integrated between *pyrC* and *purB* in some strains (209), might account for this distribution of cotransduction frequencies. However, it now appears that e14 may integrate at a locus clockwise of *purB* (C. W. Hill, personal communication).

It is to be hoped that with the techniques now available for mapping, many of the above-mentioned uncertainties will be resolved within the next few years.

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